# Undergraduate Student Competition:
# ASAS Undergraduate Student Poster Competition

**W158 Comparison of pre-race behaviors of Thoroughbred race horses on finish order and finish type.** A. McDuff*, K. William, J. Gregory, and C. E. Ferguson, *McNeese State University, Lake Charles, LA.*

This study compared various pre-race behaviors of Thoroughbred (TB) race horses (n = 1018) at Delta Downs (Vinton, LA) with their performance. The horses were evaluated based on their behavior by 4 experienced horse persons and the pre-race period was divided into 3 sections: pre-saddling (BSAD), which was the time the horse entered the saddling paddock until the saddling, saddling (SAD), which was the time from saddling until the jockeys prepared to mount the horse, and post-parade (POSTP), which consisted of the time the jockey mounted and rode the horse in the parade. The behavior was classified as calm, nervous, or ready and they were also scored numerically from 1 to 5 with 1 being only minimal movement and 5 being a horse that reared, flipped over or pawed several times during the each evaluation period. The horses received a separate behavior type and numerical score for BSAD, SAD and POSTP. Following completion of the race the horses finish order and method of finishing the race (running, tired, or pulled-up) was recorded. Statistically evaluations were performed in SAS and chi-squared analysis was performed to determine statistical differences. Horse scored as nervous during BSAD were more likely ($P < 0.001$) to finish the race tired (68%) compared calm or ready horses (34% and 35%), respectively. Being nervous during BSAD significantly ($P < 0.006$) decreased the horses chances of finishing first to third (17%) compared with calm or ready horses (36% and 38%), respectively. More ($P < 0.0001$) horses that were nervous during SAD finished tired (63%) compared with calm or ready horses (31% and 36%), respectively. Also, horses that were nervous during POSTP were more likely ($P < 0.004$) to run tired (59%) compared with calm or ready horses (34% and 35%), respectively. The BSAD, SAD and POSTP behavior score did not affect finish type ($P < 0.4$, $P < 0.14$, $P < 0.76$) or the percent finishing fourth or better ($P < 0.18$, $P < 0.56$, $P < 0.26$), respectively. Horses with no chain or it used as a regular lead shank were more likely ($P < 0.01$) to run first to fourth (64%) compared with horses with a chain used over their nose or in their lip (47%).

**Key Words:** horse racing, Thoroughbred, behavior

**W159 Alleviation of pain associated with disbudding.** A. Mathias*, J. Gilliam, D. Stein, and M. Calvo-Lorenzo, *Oklahoma State University, Stillwater.*

Disbudding, the removal of the horn buds of a calf, is a necessary management procedure because it eliminates costs associated with horns and improves safety. However, disbudding is known to cause pain and distress in calves. Extra-label use of some pharmaceuticals allows for some of the alleviation of the pain and distress, but it is not the best way. A FDA-approved pharmaceutical would be the best option to alleviate the pain and distress, however one does not exist. Therefore, pharmaceuticals are often used extra-label to alleviate pain and distress. This study evaluates the effectiveness ethyl alcohol (EtOH) to produce a cornual nerve block, when the area surrounding the horn is numb. To test this, calves were given 1 of 4 treatments: 5 mL saline solution (SAL), solution mixture of 2.5 mL 2% Lidocaine and 2.5 mL 75% EtOH (MIX), or 5 mL 75% EtOH (ALC). The calves were needle pricked in the area surrounding the horn bud at 5, 10, 15, 20, 30, and 60 min after the treatment on d 1 to determine the onset of the cornual nerve block. To test the duration of the cornual nerve block they were pricked once daily from d 2 - 14. The behavioral response to the prick test was evaluated as either “blocked” or “not blocked.” “Blocked” was defined as no movement in response to the prick test, and “not blocked” was defined as pulling on halter, throwing head back, backing away from handler, or falling down. The study found that SAL calves exhibited “not blocked” behaviors at all needle pricking time points; all other treatments exhibited initial “blocked” behaviors at 5 min post-treatment. The study also found that the MIX and ALC treatments were effective at maintaining a cornual nerve block for 2 weeks when needle pricked daily from d 2–14. These results indicate there is potential in utilizing EtOH as a form of non-restricted pain relief for disbudding calves, which would be beneficial for management practices on farms today. Future research incorporating the removal of the horn buds after EtOH administration will further evaluate the effectiveness of EtOH as a cornual nerve block.

**Key Words:** dehorning, calf, ethyl alcohol

**W160 Factors affecting neonatal dairy calf mortality in a hot-arid environment.** E. L. Lopez Rodriguez*, M. Mellado, F. G. Veliz, M. A. de Santiago MIRAMONTES, and J. E. Garcia, *Autonomous Agrarian University Antonio Narro, Torreon, Coahuila, Mexico.*

A field study involving 7734 Holstein calves from 8 large intensive dairy herds in northern Mexico (26° N; 24.2°C mean annual temperature; same location) was conducted to determine some factors affecting early postnatal (one to 21-d of age) dairy calf mortality, and to assess its association with climatic conditions. The effects of season of birth, size of dairy operation, birth type (single or twin), sex of calves, and temperature-humidity index (THI) shortly before, during or shortly after calving were analyzed by the GENMOD procedure of SAS. The total mortality incidence was 14%. Mortality of calves was altered by the THI during birth, with a decreased ($P < 0.05$) mortality rate from 16 to 12% when THI was 81 or higher. Mortality levels were 4 percentage point higher ($P < 0.05$) in winter than all other seasons. Single-born calves had fewer deaths (14%) than twin-born calves (19%). The mortality rate was higher ($P < 0.05$) in male than in female calves (17 vs. 12%). Calves that were born in dairy operations > 1800 cows had a greater risk of dying than calves born in smaller dairies (16 vs. 13%). Both respiration rate (74.4 ± 15.6 vs. 67.8 ± 16.3; means ± SD) and heart rate (119.2 ± 19.6 vs. 113.9 ± 17.0; means ± SD) were higher ($P < 0.05$) in calves born in winter than in summer. Rectal temperature was not altered by high ambient temperature and panting was not observed in calves during high ambient temperature. It was concluded that in this particular zone characterized by an intense heat load for the most part of the year, calf mortality was not linked to high ambient temperature around calving. Instead, survival of calves was negatively affected by winter weather. Thus, efforts to protect calves from cold weather would alleviate calf losses.

**Key Words:** calf, mortality, climate

**W161 GALNT13, a positional candidate gene on bovine chromosome 2 for heifer pregnancy, is only expressed in nervous tissue.** J. N. LaMastro*[1], W. A. Khan[1,2], S. O. Peters[2,3], O. O. Ajayi[1],

M. De Donato[1,4], W. Bai[1,5], and I.G. Imumorin[1], *[1]Cornell University, Ithaca, NY, [2]University of Veterinary and Animal Sciences, Lahore, Pakistan, [3]Berry College, Mt. Berry, GA, [4]Universidad de Oriente, Cumana, Sucre, Venezuela, [5]Shenyang Agricultural University, Shenyang, China.*

Genetic improvement programs for reproductive traits have been much slower to develop than improvement programs for growth and carcass traits for reasons including low heritability of fertility traits. In our previous study, a Bayesian based association mapping combined with alignment to differentially expressed hypothalamic transcriptome from RNA-seq data helped to identify candidate genes that may be responsible for the variation in heifer pregnancy on bovine chromosome 2. One of these candidates is uridine diphospho N-acetylgalactosaminyltransferase 13 (GALNT13), belonging to a family of enzymes involved in mucin-type O-glycosylation of serine and threonine residues of polypeptide acceptors. Bovine GALNT13 has 11 exons with mixed structures in its secondary structures predicted using the GORIV tool showing that it possesses the glycosyltransferase and ricin domains. We analyzed expression of bovine GALNT13 using reverse transcriptase-PCR amplification of 290 bp from exon 1. Like its murine and human counterpart, bovine GALNT13 is expressed in brain and spinal cord and not in liver, heart, kidney and lymph node. Our results appear to support previous studies in mouse that GALNT13 is a major enzyme responsible for the synthesis of O-glycan residues in neurons, which is consistent with being expressed only in nervous tissue.

**Key Words:** GALNT13, bovine, brain

### W162 Combining ruminally protected choline and flaxseed in cattle diets to increase assimilation of n-3 fatty acids from the diet .

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Crossbred heifers (n = 108; initial BW = 285 ± 13.6 kg) were used in a randomized complete block experiment with a 2 × 2 factorial treatments arrangement to evaluate effects of ruminally-protected choline and ground flaxseed on changes in plasma concentrations of long-chain fatty acids, glucose, and L-lactate. Heifers were stratified by initial BW and allocated randomly, within strata, to 36 feedlot pens with 3 heifers/pen (9 pens/treatment). Factors consisted of level of ruminally-protected choline (C) fed at 0 or 113 g/d (Robert Morgan Inc.) and level of an extruded mixture of flaxseed, wheat middlings, vitamins, and minerals (F) fed at 0 or 10% of diet DM (Great O3 Premium Feed). Heifers were fed a basal diet (DM basis) of 25% corn silage, 15% alfalfa, 25% wet corn gluten feed, steam-flaked corn, and supplement. Cattle were fed their respective diets ad libitum at 1600 h daily. On d 0 and 14 of the study, cattle were weighed, blood was sampled via jugular venipuncture and centrifuged to recover plasma. Plasma glucose and L-lactate were measured using a YSI 2100D analyzer and fatty acid methyl esters (FAMEs) were measured by gas chromatography. Data were analyzed as a mixed model with choline, flaxseed, day, and all interactions as fixed effects, weight block as a random effect, and pen as the experimental unit. There were no significant interactions between C and F for performance or blood constituents ($P > 0.05$). Feeding C tended to improve gain efficiency (0.284 vs. 0. 313) for 0 and 113 g/d feeding levels, respectively; $P = 0.06$); but did not affect ADG, DMI, or blood constituents ($P > 0.10$). Gain, DM intake, gain efficiency, and plasma glucose and lactate were unaffected by feeding F ($P > 0.10$), but plasma concentrations of $\alpha$-linolenic acid were greater for cattle fed F compared with those without ($P < 0.01$). Ruminally protected choline yielded efficiency responses comparable to those observed in previous studies. The Great O3 feed used in this study increased plasma concentrations of n-3 fatty acids, but including choline provided no further improvement in assimilation of dietary fats.

**Key Words:** FAME, glucose, lactate

### W163 Kyphosis induced by maternal vitamin D intake is not explained by a reduction in vertebrae body mineral content of pigs at birth or weaning.

L. M. Vanderwerff*, L. A. Rortvedt-Amundson, and T. D. Crenshaw, *University of Wisconsin, Madison.*

Kyphosis, an idiopathic disease characterized by abnormal outward spinal curvature, commonly affects the 14th to 16th thoracic vertebrae. In recent experiments kyphosis was induced in young pigs produced by sows fed diets with no supplemental vitamin $D_3$ (D) throughout gestation and lactation. The current objective was to assess variation in mineral content of regions along spinal columns of pigs produced by gilts fed diets varying in D. Regions were examined to determine if a reduction in percent ash (%ash) predisposed specific vertebrae to conformational deformities associated with kyphosis. Spinal columns were collected from pigs at birth (d 0, n = 12) and weaning (d 25, n = 15). Gilts that produced the pigs were fed diets containing 0, 325, or 1,750 IU D/kg from breeding through lactation. After euthanasia, the spinal column was removed and vertebrae bodies were dissected, then extracted with ether and ashed. Data from individual vertebral bodies were grouped into regions (n = 3/region) and numbered 1 to 7 consecutively from the 1st rib through the last lumbar vertebra. Regions of 3 adjacent vertebrae were selected based on the definition of kyphosis. Differences due to maternal diets were not detected in vertebrae % ash of pigs at birth (44.4, 43.6, and 44.8%) or weaning (37.4, 37.1, and 39.9%). Vertebrae % ash decreased ($P < 0.05$) from d 0 to d 25 (44.3 vs. 38.1%) but these differences varied by region within the vertebral column (age X region interaction, $P < 0.01$) as shown below. The 6% decrease in % ash with age was due to a 4-fold increase in bone organic matrix (0.11 vs. 0.49 g) that exceeded the 3-fold increase in bone mineral (0.09 vs. 0.31 g). At d 0, the % ash was essentially constant across regions but at d 25, % ash increased, especially in the more distal regions. At d 25, % ash values in regions associated with kyphosis were greater, implying that kyphosis may result from an overgrowth of organic matrix not from a lack of matrix mineralization.

**Table 1.** Ash (%) values of different vertebral regions

|  | Vertebral region (3 vertebrae/region) |  |  |  |  |  |  | Pooled |
|---|---|---|---|---|---|---|---|---|
| Age, d | 1 | 2 | 3 | 4 | 5 | 6 | 7 | SEM |
| 0 | 43.8 | 43.8 | 44.1 | 44.3 | 44.2 | 45.0 | 44.9 | 0.07 |
| 25 | 36.5 | 37.3 | 37.6 | 38.4 | 39.0 | 39.5 | 38.5 | 0.08 |

**Key Words:** bone ash, bone matrix, vitamin D

### W164 Effect of sex, pen density and season on feedlot performance.

J. H. Moss*, C. L. Maxwell, and C. R. Krehbiel, *Department of Animal Science, Oklahoma State University, Stillwater.*

There are a variety of factors that can affect feedlot performance for both steers and heifers. The objective of this study was to quantify factors that affect DMI, ADG, and efficiency of cattle during the finishing phase. Factors that were evaluated were sex and season of cattle closeout. Trial data from 2003 to 2012, including initial BW, final BW, DMI, ADG, G:F, from the Willard Sparks Beef Research Center was compiled and analyzed. The data set consisted of 933 pens, 647 pens of steers (3,706 steers) and 286 of heifers (1,800 heifers). The effect of sex was analyzed using PROC MIXED (SAS 9.3, Cary, NC), initial

BW was used as a covariate when necessary ($P < 0.05$) to determine the difference in performance and efficiency between steers and heifers. Steers consumed 14.5% more feed (10.29 vs. 8.99, kg/d), gained 16.9% faster (1.66 vs. 1.42, kg/d), and were 3.2% more efficient than heifers (0.162 vs. 0.157; $P < 0.01$). Season was evaluated to determine the effect of seasonal variation on performance. Season was divided into 4, 3 mo periods 1(Jan-Mar), 2(Apr-Jun), 3(Jul-Sep), 4(Oct-Dec). Cattle finished in season 4 consumed 5% more feed (10.02 vs. 9.54 kg/d; $P < 0.01$) compared with the other 3 seasons. Cattle in seasons 2 and 4 had a 5.2% improvement in ADG compared with season 1 (1.61 vs. 1.53 kg/d) and an 11.0% improvement in ADG compared with season 3 (1.61 vs. 1.45; $P < 0.01$). Cattle in season 2 and 4 were 4.1% more efficient than cattle in season 1 and 3 (0.164 vs. 0.157, $P < 0.01$). A strong positive correlation existed between initial and DMI for heifers ($r^2 = 0.54$; $P < 0.01$), as well as steers ($r^2 = 0.40$; $P < 0.01$). Using PROC REG, dry matter intake for this data using only initial BW was estimated by the equation DMI, kg/d = 6.75 + (initial BW, kg*0.162) ($P < 0.01$). Actual DMI was positively correlated to predicted DMI (Eq.7–2, NRC, 2000; $r^2 = 0.40$, $P < 0.01$). The results of this study indicates that steers have increased DMI, ADG, and feed efficiency during the finishing period compared with heifers, and that cattle closed out in the spring and fall of the year experience improved feedlot performance compared with cattle closed out in the winter and summer.

**Key Words:** sex, season, feedlot performance

### W165 Phosphorus status of grazing beef cattle in Virginia's Chesapeake Bay watershed.

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Phosphorus loads in the Chesapeake Bay are a focus of environmental concern. Animal agriculture's contribution to this problem has been documented and efforts are focused on mitigating the issue. Major research and extension efforts have focused on concentrated animal feeding operations (mainly dairy and poultry); however, 400,000 beef cows are located in Virginia's Chesapeake Bay watershed counties. The objective of this study was to document phosphorus (P) supplementation in free choice minerals, soil test P, forage P and manure P levels of grazing beef cows in Virginia's Chesapeake Bay watershed. Producers could submit more than one set of samples if a full complement of samples was collected and the samples represented another land area or herd. Thirty-four producers from 2 counties cooperated with sample collection (n = 80) and completed a questionnaire related to their management practices. Soil test P values were characterized as low (14%), medium (29%), high (27%) and very high (13%) based on Virginia Cooperative Extension Soil Test guidelines. Phosphorus content of pasture forage grab samples (mean = 0.36%, SD = 0.10) was correlated to soil phosphorus levels (r = 0.42), but manure total P was lowly related (r = 0.05) to soil P values. Forage P levels were compared with Beef Cattle NRC (2001) P requirements for a 545-kg cow (peak milk, 13.6 kg/d). All forage samples were sufficient in P content to meet a dry cow's requirements, 98% met the requirements for late gestation and 87% met the peak lactation P requirement. Farm mineral supplements were categorized into 4 levels of P content (0, 1.0–2.5, 3.0–5.0 and >6.0%). Forage P content did not affect mineral selection by producers. The mean forage P content for the 4 mineral categories were 0.27, 0.37, 0.37 and 0.46%, respectively. Manure TP increased as mineral P content increased, 0.54, 0.65, 0.80 and 0.88% respectively. All farms surveyed required little or no phosphorus supplementation in regard to cow nutrient requirements. Sixty-five percent of participating cattlemen were receptive to modifying their P supplementation based on forage test results while only 6% were opposed to any modification.

**Key Words:** phosphorus, beef cattle

### W166 Effect of anabolic implants on adrenal cortisol synthesis in beef cattle.

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Implantation of anabolic steroids to increase growth rate in beef cattle affects adrenal glucocorticoid production. The mechanism by which trenbolone acetate and estrogen reduce cortisol (C) biosynthesis in heifers is not clear. The objective of this study was to determine serum C concentrations and adrenal steroidogenic enzyme mRNA levels in heifers implanted with Revalor 200. On d 0 of a 90-d finishing phase, 187 predominantly Angus heifers were randomly assigned to 3 treatments: non-implanted controls (con); Revalor 200 implant for 90 d of finishing phase (early); or Revalor 200 for last 30 d of finishing phase (late). On d 0, BW was 363, 359, and 361 kg for con, early and late treatments, respectively. At d 60, BW for early implanted heifers (458 kg) was greater ($P < 0.01$) than con (439 kg) and late implanted (436 kg) heifers. Final BW (d 90) was greater in early (519 kg) and late (510 kg) implanted heifers compared with con (492 kg). In a subset of heifers (n = 49) peripheral blood was collected to quantify serum C concentrations at d 0, 30, 60 and 90. Serum C was similar among groups at d 0 ($P = 0.65$); however, at d 30 heifers receiving implants had a marked reduction ($P < 0.01$) in serum C concentrations (31 ng/mL) compared with con (47 ng/mL) and late (48 ng/mL). At d 90, con heifers had a serum C value of 43 ng/mL compared with 25 ng/mL in both early and late implanted heifers ($P < 0.01$). At harvest (d 90) adrenal tissue was collected (n = 6/group) for mRNA analysis of steroidogenic enzymes cytochrome P450, family 21, subfamily A, polypeptide 2, cytochrome P450, family 11, subfamily B, polypeptide 1 and melanocortin 2 receptor. Despite decreased serum C in implanted heifers, no difference among treatments was detected for expression of the steroidogenic enzymes or the ACTH receptor in adrenal glands indicating other components of the hypothalamic-pituitary-adrenal axis are responsible for the observed decrease in serum C.

**Key Words:** adrenal, cortisol, implant

### W167 Expression of WNT signaling transcripts at specific stages of follicle development in bovine granulosa cells.

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Follicular maturation is a dynamic process requiring input from pituitary gonadotropins and ovarian derived factors. Members of the wingless-type mammary tumor virus integration-site (WNT) signaling pathway have been recognized to be differentially expressed and hormonally regulated in rodent ovaries, and we recently reported that WNT2 is regulated by FSH in bovine granulosa cells. However, the role and expression of WNT signaling molecules in ovarian follicle development in cattle is unknown. Therefore, the objective of this study is to characterize components of the WNT signaling pathway at specific stages of follicular development by real-time PCR. To identify gene expression changes in bovine folliculogenesis, granulosa cells and follicular fluid were collected from ovary pairs containing a stage III CL (d 11 to 17 of an estrous cycle). Granulosa cells were isolated from small (1 to 5 mm; n = 4) and large (8 to 22 mm; n = 4) follicles, and the corresponding CL (n = 3). Intra-follicular estradiol and progesterone concentrations were used to identify large dominant follicles (estradiol:progesterone >1). Real-time PCR quantification of select WNT family members was evaluated at distinct stages of development. Compared with small follicle granulosa cells, expression of the WNT transcriptional co-factor, CTNNB1 was similar in large dominant follicles ($P = 0.95$) but was decreased in the CL ($P = 0.06$). Expression of WNT ligands also demonstrated stage specific regulation as WNT2B was reduced in large dominant follicles ($P = 0.02$) but similar in CL ($P = 0.53$) compared with small follicles. A comparable pattern of expression was demonstrated for WNT5A as small follicles had greater expression compared with large follicles ($P < 0.01$) and was similar to CL ($P = 0.37$). However, WNT2 mRNA expression was unchanged throughout follicle maturation ($P = 0.47$). Previous work in our laboratory demonstrated WNT3A is antagonistic to FSH signaling in cultures of primary rat granulosa cells. Results from the current experiment indicate that WNT signaling molecules may be inhibitory to follicle development and luteinization in cattle.

**Key Words:** folliculogenesis, ovary, WNT

**W168 Solubility of copper sulfate and three sources of dicopper chloride trihydroxide.** C. S. Park* and B. G. Kim, *Konkuk University, Seoul, Republic of Korea.*

Copper sulfate ($CuSO_4$) and dicopper chloride trihydroxide (dCCTH) are widely used as Cu sources in swine diets. The objective of this study was to determine the solubility of Cu in $CuSO_4$, and 3 sources of dCCTH consisted of α-form (dCCTH-α), β-form (dCCTH-β), or a mixture of α and β-form (dCCTH-α·β) at different pH and an in vitro digestion procedure using a shaking incubator at 39°C. In Exp. 1, $CuSO_4$, dCCTH-α, dCCTH-β, and dCCTH-α·β were incubated in buffer at pH 2.0, 3.0, 4.8, and 6.8 for 4 h. Copper sulfate was completely dissolved within 15 min except at pH 6.8. At pH 2.0, solubility of Cu in dCCTH-α and dCCTH-α·β was greater (42.5 and 34.9 vs. 17.2%; $P < 0.05$) than dCCTH-β at 15 min and Cu in all dCCTH was completely dissolved at 4 h. In pH 3.0 and 4.8 buffers, all sources of dCCTH were dissolved at less than 22% and 3%, respectively, when incubated for 4 h. Copper in dCCTH sources was not dissolved at pH 6.8. Exp. 2 was conducted to determine the solubility of Cu in the same Cu sources as in Exp. 1 using an in vitro digestion assay simulating digestion procedures of pigs. All sources of Cu were completely dissolved at pH 2.0 when incubated for 2 h in a phosphate buffer. In Exp. 3, the 5 diets consisted of a control diet and diets supplemented with 250 ppm of Cu as $CuSO_4$, dCCTH-α, dCCTH-β, or dCCTH-α·β were prepared to determine the solubility of Cu during an 3-step in vitro digestion assay. Solubility of Cu in diets supplemented with $CuSO_4$ and dCCTH sources was greater ($P < 0.05$) than the control diet in step 1 and 2. These results indicate that solubility of $CuSO_4$ and dCCTH is affected considerably by pH of digesta. Among dCCTH sources, the solubility of Cu in dCCTH-α is greater than in other dCCTH sources at pH 2.0.

**Key Words:** in vitro digestion, swine, trace mineral

**W169 Effects of poor maternal nutrition on GH, IGF-I, insulin, and leptin concentrations in pregnant ewes.** M. E. Forella*, K. N. Peck, M. L. Hoffman, A. R. Fox, K. E. Govoni, and S. A. Zinn, *Department of Animal Science, University of Connecticut, Storrs.*

Maternal hormones affect fetal growth and development through their effect on nutrient partitioning and placental development. Maternal diet is one factor regulating maternal hormone concentrations. We hypothesized that during gestation, diet alters concentrations of maternal metabolic hormones. Pregnant ewes (n = 36; 12/treatment) were individually fed 1 of 3 diets [100% (CON), 140% (OVER), or 60% (RES) NRC requirements] from wk 5 of gestation until parturition. Weekly blood samples (20 mL) were obtained via jugular venipuncture and BW was measured. Concentrations of GH, IGF-I and leptin were determined by RIA. Insulin was determined by ELISA. Data were analyzed using ANOVA. By the end of gestation (wk 20), RES ewes (89.3 ± 3.6) were lighter ($P < 0.01$) and OVER ewes (119.7 ± 3.6 kg) were heavier ($P < 0.1$) than CON ewes (112.9 ± 3.6 kg). However, compared with CON ewes (0.27 ± 0.01 kg), ADG was increased ($P < 0.01$) in OVER ewes (0.35 ± 0.01 kg) and decreased ($P < 0.01$) in RES ewes (0.12 ± 0.01 kg). Concentrations of GH were greater ($P < 0.01$) in RES ewes (6.4 ± 0.6 ng/mL) than CON ewes (3.2 ± 0.6 ng/mL) and OVER ewes (2.3 ± 0.6 ng/mL). Average concentrations of IGF-I were greater ($P < 0.1$) in OVER ewes (197.7 ± 14.5 ng/mL) compared with CON (163 ± 14.5 ng/mL) and RES (146.35 ± 14.5 ng/mL) ewes, but there was no difference between CON and RES ewes ($P < 0.42$). Average concentrations of insulin were greater ($P < 0.01$) in OVER ewes (0.61 ± 0.7 ng/mL) than RES (0.31 ± 0.7 ng/mL) and CON (0.32 ± 0.7 ng/mL) ewes. Leptin averaged 2.3 ± 1.4, 1.5 ± 1.4, and 4.3 ± 1.4 ng/mL in CON, RES, and OVER ewes, respectively, but there were no differences in leptin due to diet ($P > 0.32$). In conclusion, poor maternal diet during gestation affects circulating concentrations of GH, IGF-I, and insulin, and this may contribute to developmental changes in the fetus.

**Key Words:** insulin, maternal diet, somatotropic axis

**W170 In vitro fermentation of high forage substrate with addition of direct fed microbials and/or monensin.** K. E. Roberts*, K. M. Anderson, N. M. Kenney, K. R. McLeod, and E. S. Vanzant, *University of Kentucky, Lexington.*

This study was conducted to determine in vitro ruminal fermentation characteristics with addition of direct fed microbials (DFM) and/or monensin (MON) to a high forage TMR. ANKOM RFS fermentation vessels received either 50 µg lactose (control) or 50 µg DFM containing 50,000 cfu lactic acid bacteria (LifeProducts 10G) whereas MON was applied in the feed of the inoculum donor steers. Four ruminally cannulated steers received a high forage diet either with (n = 2) or without (n = 2) 440 mg/hd/d MON. Rumen fluid for each pair of steers was combined before inoculating fermentation vessels. Gas production was measured in each vessel for 24 h. At termination, fluid samples were collected from each vessel for measurement of VFA, ammonia, and pH. The best-fit model of 10 gas production models evaluated was used to quantify gas production parameters for individual vessels. Data were analyzed with the GLM procedure of SAS with a model appropriate for a completely randomized design with treatments arranged in a 2 × 2 factorial structure. Treatments did not influence ($P > 0.10$) total VFA concentrations (m*M*) or gas production (mL). Gas production rates were decreased slightly ($P = 0.06$; 0.236 mL/min and 0.224 mL/min ± 0.004) by DFM and were unaffected by MON ($P = 0.89$). Interactions between DFM and MON were detected ($P \leq 0.08$) for NH3 concentration and molar proportions of all VFA except propionate. In the absence of MON, DFM had no influence ($P > 0.10$) on any of these variables. With MON, acetate proportion was decreased ($P < 0.06$; 56.8 vs. 53.7 ± 1.10%) by DFM, whereas molar proportions of the remaining VFA (except propionate) were increased ($P < 0.10$; 11.9 vs. 13.2 ± 0.43%; 4.4 vs. 5.2 ± 0.28%; 2.1 vs. 2.4 ± 0.09%; 4.7 vs. 5.5 ± 0.28%; for butyrate, valerate, isobutyrate, and isovalerate) by DFM, as was NH3 concentration (1.6 vs. 2.8 ± 0.43 m*M*). Although MON decreased pH slightly ($P < 0.01$; 6.86 vs. 6.73 ± 0.015), DFM had no effect ($P = 0.30$) on pH. Results indicate that the effects of DFM on VFA profiles and ammonia concentrations with in vitro fermentation of a high forage substrate were dependent on the presence of MON.

**Key Words:** direct-fed microbial, VFA, gas production

### W171 Effects of poor maternal nutrition on gene expression in bone marrow stromal cells from lambs.

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Poor maternal nutrition can reduce growth rate, reduce bone development, and increase fat deposition in offspring. Bone marrow stromal cells (BMSC) are multipotent stem cells that can differentiate into several cell types including osteoblasts and adipocytes. Poor maternal nutrition may commit these cells to the adipocyte lineage, contributing to increased adipose tissue and reduced bone; however the mechanisms are not well established. We hypothesized that poor maternal nutrition would alter gene expression in BMSC. Pregnant ewes (n = 24) were randomly assigned to a diet of 100% (CON), 60% (RES), or 120% (OVER) of NRC requirements beginning at d 114 ± 10 of gestation. Within 24 h of birth, lambs were euthanized (n = 3/treatment), BMSC were isolated from the femur, cultured until 80% confluent, and RNA was extracted using TriReagent and ethanol precipitation. Real-time reverse transcriptase (RT)-PCR was used to determine mRNA expression. Data were analyzed by ANOVA. We did not observe an effect of treatment on markers of adipogenesis [CCAAT-enhancer binding protein (CEPB)-α, proliferation-activation receptor (PPAR)-γ, Pref-1; $P \geq 0.29$]. Maternal diet did not affect runt-related transcription factor (Runx)2 ($P \geq 0.45$), a key transcription factor in osteoblast differentiation, as well as various transcription factors involved in osteoblast development [dickkopf-related protein (DKK)2, low density lipoprotein receptor-related protein (Lrp)4, Lrp5, glycogen synthase kinase (GSK)-β and β-Catenin; $P \geq 0.3$]. mRNA expression of T-box (Tbx)-3, a key transcription factor in development and osteoblast function, tended ($P = 0.1$) to be reduced 1.6 ± 0.2-fold in RES. Expression of P2Y14 receptor, a key factor in lineage commitment of BMSC, was reduced 3.8 ± 0.1-fold in OVER ($P = 0.03$). Expression of CEBP-β was reduced 2.0 ± 0.1 and 2.2 ± 0.1-fold in RES and OVER, respectively ($P \leq 0.02$). In conclusion, poor maternal nutrition during gestation alters the expression genes involved in the commitment of BMSC to osteoblast and adipocytes cell lineage, which may contribute to altered body mass and composition of offspring.

**Key Words:** maternal nutrition, bone marrow stromal cells, sheep

### W172 Effects of maternal dietary yeast supplementation on foal growth and development.

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Dietary yeast supplementation in horses has been reported to influence nutrient digestibility and milk production in mares. Altering the nutrient composition of the milk from mares may influence the growth of their foals. The objective of this study was to determine if dietary yeast supplementation of the maternal diets would influence foal growth and development. Eight Quarter Horse mares (14.5 ± 7.5yr) were randomly assigned to one of 2 groups: Yeast or Control. All mares received 0.5% BW of a 16% CP pelleted concentrate, with water and mixed grass hay ad libitum. Mares in the yeast treatment group were fed a targeted dose of 1 g/ 45.4 kg of BW per day of a live culture of *Saccharomyces cerevisiae* for a period of 180 d. Growth measurements (body weight, body length, heart girth, wither and hip height, upper and lower leg length, and front/rear cannon bone circumference) were taken on d 0, 7, 14, 21, 28, 35, 42, 49, 56, 70, 84, 98, 112, 126, 140, 154 and 168. Data were analyzed using the PROC Mixed procedure of SAS. Average daily gain (ADG) of the foals was not influenced by the addition of yeast to the maternal diets. Hip height and wither height were highly correlated (r = 0.99). Although upper leg length and wither height were highly correlated (r = 0.93), lower leg length and wither height were not (r = 0.72). No significant differences in foal growth and development due to dietary yeast supplementation of the

**Key Words:** foal, growth, yeast

### W173 Effects of poor maternal nutrition during gestation on gene expression in renal adipose tissue of lambs.

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Poor maternal nutrition impairs postnatal growth and development of the animal, particularly decreasing carcass quality with an increase in fat deposition. We hypothesized that poor maternal nutrition would alter expression of key genes involved in adipogenesis in lambs. Thirty-six multiparous Dorset (n = 25), Shropshire (n = 7), and Southdown (n = 4) ewes were individually housed and fed either 100% (CON), 60% (RES), or 140% (OVER) of requirements for ewes pregnant with twin lambs (NRC, 1985) starting at d 31 ± 1.3 of gestation. Lambs were euthanized within 24 h after birth (n = 18) and perirenal adipose tissue was collected immediately and snap frozen in liquid nitrogen. Gene expression was determined by RNA extraction using Tri-Reagent, an RNeasy Mini Kit, and real-time reverse transcriptase-PCR. Data were analyzed using ANOVA with significance considered as $P \leq 0.05$. To determine if maternal diet affected markers of adipogenesis, we quantified expression of peroxisome proliferator-activated receptor gamma (PPAR-γ) and CCAAT/enhancer binding protein β (CEBP-β). We did not observe a change in expression of either gene in lambs born to RES and OVER ewes relative to controls at birth ($P \geq 0.27$). In addition, we did not observe an effect of maternal diet on glucose transporter type 4 (GLUT-4), a marker of nutrient uptake, in RES and OVER lambs relative to controls at birth ($P = 0.17$). Maternal diet did not effect adiponectin (ADIPOQ), a marker of energy homeostasis, in RES and OVER groups relative to controls ($P = 0.07$). These findings suggest that during fetal development, poor maternal nutrition does not alter expression of key markers of adipogenesis. Further analysis is needed to determine if poor maternal nutrition alters gene expression in adipose tissue at later stages of development when fat accretion is more rapid.

**Key Words:** maternal nutrition, adipose tissue, sheep

### W174 Uterine flux of estrone sulfate in an ovine maternal nutrient restriction model during melatonin supplementation.

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Previous data from our laboratories showed an increase in uteroplacental secretion of progesterone and estradiol 17β in nutrient restricted vs. adequate fed ewes. The current objectives were to examine the effects of dietary melatonin supplementation and nutritional plane on uteroplacental estrone sulfate flux and placental protein expression of steroidogenic acute regulatory protein (StAR) and aromatase. From d 50 to 130 of gestation, 31 primiparous ewes received 100% (ADQ) or 60% (RES) of nutrient requirements and were supplemented with 5 mg of melatonin per day (MEL) or no melatonin (CON). At d 130, uterine artery blood flow (BF) was determined under general anesthesia. Blood samples were collected from maternal saphenous artery, gravid uterine vein, umbilical artery, and umbilical vein. Estrone sulfate was not detected in the umbilical vein or umbilical artery samples (concentration ≤0.01 ng/mL). Uterine flux of estrone sulfate was calculated as maternal arterial-venous difference × uterine BF. Maternal artery estrone sulfate was increased ($P < 0.01$)

in RES (5.3 ± 1.4 ng/mL) vs. ADQ (0.7 ± 0.3 ng/mL) ewes. Similarly, uterine vein estrone sulfate was increased ($P < 0.05$) in RES (5.1 ± 1.5 ng/mL) vs. ADQ (1.5 ± 0.7 ng/mL) ewes. Maternal arterial-venous difference of estrone sulfate was increased ($P = 0.01$) in CON-RES (1.9 ± 1.0 ng/mL) vs. CON-ADQ (−1.1 ± 1.0 ng/mL), while MEL-RES (−2.1 ± 1.0 ng/mL) was not different ($P > 0.50$) from CON-ADQ. Uterine flux of estrone sulfate was decreased ($P < 0.01$) in MEL-RES (−3.4 ± 1.4 µg/min) vs. CON-RES (2.2 ± 1.4 µg/min), while neither was different ($P \geq 0.07$) from CON-ADQ (−1.5 ± 1.5 µg/min). Placental StAR protein expression was increased ($P < 0.05$) in RES vs. ADQ ewes at d 130, while placental aromatase protein was not different ($P > 0.60$) across all treatment groups. Maternal nutrient restriction interacted with dietary melatonin supplementation to alter uterine flux of estrone sulfate. Moreover, the previously observed increase in steroid secretion from nutrient restricted dams is associated with an increase in placental StAR protein.

**Key Words:** estrone sulfate, melatonin, uterine flux

**W175 Reproductive indices of quail hatching eggs under semi-intensive management system.** O. T. F. Abanikannda, A. M. Adeyeye*, A. O. Leigh, and A. A. Olubunmi, *Lagos State University, Ojo, Lagos, Nigeria.*

The supply of day old chicks is very important for successful hatchery operations and the future of quail production, breeding and management. This is predicated not only on the number produced but also the fertility and hatchability of the eggs. Fertility and hatchability are 2 major indices for assessing reproductive performance which are mostly sensitive to environmental and genetic influences. This study was aimed at assessing the fertility and hatchability of quail eggs under semi-intensive management. A total of 985 eggs were sourced from a quail farm in the Savannah region of Nigeria. The breeders were kept in cages and were freely pen-mated with a sex ratio of one male to 5 female birds. Eggs were cleaned, labeled, measured, fumigated, incubated and classified as fertile or not fertile after incubation. Measurements included egg weight, length, width, vertical and horizontal circumferences, while computed indices were egg density, surface area and volume (Table 1). All statistical analyses (exploratory, correlation and logistic fit) were done with JMP$^{(R)}$ software. Fertility was 74.92%, while hatchability was 67.82% in the entire study but 90.51% within the fertile eggs group. There was no statistical significance ($P > 0.05$) in mean of all variables in the 2 groups (fertile and not fertile) and a further logistic fit of the 2 groups based on the measures was not significant ($P > 0.05$). In a similar way, hatchability was not significantly influenced by the pre-hatch measures of the eggs. It can be concluded from the study that physical characteristics of the eggs as reflected by the measured variables and indices was not the significant factor in the determination of the fertility and hatchability of the eggs.

**Table 1.** Descriptive statistics of measured variables

| Variable | Fertile | Not fertile |
|---|---|---|
| Sample size (no.) | 738 | 247 |
| Egg weight (g) | 9.90 ± 0.03 | 9.93 ± 0.06 |
| Egg length (mm) | 30.46 ± 0.05 | 30.62 ± 0.09 |
| Egg width (mm) | 24.54 ± 0.04 | 24.49 ± 0.04 |
| Horizontal circumference | 8.37 ± 0.02 | 8.34 ± 0.02 |
| Vertical circumference | 9.25 ± 0.02 | 9.23 ± 0.03 |
| Egg density | 1.05 ± 0.01 | 1.05 ± 0.01 |
| Egg surface area | 22.61 ± 0.06 | 22.66 ± 0.10 |
| Egg volume | 10.33 ± 0.05 | 10.34 ± 0.07 |

**Key Words:** fertility, hatchability, logistic fit

**W176 Effects of maternal 25-hydroxycholecalciferol (25OHD3) supplementation on fetal bone development in pigs.** K. K. McFadden*[1], M. L. Hoffman[1], J. D. Starkey[2], J. D. Coffey[2], E. A. Hines[2], C. W. Starkey[2], and K. E. Govoni[1], [1]*University of Connecticut, Storrs,* [2]*Texas Tech University, Lubbock.*

Lameness in pigs is often due to poor bone development and creates a major health issue for the swine industry. The majority of bone development occurs during fetal and early postnatal development and vitamin D is required for proper bone development. It has been shown in swine that 25OHD3, a metabolite of vitamin D, is more bioavailable than vitamin D$_3$. We hypothesized that providing vitamin D as 25OHD3 to pregnant gilts would increase markers of bone formation in the bones of fetuses. Forty PIC Camborough-22 gilts were randomly assigned to one of 2 corn-soybean meal-based diets. The control diet contained 2,500 IU of vitamin D$_3$ per kg of diet. The experimental diet contained 500 IU D$_3$ per kg of diet plus 50 µg of Rovimix Hy-D (DSM Nutritional Products Ltd., Basel, Switzerland) the 25OHD3 form. Beginning 43 d before gestation, gilts were fed 2.7 kg of their assigned diet once a day until 90 d of gestation. At d 90 ± 1 femurs from the 2 median BW fetuses per gilt (1 male and 1 female) were collected (n = 22: control; n = 28: 25OHD3). mRNA was extracted from the mid-diaphysis for gene expression analysis using real time-reverse transcriptase (RT)-PCR. Data were analyzed using ANOVA with significance considered at $P \leq 0.05$. Specifically, we evaluated mRNA expression of markers of bone formation [osteocalcin, alkaline phosphatase (ALP), and type I collagen], as well as, vitamin D receptor, parathyroid hormone receptor (PTHR), and fibroblast growth factor-23 (FGF-23), molecules critical for bone development and known to interact with the vitamin D pathway. We did not observe an effect of maternal 25OHD3 supplementation on the expression of any of the genes evaluated ($P = 0.32$). In addition, we did not observe an effect of gender ($P = 0.25$) or a treatment × gender interaction ($P = 0.46$). These data suggest that maternal supplementation with 25OHD3 does not alter the expression of these genes at this time during fetal development (90 d of gestation). Further studies are needed to determine if maternal vitamin D supplementation will affect markers of bone formation later during fetal development and postnatal growth.

**Key Words:** vitamin D, swine, bone

**W177 Pituitary genomic expression profiles of steers are altered by grazing of high (HE) versus low (LE) endophyte-infected pastures.** R. M. Hegge*, J. A. Boling, and J. C. Matthews, *University of Kentucky, Lexington.*

Consumption of ergot alkaloids in endophyte-infected tall fescue induces a distinct set of physiological and whole-animal performance parameters collectively known as “fescue toxicosis.” It is estimated that fescue toxicosis-associated animal performance losses cost cattle farmers about $1 billion annually. Many of these parameters, such as decreased fertility and milk production are consistent with impairment of pituitary functions. The goal of this study was to test the overall hypothesis that consumption of endophyte-infected tall fescue would alter pituitary genomic expression profiles, including genes involved with prolactin (PRL) metabolism, a known marker of fescue toxicosis. Total RNA was extracted from pituitaries of 16 Angus-cross steers (BW = 266 ± 10.9 kg) that had been randomly assigned (n = 8) to graze either HE or LE pastures for 89 d, and for which serum PRL levels of HE steers was only 10% of LE steers (JAS, 2009, 87:748–760). RNA was subjected to microarray analysis using a custom platform (WT Btau 4.0 Array, Affymetrix). Raw expression intensity values were adjusted using Robust Multichip Averaging and then normalized using the GeneChips and Media Polish Summarization algorithms (Partek). Pearson (linear)

Correlation Analysis revealed a high (>0.98) correlation among all chips. ANOVA testing found differential ($P \leq 0.001$) expression of 592 RNA transcripts in HE vs. LE pituitaries. Hierarchical clustering analysis (Partek) of differentially-expressed genes revealed that each animal segregated within its respective treatment group. Bioinformatic analysis identified decreased (17 to 63%) expression in HE steers of genes for prolactin signaling and regulation of lactotroph, gonadotroph, and thyrotroph proliferation (GPR101, DRD2, PCSK1, PRL, PRLR), and altered expression of another 13 genes for gonadotropin releasing hormone-mediated signaling. In conclusion, steers grazing HE pastures had altered pituitary genomic profiles, in a manner consistent with reduced blood PRL and altered whole-body metabolism, hallmarks of fescue toxicosis.

**Key Words:** pituitary, gene expression, ergot alkaloid

### W178 Excess estrus in meat goats: 1-year summary.

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Excess estrus (EE) occurs when animals exhibit behavioral estrus, or standing heat, after conception. Excess estrus can occur frequently in some domestic farm animals; however, information regarding its frequency in goats is limited. The causes and effects of EE on the reproductive cycle and pregnancy in goats have not previously been studied. The objective of this project was to determine the frequency of EE in meat goats. Hormone profiles of estradiol-17β ($E_2$) and progesterone ($P_4$) during pregnancy and quantity of embryonic and fetal losses (near d 25, 40, 60, and 110) were recorded to determine if does displaying EE were more prone to reproductive dysfunction. In winter 2011, ultrasonographic examination was used to determine pregnancy in 132 bred Boer and Boer-cross does. One vasectomized buck fitted with a marking harness was placed with does following breeding to detect does displaying EE (EE does). Does were checked for breeding marks daily. Results of this study indicate that of 105 does confirmed pregnant, 21 (20%) showed EE at least once during pregnancy. Concentrations of $E_2$ and $P_4$ were lower in EE does compared with does not displaying EE near d 25 of pregnancy (5.9 vs. 7.3 pg/mL; 7.5 vs. 10.8 ng/mL, respectively). Concentrations of $P_4$ remained lower in EE does through d 40 (8.7 vs. 10.2 ng/mL) and tended ($P = 0.07$) to remain lower through d 60 (10.2 vs. 11.9 ng/mL) of pregnancy. On a percentage basis, fetal and embryonic losses were greater in EE does (29% vs. 15%); however, there was not enough animals to determine significance. Of does kidding, kidding rate of EE does compared with does that did not show EE was not different (1.6 vs. 1.5 kids/doe, respectively; $P = 0.72$).These results suggest that EE may occur in a significant portion of pregnant meat goats and may be associated with differences in embryonic and/or fetal losses of these animals. This project was supported by USDA-NIFA Cooperative agreement.

**Key Words:** goat, estrus, behavior

### W179 Physicochemical analyzes of Longissimus dorsi muscle for checking the quality of meat from cattle Nellore (*Bos indicus*) selected for production.

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Tenderness is a major quality attribute of beef that affects consumer satisfaction, consumption habits and retail preferences. Hence, breeding programs that focus on meat tenderness are important for Brazil given the prevalence of *Bos indicus* breeds in the cattle industry [1]. The present work aims to determine traits in meat quality in Longissimus dorsi muscle of Nellore cattle from 10 farms in 5 Brazilian states that currently are selecting for meat tenderness traits in their breeding programs including analysis shear force (SF), rib eye area (REA), fat thickness (FT), myofibrillar fragmentation index (MFI) and total lipids (TL). The results of the analysis in this study show verified average and standard deviation for each analysis and the correlation of this with the value of shear force. It is the average value and standard deviation of 4.3 ± 1.25 for SF analysis, which confirms the tenderness of the meat in question since it did not exceed the limit accepted for the meat to be considered tender, ie, 4.5 kg [2]. The MFI value found was heavily influenced by postmortem, where the meat showed satisfactory average 63.19 ± 16.26 denoting high tenderness of the analyzed meat, as Culler et al. (1978) [3] values above 60 to qualify as tender flesh. It has been shown a significant correlation ($P < 0.01$) between SF and MFI, as these characteristics are inversely proportional. It has also been found significant correlations ($P < 0.05$) for the analysis of REA (65.49 ± 7.98) and TL (0.76 ± 0.36). For FT (5.26 ± 3.2) there was not a significant correlation ($P < 0.05$) with SF. Therefore, the use of physical and chemical analysis and correlations with shear force, can be used as a tool in verifying the quality of beef, mainly for Nellore (*Bos indicus*), showing a herd with a deficit for such.

**Key Words:** meat tenderness, myofibrillar fragmentation index, shear force

### W180 Bioanalytical methods for calcium proteomic study on tenderness Longissimus muscle of Nellore cattle (*Bos indicus*).

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The calpain system is a complex of proteases activated by calcium as the μ-calpain and m-calpain and its endogenous inhibitor, the calpastatin and are related to proteolysis and meat tenderness [1]. This study examines the separation of skeletal muscle proteins by 2D-PAGE and performing the identification of calcium ions in the protein spots by x-ray fluorescence (SR-XRF) for the 20 Nellore cattle (*Bos indicus*) contrasting meat tenderness: tough (TO) and tender (TE) meat animals. A third group (PI) with Piedmontese cattle (*Bos taurus*) was used as a comparative model of meat tenderness degree. The 3 groups were selected according by the rib eye area and backfat as well the shear force values [2]. The resolution of the gels (matching > 50%) and the image analysis between groups TO, TE and PI showed a correlation between gels of (n = 3) 82%, 54% and 53%, respectively. The average numbers of protein spots in repetitions gels were 176 ± 22, 172 ± 31 and 204 ± 33 for the groups TO, TE and PI, respectively. This standard deviation below 20% can be regarded as a good indication of the proteins fractionation by 2D-PAGE [3]. In the study images of the gels were estimated correlations between protein spots for the groups. The correlation between the spots of the protein was varied in the different groups TE and PI ($R > 0.85$) as well the gels of the TO and PI groups ($R > 0.73$). In the qualitative assessment of calcium ions by SR-XRF were randomly chosen 60 protein spots from the experimental groups, with molar weight (MW) between 20 and 97 kDa [4]. There was higher detection (56%) of calcium by SR-XRF in protein spots TE group, a factor that may be indicative of proteolytic activity in meat after slaughter. The 2D-PAGE in the evaluation study of the calpain system was effective in the fractionation of proteins present in Longissimus muscle. The correlations obtained in the 2D gels indicated that the procedures for extraction of total protein were efficient and preserved the metal-protein structure. However, it was possible to make a detection of calcium in protein spots by SR-XRF with MW between 20 and 97 kDa.

**Key Words:** calpain system, 2D-PAGE, shear force

**W181 The effects of selecting for the myostatin F94L polymorphism on reproductive traits in pubertal heifers.** E. D. Forbes*[1], O. L. Swanson[2], A. K. McNeel[3], R. G. Tait Jr.[3], T. P. L. Smith[3], G. L. Bennett[3], T. A. Hoagland[1], S. A. Zinn[1], C. A. Lents[3], G. A. Perry[2], and R. A. Cushman[3], *[1]University of Connecticut, Storrs, [2]South Dakota State University, Brookings, [3]US Meat Animal Research Center, Clay Center, NE.*

The myostatin F94L polymorphism influences carcass traits in steers; however, the influence of this polymorphism on female reproductive performance should be characterized as part of using it for marker assisted selection. Results from USMARC indicate that heifers that are homozygous for the L allele (L) reach puberty later than heifers that are homozygous for the F allele (F, wild-type), but no one has investigated the influence of this polymorphism on reproductive function in pubertal heifers. We hypothesized that reproductive function would be decreased in heifers that were L. Homozygous heifers that were pubertal (n = 5/genotype) were synchronized with 2 shots of PFG2a given 11 d apart and observed every 4 h for behavioral estrus with the aid of estrus detection patches. Heifers were slaughtered on d 4 after estrus, and the uterus, ovaries, and anterior pituitary were collected, measured, and weighed. A representative piece of one ovary was fixed for histological evaluation, and a sample of subcutaneous adipose was collected and frozen to measure relative levels of chemerin mRNA, a marker of adiposity. Follicular fluid was aspirated from all small follicles (1–5 mm), pooled within heifer, and frozen. Data were analyzed using a MIXED model with genotype as a fixed effect. Heifers that were F had lighter birth weights than heifers that were L ($P = 0.04$), but there was no difference in weaning weight, slaughter weight, or chemerin mRNA levels in the adipose. Heifers that were L exhibited behavioral estrus 14 h sooner after PGF2a than heifers that were F ($P = 0.06$). There was no difference in reproductive organ measurements or numbers of follicles in the ovaries between genotypes. Follicular fluid estradiol concentrations tended to be greater in L heifers than F heifers ($P = 0.10$). Reproductive tract development is not altered in heifers homozygous for the L allele, although they reach puberty later. A shorter time from PGF2a to estrus indicates that timing of insemination in timed-AI protocols may need to be altered for L heifers. USDA is an equal opportunity provider and employer.

**Key Words:** heifer, myostatin, puberty