($P < 0.01$), but was not affected by WQ ($P = 0.39$). There was no SBM × WQ interaction for total tract OM digestibility (TTOMD; $P = 0.69$). SBM linearly increased TTOMD ($P < 0.01$), and LS had lower TTOMD than HS ($P < 0.01$; 55.4 vs. 59.3% for LS and HS, respectively). Nitrogen balance was not affected by SBM × WQ interaction ($P > 0.12$), but N utilization (N-retained/N-intake ratio; $P < 0.01$) was. Regardless of WQ, we observed that SBM exerted a quadratic and linear response for N utilization ($P = 0.01$) and balance ($P < 0.01$). In LS, N balance and N utilization became positive at 0.25% of SBM, but in HS were positive only at the two greatest level of SBM (0.75 and 1.00%). In conclusion, according to our results lambs fed low-quality forage require greater levels of protein supplementation to maximize total digestible OM intake, N balance, and N utilization when they drink high-salt water compared to those drinking low-salt water.

Key Words: nitrogen balance, supplementation, saline water

MEAT SCIENCE AND MUSCLE BIOLOGY

0878 Chemical composition and expression of genes involved in lipid metabolism in the muscle of Nellore and Angus young bulls fed whole shelled corn diet.

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The objective was to evaluate expression of genes involved in lipid metabolism and chemical composition of *longissimus dorsi* (LD) muscle of Nellore and Angus bulls fed whole shelled corn (WSC) or a ground corn (GC) diet. Twenty-eight bulls with average initial body weight of 378 ± 8.7 kg were used in a completely randomized design and arranged as a 2 × 2 factorial (2 breeds and 2 diets). The GC diet had 30% corn silage and 70% of a concentrate based on corn and soybean meal. The WSC diet had 85% whole shelled corn and 15% of a pellet based on soybean meal and minerals. After being harvested, samples were taken from the LD muscle between the 12th and 13th ribs for centesimal composition analyses and gene expression, which was analyzed by RT-qPCR. The model included the fixed effects of breed, diet, and their interaction. Expression of *PPARA* was greater in the LD of Nellore bulls (Table 1; $P < 0.01$) and also when bulls were fed the WSC diet ($P = 0.04$). Opposite results were found for *SREBF1* expression, which was less when bulls were fed the WSC diet ($P < 0.01$) and less in Nellore bulls ($P = 0.03$). *PPARG* and carnitine palmitoyl transferase 2 (*CPT2*) expression was downregulated in the LD muscle of Nellore bulls fed WSC and upregulated in the LD of Angus fed the same diet. Expression of lipoprotein lipase (*LPL*), fatty acid binding protein 4 (*FABP4*), acetyl CoA carboxylase (*ACACA*), and stearoyl-CoA desaturase (*SCD1*) was greater ($P < 0.05$) in the LD of Nellore bulls fed the GC diet. However, diets did not affect the expression of these genes in the LD muscle of Angus bulls. Fatty acid synthase (*FASN*) expression was greater in the LD of Nellore bulls ($P < 0.01$) and when animals were fed WSC ($P < 0.01$). Expression of acyl-coenzyme A oxidase 1 (*ACOX*) was greater for Angus fed WSC ($P = 0.04$). Meat from Angus bulls had greater intramuscular fat than meat from Nellore bulls (4.95 and 4.30; $P = 0.05$). However, there was no effect ($P > 0.05$) of diet on intramuscular fat. Moisture and protein were not affected ($P > 0.05$) by diet and breed. In conclusion, expression of *PPARA* and *SREBF1* have opposite regulation mechanisms in bovine muscle, regardless of the subspecies. Diets affected the expression of some genes involved in lipid metabolism differently in Nellore and Angus bulls.

Key Words: lipogenesis, marbling, *PPAR*, *SREBF1*, transcription factor

Table 0878.

Table 1. Expression of genes involved in lipid metabolism in the *longissimus dorsi* muscle of Nellore and Angus young bulls fed whole shelled corn (WSC) and ground corn (GC) diet.

	Nellore		Angus			*P*		
Genes	GC[1]	WSC[2]	GC	WSC	SEM	Breed	Diet	B*D
PPARA	3.78	4.72	1.00	2.83	0.32	<0.01	0.04	0.22
PPARG	2.61 b	1.00 c	2.8 b	5.67 a	0.33	<0.01	0.86	<0.01
SREBF1	5.25	1.00	5.71	2.61	0.28	0.03	<0.01	0.10
LPL	3.78 a	1.00 c	1.77 b	1.36 bc	0.29	0.04	<0.01	0.01
FABP4	13.47 a	1.00 c	8.93 b	10.16 b	0.86	0.34	<0.01	<0.01
ACACA	7.16 a	1.00 c	3.37 b	1.84 b	0.45	1.00	<0.01	<0.01
FASN	3.87	4.34	1.00	1.83	0.22	<0.01	0.01	0.16
SCD1	3.18 a	1.00 c	1.95 b	1.67 b	0.21	0.91	<0.01	0.02
CPT2	7.2 a	1.00 d	2.02 c	2.87 b	0.27	0.92	<0.01	<0.01
ACOX	1.33 c	1.00 c	2.67 b	5.29 a	0.38	<0.01	0.52	0.04

[1]GC: Diet containing 30% roughage and 70% concentrate
[2] WSC: Diet with 85% whole shell corn and 15% of a *pellet* based on soybean meal and minerals

0879 Effects of arachidonic acid and prostaglandins on proliferation, differentiation, and fusion of bovine myoblasts. X. Leng* and H. Jiang, *Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg*.

Arachidonic acid (AA) is a major lipid component of the plasma membrane and the precursor of prostaglandins (PG) in skeletal muscle. The objective of this study was to determine the effects of AA and its major PG derivatives PGE_2, $PGF_{2\alpha}$, and PGI_2 on the proliferation, differentiation, and fusion of bovine myoblasts. Satellite cells were isolated from 6 Angus or Angus crossbred steers (experimental unit) and were expanded as myoblasts in growth medium for a week before being used in the following tests. In the proliferation test, myoblasts were cultured in growth medium with 10 μM AA, 1 μM PGE_2, 1 μM $PGF_{2\alpha}$, 1 μM PGI_2, or vehicle control for 24 h. Proliferating cells were identified by EdU labeling. This test revealed that AA, PGE_2, $PGF_{2\alpha}$, and PGI_2 each increased the number of proliferating myoblasts by 13%, 24%, 16%, and 16%, respectively, compared to the control ($P < 0.05$). In the differentiation and fusion test, myoblasts were induced to differentiate and fuse into myotubes in the presence of the aforementioned treatments or control, for 24, 48, and 72 h. The differentiation status of myoblasts was assessed by reverse transcription-quantitative PCR of myogenin (*MYOG*), myosin heavy chain 3 (*MYH3*), and muscle creatine kinase (*CKM*) mRNAs, which are markers of differentiated myoblasts. The fusion level of myoblasts was estimated by calculating the percentage of nuclei located in myotubes, i.e., fusion index. Compared to the control, AA increased *MYOG* mRNA expression at 24 and 48 h, *MYH3* mRNA expression at 24 and 48 h, and *CKM* mRNA expression at 24, 48, and 72 h of differentiation ($P < 0.05$); PGE_2 increased *MYOG* mRNA expression at 24 and 72 h, and *MYH3* mRNA expression at 72 h of differentiation ($P < 0.05$); $PGF_{2\alpha}$ increased *CKM* mRNA expression at 72 h of differentiation ($P < 0.05$); and PGI_2 had no effect on mRNA expression of any of the three markers at any of the three times of differentiation. Compared to the control, PGE_2 increased the fusion index by 14% ($P < 0.05$) but the remaining treatments had no effect on this index. In conclusion, this study demonstrates that AA, PGE_2, $PGF_{2\alpha}$, and PGI_2 stimulate the proliferation, that AA and PGE_2 stimulate the differentiation, and that PGE_2 stimulates the fusion of bovine myoblasts in vitro.

Key Words: cattle, myoblasts, prostaglandins

0880 Influence of zinc amino acid complex and ractopamine hydrochloride supplementation on the sarcoplasmic protein profile of finishing steers. O. N. Genther-Schroeder*[1], E. Huff-Lonergan[1], M. E. Branine[2], and S. L. Hansen[1], [1]*Iowa State University, Ames,* [2]*Zinpro Corporation, Eden Prairie, MN*.

The objective of this study was to determine if Zn amino acid complex (ZnAA) and ractopamine hydrochloride (RH) supplementation affect the protein profile of the *longissimus dorsi* muscle of finishing steers. Twenty-four steers (477 ± 5.3 kg; SD) were fed a corn-based finishing diet in pens equipped with GrowSafe bunks to measure individual intake, as a part of a 2 × 2 factorial of ZnAA and RAC supplementation. All steers were supplemented with 60 mg Zn/kg diet DM as $ZnSO_4$ and were assigned to receive either 0 (CON) or 60 mg supplemental Zn/kg DM from ZnAA (ZN; $n = 12$ steers per treatment) for 56 d. On d 56 steers were equally assigned within treatments to receive RH at 300 mg·steer^{-1}·d^{-1} for 0 (NoRAC) or 28 d (RAC) before harvest ($n = 6$ steers per treatment). Muscle biopsies were collected from steers after 14 d of RAC supplementation. Four steers per treatment were selected to have sarcoplasmic extracts from muscle biopsy samples analyzed using 2D Difference-in-Gel Electrophoresis (2D-DIGE). Separate 2D-DIGE experiments were performed for the individual comparisons of CON+NoRAC vs. ZN+RAC (Exp. 1; $n = 4$ per treatment) to evaluate the effect of both RAC and ZnAA supplementation and CON+RAC vs. ZN+RAC (Exp. 2; $n = 4$ per treatment) to evaluate the effect of ZnAA supplementation within RH-fed steers. Proteins were selected based on relative abundance and were identified using mass spectrometry. In Exp. 1, abundance of isoforms of pyruvate kinase was decreased 20–25% ($P \leq 0.04$) in ZN+RAC, relative to CON+NoRAC steers. Phosphoglucomutase-1 abundance was decreased by 63% ($P < 0.0001$), phosphoglycerate mutase-2 was decreased by 21% ($P = 0.02$), and glyceraldehyde 3-phosphate dehydrogenase tended to be increased by 71% ($P = 0.06$) in ZN+RAC steers, relative to CON+NoRAC. In Exp. 2, phosphoglucomutase-1 abundance tended to be decreased by 60% ($P = 0.09$) and phosphoglycerate mutase-2 tended to be decreased 21% ($P = 0.06$) in ZN+RAC steers relative to CON+RAC steers. Decreases in phosphoglucomutase-1 and phosphoglycerate mutase-2 abundance in both experiments suggest these may be effects elicited by ZnAA supplementation. Changes in abundance of pyruvate kinase and glyceraldehyde 3-phosphate dehydrogenase were found only in the CON+NoRAC vs. ZN+RAC comparison and might be elicited by RH supplementation. These differences indicate that ZnAA and RH supplementation alter the protein abundance of enzymes involved in carbohydrate metabolism in skeletal muscle.

Key Words: ractopamine hydrochloride, zinc, 2D-DIGE

0881 Survey of attitudes for millennials who do not consume lamb. K. R. Wall[*1] and C. R. Kerth[2], *[1]Texas A&M University, College Station, [2]Texas A&M University Animal Science Department, College Station.*

Lamb consumption consists of the smallest percentage of red meat consumption in America. Our objective was to estimate how many Americans do not consume lamb and describe attitudes as to why not. The online survey consisted of demographic information and lamb consumption patterns and experiences. Participants were invited to complete the survey if they were within the millennial population (ages 18–34) and residing in the U.S. Participants (n = 2473) were 34.5% male, 65.5% female; 15.9% were ages 18–24, 83.2% were 25–34, and 0.9% were 35; 85.0% were Caucasian (non -Hispanic), 8.8% Latino or Hispanic, 3.0% Asian or Pacific Islander, 1.3% African American, and 1.8% other. Household income was 7.4% $24,999 or less, 17.9% $25,000–49,999, 20.8% $50,000–74,999, 19.5% $75,000–99,999, and 36.4% made $100,000 or more; 10.3% were not employed, 9.6% were employed part-time, and 80.0% were full-time. Participants reported consumption of the following protein sources either away from or at home: 92.3% chicken, 88.8% beef, 79.0% pork, 79.8% fish, 11% lamb, 92.6% eggs, and 25.8% soy-based products. 70.8% of the participants claimed to have eaten lamb before, and of these participants (n = 1719), 70.8% selected having a positive eating experience with lamb. Although 47.2% of the participants were uncertain how the lamb was prepared, braising (19.1%), grilling outside (12.5%), and panfrying (8.6%) were the most common methods of preparation. 65.1% of the participants would be willing to try lamb again, 23.2% selected maybe, and 11.6% would not be willing to try lamb again. Of the participants who had not tried lamb before (n = 716), 60.8% would be willing to try lamb. If lamb flavor were to be improved, 22.4% of the participants would definitely and 47.1% might consume more lamb. If lamb tenderness were to be improved, 23.7% of the participants would definitely and 44.8% might consume more lamb. If the eating quality of lamb were to be more consistent, 24.8% of the participants would definitely and 43.8% might consume more lamb. If lamb were to be implemented into the fast-food industry, 22.1% of the participants would definitely and only 22.8% might consume more lamb. While 72.8% of the participants selected they had never looked to buy lamb at their local grocery store, 14.4% selected lamb is hard to find and 5.1% selected finding lamb was hit or miss. Opportunities exist to increase the consumption of lamb by converting the millennial non-consumers of lamb.

Key Words: lamb, millennial, consumer

0882 Survey of attitudes for millennial lamb consumers. K. R. Wall[*1] and C. R. Kerth[2], *[1]Texas A&M University, College Station, [2]Texas A&M University Animal Science Department, College Station*.

As the interest in experiencing different foods increases among the millennial population, lamb consumption may be becoming more prominent. Our objective was to determine the attitudes of millennial consumers of lamb products by conducting an online survey. Participants were selected within the millennial population (ages 18–34) and residing in the U.S. Participants (n = 3292) reported consumption of the following protein sources either away from or at home: 99.4% chicken, 97.3% beef, 90.9% pork, 93.0% fish, 77.9% lamb, 96.9% eggs, and 35.5% soy-based products. 15.0% of participants eat lamb frequently (at least once every 2 wk), 24.1% eat lamb once a year, 30.0% eat lamb once every 6 mo, 31.0% eat lamb once every 3 mo. Participants reported eating lamb most frequently in the winter (December–February) at 35.0%, and 22.0% consume the most lamb in the month of December. When asked where consumers consume the most lamb, 66.0% responded away from home, and 23.0% responded at home. On a 5-point scale, 90.0% selected their experience consuming lamb has been "excellent" or "good," and 92.0% answered being satisfied with the eating quality of lamb at least 3 out 5 times. Only 34.0% of the consumers reported growing up eating lamb, and 94.0% selected having a positive first experience consuming lamb. Consumers declared choosing lamb over other protein sources 63.0% of the time due to flavor. When asked what origin of lamb consumers preferred, 78.0% selected no preference and only 11.0% selected American lamb. Consumers were prompted to distinguish between lamb and mutton, and 56.0% were "uncertain, they never tried both," whereas 33.0% selected that there are distinct differences. If lamb flavor were to be improved, 34.0% of the participants would definitely and 48.0% might consume more lamb. If lamb tenderness were to be improved, 35.0% of the participants would definitely and 46.0% might consume more lamb. If the eating quality of lamb were to be more consistent, 39.0% of the participants would definitely and 42.0% might consume more lamb. If lamb were to be implemented into the fast-food industry, 36.0% of the participants would definitely and 32.0% might consume more lamb. While 56.0% of the participants selected they had never looked to buy lamb at their local grocery store, 44.0% selected lamb is hard to find or that it was hit or miss. These data can be used to increase consumption among the millennial population.

Key Words: lamb

0883 A histologic and ultrastructural study of Wooden Breast Disease in modern broiler chickens.

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Wooden Breast Disease (WBD) is a novel muscle disorder in the poultry industry observed to frequently affect the breast muscles of high-yielding modern broilers. Characterized by extreme stiffening of the breast muscles on palpation of the pectoral region, WBD is known to result in significant economic loss in the poultry industry and may potentially cause behavioral alterations and reduced welfare in birds. To examine tissue changes associated with onset and pathogenesis of this disorder, a time-series experiment was conducted using chickens from a high-breast-muscle-yield, purebred commercial broiler line. Birds were raised for a period of 6 wk, and breast muscles sampled on a weekly basis from selected birds and processed for light and transmission electron microscopy. Histologic presentation indicated presence of focal single-myofiber degeneration and hyalinization in the second week, preceding inflammatory reaction that started in the third week. Lesions in the fourth week were generally characterized by multifocal to diffuse muscle fiber degeneration and necrosis accompanied by increased inflammatory cell infiltration. Lesions in the fifth and sixth week were characterized by diffuse muscle fiber damage, fibrosis, fatty infiltration including granulomatous tissue encompassing lipid droplets, and irregular myofiber regeneration. Ultrastructural examination showed fibrosis with dense regular collagen fibers, irregular Z-discs, myofibril splitting, displacement, and degeneration, including mitochondrial degeneration. This study therefore demonstrates that WBD exhibits an early onset in modern broilers and appears to assume a progressive course with acute inflammatory phase occurring in the earlier stages and chronic inflammation and fibrosis in the later stages of the disease course.

Key Words: broiler chickens, Wooden Breast Disease, transmission electron microscopy

0884 High-energy forage and feedlot finishing impact on beef consumer acceptability and sensory characteristics in the upper Midwest.

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The objective of this study was to determine consumer acceptability and sensory attributes of beef longissimus thoracis steaks from finishing steers grazing high-energy forages vs. fed a conventional feedlot diet. Steaks were from 32 steers fed 1 of 4 treatment diets including: mixed pasture (MIX); simple cereal grain/brassica mixture (SIMP); complex cereal grain/brassica mixture; and conventional feedlot ration (FLOT). All steers grazed a perennial mixed pasture diet before being assigned a treatment. Steers (n = 8) were fed FLOT diet for 92 d. Steers in the MIX (n = 8), SIMP (n = 8), and COMP (n = 8) grazed respective pastures for 76 d. Steers from all treatments were slaughtered on the same day. Carcasses were aged 7 d before fabricating 2.54-cm thick steaks. Vacuum packaged steaks were aged for an additional 7 d and frozen (−20°C) until evaluation for marbling score, instrumental color, pH, and Warner Bratzler shear force. Consumer panelists (n = 106) evaluated fresh steaks aged 15 d for flavor, texture and firmness, juiciness, and overall acceptability using a 9 point hedonic scale (1 = dislike extremely, 9 = like extremely). Data were analyzed with Proc Mixed and Proc ANOVA (SAS 9.4) for sensory characteristics and consumer acceptability, respectively. Marbling scores of steaks from FLOT steers (524.58) were greater ($P < 0.01$) compared to MIX (447.50), SIMP (437.50), and COMP (427.50) steers. There were no treatment differences ($P > 0.05$) for instrumental color, pH, and Warner Bratzler shear force. There were no correlations ($P > 0.05$) between marbling and Warner Bratzler shear force. Consumer panel results indicated that steaks from steers fed the FLOT diet had more preferable ($P < 0.05$) texture and firmness as well as overall acceptability (7.00 and 6.61) when compared to MIX (6.30 and 6.08) but were not different from COMP (6.63 and 6.21) and SIMP (6.69 and 6.51). Panelists detected no treatment differences ($P > 0.05$) in the hedonic ratings of flavor or juiciness. Results indicate that steaks from steers finished on high-energy forages are comparable to those finished on a conventional feedlot diet. Additionally, the brassica-rich forage diets did not impart any noticeable off-flavors in the steaks when compared to steaks from diets without brassicas.

Key Words: sensory, forage-finished, consumer panel

0885 Effect of growth-promoting technologies on the proteome of bovine *Longissimus lumborum*.

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The objective of this study was to identify the extent to which the protein profile of bovine *Longissimus lumborum* (LL) muscle in beef cattle is influenced by growth-promoting technologies (GP) during the finishing period. Crossbred heifers (n = 66) from two harvest groups were fed a conventional feedlot diet, blocked by BW, and randomly assigned to 1 of 3 treatments: no GP (CON, n = 22); implant, no ractopamine hydrochloride (IMP, n = 22); and implant and ractopamine hydrochloride (COMBO, n = 22). Heifers assigned to the IMP treatment were administered an implant containing 200 mg trenbolone acetate and 20 mg estradiol on d 0 of the study, and

the COMBO group received the same implant protocol as the IMP group, in addition to being fed 400 mg·d^{-1}·heifer $^{-1}$ of ractopamine hydrochloride for the final 28 d before harvest. Heifers were harvested on d 90 of feeding, and a section of the LL was removed (n = 66) 1 h post mortem, placed on dry ice, and stored at −80°C. A subset (n = 6) from each treatment from the first harvest group was randomly selected for proteome analysis by two-dimensional difference in-gel electrophoresis (2D DIGE) coupled with mass spectrometry (MS) to identify proteins of interest. Peptide identifications with > 95% probability with at least 2 identified unique peptides were accepted. Twenty-five spots selected in the sarcoplasmic fraction corresponding to 21 proteins differed in relative abundance among growth promoting programs. Nine spots from the myofibrillar fraction corresponding to 6 proteins were also identified to be different among treatment groups. Increased abundance (P < 0.05) of identified proteins in sarcoplasmic and myofibrillar fractions of the LL muscle from heifers subjected to the COMBO treatment when compared with the LL from CON included metabolic enzymes (creatine kinase M-type, triosephosphate isomerase, β-enolase), oxidative resistant proteins (peroxiredoxin-6, peroxiredoxin-2, protein deglycase DJ-1), muscle recovery proteins (myosin binding protein H, eukaryotic translation initiation factor 5A-1), and chaperone proteins (heat shock 70 kDa protein 1A). The results demonstrate that growth promoting technologies alter the protein profile of bovine muscle and suggest several metabolic pathways that are influenced by management practices that use these technologies. These pathways include metabolic processes, oxidative stress, and apoptosis cascades that can have an impact on growth efficiencies and meat quality in beef cattle.

Key Words: bovine, muscle, proteome

0886 Effects of post-weaning exposure to a high-concentrate diet vs. pasture on live performance, carcass characteristics, and meat quality of early harvested steers.

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Twenty Angus steers (261 ± 21.5 kg) were used to evaluate the effect of post-weaning feeding strategy on live performance, carcass characteristics, and meat quality. Steers were randomly assigned to one of two feeding treatments: high-concentrate based diet (cracked corn, corn silage, and soybean meal [F]) or high-quality pasture (winter annuals, alfalfa, and non-toxic fescue [P]) for 127 d. At slaughter, subcutaneous adipose tissue samples were collected from each steer and flash frozen for later analysis. The 6–12 rib section of each carcass was collected for further analysis on Day 2 post-harvest. Steers consuming a high-concentrate based diet had a greater overall ADG than P ones (1.36 vs. 0.68 kg/d; P < 0.0001) resulting in heavier final BW and HCW, and greater dressing percentage (P < 0.001). Steers consuming grain had larger ribeye area (P = 0.0006) and more fat at the 12th rib (P < 0.0001) than steers on forages, whereas there were no differences for KPH and calculated yield grade (P = 0.22). The high-concentrate based diet resulted in much greater marbling scores than grazing high-quality forages (P < 0.0001; 448 vs. 240). Despite the increased marbling, there was no difference in longissimus muscle (LM) b* (P = 0.956), whereas LM from F were brighter and more red (greater a*; P < 0.003). Both subcutaneous L* and b* were not different between treatments (P = 0.20), whereas subcutaneous a* was greater for F than P (P = 0.0018). Fat cell sizes of subcutaneous tissue were larger in perimeter and area for F (P < 0.0001) whereas P had a greater fat cell number (P < 0.0001). Steers on F had greater LM total lipid (P < 0.0001), whereas P resulted in greater moisture, nitrogen, and ash (P < 0.0001). There were no differences in SFA or PUFA n-6 in LM (P = 0.49) whereas F had greater MUFA (P = 0.0037) and P had greater PUFA and PUFA n-3 percentages (P < 0.01) resulting in a more desirable PUFA n-6/PUFA n-3 ratio (P = 0.0003; 1.46 vs. 7.35 for P and F, respectively). This suggests that exposure to high-concentrate based diets early in the finishing process results in increased performance and carcass quality, along with deposition of intramuscular adipose tissue.

Key Words: grain, pasture, meat quality

0887 Effects of post-weaning exposure to a high-concentrate diet vs. pasture on carcass ultrasound, plasma insulin and glucose, and gene expression of lipogenic enzymes of early harvested steers.

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Twenty Angus steers (261 ± 21.5 kg) were used to evaluate the effect of post-weaning feeding strategy on plasma insulin and glucose levels and gene expression of lipogenic genes. Steers were randomly assigned to one of two feeding treatments: high-concentrate based diet (cracked corn, corn silage, and soybean meal [F]) or high-quality pasture (winter annuals, alfalfa, and non-toxic fescue [P]) for 127 d. Blood samples were collected at 21-d intervals. At slaughter, s.c. adipose tissue samples were collected from each steer and flash frozen in optimal cutting temperature compound for later histology. Steers consuming a high-concentrate based diet had a greater overall ADG (1.36 vs. 0.68 kg/d for F and P, respectively; P < 0.0001) resulting in heavier final BW and HCW (P < 0.001). There was an interaction of treatment and time for ultrasound ribeye area (REA) and 12th-rib fat thickness (P < 0.014) as F resulted in increased REA and fat deposition over time whereas P did not differ over time. Similarly, there was a treatment by time interaction for plasma insulin with insulin levels of steers consuming a high-concentrate based diet increasing over time while steers grazing forages did not. There was no interaction of treatment and time on glucose (P

= 0.469) whereas steers on F had greater plasma glucose than those on P ($P < 0.0001$). RefFinder was used to evaluate reference gene candidates. Thy1 was selected as the most stable reference gene. There was no difference in the expression of acetyl CoA carboxylase, elongase-6, leptin, or glucose transporter type 4 ($P > 0.14$). Fatty acid synthase and stearoyl CoA desaturase-9 were upregulated by 16- and 81-fold, respectively for steers on F when compared to P ($P < 0.002$). Additionally, steers receiving a high-concentrate based diet had a 42-fold increase in mRNA of elongase-5 compared to steers grazing high-quality forages ($P = 0.0006$) and threefold more expression of lipoprotein lipase ($P = 0.011$). Early exposure of steers post-weaning to high concentrate diets increased the ratio of insulin to glucose and marbling deposition with greater expression of lipogenic genes.

Key Words: gene expression, insulin, glucose

0888 Effects of dietary coated cysteamine hydrochloride on meat quality in finishing pigs. H. Liu[*1], M. Bai[1,2], K. Xu[1], B. Zou[3], R. Yu[3], Q. Xi[2], and Y. Yin[1,2], *[1]Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha, China, [2]College of Animal Science, South China Agricultural University, Guangzhou, China, [3]King Techina Group, Hangzhou, China*.

Cysteamine is used as a feed supplement in animal production to promote growth rate and improve feed efficiency. Coated cysteamine hydrochloride (CC) target releases cysteamine in small intestine and protects gastrointestinal mucosa from oxidative damage. However, little information is known regarding the effects of CC supplementation in carcass characteristics and meat quality. The aim of present study was to investigate potential effects of cysteamine supplementation on growth performance, carcass characteristics, and meat quality in finishing pigs. A total of 144 crossbred finishing pigs (87.60 ± 0.20 kg) were assigned randomly to one of the two dietary groups, with eight pens/group (nine pigs/pen). Pigs were fed with a basal diet containing 0 (control) and 70 mg/kg CC for 29 d. The CC was supplied by King Techina Group (Hangzhou, China), containing 27% cysteamine hydrochloride. One pig from each pen was selected randomly to be killed by exsanguination after electrical stunning. A longissimus dorsi sample was collected and stored at 4°C for meat quality measurement. Muscle pH was determined by the electrometric method using a Testo 205 thermometer (Testo, Germany) at 1 h, 24 h and 48 h postmortem Meanwhile, meat color (L* = lightness, a* = redness, b* = yellowness) was measured by a chromameter at 24 h and 48 h after slaughter. The meat tenderness of the longissimus dorsi was measured with a tenderometer, and longissimus dorsi heme pigment estimation (myoglobin, oxygen-myoglobin, and metmyoglobin) was conducted based on Krzywick's method (1982). MDA was determined by commercial reagents (Nanjing Jiancheng Bioengineering Institute, Nanjing, China) according to the manufacturer's instructions. We find that dietary CC has tended to increase average daily gain and decrease feed conversion rate ($0.05 < P < 0.1$). Compared with the control diet, supplementation of CC increased carcass weight, lean rate, and eye muscle area of finishing pigs by 8.9%, 15.9%, and 11.9%, respectively. Dietary CC increased the tenderness of the longissimus dorsi significantly ($P < 0.05$). There were no significant differences in the meat color lightness and yellowness, content of oxygen-myoglobin, metmyoglobin, and MDA between groups. But the redness of meat color and the relative contents of myoglobin increased with CC supplementation ($P < 0.05$). Collectively, 70 mg/kg coated cysteamine hydrochloride diet shows a positive effect on growth performance, tenderness, and meat quality in finishing pigs; in particular, coated cysteamine hydrochloride improves the meat color by regulating the content of myoglobin in the longissimus dorsi.

Key Words: cysteamine, finishing pigs, meat quality

0889 Meat quality of lambs fed diets containing different levels of residual frying oil. M. Capelari[*1], E. L. T. Peixoto[2], E. S. Moura[3], E. L. A. Ribeiro[3], and I. Y. Mizubuti[3], *[1]Michigan State University, East Lansing, [2]Universidade Federal do Sul e Sudeste do Pará, Maraba, Brazil, [3]Universidade Estadual de Londrina, Londrina, Brazil*.

The objective of this study was to evaluate the effect of feeding different levels of residual frying oil (RFO) on meat quality traits of confined lambs. Forty growing male lambs (21.0 ± 3.4 kg initial BW) were randomly allocated to 5 pens, each representing an experimental treatments (0, 20, 40, 60, and 80 g of RFO/kg of diet DM; 8 replications per treatment) in a completely randomized block design. Animals were fed ad libitum, twice daily, a 60:40 forage-to-concentrate basal diet consisting of sorghum silage, ground corn, soybean meal, and mineral and vitamin premix and formulated to be isonitrogenous and isocaloric among treatments. After 70 d, animals reached average BW of 35 kg and were transported to a slaughterhouse. Total *Longissimus dorsi* samples were taken from all animals, subdivided into 6 equal parts and transported to the meat science laboratory of Universidade Estadual de Londrina, where they were submitted to analysis of shear force, coloration and pH, marbling, water loss by pressure, sensory analysis, and lipid oxidation. Data was tested for normal distribution and submitted to analysis of variance and regression analysis with 5% significance level. There was a linear effect of RFO inclusion on shear force (2.72 vs. 3.84 kgf for 0 and 80 g RFO/kg DM, respectively; $P < 0.01$). However, even with the increase effect on shear force with higher inclusions of RFO, in the sensory test, samples were classified as high tenderness. Lipid oxidation, color parameters and pH, chemical composition, and

sensory attributes did not differ among levels of RFO inclusion in the diet. The inclusion of RFO in lamb diets up to 80 g/Kg DM did not affect meat quality.

Key Words: shear force, *Longissimus dorsi*, lipid oxidation

0890 Sensory properties of meat of Nellore cattle fed different levels of lipid-based diets.

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Use of agroindustrial by-products in the feed of animals should be analyzed for better understanding of their impacts on cattle meat quality. The objective of this study was to determine the effect of the dietary inclusion of lipid-based diets on the sensory properties. The study was performed on a farm in Aguaí, SP, Brazil. A group of 39 uncastrated Nellore cattle was enclosed in individual pens. The animals were 36 mo old, and the initial mean live weight was 494.1 ± 10.1 kg. Animals were randomly assigned to one of three treatments, based on dry matter: feed with control diet 2.50% cottonseed (CD), feed with 11.50% cottonseed (CS), and feed with 3.13% cottonseed added of 1.77% protected lipid (PL). After 63 d mean final live weight was 577.01 ± 11.34 kg. Then, part of the *M. longissimus thoracis* of each animal was removed between the 12th and 13th rib of the left half carcass. The samples steaks were 2.5 cm thick and were stored frozen in a freezer at −18°C. Sensory analysis was performed after samples were thawed in the refrigerator (± 20 h at 2.5 ± 0.5°C) and heated on automatic superposed grills. At an internal temperature of 71°C, the steak was removed from the grill and heated in a microwave oven for 30 s until the temperature reached 50°C. Immediately after, they were randomly distributed to the panelists in sterile Petri dishes codified with four-digit numbers. Sensory evaluations were conducted using 11 trained panelists. Sensory tests used a 9-point scale: aroma intensity (ranging from absent to extremely intense), strange aroma (ranging from absent, 1, to extremely strong, 9), flavor (ranging from extremely bad to extremely good), strange flavor (ranging from absent, 1, to extremely intense, 9), tenderness (ranging from extremely tender, 1, to extremely hard, 9), juiciness (ranging from extremely dry, 1, to extremely juicy, 9), color (ranging from bright cherry red to dark red), and overall appearance (ranging from very bad to very good). The intensity of the aroma (mean 5.66), strange aroma (mean 2.27), flavor (mean 6.09), strange flavor (mean 1.85), juiciness (mean 5.36), color (mean 5.60), and overall appearance (mean 6.48) were similar between treatments, except for tenderness ($P <$ 0.05) while for CD and CS mean 5.16 versus 6.36 for PL. The addition of PL in the diets of finishing cattle led to less tender meat. Acknowledgments for financial support in Brazil: IFGOIANO, FAPEG, and CNPq.

Key Words: beef quality, protected fat, whole cottonseed

0891 Genome-wide efficient mixed-model study for meat quality in Nellore cattle.

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The quality of meat, which includes several traits such as tenderness, juiciness, and fat thickness, is essential for the beef industry. Previous genome-wide association studies (GWAS) using Bayesian methods have shown that Brazilian Nellore cattle have enough genetic variation for improvement of these traits. Thus, the aim of this study was to further identify quantitative trait loci (QTL) associated with meat-quality-related traits in Nellore beef cattle by using the univariate linear mixed model (LMM) approach implemented in the GEMMA software and compare it with our previous GWA studies performed using Bayesian approaches. A total of 387 Nelore steers comprising 34 half-sib families were genotyped using the IlluminaBovineHDBeadChip. We analyzed the association between markers and Warner-Bratzler shear force, backfat thickness, ribeye muscle area, scanning parameters lightness (L*), redness (a*), and yellowness (b*) to ascertain color characteristics of the meat, water-holding capacity, cooking loss, muscle pH, myofibrillar fragmentation index, saturated fat sum, omega-6 fatty acids sum, omega-3 fatty acids sum, and ethereal extract. These phenotypes were measured in the Longissimus dorsi muscle between the 11th and 13th ribs collected at slaughter. We identified fifty-three genomic regions that each contained at least one single nucleotide polymorphism (SNP) that showed a significant association with meat quality traits (1-Mb SNP windows). Highlighted, we found regions associated with three genes—neuronal growth regulator 1 (NEGR1, chr03: 70884613–71949611), dynamin 3, and phosphatidylinositol glycan anchor biosynthesis class C (DNM3/PIGC, chr16: 37340706–38007593)—related to lipid metabolism and obesity. Our results provide a better understanding of QTL regions associated with meat quality unexplored in our previous Bayesian approach.

Key Words: GWAS, Nellore, meat quality

0892 Comparison of carcass and sensory traits and contents of fatty acids and volatile compounds in Longissimus dorsi of three cattle breeds.

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This study was performed to compare carcass and sensory traits, physicochemical composition, fatty acid (FA) contents, and volatile compounds in Longissimus dorsi (LD) of Korean cattle, Holstein, and American Angus. A total of 36 steer LD samples were obtained from Korean cattle (n = 12), Holstein (n = 12), and American Angus (n = 12) with quality grade (QG) 1+, QG 2, and Choice grade, respectively. Korean cattle had the highest ($P < 0.05$) contents of intramuscular fat and reducing sugar but the lowest ($P < 0.05$) shear force values. Korean cattle revealed the highest ($P < 0.05$) sensory traits (flavor, tenderness, juiciness, and overall acceptance), and these traits were positively correlated with fat ($0.95 \leq r \leq 0.99$; $P < 0.001$) and reducing sugar contents ($0.55 \leq r \leq 0.63$; $P < 0.001$). Korean cattle had the highest ($P < 0.05$) contents (g/100 g LD) of most of the FAs, including palmitic acid, stearic acid, oleic acid, saturated fatty acids, monounsaturated fatty acids, and unsaturated fatty acids, and these FA contents were positively correlated ($0.65 \leq r \leq 0.78$; $P < 0.001$) with all sensory traits. Korean cattle had the highest ($P < 0.05$) concentrations of several volatile compounds, including acetaldehyde, 2-methyl butanal, 3-methyl butanal, 2,3-butanedione, and 3-hydroxy-2-butanone, and these compounds were positively correlated ($0.56 \leq r \leq 0.81$; $P < 0.001$) with all sensory traits, whereas Angus had the highest ($P < 0.05$) concentrations of pentanal, hexanal, and n-pentane. In conclusion, the LD contents of fat, reducing sugar, and FAs, the concentrations of LD volatile compounds, and sensory traits varied among breeds of cattle. Sensory traits had positive correlations with contents of fat, reducing sugars, and most of the FAs, and these showed positive or negative correlations with several volatile compounds.

Key Words: cattle breed, reducing sugar, volatile compound

0893 Label-free MS^E proteomic analysis of the bovine skeletal muscle: New approach for meat tenderness evaluation.

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Meat tenderness is an important trait for beef consumer satisfaction and presents a large individual variation among animals. Meat from Nellore cattle is less tender, resulting in lower economic value. Although many biochemical factors associated with meat tenderness have been studied, the alterations in the muscle proteome profile that reflect the biological complexity of the tenderness process remain unclear. The aim of this study was to investigate pathways and biological mechanisms associated with meat tenderness in one Nellore steer population using label-free proteomic approach by high definition mass spectrometry with HDMS^E acquisition. We evaluated differential protein expression in the *Longissimus dorsi* muscle, collected at 20 min. postmortem, from 10 animals with lower and 10 with higher values of shear force at the seventh day postmortem. The proteome analysis was performed using the nanoACQUITY UPLC Synapt HDMS G2-S system (Waters, Manchester, UK), and the data were processed using Waters Progenesis QI for proteomics software. A Nellore transcriptome database build from RNaseq data from the *Longissimus dorsi* muscle was used to identify the proteins. A total of 5016 proteins were identified, of which 3311 were quantified and 1816 were present in at least 8 out of 10 biological replicates. Among these, 125 proteins were differentially expressed (DE, $P < 0.05$), 66 proteins presented as downregulated, and 59 as upregulated in the group of animals with lower values of shear force. Functional annotation analysis of the list of DE proteins using DAVID identified two pathways (KEGG): pyruvate metabolism and viral myocarditis; catabolic processes, such as glucose, hexose, carbohydrate, and monosaccharide; and molecular functions, such as actin binding, cytoskeletal protein binding, and calcium ion binding. These results provide a comprehensive protein profile of the skeletal muscle and indicate that changes in energy metabolism and cytoskeletal structure of muscle could influence meat tenderness.

Key Words: beef cattle, mass spectrometry, proteome

0894 Carcass grading effects on the fatty acid and amino acid composition of pork loin from Duroc pigs. J. Álvarez-Rodriguez[1], R. Ros-Freixedes[1], S. Gol[1], E. Henríquez-Rodríguez[1], R. N. Pena[1], L. Bosch[2], J. Estany[1], F. Vilaró[3], and M. Tor*[1], *[1]University of Lleida, Agrotecnio Center, Lleida, Spain, [2]Universitat de Girona, Girona, Spain, [3]University of Lleida, Lleida, Spain.*

Eighty purebred Duroc pigs slaughtered at 210 d of age were used to evaluate the effect of carcass grading according to lean content (R, 45–50%, n = 18; O, 40–45%, n = 28; P, < 40%, n = 34) on the fatty acid and amino acid composition of fresh pork loins. The crude protein content of loin was higher while the intramuscular fat content was lower in R carcasses than in the rest ($P < 0.05$). Carcass group had a major effect on fatty acid composition, with R carcasses showing lower MUFA and greater PUFA content than the rest of groups ($P < 0.05$) and with similar SFA content across groups ($P > 0.05$). Amino acid composition was not affected by carcass grading except for a tendency for isoleucine and glycine to have lower levels in P and R carcasses, respectively ($P < 0.1$). The balance of amino acids in the pork loin was compared with the recommended balance of indispensable amino acids for adults (WHO/FAO/UNU) by expressing the relevant amino acids relative to lysine and then calculating the proportion of the recommended amount of each amino acid that was provided by a sample containing the recommended amount of lysine. The balance of indispensable amino acids was less than ideal, with valine being the limiting amino acid by about 30–35%,

Table 0894.

Chemical composition of fresh loins (24 h post-mortem) from Duroc barrows according to carcass commercial grading

	R (45-50% lean)	O (40-45% lean)	P (<40% lean)	P-value
Dry matter, g/kg	282.7±2.7	287.2±2.2	286.5±2.0	0.40
Crude protein, g/kg	217.0±2.0a	214.3±1.6b	210.9±1.5b	0.05
Intramuscular fat, g/kg	31.8±2.5b	40.7±2.0a	43.2±1.9a	0.002
∑MUFA, g/kg fatty acids	492.0±4.0a	501.7±3.2ab	508.8±3.0b	0.006
∑SFA, g/kg fatty acids	391.4±4.5	403.2±3.6	402.1±3.4	0.10
∑PUFA, g/ kg fatty acids	116.5±3.6b	95.1±2.9a	89.1±2.7a	<0.0001
Amino acids, g/16 g N				
Lysine	8.48±0.29	8.43±0.23	8.62±0.22	0.83
Methionine	1.95±0.08	2.06±0.07	2.08±0.06	0.46
Threonine	4.68±1.00	4.80±0.08	4.85±0.07	0.45
Valine	4.96±0.11	5.09±0.09	4.94±0.08	0.45
Isoleucine	4.54±0.09	4.56±0.07	4.34±0.07	0.09
Leucine	9.29±0.13	9.42±0.11	9.20±0.10	0.34
Histidine	5.16±0.17	5.16±0.14	5.15±0.13	0.99
Phenylalanine	3.82±0.04	3.89±0.04	3.83±0.03	0.39
∑EAA	42.9±0.7	43.4±0.6	43.0±0.5	0.80
Cistine	0.97±0.04	0.97±0.03	0.96±0.03	0.99
Hydroxyproline	0.27±0.02	0.28±0.01	0.26±0.01	0.63
Proline	3.76±0.06	3.84±0.05	3.80±0.04	0.53
Alanine	5.21±0.10	5.27±0.08	5.14±0.08	0.52
Arginine	5.97±0.07	6.01±0.06	5.90±0.05	0.35
Aspartic acid	10.34±0.26	10.79±0.21	10.73±0.20	0.37
Glutamic acid	15.47±0.30	15.89±0.25	15.48±0.23	0.42
Glycine	3.92±0.08	4.15±0.06	4.03±0.06	0.06
Serine	4.13±0.08	4.28±0.06	4.28±0.06	0.26
Tyrosine	3.34±0.10	3.22±0.08	3.33±0.08	0.53
∑NEAA	53.4±0.6	54.7±0.5	53.9±0.5	0.27
Total	96.25±1.22	98.09±0.99	96.90±0.92	0.47

MUFA= monounsaturated fatty acids (C16:1n-7; C17:1n-7; C18:1n-9; and C20:1n-9); SFA= saturated fatty acids (C10:0; C12:0; C14:0; C16:0; C17:0; C18:0; and C20:0); PUFA=polyunsaturated fatty acids (C18:2n-6; C18:3n-3; C20:2n-6; C20:3n-6; C20:4n-6; C20:4n-6 and C22:6n-3). EAA= essential amino acids (Lysine, Methionine, Threonine, Isoleucine, Valine, Phenylalanine, Leucine and Histidine); NEAA= non-essential amino acids (Cistine, Arginine, Hydroxyproline, Tyrosine, Alanine, Glycine, Glutamic acid, Serine, Proline, and Aspartic acid). Within each row, different letter denotes statistical differences among carcass grading categories (P<0.05).

indicating that consumption of 144–151 g of pork loin would be needed to match 100 g of a sample with the recommended balance of the indispensable amino acids. The amount of Duroc pork meat that would need to be consumed to get a satisfactory balance of amino acids was highest in the P (< 40% lean) carcass grade group. In conclusion, in the Duroc swine breed, carcass adiposity modifies the fatty acid profile of meat but hardly affects the amino acid balance of raw loin.

Key Words: swine, intramuscular fat, amino acid.

0895 The longissimus thoracis muscle proteome in Alentejana bulls as affected by growth pattern.

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Beef production is an important economic activity worldwide. In southern Europe there are two major types of beef production systems based on the growth pattern the animals are subjected to: continuous versus discontinuous growth (CG vs. DG). The first can be characterized as more intensive with the animals being finished on concentrate and imported feedstuffs, while the second? The objective of this work is to conduct a comparison between the protein expression profiles of the longissimus thoracis (LT) muscle in CG and DG animals using label-free quantitative proteomics. Forty purebred *Alentejana* male calves (9 mo old, 239 kg live weight) were randomly allocated to two distinct feeding regimens: CG and DG. CG animals were fed ad libitum on concentrates plus grass hay throughout the trial and slaughtered at 18 mo of age. DG animals were only fed ad libitum on hay from 9 to 15 mo of age and then fed the same diet provided to the CG group (concentrates plus hay) until 24 mo of age. Animals were slaughtered and the LT muscle sampled. Samples (100 μg) were added to 500 μL of ammonium bicarbonate 50 mM, urea 8M, thiourea 2M buffer and homogenized and centrifuged and the supernatant recovered. Proteins were trypsin digested (FASP protocol) and desalted, and peptides were loaded onto reverse-phase C18 columns and analyzed on an LTQ-Orbitrap Velos mass spectrometer. Protein identification and label-free quantification were performed using Mascot (Matrixscience) and Progenesis (Nonlinear Dynamics). The study identified a total of 531 different proteins in the bovine LT muscle, with 26 showing differential expression, of which 25 were overexpressed in the CG group. Several of these proteins (e.g., myozenin-2, myosin regulatory light chain 2, glyoclythic pathway enzymes, and 14-3-3 protein zeta/delta) could be proposed as markers of a more intensive growth pattern that slaughters cattle at a younger age. The myosin binding protein H was the only protein having the higher expression in the DG group, suggesting that this protein may be putatively used as a marker of quality associated to discontinuous growth.

Key Words: growth pattern, longissimus thoracis muscle, proteome

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0896 Ferulic acid in diets of heifers and its effect on the oxidative stability of meat stored in refrigeration.

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Ferulic acid (FA) is a naturally occurring compound with important antioxidant activity. Therefore, it could be an interesting alternative to improve the shelf life of meat. The aim of this study was evaluate the oxidative stability in meat from commercial heifers supplemented with 5 or 10 ppm of FA by 30 d. Two hundred seventy heifers (480 ± 10 kg) in the finishing phase were fed with a basal diet (20:80 forage : concentrate ratio). Treatments were Control (without additive), 5 ppm of ferulic acid (FA5), and 10 ppm of FA (FA10) per kg of body weight, assigned randomized to 90 animals per treatment by 30 d. Finishing the feeding phase, animals were slaughtered and a section of the *Longissimus thoracis* muscle (LT) was collected between 4th and 12th rib (n = 9 per treatment). The LT muscle was sliced (1-inch thickness) for oxidative stability analysis for 0, 7, 10, and 14 d of storage. Objective color variables and pH were evaluated with a Minolta colormeter and Hanna pH meter, respectively; thiobarbituric acid-reactive substances (TBARS) and metmyoglobin were evaluated by spectrophotometry. A descriptive sensory test was done according to the guidelines of AMSA, and attributes, such as loss of fresh flavor, loss of fresh odor in cooked meat, and color and discoloration in raw meat, were evaluated. All data were analyzed by GLM-ANOVA with a 3 × 4 factorial arrangement considering as fixed effects the treatments and storage time using the statistical package NCSS 2007. There were no effects of FA supplementation or interaction to a*, b*, hue angle, and pH ($P > 0.05$), where the values were normal for fresh beef. L* values were higher in FA5 (40.48) and FA10 (41.03) compared with Control (38.91) ($P < 0.05$). On overall storage time, FA10 caused an increase in lipid oxidation of beef (TBARS values) compared with Control and FA5 ($P < 0.05$); while metmyoglobin values were lower in FA10 than FA5 and Control ($P < 0.05$). No differences were detected between treatments for sensory attributes ($P > 0.05$), which were qualified with high values. Results indicated that the doses of FA used in finished diets for heifers had no antioxidant effect.

Key Words: ferulic acid, shelf life, meat oxidation

0897 Label-free quantification of myosin isoforms in porcine skeletal muscles. J. Y. Jeong*[1], H. S. Yang[2], J. K. Seo[2], H. W. Yum[2], and G. D. Kim[1,3], [1]*Institute of Agriculture & Life Science, Gyeongsang National University, Jinju, The Republic of Korea,* [2]*Division of Applied Life Science (BK21 plus), Gyeongsang National University, Jinju, The Republic of Korea,* [3]*Department of Animal Sciences, University of Illinois Urbana-Champaign, Urbana*.

Myosin isoform (myosin heavy chain, MHC) in skeletal muscles has been usually qualified and quantified by electrophoresis, immunoblotting, and immunohistochemistry. However, it was difficult to clearly analyze myosin isoforms due to high homology among myosin isoforms. In the present study, label-free quantification (LFQ) was studied to both identify and quantify porcine myosin isoforms. *Longissimus thoracis* (LT), *psoas major* (PM), and *semimembranosus* (SM) muscles were taken from three pigs (180 ± 1 days old, female, 109.2 ± 2.4 kg slaughter weight) at 24 h postmortem in a slaughter house. Myofibrillar protein, which was isolated with rigor buffer (75 mM KCl, 10 mM K_2HPO_4, 2 mM $MgCl_2$, 2 mM EGTA, pH 7.0), was loaded onto sodium dodecyl sulfate-polyacrylamide gel electrophoresis. MHC bands were cut and in-gel digested with trypsin. Spectra were obtained by analysis of liquid chromatography (LC)-mass spectrometry (MS). LFQ was performed using MaxQuant software (ver. 1.5.3.30, Max-Planck Ins., Germany). Four myosin isoforms—myosin-1 (MHC 2x), myosin-2 (MHC 2a), myosin-4 (MHC 2b), and mysoin-7 (MHC I/slow)—were identified, and their matched peptides were 193.3, 154.7, 201.2, and 77.1, respectively. Unique peptides among the matched peptides were selected for quantification of each myosin isoform. The spectral count and summed MS intensity of selected peptide were evaluated. Similar patterns were found in the relative spectral count and relative peak intensity regardless of muscle types. LT and SM muscles had a higher composition of myosin-4 than PM muscle ($P < 0.05$), whereas myosin-7 was higher in PM than the others ($P < 0.05$). Myosin-1 and myosin-2 were relatively lower than myosin-4 and myosin-7 ($P < 0.05$). These LFQ results showed a similar trend to previous reports, which observed the composition of myosin isoforms or myosin heavy chain-based fiber compositions in porcine skeletal muscles. Therefore, LFQ can be a useful approach to overcome the problem of myosin quantification caused by high homology among their isoforms.

Key Words: label-free quantification, myosin, pig

0898 Identification of novel genes and mechanisms involved in bovine myogenic differentiation. H. Jiang*[1], R. Settlage[2], X. Leng[1], and Y. Hou[1], [1]*Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg,* [2]*Biocomplexity Institute, Virginia Tech, Blacksburg*.

Myogenic differentiation, whereby the mononuclear myoblasts differentiate into the multinucleate myotubes, is a critical step in the formation of skeletal muscle. The objective of this study was to identify genes and pathways that regulate myogenic differentiation in cattle. Satellite cells, the myogenic progenitor cells in adult skeletal muscle, were isolated from 4 Angus crossbred steers (experimental unit). The isolated satellite cells were first propagated as myoblasts in growth medium containing 10% fetal bovine serum and then induced to differentiate into myotubes in differentiation medium containing 2% horse serum. Transcriptomes in myoblasts immediately before and 48 h after induction of myogenic differentiation were analyzed by RNA sequencing (RNA-seq). The RNA-seq analysis identified a total of 5538 transcripts that were differentially expressed (counts > 20; the false discovery rate-adjusted $P < 0.05$) between the two conditions. Of these transcripts, 2937 were upregulated and 2601 downregulated in differentiated myoblasts compared to undifferentiated myoblasts. Expression patterns for 20 of these genes were verified by reverse transcription-quantitative PCR. The list of genes upregulated in differentiated myoblasts included myogenin and myogenic factor 6, which are known to stimulate myogenic differentiation, and sex determining region Y-box 6 (SOX6) and growth hormone releasing hormone (GHRH), whose roles in myogenic differentiation are unknown. The list of genes downregulated in differentiated myoblasts included myostatin and myogenic differentiation family inhibitor (MDFI), which are known inhibitors of myogenic differentiation, and ZNF469 and SOX9, which are not known to be involved in myogenic differentiation. Functional annotation clustering analysis (DAVID 6.7) of 1107 transcripts upregulated $\geq$ twofold in differentiated myoblasts revealed enrichment (false discovery rate < 0.05) in contractile fiber, sarcoplasmic reticulum, calcium signaling, muscle contraction, cell adhesion, and steroid biosynthesis. Functional annotation clustering analysis of 817 transcripts downregulated $\geq$ twofold in differentiated myoblasts revealed enrichment (false discovery rate < 0.05) in cell cycle, microtubule cytoskeleton, growth factor binding, and ATP binding. Overall, this study not only confirms known factors and pathways that control myogenic differentiation but also suggest novel genes and mechanisms that may contribute to myogenic differentiation in cattle.

Key Words: cattle, muscle, myogenic differentiation

0899 Omega-3 and omega-7 oil supplementation on tissue fatty acid accumulation. S. K. Duckett*, I. F. Furusho-Garcia, M. F. Miller Jr., B. M. Koch, and G. Volpi Lagreca, *Clemson University, Clemson, SC*.

Eighteen Southdown ewe lambs (42 + 5.6 kg BW) were used to assess the effects of n-3 and n-7 oil supplementation on tissue accumulation of these fatty acids. Lambs were blocked by weight and randomly assigned to one of three treatments: 1) control (CON), no oil supplement, 2) flaxseed oil (FLAX; 56% C18:3 n-3) supplementation at 0.1% of BW, or 3) Provinal® oil (PO; 56% C16:1 n-7) supplementation at 0.1% of BW. All lambs were fed ad libitum the same basal diet consisting of 75% soybean hull pellets and 15% alfalfa pellets. Lambs were fed the treatment diets for 60 d individually. Overall average daily gain was reduced by PO compared to FLAX ($P < 0.05$). Hot carcass weights were also reduced by 12% for PO vs. FLAX ($P < 0.05$). Lambs in the PO treatment had a lower ($P < 0.01$) dressing percentage than CON or FLAX. Total lipid content of the LM was highest ($P < 0.05$) for FLAX and lowest ($P < 0.05$) for PO. Supplementation with PO increased palmitoleic (C16:1 n-7), cis-11 vaccenic (C18:1 cis-11), eicosapentaenoic (C20:5; EPA, n-3), and docosahexaenoic (C22:6; DHA, n-3) acids compared to CON or FLAX ($P < 0.01$). Supplementation of FLAX increased linolenic (C18:3 n-3) acid compared to CON or PO ($P < 0.1$). These changes in individual fatty acid concentrations with oil supplementation resulted in increased ($P < 0.01$) omega-3 fatty acid concentrations (+69%) and a lower (*P*..?) ratio of n-6 to n-3 compared to CON (3.13 for FLAX and PO vs. 5.02 for CON). In conclusion, supplementation with PO increased palmitoleic acid (+95%), cis-11 vaccenic acid (+77%; a known elongation product of palmitoleic acid), EPA (+104%), and DHA (+150%) compared to CON or FLAX. Flaxseed oil supplementation increased linolenic acid (+113%) but did not further convert this n-3 fatty acid into EPA, DPA, or DHA.

Key Words: lamb, n-7 fatty acids, n-3 fatty acids, oil supplementation

0900 Supplementation of glycerol or fructose via drinking water of pasture-fed lambs. G. Volpi Lagreca, I. F. Furusho-Garcia, B. M. Koch, M. F. Miller Jr., and S. K. Duckett*, *Clemson University, Clemson, SC*.

Eighteen wether lambs (40.1 ± 7.4 kg BW, 4.9 mo.) were used to assess the impact of glycerol or fructose supplementation via drinking water on animal performance and tissue glycogen content. Lambs were blocked by BW and allocated to alfalfa paddocks (2 hd/paddock, 3 paddocks/treatment). Each paddock within block was assigned randomly to drinking water treatments for 30 d: 1) control (CON), 2) 120 g fructose/L (FRU), or 3) 120 g glycerol/L (GLY). Lambs grazed alfalfa for 28 d and then were fasted in pens for 2 d before slaughter with access to water treatments only. Glycogen content was measured in the *Longissimus* muscle (LM) and *Semitendinosus* muscle (ST) at 30 min, 1, 2, 3, 4, 5, 6, 12, and 24 h postmortem. Data were analyzed using PROC MIXED of SAS. Daily water intake (3.5 L/animal/day) did not differ between treatments ($P > 0.05$). During the 28-d grazing period, ADG was greater ($P < 0.05$) for GLY (0.200 kg/an/d) compared to CON (0.116 kg/an/d) or FRU (0.078 kg/an/d). During the 2-d fasting period, BW shrink was lower ($P < 0.05$) for GLY (−0.392 kg/an/d) compared to CON (−1.680 kg/an/d) or FRU (−1.340 kg/an/d). HCW was greater ($P < 0.05$) for GLY compared to FRU (22.7 vs. 17.6 kg) and tended to be greater ($P = 0.06$) for GLY compared to CON. There was a treatment x time interaction ($P = 0.003$) in the LM; glycogen content was greater ($P < 0.05$) for GLY at 2 and 3 h and for FRU at 1 h compared to CON. Glycogen content in ST did not differ between treatments ($P > 0.05$). Liver glycogen content at 30 min postmortem was greater ($P < 0.01$) for GLY (5.61%) compared to FRU (1.45%) or CON (0.32%). Liver free glucose was greater for GLY, intermediate for FRU, and lower for CON ($P < 0.01$). Overall, GLY supplementation increased ADG during grazing period, reduced BW shrink during fasting, increased HCW, and increased glycogen in liver and muscle, and free glucose content in liver.

Key Words: lamb, liver, glycerol, fructose, glycogen

0901 Comparison of meat quality and fatty acid composition of grain-fed calves to grass-fed steers as an alternative beef production system in Chilean Patagonia. F. Sales*[1], R. Morales[2], R. Lira[1], L. Bravo[3], and Q. Sciascia[4], *[1]Instituto de Investigaciones Agropecuarias, Punta Arenas, Chile, [2]Instituto de Investigaciones Agropecuarias, Osorno, Chile, [3]Universidad del País Vasco, Bizkaia, Spain, [4]Leibniz Institute, Dummerstorf, Germany.*

Steers finishing in Chilean Patagonia are based on grazing lands with low nutritive value, which may lengthen the fattening phase of steers, so grain-fed calves appear as an option to reduce the farming period. However, the effect of grain inclusion in the diet on meat quality or fatty acid composition under those conditions is not clear. The aim of this study was to compare the effects on meat quality and the fatty acid profile of beef from grass-fed steers or grain-fed calves in Patagonia. Forty Angus cross steers were raised on pasture (2.0 Mcal/kg DM ME, and 11% CP) and slaughtered at 18–20 mo of age (448 ± 31.7 kg BW). On the other hand, ten calves were weaned at 9 mo of age (303 ± 8.0 kg BW) and started receiving 2.5 kg corn (3.4 Mcal EM, 8.5% CP) and 1.0 kg Cosetán® (2.95 Mcal EM, 15% CP) daily during 47 d. Meanwhile they were maintained on pasture (2.0 Mcal/kg DM ME, and 5% CP) until they reached slaughter weight (316 ± 13.9 kg BW). Animals were slaughtered the same day,

Table 0901.

Table 1. Meat quality analysis obtained from *longissimus lumborum* (lean muscle) of steers and calves that were slaughtered in Chilean Patagonia.

	STEER	CALVES	*P*-value
Body Weight in ranch (kg)	440 ± 33.0	316 ± 13.8	0.000
Slaughter Body Weight (kg)	417 ± 30.7	326 ± 13.9	0.000
Intramuscular fat (%)	7.95 ± 2.61	4.56 ± 1.18	0.000
Shear force (kgf)	2.22 ± 0.251	1.97 ± 0.298	0.030
Meat Color			
*L**	39.6 ± 1.76	42.4 ± 1.64	0.000
*a**	25.5 ± 1.83	23.2 ± 1.39	0.000
*b**	12.7 ± 1.17	12.7 ± 0.679	0.954
Fat color			
*L**	67.0 ± 1.86	65.9 ± 1.49	0.061
*a**	13.2 ± 2.03	12.9 ± 1.54	0.649
*b**	17.2 ± 1.47	14.1 ± 0.824	0.000
Fatty acid composition			
SFA (%)	47.6 ± 2.45	45.8 ± 3.22	0.120
MUFA (%)	39.0 ± 2.09	34.3 ± 1.79	0.000
PUFA (%)	7.60 ± 2.27	11.9 ± 2.91	0.001
P/S	0.162 ± 0. 0577	0.265 ± 0.0896	0.005
n-6	4.80 ± 1.36	7.88 ± 2.10	0.001
n-3	2.80 ± 0.927	3.99 ± 0.839	0.001
n-6/n-3	1.74 ± 0.155	1.96 ± 0.19	0.005
Rumenic acid (%)	0.268 ± 0.0407	0.425 ± 0.0526	0.000

SFA, saturated fatty acid; MUFA, monounsatured fatty acid; PUFA, polyunsatured fatty acid; P/S, PUFA/SFA; n-6/n-3, ratio between n-6 and n-3 PUFA.
Rumenic acid (9*c*,11*t*-18:2), principal conjugated linoleic acid.
P-value indicate significantly differences when $P \leq 0.05$.

and *Longissimus lumborum* muscle was obtained to perform meat quality and fatty acid profile analyses. A T-student was used to compare the two finishing methods (calves/grain vs. steers/pasture). As was expected, calves show lighter hot carcass weight than steers (173.9 ± 7.2 vs. 223.7 ± 17.5 kg, $P \leq 0.001$). Regarding meat quality characteristics, the color of calves' muscle was lighter (with higher *L** and lower *a** values, $P \leq 0.001$) and more tender ($P \leq 0.05$) than meat from steers. Calves' meat had lower intramuscular fat content (4.56 ± 1.18 vs. 7.95 ± 2.61%, $P \leq 0.001$), possibly because they were slaughtered younger than steers. In general, the fatty acid composition of steers' and calves' meat show healthy profiles, although calves' meat was healthier because of its higher content of polyunsaturated fatty acid, (PUFA, 11.9 ± 2.91 vs. 7.60 ± 2.27%, $P \leq 0.01$) and rumenic acid (0.425 ± 0.053 vs. 0.268 ± 0.041%, $P \leq 0.01$). However, calves' meat has a lower content of monounsatured fatty acids (MUFAs, 34.3 ± 1.79 vs. 39.0 ± 2.09%, $P \leq 0.001$) and higher n-6/n-3 ratio (1.96 ± 0.19 vs. 1.74 ± 0.155%, $P \leq 0.01$) than steers' meat. Results suggest that Patagonian beef meat has interesting quality characteristics and differs depending on the finishing methods and the slaughter age. Intramuscular fat content and fatty acid profile gave calves' meat (with an extra energy intake by grain) a higher nutritional and healthy quality compared to steers produced on pasture, which could be demanded by consumers.

Key Words: meat quality, calves' meat, beef

0902 Influence of tannins extract supplementation on lipid oxidation of beef kept in refrigerated storage.

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Steak samples of longissimus dorsi obtained from sixteen fattened bullocks (*Bos taurus* × *Bos indicus*) with 505 ± 22.23 kg final weight were used to evaluate the effect of tannin extract fed-supplementation on lipid oxidation of beef kept in refrigerated storage. Treatments were: 1) diet with 13.3% CP and 2.0 Mcal NE_m/kg DM (CTRL) and 2) CTRL plus 0.3% (DM basis) of tannin extract (TE). The tannin extract was offered from Bypro (Indunor S.A., Buenos Aires, Argentina), which contains 70% tannins. Treatments were fed during 70 d before harvesting. Bullocks were harvested in a processing plant, and after 24 h chilling at 4°C, a cross cut was performed in the longissimus dorsi of carcass left side, between 12th and 13th ribs. Beef samples were kept frozen (−20°C) until used for lipid oxidation analyses. Lipid oxidation was estimated as thiobarbituric acid-reactive substances (TBARS) and was determined at 0, 3, 6, 9, and 12 display d at 4°C. Because TBARS data were not normal ($P < 0.05$), before analyses, they were

transformed to $\log_{10}$ (n * 1000) to be normalized ($P = 0.68$). The results were analyzed by ANOVA for a completely randomized design, with a 2 × 5 factorial arrangement (two levels of factor TE: 0 and 0.3% diet DM; and five levels of factor d: 0, 3, 6, 9, and 12). The steak sample from each bullock was the experimental unit. A tendency ($P = 0.10$) for interaction TE × d was observed, where meat lipid oxidation from d 0 to d 9 was similar ($P > 0.10$) between treatments; but at display d 12, beef from TE supplemented bullocks exhibited a lower ($P < 0.05$) TBARS value than CTRL (0.04 vs. 0.11 mgMDA/kg meat^{-1} wet basis). The results suggest that supplementation of a 0.3% tannin extract to feedlot cattle may help to increase shelf life of beef by decreasing lipid oxidation.

Key Words: bovines, meat lipid oxidation, tannin

0903 Differentially expressed genes in genetically divergent Nellore steers for calcium content in the Longissimus dorsi muscle.

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Calcium is an important mineral for mammals, because it is involved in muscle contraction and neuro impulse transmission and controls the flow of substances in the cellular environment. Calcium is the major part of the mammal skeleton; it is found in great amount in milk and can be found in beef. In addition, the calcium content in bovine muscle can influence meat quality traits, such as meat tenderness, due to its importance for calcium-dependent proteases. Although calcium functions in the organism have been extensively studied, a lack of knowledge of the mechanisms regulating calcium content is still observed. In this study, we identified differentially expressed (DE) genes in genetically divergent Nellore steers for calcium content in the *Longissimus dorsi* (LD) muscle using an RNA-seq approach. From an initial population of 120 animals presenting genomic breeding value (GEBV) estimates for calcium content, we chose 10 animals in two groups selected for their extremely low or high GEBV. The analysis of RNA-seq samples using the Tuxedo suit pipeline revealed 43 DE genes, 32 upregulated in the group with low calcium content. A functional gene enrichment analysis performed by DAVID software indicated 10 functional clusters involved in membrane and extracellular matrix proteins, cell and tissue adhesion, skeleton, neurological system and cartilage development, calcium, carbohydrate and metal binding, and sensorial and sound perception. Gene functions, such as cell and tissue adhesion, and calcium, carbohydrate, and metal binding are related to meat tenderness due to their role in the rigor mortis process and in muscle contraction through the interaction with troponin. Among the upregulated genes in the low calcium content group, we found the collagen genes *COL11A1* and *COL11A2* involved in skeletal morphogenesis and associated with several genetic syndromes related to abnormal calcium deposits in humans. *COL11A1* is downregulated in female Quinchuan cattle, which might explain part of the higher tenderness in this sex, since there is a negative correlation between this trait and collagen. In *Bos taurus coreanae* both genes are upregulated in intramuscular fat in comparison with subcutaneous fat, along with integrins, calcium dependent proteins that are related to cellular adhesion. These are intermediate results and further experiments will allow the exploration of the genetic findings influencing muscle calcium concentration in Nellore cattle. The results will provide a more comprehensive picture of gene expression associated with calcium content in bovine muscle.

Key Words: *Bos indicus*, calcium, RNA-Seq

0904 Fatty acid profile and gene expression of lipogenic transcription factors in the muscle of Nellore bulls fed processed soybean.

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The objective was to evaluate the fatty acid profile and gene expression of *PPARA*, *PPARG*, and *SREBF1* in the muscle of Nellore bulls fed ground or extruded soybean. Sixty crossbred Nellore young bulls, with initial average weight of 320 ± 8.12 kg, were distributed in a completely randomized design. The animals were placed in 12 pens, with 3 treatments, 5 animals per pen, and 4 replications, and therefore pens were the experimental units. The bulls were fed the following diets: diet without soybean inclusion (NSB), ground soybean diet (GSB), and extruded soybean diet (ESB). These diets containing corn silage as forage (40% DM), 14% CP, and 2.4, 6.1, and 6.3% of ether extract (EE), respectively. Soybean content was 20.4% in both ground and extruded soybean diets. Bulls were slaughtered at an average of 442 ± 10.4 kg. After being harvested, samples were taken from the *longissimus dorsi* (LD) muscle of 24 bulls randomly, 2 bulls from each pen, between the 12th and 13th ribs for fatty acid analyses, using gas chromatography, and gene expression, which was analyzed by RT-qPCR. The model included the fixed effect of diet and was analyzed using the GLM procedure in SAS 9.4. Muscle of bulls fed soybean diets, regardless of processing, had lower

concentrations ($P < 0.05$) of C12:0 and the CLA C18:2 c9, t11; and higher ($P < 0.05$) concentrations of C18:0. The C14:0 content was higher ($P < 0.05$) in the muscle of bulls fed NSB, compared to those receiving GSB. The concentration of C18:1 *trans* isomers were higher ($P < 0.05$) in the muscle of bulls fed GSB compared to those fed ESB and NSB. On the other hand, C18:1 c9 content in the muscle of bulls fed GSB was lower ($P < 0.05$) compared to the muscle of bulls fed the other diets. LD muscle of bulls fed soybean diets, regardless of processing, had greater concentrations of saturated fatty acids. Polyunsaturated fatty acid content was lower ($P < 0.05$) when bulls were fed ESB. Gene expression of *PPARA* and *PPARG* was not affected by diet ($P > 0.05$). However, expression of *SREBF1* was greater ($P < 0.05$) in the muscle of bulls fed ESB. In conclusion, extrusion of soybean contributes to the greater biohydrogenation of polyunsaturated fatty acids and consequently greater expression of the gene *SREBF1*. The use of ground or extruded soybean does not increase CLA C18:2 c9, t11 content in beef cattle muscle.

Key Words: CLA, extruded soybean, *PPAR*, *SREBF1*

0905 Heat shock protein expression differs in 14 d aged longissimus lumborum in agreement with Warner-Bratzler shear force values. N. E. Ineck*, R. G. Christensen, S. M. Quarnberg, J. McClellan, J. F. Legako, and K. J. Thornton, *Utah State University, Logan*.

Despite similar production practices, beef cattle exhibit undesirable variation in the rate and extent of postmortem proteolysis lending to inconsistencies in tenderness. The objective of this study was to determine whether heat shock proteins (HSP) play a role in postmortem proteolysis and thus, development of tenderness. To address this, HSP expression was determined in the longissimus lumborum after 14 d of aging. A total of 32 samples were placed into either a more tender (MT; $n = 16$) or less tender (LT; $n = 16$) group based on previous Warner-Bratzler shear force (WBSF) values. Western blot analyses were then completed to determine expression of two different HSP: HSPβ1 and HSP70. Statistics were completed using Proc MIXED in SAS to determine whether HSP expression varied between MT and LT samples; the model included tenderness as a fixed effect and gel and sample as random effects. Spearman-Pearson correlations were also completed in SAS to determine whether WBSF value and HSP expression were related. The two tenderness groups had different ($P < 0.001$) WBSF values; the MT group had an average WBSF value of 1.9 kg, while the less tender group had an average WBSF value of 5.5 kg. Less tender samples showed increases ($P = 0.03$) in HSPβ1 when compared to the MT samples. Furthermore, there was a correlation ($R = 0.5238$, $P = 0.008$) between WBSF value and HSPβ1 expression. No differences ($P = 0.49$) in HSP70 expression were observed between the MT and LT groups. There was no ($R = 0.031$, $P = 0.89$) correlation identified between WBSF values and HSP70 expression. These data demonstrate that HSPβ1 expression in meat samples from the longissimus lumborum after 14 d aging may play a role in postmortem proteolysis, and thus development of tenderness. Further research is needed to improve our understanding of how HSP are involved in the postmortem proteolysis process.

Key Words: heat shock proteins, tenderness, Warner-Bratzler shear force

MEAT SCIENCE AND MUSCLE BIOLOGY SYMPOSIUM: SCIENCE OF RED MEAT CONSUMPTION

0906 Beef's role in a healthy diet. J. N. Martin*, D. R. Woerner, R. Delmore, K. E. Belk, and J. D. Tatum, *Colorado State University, Fort Collins*.

Although red meat has long been established as a tremendous source of essential nutrients, its posed contributions to heart disease, obesity, and various cancers have resulted in growing criticism of its role in the diet. This widespread criticism and posited associations to negative health outcomes have fostered an overall decrease in the consumption of red meats in the U.S. over the past several decades. Although this decrease hasn't resulted in overt and direct improvements to human health, its absence has highlighted the vital nutritional role of lean, red meat in the diet. Concurrently, the entirety of the meat industry has steadfastly pursued investigating—and further, communicating—the nutritional profile and health value of red meats. A noteworthy example of efforts to demonstrate the nutritional advancement of red meats has been the remarkable progress on reducing the total available fat in consumed red meat products. Through targeted efforts in animal husbandry and processing innovation, the meat industry has reduced the total fat available from red meats by up to 70% in the past three decades. Furthermore, multiple industry efforts have addressed concerns regarding the fatty acid profile of red meats by demonstrating the relatively high proportion of unsaturated fatty acids and the cardiovascular neutrality of certain saturated fatty acids (i.e., stearic acid) in red meats. Likewise, although the value of red meat proteins has been long established, recent investigations of their role in weight loss and weight maintenance have highlighted their beneficial contributions to the diet and long-term health. Similarly, the exclusion of red meats in certain dietary patterns has been demonstrated to exacerbate iron deficiency and sarcopenia. Overall, the totality of data regarding the nutritional profile of red meat suggests that criticisms of its inclusion in dietary recommendations are unwarranted. Instead, the body of evidence suggests that negative health outcomes are complex, yet the inclusion of lean, red meats in a balanced diet can promote health and well-being.

Key Words: health, nutrition, red meat