102 Timing of exposure to high-concentrate diets vs. pasture on lipogenic enzyme gene expression of steers at slaughter. Brandon M. Koch*[1], Emanuel A. Oliveira[2], and Susan K. Duckett[1], *[1]Clemson University, Clemson, SC, [2]Universidade Estadual Paulista, Jaboticabal, SP, Brazil.*

Forty Angus steers (278 ± 21.4 kg) were used to evaluate the effect of feeding strategy during stocker (P1) and finishing (P3) phases on the relative mRNA expression of lipogenic enzymes. Steers were randomly assigned to 2 feeding treatments during P1 (111 d): high-concentrate diet (cracked corn, corn silage, and soybean meal) or high-quality pasture (winter annuals, alfalfa, and non-toxic fescue). An intermediate phase (P2) consisted of 98 d where all steers grazed high-quality pastures. At the start of P3 (until 568 kg BW), each group from P1 was randomly divided into 2 groups that received either a high-concentrate diet or grazed high-quality pastures resulting in 4 treatments (FPF, FPP, PPF, PPP). At slaughter, s.c. adipose tissue samples were collected from each steer and flash frozen for later analysis. No differences were observed for the relative expression of Acetyl CoA carboxylase, carnitine palmitoyltransferase 1A, or glucose transporter type 4 mRNA ($P > 0.162$). An interaction between P1 and P3 ($P = 0.048$) was observed for stearoyl CoA desaturase (SCD) mRNA with 107-, 140-, 10-fold increases for FPF, PPF, FPP, respectively, compared with PPP. Steers on a high-concentrate diet during P3 had greater relative expression of fatty acid synthase (FASN) mRNA ($P < 0.001$) with 59- and 21-fold increases for FPF and PPF treatments, respectively compared with PPP. Similarly, elongase-5 (ELOVL5) and elongase-6 (ELOVL6) mRNA expression increased ($P < 0.001$) when finished on a high-concentrate diet, with FPF and PPF treatments having 18- and 10-fold increases, respectively, for ELOVL5, and 8 and 5-fold increases, respectively, for ELOVL6, when compared with PPP. Adiponectin receptor 1 adipocyte protein 2, and lipoprotein lipase expression were all downregulated when cattle received a high-concentrate diet during P1 ($P < 0.018$). Glycerol-3-phosphate acyltransferase was highly upregulated when steers were finishing on a high-concentrate diet ($P < 0.001$; 56- and 33-fold increase for FPF and PPF, respectively, when compared with PPP). Feeding high-concentrate diets upregulates key lipogenic genes that enhance MUFA content of beef.

Key Words: gene expression, lipogenic

103 Effects of high-concentrate diets during stocker and finishing phase on lipid fractions in longissimus muscle. Adriana Pordomingo, Gabriela Volpi Lagreca, Brandon M. Koch, and Susan K. Duckett*, *Clemson University, Clemson, SC.*

Twenty Angus steers (278 ± 21.4 kg BW) were used to evaluate the effect of high concentrate diets during stocker and finishing phases on lipid fractions [neutral lipid (NL), phospholipid (PhL) and free fatty acid (FFA)] in longissimus muscle. Steers were randomly assigned to 2 treatments: (1) high quality forage grazed during all phases (PAST) or (2) high concentrate diets fed during early stocker (111 d) phase and finishing phase (77 d) with an intermediate period on high quality forage (98 d) between stocker and finishing periods (FPF). Steers were slaughtered at a similar live weight endpoint (568 kg BW). Longissimus muscle samples were obtained from each animal. Lipids were extracted from the LM, separated into lipid fractions (NL, PhL, and FFA) and fatty acid composition of each fraction analyzed by GLC. Feeding of high concentrates during the stocker phase and finishing phase increased ($P < 0.05$) total fatty acid content of the LM compared with PAST (4.96% vs. 3.38%, respectively). On a gravimetric basis, FPF had greater NL and FFA content than PAST. However on a percentage basis, the lipid fractions were similar ($P > 0.05$) between PAST and FPF. Overall, the LM contained 93.7% NL, 5.0% PhL, and 1.6% FFA. In the NL, FPF had greater ($P < 0.05$) concentrations of MUFA, n-6 PUFA, and n-6 to n-3 ratio of PUFA compared with PAST. The PAST had greater ($P < 0.05$) concentrations of n-3 fatty acids in NL than FPF. In the PhL, PAST had greater ($P < 0.05$) MUFA and n-3 PUFA compared with FPF. The PhL fraction of FPF had greater ($P < 0.05$) concentrations of n-6 PUFA and higher ratio of n-6 to n-3 PUFA. Fatty acid composition of FFA fraction did not differ ($P > 0.05$) between treatments. These results indicate that PAST finished beef has increased n-3 PUFA concentrations in the LM due to greater accumulation of n-3 PUFA in both NL and PhL fractions and not because of a greater PhL contribution to the total lipid fraction.

Key Words: beef, high concentrate diet, fatty acid

104 Feeding microalgae meal *(Schizochytrium limacinum* CCAP 4087/2) to finishing cattle I: Effects on visceral and subcutaneous adipocyte size and *Longissimus lumborum* muscle fiber characteristics. Kelsey J. Phelps*[1], John M. Gonzalez[1], Derris D. Burnett[1], Christian A. Alvarado-Gilis[1], Mathew A. Vaughn[1], Caleb P. Weiss[1], Cadra L. Van Bibber-Krueger[1], Justin E. Axman[1], Jake D. Thieszen[1], Kate A. Jacques[2], and James S. Drouillard[1], *[1]Kansas State University, Manhattan, KS, [2]Alltech Inc., Nicholasville, KY.*

The objective of this study was to examine effects of feeding microalgae meal *(*MA*; Schizochytrium limacinum* CCAP 4087/2) on visceral adipocyte, subcutaneous adipocyte, and *Longissimus lumborum* (LL) muscle fiber characteristics. Heifers (36 pens; 8 heifers/pen) were blocked by initial pen BW (4014 ± 223 kg) and assigned within strata to 1 of 4 treatments. Treatments consisted of 0, 50, 100, and 150 $g \cdot heifer^{-1} \cdot d^{-1}$ of MA (Alltech Inc., Nicholasville, KY) added to a basal diet consisting of steam-flaked corn, wet corn gluten feed, alfalfa hay, glycerin, and supplement. Heifers were harvested on d 89 of the study and visceral and subcutaneous adipose tissue were collected from approximately the 13th rib of 3 heifers selected at random from each pen. The strip loin from the left side of the same randomly selected heifers was removed and transported to Kansas State University for analysis. One 1.27-cm steak was removed from the 13th-rib end of each loin for measurement of muscle fiber characteristics of the LL. There were no treatment × depot interactions for cross-sectional area or diameter of subcutaneous and visceral adipocytes ($P > 0.33$). Increasing MA in the diet did not affect cross-sectional area or diameter of visceral or subcutaneous adipocytes ($P > 0.56$) and did not affect distribution of LL myosin heavy chain type I, IIA, and IIX muscle fibers or cross-sectional area of fibers ($P > 0.16$; Table 1). Supplementing microalgae meal does not affect visceral and subcutaneous adipocyte size or muscle fiber characteristics of the LL.

Contd.

Table 1 (Abstr. 104). Cross-sectional area (μm^2) of adipocytes and muscle fibers in heifers fed microalgae meal

Item	Algae, g·heifer^{-1}·d^{-1} DM				SEM
	0	50	100	150	
Subcutaneous adipocyte	9,962	9,395	9,632	9,899	523
Muscle fiber					
Type I	2,601	2,321	2,289	2,521	119
Type IIA	2,794	2,692	2,710	2,676	139
Type IIX	4,171	3,809	3,954	4,020	181

Key Words: omega-3, adipocyte, muscle fiber type

105 Feeding microalgae meal *(Schizochytrium limacinum* CCAP 4087/2) to finishing cattle II: Effects on *Longissimus lumborum* fatty acid profile and meat quality. Kelsey J. Phelps*[1], John M. Gonzalez[1], Christian A. Alvarado-Gilis[1], Derris D. Burnett[1], Mathew A. Vaughn[1], Sara M. Ebarb[1], Caleb P. Weiss[1], Cadra L. Van-Bibber Krueger[1], Justin E. Axman[1], Kate A. Jacques[2], and James S. Drouillard[1], *[1]Kansas State University, Manhattan, KS, [2]Alltech Inc., Nicholasville, KY.*

Effects of feeding microalgae meal *(*MA; *Schizochytrium limacinum* CCAP 4087/2) on fresh meat quality were examined. Heifers (36 pens; 8 heifers/pen) were blocked by initial pen BW (4014 ± 223 kg) and assigned within strata to 1 of 4 treatments. Heifers were fed diets containing steam-flaked corn, wet corn gluten feed, alfalfa hay, glycerin, supplement, and 0, 50, 100 or 150 g·d^{-1} MA (Alltech, Inc., Nicholasville, KY). Heifers were harvested on d 89 of the study and strip loins were collected from 3 randomly selected heifers per pen. One 1.27-cm steak was removed from the 13th-rib end of each loin for fatty acid analysis. Loins were weighed, vacuum packaged, and aged for 14 d. Loins were reweighed and fabricated into 2.54-cm steaks for analysis of lipid oxidation and color stability during retail display, Warner-Bratzler shear force, and sensory attributes. Feeding MA did not affect concentrations of C16:0, C18:0, C18:3n-3, or total fatty acids within loins ($P > 0.16$), but increased concentrations of C18:2n-6c and C20:5n-3 (linear, $P < 0.01$) and C22:5n-3 and C22:6n-3 (quadratic, $P < 0.02$). There were treatment × day interactions for all color attributes and TBARS during display ($P < 0.01$). From d 0 to 2 of display, increasing MA decreased L* (linear, $P < 0.03$). For the remainder of display, increasing MA tended to decrease L* (quadratic, $P < 0.07$). From d 2 to 4 of display, increasing MA decreased a* (linear, $P < 0.04$). For the remainder of display, increasing MA decreased a* (quadratic, $P < 0.02$). Surface oxymyoglobin decreased and surface metmyoglobin increased with increased MA (d0–4, linear, $P < 0.05$; d5–7 quadratic, $P < 0.04$), and lipid oxidation was elevated on d 0 and 7 of display with increased MA (quadratic, $P < 0.01$). Treatments did not affect loin purge loss, loss of weight during cooking, or shear force ($P > 0.15$). For sensory panel, off-flavors increased (quadratic, $P < 0.01$) with increased MA. Increases in measures of oxidation in response to feeding microalgae meal suggest that it may be prudent to include antioxidants in diets of microalgae-fed cattle to preserve oxidative stability of meat.

Key Words: omega-3, color, sensory

106 Intratesticular injection of zinc solution effectively castrates male pigs without affecting pork quality. Jason K. Apple*[1], Tsung-Cheng Tsai[1], Hae-Jin Kim[1], Min Wang[2], Brian P. Corbett[2], Tim M. Johnson[1], and Charles V. Maxwell[1], *[1]Department of Animal Science, University of Arkansas Division of Agriculture, Fayetteville, AR, [2]Ark Science Inc., Irvington, NY.*

Zinc gluconate neutralized by Arg (Zeuterin; Ark Science Inc., Irvington, NY) is directly injected into the testes of dogs and has a 99.6% sterility rate; thus, a study was designed to test the effects of intratesticular injections of a Zn solution (Testrin (T); Ark Science Inc.) as a method of castration in swine. Within 10 litters, 7-d-old male pigs (birth weights of 1 kg, or greater) were assigned randomly to 1 of 3 intratesticular T dosages: 0.15 (n = 1/litter), 0.20 (n = 2/litter), or 0.30 mL/testicle (n = 2/litter). Scrotal area was thoroughly cleansed before T was administered by deep intratesticular injection using a sterile syringe and a sterile 28-gauge (1.26-cm long) needle. A surgically-castrated male (B) and an intact female (G) from each litter were designated as industry controls. Pigs were weaned at 21 d, mixed, and subsequently moved first to an off-site nursery then to a grower-finisher unit. Live weights were recorded at birth, weaning, and at the end of the study to calculate ADG, and scrotums were palpated monthly to monitor testicle growth. One month after injection, the proportion of pigs receiving 0.15, 0.20, and 0.30 mL/testicle with at least 1 testicle was 88.9, 95.0, and 70.0%, respectively, and declined to 55.6 (end of trial), 40.0 (end of trial), and 0% (4 mon after injection), respectively. Testrin-injected pigs were heavier ($P < 0.05$) at weaning than B, but neither pre-weaning ($P = 0.549$), post-weaning ($P \geq 0.185$), nor overall ADG ($P = 0.262$) differed among treatments. Carcasses of T-pigs were heavier ($P = 0.015$) than B, but fat depths, LM area, and calculated fat-free lean yield were similar ($P \geq 0.333$) among treatments. Although the LM from G and males treated with 0.20 mL T/testicle were darker (lesser L* value; $P < 0.05$) than the LM from B, LM color ($P \geq 0.071$), drip and cooking losses ($P \geq 0.370$), marbling ($P = 0.164$), firmness ($P = 0.185$), and shear force values ($P = 0.378$) did not differ among T-treated males, B, and G. Results indicated that male pigs can be effectively castrated by intratesticular injections of 0.30 mL T/testicle, and produce carcasses of equal composition and quality to B and G.

Key Words: castration, intratesticular injection, pork quality

107 Prediction of red meat yield and trimmable fat yield from beef carcasses utilizing bioelectrical impedance analysis. Angela N. Schmitz*[1], Lee-Anne J. Walter[1], Wade T. Nichols[2], John P. Hutcheson[2], and Ty E. Lawrence[1], *[1]West Texas A&M University, Canyon, TX, [2]Merck Animal Health, Summit, NJ.*

An experiment was performed utilizing bioelectrical impendence technology (BIA) to predict red meat and trimmable fat yields for over-finished beef carcasses. Fifty-six single-sired steers were finished to above typical slaughter weights (603.5 kg ± 48.1 kg; 2.0 ± 0.7 cm 12th rib back fat) before harvest. After a 24-h chill period, standard grading procedures were used to derive a calculated yield grade for each animal (3.7 ± 0.9). Measures of BIA [resistance (Rs, 160.2 ± 16.5 ohms), reactance (Xc, 44.6 ± 4.8 ohms)] were quantified by introducing an alternating electrical current between positive (detector) and negative (source) electrodes placed at opposite ends of the right side of each carcass. Source electrodes introduced current through the carcass and detector electrodes detected any decrease in voltage caused by resistance to electrical current. Other measured variables included temperature (Tp, 3.1 ± 0.7°C), length between electrodes (L, 118.7 ± 5.1 cm), and hot carcass weight (HCW, 381.0 ± 32.8 kg). Impedance (I; $(Rs^2 + Xc^2)^5$; 166.3 ± 17.0) electrical volume (EVOL; L^2/Rs; 89.4 ± 16.8), resistive density (RsD; $RSW^2/(L^2/Rs)$; 392.4 ± 63.0), and reactive density (XcD; $RSW^2(L^2/Xc)$; 108.9 ± 16.3) were derived from measured variables. Correlations were calculated between dependent and independent variables. Stepwise regression procedures were used to develop models for prediction of percentage red meat yield (RMY%) and trimmable fat yield (TFY%). Pearson correlation coefficients indicate that RMY was

highly correlated ($P < 0.05$) to RsD (r = −0.65), XcD (r = −0.51), Tp (r = −0.46), HCW (r = −0.39), EVOL (r = 0.30), Rs (r = −0.30), and I (r = −0.28) whereas FY was correlated ($P < 0.05$) with RsD (r = 0.75), XcD (r = 0.60), HCW (r = 0.57) and Tp (r = 0.50). Regression models indicate that 65% and 72% of the variation in RMY% and TFY% may be attributed to BIA measures. By comparison, the calculated USDA yield grade accounted for 50.0% and 61.0% of the variation in RMY% and TFY%, respectively. These results suggest that BIA technology can be utilized as a predictor of beef carcass composition.

Key Words: beef, bioelectrical impendence technology (BIA), zilpaterol

108 Dietary lysine affected the expression of genes related to lipid metabolism in skeletal muscle of finishing pigs. Taiji Wang*, Naresh Regmi, Jean M. Feugang, Mark A. Crenshaw, John R. Blanton Jr., and Shengfa F. Liao, *Department of Animal and Dairy Sciences, Mississippi State University, Mississippi State, MS.*

It has been reported that some amino acids can function as signaling molecules to regulate skeletal muscle growth in mammals. This study was conducted to identify those genes that may be regulated by amino acid lysine and responsible for muscle growth and meat quality of pigs. Nine crossbred barrows (94.4 ± 6.7 kg BW) were randomly allotted to 3 dietary treatments (3 pigs/treatment). Three corn and soybean-meal based diets were formulated to meet the NRC (2012) requirements for nutrients except for lysine, whose concentrations were 0.43, 0.71, and 0.98% for Diets 1 (lysine deficient), 2 (lysine adequate), and 3 (lysine excess), respectively. After 5 weeks on trial, pigs were killed and muscle samples collected from *longissimus dorsi* (between the 10th and 12th ribs). Total RNA was extracted from 50 mg of each sample using a TRIzol reagent. Porcine Gene 1.0 ST Array (Affymetrix, Inc.) was used to quantify the expression levels of 19,211 genes. Raw microarray data were normalized with gcRMA algorithm and analyzed with ANOVA using Partek Genomics Suite (Partek Inc.). A total of 674 transcripts were differentially expressed ($P < 0.05$); 60 out of 131 transcripts ($P < 0.01$) belong to 59 genes and 71 were unannotated. GO Enrichment analysis of this 59-gene set identified 11 genes in 5 categories of molecular functions: binding, catalytic activity, transcription regulator activity, transporter activity, and molecular transducer activity. Interestingly, 4 genes are associated with lipid metabolism: PSPH: lipid binding and key enzyme for serine (precursor of phospholipids and glycolipids) synthesis; CFD: stimulating glucose transport for triglyceride accumulation and inhibiting lipolysis; ME1: associated with backfat thickness and meat quality; SCD: playing a key role in intramuscular fat formation. It appears that lysine can regulate the expression of multiple genes, and at least 4 genes are related to lipid metabolism. Further studies are needed to elucidate the association of dietary lysine level with the expression levels of these genes and the gene network for lipid metabolism. (Supported by USDA Hatch/Multistate Project 233803)

Key Words: lysine, muscle, gene expression

109 Transcriptomic and metabolomic assessment of growth promoter effects on porcine muscle growth. John Brameld*[1], Kevin Ryan[1], Hannah Williams[1], Doug Harris[2], David Brown[1], Richard Emes[1], Tom Giles[1], Chungui Lu[1], Charlie Hodgman[1], and Tim Parr[1], *[1]University of Nottingham, Nottingham, UK, [2]Zoetis, Kalamazoo, MI.*

This study compared the effects of growth hormone (GH) and β-adrenergic agonist (BA) on porcine muscle transcriptome and blood metabolome. Duroc × (Landrace × Large White) gilts (77 ± 7.1 kg, n = 165) were all fed a high protein/energy diet ad libitum, with the GH group receiving an intramuscular injection, 10mg once every 2d of porcine GH (Reporcin, Zamira), the BA group receiving Ractopamine at 20mg/kg feed, whereas the control group just had feed. Pigs were treated for 1, 3, 7, 13d (n = 10 per treatment for each period) and 27d (n = 15 per treatment for each period). After each treatment period muscles were harvested and blood collected, then plasma immediately prepared. The remaining carcass was incinerated. Plasma was analyzed by Metabolon's biochemical platform technology. Total RNA from LD was extracted and subjected to transcriptome analysis (Agilent pig microarray) followed by gene cluster analysis using MaSigPro. Gene expression was verified by quantitative RT-PCR. Protein expression was determined by Western blot. Treatment groups were compared by 2-way ANOVA (Genstat). The BA treatment increased Vastus Lateralis weight ($P < 0.001$), and induced a switch to faster muscle fiber type in Longissimus dorsi (LD), as myosin heavy chain isoform IIB gene expression was increased ($P < 0.001$). Within 1d of treatment plasma fatty acids were increased in BA, but not GH ($P < 0.05$). Both GH and BA decreased certain plasma amino acids, such as lysine ($P < 0.05$), but only GH decreased the concentration of others, such as serine ($P < 0.05$) and glycine ($P < 0.05$). Only GH increased glucose ($P < 0.05$) but there was no effect of either GH or BA on lactate ($P > 0.1$). Predominant effect of treatment was a BA coordinate increase in LD serine synthesis pathway gene expression (PHGDH, $P < 0.001$; PSAT, $P < 0.001$; PSPH, $P < 0.001$) by 3d, which was confirmed at the protein level, as PHGDH was increased with BA at 7d ($P < 0.001$). The effect of GH and BA treatment on metabolism appears to lead to differential effects on muscle mass, with BA potentially elevating serine synthesis, which could lead to the generation of metabolites required for growth.

Key Words: growth promoters, pig, transcriptomics

110 Molecular factors underlying the discrepancy of marbling between Nellore and Angus beef. Taiane Martins[1], Walmir Silva[1], Letícia Sanglard[1], Ivan Carvalho Filho[1], Ygor Cassani[1], Nick Serão[2], Mario Chizzotti[1], Marcio Ladeira[3], and Marcio Duarte*[1], *[1]Federal University of Vicosa, Vicosa, MG, Brazil, [2]Iowa State University, Ames, IA, [3]Federal University of Lavras, Lavras, MG, Brazil.*

Studies have reported that intramuscular adipogenesis and fibrogenesis may concomitantly occur in skeletal muscle of beef cattle. Thus, we hypothesized that the discrepancy of intramuscular fat content in beef from Nellore and Angus bulls was associated with differences in intramuscular adipogenesis and fibrogenesis during the finishing phase. To test our hypothesis, longissimus muscle samples of Nellore (n = 6; BW = 372.5 ± 37.3 kg) and Angus (n = 6; BW = 382.8 ± 23.9 kg) bulls with 20 mo of age were collected for analysis of gene and protein expression, and chemical quantification of intramuscular fat and collagen. Least squares means were estimated for the effect of breed and differences were considered at $P \leq 0.05$. A greater intramuscular fat content was observed in skeletal muscle of Angus compared with Nellore cattle ($P < 0.01$). Despite the lack of differences in gene expression of adipogenic markers *Zfp423* ($P = 0.62$), *PPARγ* ($P = 0.42$), and *C/EBPα* ($P = 0.14$), a greater protein expression of PPARγ was observed in skeletal muscle of Angus compared with Nellore cattle ($P = 0.05$). A greater abundance of adipo/fibrogenic cells, evaluated by the PDGFRα content, was observed in skeletal muscle of Angus than Nellore cattle ($P = 0.05$). No differences in fibrogenesis were observed in skeletal muscle of Angus and Nellore cattle, which is in accordance with the lack of differences in intramuscular collagen content in beef from both breeds ($P = 0.16$). These findings demonstrate that difference in intramuscular fat content

is associated with a slightly enhanced adipogenesis in skeletal muscle of Angus compared with Nellore cattle, but no difference in fibrogenesis.

Key Words: adipocyte, collagen, intramuscular fat

111 Effect of rearing system on meat quality, lipid, and amino acid profiles of lambs. Jian-min Chai[1], Hai-chao Wang[1], Qi-yu Diao[1], Kai-dong Deng[2], Yan Tu[1], Min-li Qi[1], and Nai-feng Zhang*[1], *[1]Feed Research Institute of Chinese Academy of Agricultural Sciences, Key Laboratory of Feed Biotechnology of the Ministry of Agriculture, Beijing, China, [2]College of Animal Science, Jinling Institute of Technology, Nanjing, Jiangsu, China.*

To determine the effect of rearing system on meat quality, lipid and amino acid profiles of lambs, 24 Hu lambs (12 rams and 12 ewes) were randomly divided into 2 treatments: ewe-reared (ER) or weaned at d 10 and fed milk replacer (MR). Ewe milk or MR was available from 0 to 60 d and a creep feed was offered ad libitum to all lambs from d 15 to 90. The fatty acid and amino acid composition of the diet and meat samples were determined by gas chromatography and automated dedicated amino acid analyzer, respectively. All data were analyzed using *t*-test procedure of SAS. Lambs fed MR had a greater growth rate ($P = 0.03$) and creep feed intake ($P < 0.001$) than those in ER treatment. Lambs fed MR had a greater harvest weight ($P = 0.003$), HCW ($P = 0.004$) and fat thickness over L *dorsi* ($P = 0.05$) compared with those of ER treatment. The meat of lambs in MR treatment had lesser L* ($P = 0.04$) and b* ($P = 0.02$). There was no difference ($P = 0.82$) in a* values between the 2 treatments. Lambs fed MR had greater ether extract content ($P = 0.003$) than that in ER treatment. No differences were found in crude protein ($P = 0.58$) and ash ($P = 0.11$) between 2 treatments. The content of unsaturated fatty acids and monounsaturated fatty acids in meat were greater ($P = 0.02$) for MR treatment compared with ER treatment. On the contrary, the proportion of saturated fatty acids in ER treatment was greater ($P = 0.03$) than that in MR treatment. The proportion of C14:0 of ER lambs was greater ($P = 0.01$) than that in MR treatment, while the proportion of C18:0 ($P = 0.003$), C18:2 ($P = 0.04$), C18:3 ($P = 0.008$) and the ratio of polyunsaturated fatty acids ($P = 0.002$) and saturated fatty acids (P/S) ($P = 0.03$) were lesser than those of MR treatment. The proportion of leucine ($P = 0.003$), alanine ($P < 0.001$), tyrosine ($P = 0.002$), and proline ($P < 0.001$) were greater, while histidine ($P = 0.014$) was lesser for lambs of MR treatment compared with those of ER treatment. In conclusion, the MR rearing system could increase meat production and improve the proportion of lipid and amino acid profiles of lambs.

Key Words: meat quality, lipid, amino acid profile

112 The effects of growth-promoting agents on ovine metabolism and growth. Shaker Al-Doski*[1], Tim Parr[1], Krystal Hemmings[3], Zoe Daniel[1], David Brown[1], Doug Harris[2], Chungui Lu[1], Charlie Hodgman[1], Sean May[1], and John Brameld[1], *[1]University of Nottingham, Nottingham, UK, [2]Zoetis, Kalamazoo, MI, [3]University of Derby, Derby, UK.*

This study sought to investigate the short-term effects of bovine growth hormone (GH) and β-adrenergic agonist (βA), on lamb liver and muscle, particularly protein and energy metabolism. Wether lambs (120 d old) were all fed a high protein/energy diet ad libitum, with the GH group (n = 10) receiving a single subcutaneous injection of bovine GH (Posilac, Monsanto, 3.75mg/kg BW) on d 1; the βA group (n = 10) receiving βA (cimaterol) at 10mg/kg in the feed, whereas the control group (C, n = 11) only had ad libitum feed. After 6 d sheep were slaughtered blood was collected, plasma immediately prepared, and subsequently analyzed using Metabolon's biochemical platform technology. Samples of Longissimus dorsi (LD) and Supraspinatus (SS) muscles were snap frozen in liquid nitrogen and stored at −80°C until analysis, the remaining carcass was incinerated. From extracted total RNA first strand cDNA was generated using random primers. Gene expression was determined by quantitative RT-PCR analysis relative to total cDNA, as measured using oligreen. Protein expression was determined by Western blot. Treatment groups were compared by one-way ANOVA (Genstat) and post hoc Dunnett's test. Although there were no significant effects of βA and GH in body weight of lambs ($P = 0.122$), βA, but not GH, significantly increased the weights of both SS ($P < 0.01$) and ST ($P < 0.05$). In the blood, GH significantly increased the concentration of more fatty acids than βA ($P < 0.05$), both GH and βA significantly decreased certain plasma amino acids ($P < 0.05$). Treatment with βA, but not GH, increased mRNA expression of genes involved in glycolysis ($P < 0.05$) and the serine synthesis pathway ($P < 0.05$) in both SS and ST, but decreased expression of genes in the TCA cycle ($P < 0.05$). Effects on the serine pathway were confirmed as protein levels for PHGDH were significantly increased with βA ($P < 0.001$). It appears that GH and βA have differential effects on metabolism that lead to differential effects on muscle mass over this short time frame. Treatment with GH has wider effects on whole body metabolism, while βA appears to have more specific effect on both muscle metabolism and its growth.

Key Words: growth promoter, sheep, transcriptomics