W219 Myogenic regulatory factors are increased in bovine satellite cells by polyamines and their precursor amino acid ornithine. Kara J. Thornton[2], Stephen C. Tamm*[1], Samantha L. Faulkner[1], and Gordon M. Murdoch[1], [1]*University of Idaho, Moscow, ID,* [2]*University of Minnesota, Minneapolis, MN.*

Skeletal muscle is unique in its growth and developmental characteristics in that normal hypertrophy is carried out through activation and fusion of satellite cells (SC) surrounding individual muscle fibers. These SC are responsive to signals from their extracellular environment especially growth factors and nutrients. Polyamines (PA) are a class of small, positively charged molecules that favorably affect growing cells through somewhat undefined physiological mechanisms. Polyamines exist in mammalian species primarily as ornithine derivatives. Abnormalities in polyamine metabolism are associated with irregular development in mammals emphasizing their critical role as regulators of growth. To test the direct effect of PA on skeletal muscle development, primary bovine SC cultures were differentiated in media containing either methionine (10 m*M* control 1), ornithine (10 m*M*), putrescine (5 m*M*), spermine (0.5 m*M*), or no supplement (control 2). SC were differentiated as a monoculture (MC) as well as in coculture (CC) alongside preadipocytes isolated from bovine intramuscular fat depots. This coculture provided a more realistic environment of that which would surround skeletal muscle and impact SC activity. Following treatment, SC were isolated from CC using laser micro-dissection technique. SC populations were analyzed for temporal expression of the myogenic regulatory factors (MRF) *MyoD*, *Myf5*, and *Myf4* (myogenin) to identify differentiating cells along with the genes *Pax7* and *Spry1* representative of quiescent cells. Protein isolation and Western Blot analyses were also performed to measure protein expression in a temporal manner. Exposure of SC's to PA in CC resulted in upregulation of *MyoD* ($P = 0.05$), *Myf5* ($P = 0.02$), and *Myf4* ($P = 0.09$) and attenuation of *Pax7* ($P = 0.10$) and *Spry1* ($P = 0.07$). Statistics generated in SAS (Cary, NC) using PROC MIXED procedure. Treatment was included as a fixed effect. These results suggest that ornithine metabolism and polyamine metabolites can affect bovine skeletal muscle myogenesis, and may therefore be promising as candidates for natural means of promoting growth of lean tissue in cattle.

Key Words: polyamine, satellite cell, myogenic regulatory factor

W220 Muscle gene expression patterns in finishing steers supplemented with dietary Amaize *(Aspergillus oryzae* extract). Daniel E. Graugnard*[1], Kristen M. Brennan[1], Allison C. Smith[1], Sonia J. Moisá[2], and Juan J. Loor[2], [1]*Alltech Center for Animal Nutrigenomics and Applied Animal Nutrition, Nicholasville, KY,* [2]*Department of Animal Sciences, University of Illinois, Urbana, IL.*

We evaluated the effect of dietary *Aspergillus oryzae* extract on gene expression profiles in the *Longissimus lumborum* from finishing steers. Cross-bred (Simmental × Angus) yearling steers were randomly assigned to one of 2 groups (n = 10/treatment). From receiving until d21, starter and step-up diets were fed to acclimate steers to a traditional mid-west finishing diet. Steers were then fed *ad libitum* to meet or exceed NRC requirements until slaughter (d140): basal diet with or without 5 g/hd/d of *A. oryzae* extract (Amaize, Alltech Inc., Nicholasville, KY) containing α-amylase (AMZ). On d90, *Longissimus lumborum* tissue was collected for gene expression analysis. Serum was collected at d 40, 90 and 140 for analysis of metabolites (BHBA, glucose, insulin, urea). Data from blood metabolites was analyzed using a mixed model. Gene expression was profiled using the Affymetrix Bovine Gene 1.0 ST Array. Performance did not differ between treatments. Hierarchical clustering indicated a treatment effect ($P < 0.05$) of the AMZ-supplemented group compared with the control. A total of 1148 genes were differentially affected ($P < 0.05$; 430 upregulated; 718 downregulated) between treatments. The genes affected, enriched ($P < 0.05$) and activated several pathways, including IGF-1 signaling, insulin receptor signaling, valine degradation, and VDR/RXR activation. The pathways activated are involved in the regulation of muscle development and growth. Blood metabolites indicated greater levels of BHBA, urea and insulin ($P < 0.05$) at d40 in AMZ-supplemented steers. Only insulin remained at a greater concentration in the AMZ group than the control throughout the experiment. In conclusion, AMZ supplementation in the finishing diet affects muscle gene expression and insulin metabolisms, potentially causing a positive effect for the development of skeletal muscle in finishing steers.

Key Words: amylase, muscle, cattle

W221 Investigation of effects of maternal nutrition intensification and fetal sex on development of skeletal muscle of bovine fetuses. Tathyane RS Gionbelli*[1,2], Polyana P. Rotta[2], Cristina M. Veloso[2], Marcos I. Marcondes[2], Sebastiao C. Valadares Filho[2], Bruno C. Carvalho[3], Joao V. R. Lovatti[2], Camila S. Cunha[2], Marco A. S. Novais[2], Marcio S. Duarte[2], and Mateus P. Gionbelli[1], [1]*University of Lavras, Lavras, Minas Gerais, Brazil,* [2]*University of Viçosa, Viçosa, Minas Gerais, Brazil,* [3]*Embrapa Dairy Cattle, Brazilian Corporation of Agricultural Research, Coronel Pacheco, Minas Gerais, Brazil.*

This study aimed to evaluate the effects of maternal feeding level (MN) and fetal sex (FS) on skeletal muscle development of bovine fetuses at different stages of gestation (SG). Fourty-4 multiparous, dry Holstein × Gyr cows with average initial body weight of 480 ± 10 kg were fed either restricted feeding at 1.15% of body weight (CO, n = 24) or ad libitum (ON, n = 20) with the same diet (93% corn silage and 7% concentrate; 111 g/kg of CP and 674 g/kg of TDN). Eleven cows of each dietary treatment were slaughtered at 139, 199, 241 and 268 d of gestation. Fetuses were necropsied to evaluate the development of skeletal muscle. Data were analyzed by MIXED procedure of SAS considering the fixed effects of MN, FS and SG (2 × 2 × 4 factorial). Modifications in gene expression of skeletal muscle of fetuses were observed in function of MN and FS despite the lack of effect of MN ($P = 0.330$) and FS ($P = 0.518$) on fetal weight. The muscle mRNA expression of myogenic markers β-catenin and MyoD was greater in male than in female fetuses, as well the expression of all adipogenic markers evaluated (Zfp423, C/EBPα and PPARγ), 3 of the 4 fibrogenic markers evaluated (Collagen I, Collagen III and Fibronectin) and the number of myocytes in muscle. Marginal effects of MN were observed on mRNA expression as well on the phenotypic indicators of myogenesis, adipogenesis and fibrogenesis. At the mid-gestation (139 DG) β-Catenin, Zfp423 and PPARγ expression and myocytes number were greater in ON than in CO fetuses and in males than in females, but these differences were not observed at subsequent SG. Fat content of fetal muscle was not affected by MN and FS. Almost all myogenic, adipogenic and fibrogenic markers were less expressed in late gestation than in mid-gestation, however collagen deposition, fat and crude protein content of fetal muscle were greater at late gestation than in mid-gestation. The MN changed gene expression of myogenic, adipogenic and fibrogenic markers at mid-gestation (greater in ON than in CO) but some compensatory gene expression made the effect of MN not significant in late gestation.

Key Words: adipogenesis, fetal programming, fibrogenesis

W222 High-energy diet reduced myogenic gene expression of Hanwoo steers fed to three different endpoints. K. Y. Chung*, S. S. Chang, H. S. Kim, E. M. Lee, H. J. Kim, and H. S. Kang, *Hanwoo Research Institute, NIAS, Pyeongchang, Korea.*

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