treatment, suggesting that the NE value of diets containing WEP might have been higher than estimated. Other factors such as Na and Cl concentration may limit the practical inclusion rate of WEP in pig diets. A study examining the impact of feeding a constant rate of WEP would further clarify the impact of this feedstuff on pig performance.

Key Words: growing pigs, byproduct feeds, feed intake

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502 Low-Stress Sampling and Cortisol Concentrations in Periparturient Sows. M. J. Goering*, J. M. Mumm, M. J. Coffin, E. M. Bortoluzzi, L. A. Ruiz, L. E. Hulbert, *Kansas State University, Manhattan, KS*

The most common method of cortisol sample collection for sows is jugular venipuncture, which requires restraint via snaring. Snaring can be an added stressor to sows, especially during the periparturient phase, when cortisol concentrations are already elevated and variable responses are expected. Therefore, the objectives of this study were to determine the variation of stress-responses to farrowing using less-invasive sample collection methods (saliva vs. low-volume ear vein blood). Samples were collected from 10 multiparous sows (DNA Genetics; K-State Swine Research Center) at -1 and +1 d relative to farrowing. Sows were offered a 51 cm cotton-rope to chew on and 300 uL of blood was drawn after ear venipuncture using a 26 gauge needle and syringe treated with heparin. After centrifugation, saliva and plasma were harvested from solid-particles and blood cells then immediately frozen at -20°C until cortisol concentration analysis using a commercially available ELISA kit (Detect X Cortisol Assay; Arbor Assays, Anne Arbor, MI). Sows tended, ($P = 0.06$) to have less ear-vein plasma cortisol concentrations at -1 than +1 d relative to parturition, but differences in cortisol concentrations were not detected from saliva samples ($P = 0.67$). The range of cortisol concentration was greater in the plasma-samples than the salivary samples (19.17 to 55.50 vs. 0.69 to 6.14 ng/mL, respectively). Nonetheless, CV% was lower among plasma than salivary samples (24.8 vs. 67.3%). If a treatment is expected to cause a 25% change in cortisol secretion, then only 21 sows will be needed per treatment if plasma is measured, whereas 152 pigs will be needed if saliva is measured. Therefore, the preferred sample collection method for future experiments involving periparturient sows will be ear-venipuncture, rather than salivary collection.

Key Words: Glucocorticoids, Swine, parturition

POSTER SESSION II: UNDERGRADUATE STUDENT POSTER COMPETITION II

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503 Defining the Minimum Inhibitory Concentration of Synthetic and Commercial Medium Chain Fatty Acid Based Products Against Salmonella Typhimurium. E. W. Sylvester*[,1], R. A. Cochrane[1], R. G. Amachawadi[1], S. Remfry[1], A. B. Lerner[1], T. G. Nagaraja[1], J. R. Pluske[2], M. C. Niederwerder[3], C. B. Paulk[1], C. R. Stark[1], J. C. Woodworth[1], S. S. Dritz[1], M. D. Tokach[1], J. M. DeRouchey[1], R. D. Goodband[1], C. K. Jones[1], *[1]Kansas State University, Manhattan, KS, [2]Murdoch University, Western Australia, Australia, [3]Department of Diagnostic Medicine/ Pathobiology, Kansas State University, Manhattan, KS*

Research has confirmed that a 2% inclusion rate of a blend of C6:0, C8:0, and C10:0 in swine diets and ingredients can reduce *Salmonella enterica* serotype Typhimurium. However, it is unclear how the chain length and concentration of medium chain fatty acids (MCFA) impacts bacteriostatic properties. This can be tested through a minimum inhibitory concentration (MIC) benchtop assay, which identifies the lowest concentration of a chemical that prevents visible growth of a bacterium. The objective of this set of experiments was to utilize MIC as a mechanism to screen commercial or developmental feed additives containing MCFA for potential to mitigate *Salmonella* Typhimurium. First, the MIC of four synthetic MCFA treatments (C6:0, C8:0, C10:0, and 1:1:1 ratio of C:6:C8:C10 blend) was determined for *Salmonella* Typhimurium. The MIC of each treatment was conducted in a modified microbroth dilution and had three replicates. The MIC of C6:0 and C8:0 (0.4 and 0.5%, respectively) were similar ($P > 0.05$) to one another, but lower ($P < 0.05$) than the MIC of C10:0 or the blend of C6:C8:C10 (0.6% and >1.0%, respectively). It was therefore hypothesized that products containing high concentrations of C6:0 or C8:0 would have the greatest potential to mitigate *Salmonella* Typhimurium. Next, the fatty acid profile of 24 feed additive products that were commercially developed or in the development process and containing MCFA was determined via gas chromatography. As a result, four products in the development phase from varying companies plus coconut oil were selected as having a high potential for mitigating *Salmonella* Typhimurium based on their C6:0 and C8:0 levels. Development products 1, 2, 3, 4, and coconut

oil contained 29.5, 43.1, 27.4, 0.98, and 6.82 mg/g of C6:0 and 123.20, 610.3, 248.7, 227.1, and 72.0 mg/g of C8:0, respectively. The MIC of these products vs. *Salmonella* Typhimurium was then determined. The MIC of Product 1 and Product 2 (0.5% and 1.3%, respectively) were similar ($P > 0.05$) to one another, but lower ($P < 0.05$) than the MIC of Products 3 or 4 (3.8% and 4.3%, respectively). All four products had a lower ($P < 0.05$) MIC than coconut oil (> 5.0%). In summary, current or future feed additives containing high concentrations of C6:0 and C8:0 appear to be more effective at mitigating *Salmonella Typhimurium* than those containing C10:0. Furthermore, it is hypothesized that free MCFA have greater antibacterial potential than those in triglyceride form.

Key Words: Salmonella Typhimurium, Medium Chain Fatty Acids, Swine

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504 Identification and Expression Profiling of Novel microRNAs in Pig Fetal Skeletal Muscle. L. M. Ford*[,1], R. J. Corbett[2], K. R. Daza[1], N. E. Raney[1], C. W. Ernst[1], *[1]Department of Animal Science, Michigan State University, East Lansing, MI, [2]Genetics Graduate Program, Michigan State University, East Lansing, MI*

MicroRNAs (miRNAs) are a class of noncoding RNAs known to post-transcriptionally regulate gene expression through binding with target mRNAs, ultimately affecting a multitude of biological processes and phenotypes. It has been documented that miRNAs influence skeletal muscle development; however lack of miRNA annotation in pigs hinders understanding of molecular mechanisms underlying this process. We sought to identify novel miRNAs in fetal *longissimus dorsi* (LD) muscle and compare expression of these miRNAs at 41 days gestation (dg) and 70 dg (n=3 per stage), representing primary and secondary fetal myogenesis. Total RNA was isolated from LD samples of fetuses obtained from Yorkshire x Landrace gilts. Small-RNA sequencing was performed on the Illumina HiSeq 4000 platform, generating 30-60 million 1x50 reads per sample. High-quality reads were aligned to the *S. scrofa* reference genome (v11.1), and mapping and prediction of novel miRNAs was performed using miRDeep2. Predicted miRNAs with significant randfold p-values, miRDeep2 scores >7, and total read counts per million ≥1 for each sample were retained. Annotated human miRNAs with ≤2 mismatches with common and stage-specific novel miRNAs were found using miRBase. Differential expression analysis was performed on novel miRNAs using DESeq2. TargetScan was used to find conserved targets of human miRNAs with sequence identity to differentially expressed (DE) pig miRNAs. At 41 dg and 70 dg, 83 and 73 novel miRNAs were predicted in at least two samples, respectively. Of these, 59 were common to both stages. We identified 10 DE miRNAs (|log2 fold change|>1 and adj.p<0.05), nine of which were downregulated and one upregulated. One novel DE miRNA had 95% identity (1 mismatch) with a known pig miRNA (ssc-miR-26a). miR-26a has been found to play a major role in repression of myogenesis through the TGF-β/BMP signaling pathway in mice. In addition, six DE miRNAs had ≤2 mismatches with the known human miRNAs: miR-188-5p, miR-200ab-5p, miR-3194-5p, miR-33a-5p, miR-34b-5p, miR-93-5p. miR-34b has been shown to play a role in muscle cell differentiation during development in C2C12 mouse myoblast cells. Targets of DE miRNAs were enriched for Gene Ontology terms and KEGG pathways related to skeletal muscle development including axon guidance, regulation of actin cytoskeleton, Wnt signaling pathway, and cadherin binding involved in cell-cell adhesion. This study identified novel pig miRNAs with putative roles in myogenesis as supported by research in model organisms. Future efforts will analyze specific gene targets and their roles in skeletal muscle development.

Key Words: Skeletal Muscle, Pig, MicroRNAs

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505 Toxic Fescue Exposure Alters Vaginal Microbial Communities of Crossbred Beef Cows. A. E. Ratton*[,1], S. Chewning[1], L. R. Meyer[1], J. A. Atchley[1], J. G. Powell[1], J. D. Tucker[2], D. S. Hubbell, III[2], J. Zhao[1], J. E. Koltes[3], *[1]Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville, AR, [2]Livestock and Forestry Research Station, Division of Agriculture, University of Arkansas, Batesville, AR, [3]Department of Animal Science, Iowa State University, Ames, IA*

Consumption of toxic fescue by beef cattle results in adverse physiological effects such as: reduced reproductive success, vasoconstriction, poor body condition, hyperthermia, decreased prolactin, and reduced hair shedding. The purpose of this study is to characterize bacterial community of the reproductive tract in animals grazing toxic or novel fescue and determine the microbiota's relationship to host phenotype. One-hundred fall-calving crossbred cows were allocated to graze toxic fescue (toxic: n=50) or novel (non-toxic: n= 50) fescue pastures for five months (March-August). Treatments were blocked by sire breed (Charolais or Hereford) and