species fecal microbiota transplantation experiments to demonstrate that a human gut associated microbiota can colonize and be maintained within the gnotobiotic pig. The pigs derived through cesarean sectioning were divided into 3 treatment groups and were inoculated with either an obese human gut microbiota , lean gut microbiota,, or a conventional pig microbiota. The pigs with an obese donor microbiota were fed a 40% fat and carbohydrate diet and the pigs that received a lean or conventional pig microbiota was maintained on a 5% fat and carbohydrate diet. Fecal samples were collected weekly to monitor establishment of the gut microbial community. At 7 wk of age, 2 pigs from each treatment were cecum cannulated to evaluate the effect of cannulation on the microbial community structure. The pigs were maintained for an additional 2 wk before euthanization. Microbial community was evaluated using 16S rRNA sequencing using an ION Torrent Personnel Genome machine. This pilot study demonstrated that germfree piglets receiving the human microbiota developed a donor like microbial community each similar to the respective obese or lean donor (PERMANOVA $P < 0.05$) with minimal animal-to-animal variation. Comparison of the microbiotas of humans, germfree pig recipients of (obese, lean, and conventional), revealed that the microbiota of germfree piglets receiving human microbiota was more similar to human donor microbiota than conventionally raised pigs suggesting the establishment of a human gut flora within the pig (PERMANOVA, $P < 0.05$). The humanized pig model has potential to help understand structure function relationships of the human microbiome. With the cecum cannulation, longitudinal sampling can be performed at the site of microbial action allowing the investigation of microbial gene expression. This model will provide an opportunity to better understand how microbial gene expression effects host gene expression and in turn host physiology.

Key Words:16S human microbiota, microbiota transplantation, pig model

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444 **Gross morphology, morphometric characteristics, and sequential changes in digesta fiber fractions of gastrointestinal tract segments from high postpartum piglet mortality extensively reared swine.** S. N. Carr*, Q. S. Baptiste, *Berea College, Berea, KY.*

The gross morphology, morphometric characteristics, and sequential changes in digesta fiber fractions of gastrointestinal tract segments harvested from high postpartum piglet mortality (21.79%) of extensively reared swine were investigated. Swine had access to forage with moderately high NDF (50 to 60%) and ADF (30 to 43%) throughout this study and consumed a basal diet of corn and soybean with added minerals. Harvested stomach was dissected and emptied of its content (900 g of digesta) via a 4cm incision in the cardiac/oesophageal region. Stomach volume was 4,540 mL and its empty weight (579.14 g) was below that reported for concentrate fed intensively reared swine (0.64% vs. 1.20% of BW). In addition, a conspicuous 6.5 cm long fingerlike sacculation and segmentation of the fundus was visible both externally and along the inner walls of the dissected stomach. The length of the small intestine (18.69 m) was equivalent to average values reported for adult swine (18 m). The large intestine length (455 cm) was greater than 50% of the value reported for adult swine (750 cm). Stomach, caecum (proximal, medial and distal regions), and colon digesta were sampled and analyzed for DM, NDF and ADF content. Stomach digesta NDF and ADF (24.53 and 12.98%) reflected the values expected for extensively reared swine consuming soybean meal and corn concentrate. NDF and ADF values of caecum proximal (32.47 and 16.67%), medial (35.98 and 19.24%), and distal (31.78 and 16.69%) regions were higher than those of a composite colon digesta sample (25.47 and 13.06%). The DM values of caecum proximal (14.70%), medial (16.10%), and distal (19.44%) regions were lower than those of a composite colon digesta sample (23.19%). Hence, extensively reared swine display intestinal morphology and morphometric characteristics which indicate the need for caecal digestion and colon absorption of nutrients. However, even these modifications may be inadequate to meet nutrient requirements of gestating extensively reared swine, as evidenced by high early postpartum piglet mortality rates of this study's herd.

Key Words: GIT, morphology, mortality

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445 **Effects of detoxifying agents on growth performance of nursery pigs fed deoxynivalenol-contaminated wheat.** H. L. Frobose*[1], E. W. Stephenson[1], M. D. Tokach[1], J. M. DeRouchey[1], R. E. Musser[2], S. S. Dritz[1], R. D. Goodband[1], J. C. Woodworth[1], J. L. Nelssen[1], *[1]Kansas State University, Manhattan, [2]NUTRIQUEST, Mason City, IA.*

A total of 238 barrows and gilts (PIC 327 × 1,050; initially 13.4 ± 1.8 kg) were used in a 21-d study to evaluate the effects of detoxifying agents on the growth performance of nursery pigs fed diets contaminated with deoxynivalenol (DON). Pens of pigs were allotted by BW to 1 of 5 treatments in a completely randomized design with a 2 × 2 + 1 factorial arrangement, with main effects of DON (4 mg/kg) and Product D (Nutriquest, Mason City, IA). A fifth treatment was included to confirm the effectiveness of 1.0% sodium metabisulfite (SMB; $Na_2S_2O_5$) in DON-contaminated diets. There were 6 or 7 replicate pens/treatment and 7 pigs/pen. Naturally DON-contaminated wheat (6 mg/kg) replaced non-contaminated wheat in diets to achieve desired dietary DON concentrations. Basal ingredients were tested for mycotoxin and amino acid content prior to diet manufacturing. Diets were pelleted at 85°C with a 45 s conditioning time. Analyzed DON levels were 92% lower when pelleted with SMB, but otherwise DON matched formulated levels, although low levels of fumonisin (<1 mg/kg) were also present. Overall (d 0 to 21),

Table 445.

Formulated DON, mg/kg:	<0.5	<0.5	4.0	4.0	4.0	
Additive:	None	Product D	None	Product D	SMB	SEM
Analyzed DON, mg/kg	0.04	0.06	4.10	4.23	0.35	
d 0 to 21						
ADG, g	498	510	404	363	543	13.2
ADFI, g	798	805	702	639	772	18.3
G:F	0.625	0.634	0.576	0.567	0.704	0.011
Final BW, kg	23.9	24.2	22.1	21.1	24.8	0.30

a DON × Product D interaction was observed for ADG ($P < 0.05$) with a tendency for an interaction for ADFI ($P < 0.06$). As anticipated, DON reduced ($P < 0.001$) ADG and ADFI by 20 and 12%, respectively, but the interaction was driven by poorer growth performance when Product D was incorporated into DON diets. Additionally, pigs fed DON diets had 9% poorer G:F ($P < 0.001$). Deoxynivalenol-associated reductions in ADG were most distinct (89%) during the initial period (39 vs. 329 g from d 0 to 3), and least marked (18%) during the final period (497 vs. 607 g from d 14 to 21). Adding SMB increased ($P < 0.01$) ADG, ADFI and G:F compared to pigs fed DON-contaminated diets, and also increased ($P < 0.02$) ADG and G:F compared to pigs fed DON-free diets. Overall, Product D was not effective in DON-contaminated diets. While SMB appears promising to restore performance in pelleted DON-contaminated diets, additional research is necessary to clarify the response.

Key Words: deoxynivalenol, mycotoxin, sodium metabisulfite

446 **Characterization of microbial community structure during Salmonella shedding in beef cattle.**

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Food animals are a major reservoir for zoonotic transmission of *Salmonella* through contaminated foods. In particular, asymptomatic carriers play an important role in *Salmonella* propagation in cattle and in contaminated foods because they are not easily identified and isolated. Minimizing the number of such animals would have a significant impact on lowering incidence of Salmonella contamination in beef in a production setting. Depending on the serotype and other unknown factors, *Salmonella* can cause either a symptomatic infection in cattle or the organism can colonize the animals asymptomatically, converting the animal to a carrier state where the organism can be dispersed quite efficiently throughout the environment. We hypothesize that competition between pathogens and non-pathogens for nutrient resources is important for limiting disease incidence and pathogen colonization. Therefore, competitive exclusion may be a viable strategy to reduce or control pathogenic Salmonella populations. However, our knowledge about the fecal microbial community is limited as 99% of the bacteria in the rumen or feces have not been cultured or isolated, hindering the opportunity to identify competitor. As a first step toward identifying competitor microbial species, we used selective microbiological culture methods and molecular methods to identify *Salmonella* high-shedders and low-shedders among 225 beef steers over 4 time periods. Based on shedding numbers 48 high-shedders ($>10^3$ *Salmonella* cfu/g of feces) and 48 low shedders ($<10^2$ cfu/g of feces) were phenotyped for gut microbial composition using 16s rRNA based amplicon sequencing. A total of ~10,000,000 high-quality DNA sequences generated through Ion Torrent semi-conductor based sequencing was used to evaluate microbial community composition. Bioinformatic analysis of the sequences from high-shedders and low-shedders indicated significant variations in microbiome composition between high and low shedders. It was revealed that members of the phylum *Bacteroidetes* were more abundant in the high-shedders, while members of the phylum *Firmicutes* were more abundant in the low-shedding animals. Furthermore, the analysis showed that 8 operational taxonomic units (OTUs) were significantly more abundant in low-shedders than in high-shedders. These OTUs represented candidate members of the microbiome that can be used as direct fed microbials (DFM) to reduce Salmonella shedding. These results provide new insight into bacterial populations that are present in the feces of *Salmonella* shedding cattle.

Key Words: 16S bacterial community, dysbiosis, *Salmonella*