

arrangement with 2 diet types (low- or high-fiber) and 2 levels of DFM [0 or 60 g DFM (2.4×10^{12} CFU/kg feed)/MT feed]. Pigs were fed their respective treatment diets during periods 2, 3, and 4, but during periods 1, 5, and 6, all pigs were fed the low-fiber diet without DFM. Each period lasted 14 d and involved a 5 d adaptation period, total collection of feces and urine from d 6 to 11, and ileal digesta collection on d 13 and 14. Contrasts were used to compare periods within each treatment group and results for all treatment groups for periods 2, 3, and 4 were analyzed as repeated measures using PROC MIXED of SAS. Results indicated AID of starch and ATTD of DM, GE, ADF, and NDF increased ($P \leq 0.05$) as period increased, regardless of diet type. This corresponded with an increase ($P \leq 0.05$) in DE and ME from 3357 to 3383 and from 3132 to 3199 kcal/kg, respectively, from periods 2 to 4. Pigs fed high-fiber diets during periods 2, 3, and 4 had reduced ($P \leq 0.05$) AID of most AA, ATTD of GE and NDF, and DE and ME compared with low-fiber diets fed during periods 1, 5, and 6. Addition of DFM to the high-fiber diet did not ameliorate the negative effects of fiber on digestibility, but addition of DFM to the low-fiber diet increased ($P \leq 0.05$) the AID of ADF, NDF, Lys, Phe, and Glu by 18.1, 21.7, 1.9, 2.5, and 2.2%, respectively. When DFM were withdrawn from the low-fiber diet, digestibility values were not maintained, indicating that DFM must be fed continuously to exert beneficial effects and that no carry-over effects are expected. In conclusion, AID of starch and ATTD of fiber and energy increased as pig BW increased, but digestibility values of energy and nutrients were reduced by increased fiber in the diets, although the AID of some nutrients were improved by addition of DFM to the low-fiber diet.

Key Words: dietary fiber, direct-fed microbial, pigs

162 Improved growth performance of nursery pigs fed diets supplemented with a *Bacillus subtilis*-based direct-fed microbial feed additive.

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Three experiments were done to determine the efficacy of a *Bacillus subtilis*-based direct-fed microbial (DFM) feed additive for improving growth performance of nursery pigs. All experiments were done with PIC 337 × C29 terminal pigs weaned at approximately 20 d of age and 6 kg body weight. In all experiments, pens of pigs were blocked by weight and randomly allotted to experimental treatments from within block (replicate). Experiment 1 compared the DFM (Visano Nursery, JBS United, Inc.) to a control in corn-SBM diets with 14 replicates of 10–12 pigs/pen from 7 to 27 d postweaning. All pigs were fed a common complex Phase 1 nursery diet before the start of this experiment. Experiment 2 compared the DFM to a control in corn-SBM-DDGS diets with 11 replicates of 25–28 pigs/pen from 1 to 41 d postweaning. Experiment 3

compared the DFM to a control and a medicated feed additive (MFA)-containing treatment in corn-SBM-DDGS diets with 11 replicates of 10–12 pigs/pen from 1 to 38 d postweaning. The MFA consisted of 55 mg/kg carbadox from d 1–7, 441, and 38 mg/kg CTC and tiamulin, respectively, from d 8–21, and 28 mg/kg carbadox from d 22 to 38. The DFM was supplemented to final diets at 0.05% of complete feed from a premix of analyzed cfu concentration. Body weights, weight gain, feed intake, and feed efficiency metrics were collected in each experiment, and data were analyzed as a randomized complete block design. In Experiment 1, there was a trend ($P < 0.10$) toward a lower feed/gain ratio (1.4%; 1.41 vs. 1.39 kg/kg) in the DFM treatment group. In Experiment 2, supplementation of the *Bacillus* DFM increased ($P < 0.05$) growth rate by 5% (0.36 vs. 0.34 kg/d) and increased ($P = 0.06$) d 41 body weight by 0.5 kg. In Experiment 3, the *Bacillus* DFM increased ($P < 0.05$) growth rate by 10% over the control (0.29 vs. 0.26 kg/d) and reduced ($P < 0.05$) feed/gain ratio by 5% (1.45 vs. 1.52 kg/kg), while the medicated feed additive treatment showed 25% greater ($P < 0.05$) weight gains and 10% lower ($P < 0.05$) feed/gain ratios than the control treatment. Dietary inclusion of the *Bacillus*-based DFM was efficacious in increasing weight gain and improving overall growth performance in nursery pigs fed out to 6 wks postweaning.

Key Words: *Bacillus subtilis*, pigs, direct-fed microbial

163 Utilizing feed sequencing to decrease the risk of porcine epidemic diarrhea virus (PEDV) cross-contamination during feed manufacturing.

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Since the introduction of porcine epidemic diarrhea virus (PEDV) into the United States, feed has been identified as a vector of transmission between herds. As with other biological hazards, biosecurity at feed manufacturing facilities plays a key role in preventing cross-contamination of finished feeds. One potential method for reducing introduction of PEDV into finished feeds is through batch sequencing of diets. Therefore, the objective of this study was to determine the effects of feed batch sequencing on PEDV cross-contamination between diets. A 50 kg batch of feed was inoculated with PEDV, mixed in a 0.11 m³ electric paddle mixer and had a final concentration of 4.5×10^4 TCID₅₀ PEDV particles per g, cycle threshold (Ct) of 11. After mixing, the feed was discharged from the mixer into a bucket elevator and collected to mimic processing in a commercial feed mill. To simulate batch sequencing, 4 subsequent PEDV-free batch diets were processed through the system without equipment cleaning. Sequenced batches (1–4) were mixed, discharged, and sampled similar to the PEDV-positive

batch. Feed inoculation, processing, and batch sequencing was performed for 3 replicates with complete PEDV-decontamination of all equipment and facility between each replication. All collected feed samples were analyzed for PEDV RNA by quantitative PCR (qPCR) and infectivity by bioassay. Bioassay included a controlled challenge study using 30 crossbred 10 d old pigs to establish infectivity. All pigs (9/9) challenged with the positive treatment (feed Ct 31.7 ± 0.20 SEM) had fecal swabs with detectable PEDV RNA indicating PEDV infectivity. Infectivity was further confirmed with histopathology and immunohistochemistry (IHC). The discharge for the first sequence had less detectable PEDV RNA ($P < 0.01$, feed Ct 39.1 ± 3.4 SEM). Feed samples from the second, third and fourth sequence had no detectable PEDV RNA (Ct > 45). Infectivity was confirmed in 1 of 3 replicate batches for the first and second sequences. It is important to note, the 2nd sequence did not have detectable PEDV RNA in any feed sample. The results of this study confirm feed as a vector of PEDV transmission and is the first to demonstrate feed without detectable PEDV RNA can be infective. Furthermore, although subsequent feed batches had reduced quantities of PEDV RNA, they were still found to be infective. Therefore, feed batch sequencing should be considered a risk mitigation strategy but should not be considered a risk elimination strategy.

Key Words: feed, PEDV, sequencing

164 Evaluating the effect of manufacturing porcine epidemic diarrhea virus (PEDV)-contaminated feed on subsequent feed mill environmental surface contamination.

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With the introduction of porcine epidemic diarrhea virus (PEDV) to the United States in 2013 and the subsequent identification of feed as a route of transmission, identifying sources of feedstuff contamination and methods to reduce the risk of transmission at feed mills has become paramount. As with other biological hazards, contaminated ingredients can easily lead to cross-contamination of finished feeds and contamination throughout the facility. Therefore, the objective of this study was to monitor equipment and environmental contamination after manufacturing PEDV-positive feed and after the production of subsequent PEDV-negative feed. PEDV-positive feed (50 kg with 4.5×10^4 TCID₅₀/g, Ct 11) was mixed in a 0.11m³ paddle mixer, discharged into a bucket elevator, and collected. Following processing of the contaminated feed, 4 subsequent batches of PEDV-free feed (sequence 1–4) were processed through the mixer and bucket elevator with no decontamination between batches to mimic commercial feed production. Porcine epidemic diarrhea virus contamination

of equipment and surrounding areas were monitored via the collection of swabs that were analyzed via quantitative PCR (qPCR) for PEDV RNA. Swabs were collected from equipment and facility surfaces prior and after processing contaminated feed and after processing subsequent sequenced batch diets. Monitored areas for equipment included the interior of the mixer and bucket elevator. Facility areas included high and low foot traffic areas (concrete), floor drain (concrete), worker boot bottoms (rubber), table (metal), and door (metal). Three replications of contaminated feed and subsequent sequence batch diet processing was completed, with equipment and facility decontamination between replicates. Following qPCR analysis, Ct values ≤ 40 were considered PEDV-positive and all numerical data was converted to $\pm$ for statistical analysis via PROC MIXED procedure of SAS. The interactions feed contact surface by sequence were found to be significant ($P < 0.01$). All swabs collected from equipment surfaces after processing of PEDV-positive feed were positive for PEDV, while 16 of 18 of the collected facility swabs were positive for PEDV RNA. Following processing of the first sequence batch diet, 100% of equipment surfaces and 88.9% of facility surfaces were positive for PEDV. Surprisingly, a large percentage of equipment and facility surfaces remained PEDV-positive through the processing of the subsequent sequence batch diets. Furthermore, all swabs collected from concrete and rubber surfaces remained PEDV-positive through all processing of all diets. This study demonstrates the extent of equipment and facility contamination that could occur in a feed manufacturing facility after processing of PEDV-contaminated feed.

Key Words: PEDV, feed mill, contamination

165 To determine if hand held near infrared spectroscopy can be used to measure corn particle size, corn particle distribution and corn moisture.

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In swine production the effect of corn particle size on performance in pigs fed pelleted diets has shown that in general the finer the grind size the better the feed efficiency. Currently, to determine particle size, the most widely used methods are the onsite 3 pan sieve analysis because of its simplicity, cheapness and ease of interpretation or the 13 pan sieve analyses which is often tested off site at a laboratory. Near-infrared (NIR) spectroscopy is an analytical technique used for grain quality assessments due to its versatility and speed. Although the ability of NIR to estimate particle size is well documented, obtaining the full particle size distribution profile has not been studied in depth. The objective of this trial was to determine if a hand held near-Infrared (HHNIR) spectroscopy could be used to measure corn average particle size, moisture and par-