proved by addition of DFM to the low-fiber diet.

**Key Words:** dietary fiber, direct-fed microbial, pigs
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**162 Improved growth performance of nursery pigs fed diets supplemented with a *Bacillus subtilis*-based direct-fed microbial feed additive.**

N. R. Augspurger*[1], J. D. Spencer[1], S. Son[2], J. A. Ley[1], M. R. King[2], *[1]JBS United, Inc., Sheridan, IN, [2]Microbial Discovery Group, Franklin, WI.*

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

L. L. Schumacher*[1], R. A. Cochrane[1], J. C. Woodworth[1], A. R. Huss[1], C. R. Stark[1], C. K. Jones[1], Q. Chen[2], R. Main[2], J. Zhang[2], P. C. Gauger[2], S. S. Dritz[1], M. D. Tokach[1], *[1]Kansas State University, Manhattan, [2]Iowa State University, Ames.*

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 $m^3$ electric paddle mixer and had a final concentration of $4.5 \times 10^4$ $TCID_{50}$ 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 detectible 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 2ndsequence 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 detectible 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
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