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 \pm 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

164 Evaluating the effect of manufacturing porcine epidemic diarrhea virus (PEDV)-contaminated feed on subsequent feed mill environmental surface contamination. L. L. Schumacher*1, R. A. Cochrane¹, C. E. Evans¹, J. R. Kalivoda¹, J. C. Woodworth¹, A. R. Huss¹, C. R. Stark¹, C. K. Jones¹, Q. Chen², R. Main², J. Zhang², P. C. Gauger², S. S. Dritz¹, M. D. Tokach¹, ¹Kansas State University, Manhattan, ²Iowa State University, Ames.

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 \leq 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-Infra-red (HHNIR) spectroscopy could be used to measure corn average particle size, moisture and par-