Background

- Porcine Epidemic Diarrhea Virus was first identified in the United States in April 2013.
- The original North American PEDV strains identified in 2013 caused severe piglet morbidity and mortality and had a 99.5% nucleotide percent identity to Chinese strain AH2012.
- Recently, a North American PEDV variant-INDEL strain was identified. This spike gene deletion has been described in global PEDV strains and may correlate to a less severe clinical presentation of PEDV.
- A third porcine epidemic diarrhea virus has been identified in the United States, which has a 2 amino acid deletion in the spike gene.

Objective

To describe the identification of a third PEDV virus and its genomic relationships

Results

Figure 1 PEDV amino acid alignment representing the 114 PEDV strains. Dots represent amino acids matching the consensus sequence. Box residues represent amino acid residues not previously identified in the US PEDV strains.
Implications

- Documenting PEDV variation is important to understand the natural evolution of the virus and possibly identify portions of the genome associated with difference clinical disease presentation.
- Animal studies are required to define the effect these mutations have on clinical disease, pathogenesis, and immunity and to understand how sow exposure to a different PEDV virus correlates to protection of piglets from clinical disease.

Results

Figure 2 Complete genome phylogenetic tree of 114 PEDV strains. Strains colored blue represent US prototype strains, strains colored red represent INDEL strains, and the color green represents the newly identified S2aa-del strain.

Conclusions

- Thus far, three natural occurring American PEDV strains have been identified, the original PEDV, the PEDV with changes in the spike gene (INDEL), and the PEDV strain (S2aa-del).
- The significance of genetic changes in the American PEDV strains to clinical disease is not yet known.
- It is also unknown if the PEDV 6nt-del strain will circulate in the North American swine population.