

Request for current PEDV samples: Do we know what's out there?

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Background

PEDV was introduced to the USA in 2013 and quickly spread across the country. In the USA, two strains are present: S-indel (low pathogenic) and non-S indel (high pathogenic), which are characterized by the presence or absence of deletions in the ORF-S, respectively. Most studies investigating the evolutionary dynamics of PEDV were carried out only at the early stages of the epidemic, shortly after its introduction into the USA. In a recent study, we investigated the evolutionary dynamics of PEDV in the USA over a 10-year period, capturing changes in the composition of the viral population during the endemic phase. The clades that circulated during the epidemic period and the early endemic phase ceased to circulate after 2017, being replaced by two novel clades (Figure 1). These new clades are restricted to specific regions of the USA, with no evidence of PEDV transmission between them. However, sequencing surveillance declined gradually after the epidemic period, which may represent a limitation of this study. Given the swine industry's substantial efforts to eradicate PEDV, these findings evidence the importance of expanded surveillance to assess whether divergent clades are spreading around USA and to confirm the extinction of ancestral clades.

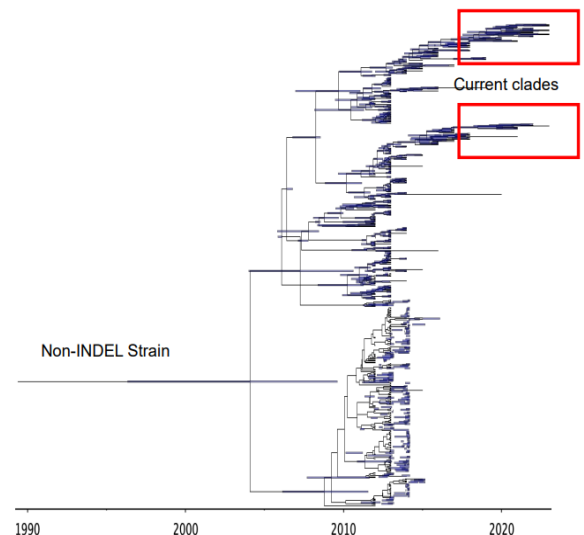


Figure 1. Time-scaled tree of PEDV spike protein for non-indel strains.

New study

Our new study aims to update and fill gaps in current PEDV genomic surveillance data, which is vital for the swine industry to advance toward disease eradication and is key to:

- confirming the extinction of older clades and genetic makeup of contemporary viruses,
- mapping the distribution of recent clades and regional movement of the virus, and
- understanding PEDV's evolutionary diversification in light of vaccine development.

However, the most recent whole genome sequences available for PEDV are from ~2017, creating a major blind spot in what strains are currently circulating in the U.S. As part of this study, **we are seeking clinical PEDV samples from the field for whole genome sequencing** to fill in the gaps on current PEDV strains.

Benefits of participation:

We will pay for whole genome sequencing. Sequences will be shared with the participant. In addition, the data will contribute to understanding PEDV epidemiology and help enable vaccine development to be tailored to contemporary strains of the virus.

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Please contact Kim VanderWaal (kvw@umn.edu) and Joao Silva (herre466@umn.edu) if you are willing to contribute a PEDV clinical sample for this project.