



UNIVERSITY OF MINNESOTA

Swine Disease Eradication Center

October 2016
Volume 5, Issue 3

www.cvm.umn.edu/sdec

SDEC Partners Research Update

Project Update: New computational analysis of historical porcine circovirus 2 sequences from the Minnesota Veterinary Diagnostic Laboratory identifies a new cluster, PCV2e

Investigators: Brendan Davies, Xiong Wang, Cheryl Dvorak, Douglas Marthaler, Michael Murtaugh

Funded by: Boehringer Ingelheim Vetmedica (BIV) and USDA National Institute of Food and Agriculture, multistate project MIN-63-112

Background

- Porcine circovirus 2 (PCV2) is associated with the postweaning, multisystemic wasting syndrome and is commonly called PCV2-associated disease (PCV2AD).
- Nearly, 80% of the pigs were infected with PCV2 prior to the 2000's outbreak in the United States
- PCV2 has been routinely sequenced by the Minnesota Veterinary Diagnostic Laboratory to investigate strain variation of the virus.

Objective

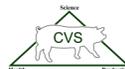
To conduct a systematic analysis of the unpublished ORF2 sequences collected at the Veterinary Diagnostic Laboratory to further understand the evolution of PCV2

Methods

- Sanger sequencing was used to generate the ORF2 of 1289 PCV2 sequences. High quality filtering and removal of the sequencing samples left 729 validated field sequences.
- Sequences were aligned and a maximum likelihood phylogenetic tree was generated.
- Whole genome sequencing was conducted on two novel PCV2 genomes, using Sanger sequencing.



SCHWARTZ
FARMS, INC.



PIC



Results

- Phylogenetic analysis of the ORF2 sequences revealed a novel genotype, tentatively named PCV2e, which were collected between 2006 and 2015 and were from Iowa, Nebraska, Minnesota, Illinois, and Mexico (Figure 1).
- PCV2e have a 12-nucleotide insertion in ORF2, encoding the capsid protein, compared to PCV2a and PCV2b.
- The closest ORF2 nucleotide percent identity in GenBank was 87% to strains from Denmark, Romania, and India.

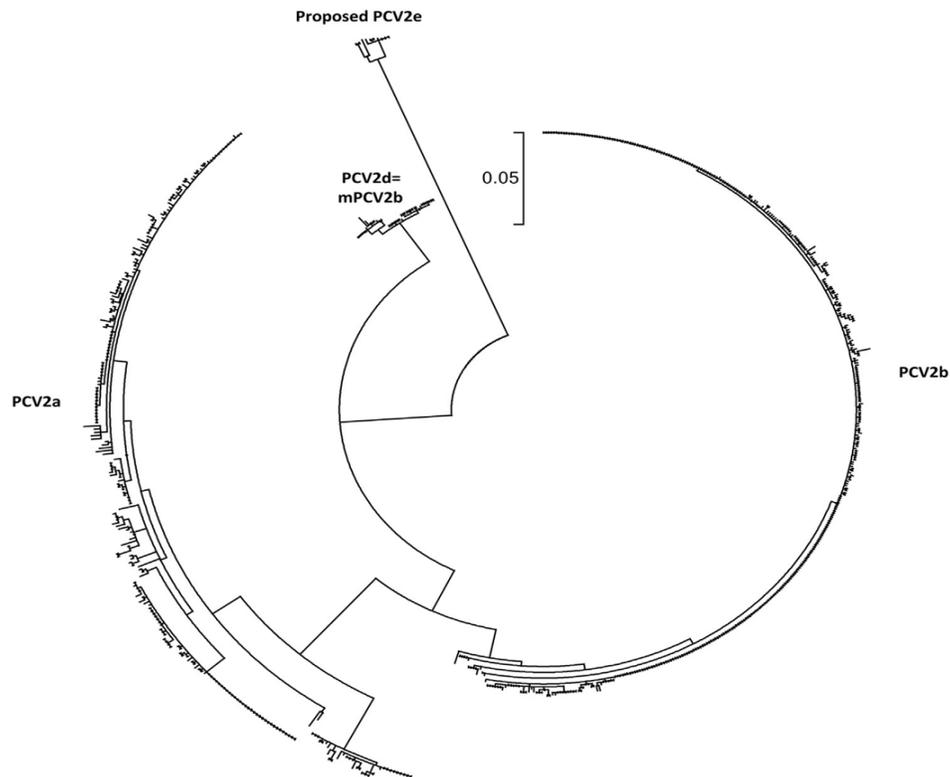


Figure 1. Phylogenetic tree of the ORF2 sequence generated from the Minnesota Veterinary Diagnostic Laboratory.

Conclusions

- Computational analysis of historical sequences in diagnostic lab databases can provide valuable information about pathogen variation and evolution.
- PCV2e was identified in 2006, is sporadically isolated, but widespread in the Midwest region of the United States, and is in Mexico.
- PCV2e is associated with PCVAD and is in healthy pigs like other PCV2.
- **Reference:** [Diagnostic phylogenetics reveals a new Porcine circovirus 2 cluster](#). Davies B, Wang X, Dvorak CM, Marthaler D, Murtaugh MP. *Virus Res.* (2016) 217:32-37. pii: S0168-1702(15)30171-4. doi: 10.1016/j.virusres.2016.02.010.