PCV2 vaccine cross-protection: Identification of sequences in successfully vaccinated field cases

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INTRODUCTION

It is necessary to evaluate emerging PCV2 isolates in both control and clinical cases in order to determine the importance and impact of novel mutations.
The primary objective of this study was to identify PCV2 isolates in herds where

- Production performance was meeting the systems' expectations
- No clinical PCVAD signs were apparent
- The organization was satisfied with vaccine

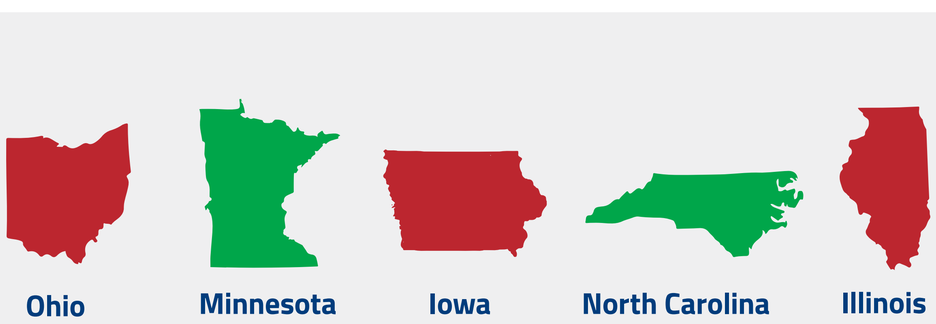
MATERIALS AND METHODS

Farms (n = 48, 10 unique systems) were selected using the following criteria:
1) Use of Ingelvac CircoFLEX® at weaning age
2) Pig owner and veterinarian were satisfied with vaccine
3) Pig performance was meeting systems' expectations
4) No clinical health issues suggestive of PCVAD present

Samples:
Serum (n = 432 samples; 23 farms)
Oral fluids (OF; n = 168 samples; 24 farms)
Lung homogenate (n = 1 sample)

Individual pig serum and OF samples were PCV2 tested (HMC, Ames, IA) using TaqMan real-time PCR reagents with a detection limit of below 3.5 genomic equivalents/reaction. Lung tissues were sent to ISU-VDL for PCV2 PCR.
Farms (n = 16) samples were targeted for lower Cq values with a PCR cycle quantity (Cq) ≤ 32 for serum (n = 16), Cq ≤ 30 for OF (n = 11) and for tissues (n = 1; Cq = 19.3) to be sent to U of MN for PCV2 capsid gene sequencing with quality analysis performed within DNAstar (Madison, WI). Each isolate was further characterized based on standards and dendrograms were created.

Figure 1: Distribution an selection criteria of farms



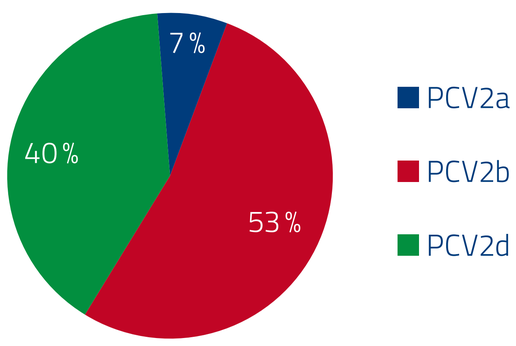
Testing criteria

- ✓ *Pigs vaccinated with a full dose of Ingelvac CircoFLEX® at weaning age*
- ✓ *Both pig owner and veterinarian were satisfied with the vaccine*
- ✓ *Pig performance was meeting the systems' expectations*
- ✓ *No clinical PCVAD signs*

RESULTS

Twenty-seven farms had PCV2 PCR positives (12, 15 and 5 from serum, OF, lung homogenate, respectively) of which 44 samples (24, 17 and 3 from serum, OF, lung homogenate, respectively) were sent for sequencing.
There was an overall 91 % sequencing success rate (87 % for serum, 94 % for OF, 100 % for tissue homogenate). Forty total samples were successfully sequenced and characterized as PCV2a (n = 3), PCV2b (n = 21) or PCV2d (n = 16).

Figure 2: Number of Sequences, n



DISCUSSION

Vaccination strategies have decreased the presence of PCV2, yet it remains in the barn environment and vaccinated populations.
Though not reflective of the population, the biased sampling of PCV2 PCR positive samples based on Cq level allowed for a more economically beneficial success rate on sequencing.
No farms with multiple sequences on samples had homologies less than 100 % (amino acid comparison), indicating that the same strain was found multiple times in the same farm in multiple pigs.
Although there were forty sequences, via capsid sequencing there was only a maximum 3 % heterology amongst these samples.
In this study, vaccinated pigs showed no clinical signs of PCVAD and met the systems' performance expectations, while still being exposed to a wide-range of modern PCV2 strains. Although mutations may occur the commercial PCV2 vaccines appear to remain efficacious.

Figure 3: Dendogram