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David Brown
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Logo Design
Ruth Cronje, and Jan Swanson;
based on the original design by Dr. Robert Dunlop

Prevalence of PCV2 viremia from 2007-2010 in a large cross-sectional US dataset.

E. Johnson, G. Cline, G. Anderson
Boehringer Ingelheim Vetmedica, Inc., St Joseph, MO

Introduction and Objectives

Porcine circovirus associated disease (PCVAD) has been described frequently in North America since 2004 and is evidenced by morbidity and mortality as well as poor growth characteristics. The objective of this analysis was to evaluate the prevalence of porcine circovirus type 2 (PCV2) viremia over a recent 4 year period.

Materials and Methods

Swine herds in the United States were cross-sectionally sampled over a four year period (2007-2010) as part of a previously described diagnostic protocol.[2] 116 projects were completed with few herds represented in two or more years. These projects were conducted for a variety of reasons including expression of clinical signs or history of poor performance in a flow. Clinical signs may or may not have been attributable to PCV2 infection or PCVAD. In addition to tests for other pathogens, cross-sectional serum samples were individually assayed for PCV2 by quantitative PCR (qPCR) at a single diagnostic laboratory. The PCV2 qPCR test detects presence and approximate quantity of PCV2 in serum samples and has a lower detection limit of $1.00X10^4$ (4 logs) viral genomic equivalents/ml. A result reported as $<1.00X10^4$ was deemed "undetected" rather than "negative" for the purposes of this analysis. Pig flows chosen for this analysis had PCV2 qPCR results from at least 10 pigs/time point in at least 4 of the following age groups: Nursery (3-7 wks), Late Nursery (8-12 wks), Early Finishing (13-17 wks), Mid-Finishing (18-22 wks), and Late Finishing (23-27 weeks).

Results

87 of 116 projects, from 83 different herds, met the inclusion criteria for this analysis. The proportion of PCV2 qPCR positive individual samples declined from 25.8% in 2007 to 6.47% in 2010. Pig Flows were categorized as positive if they contained one or more positive samples. The proportion of positive flows in each year ranged from 62.5-95.0%.

Table 1. PCV2 qPCR results by year.

	2007	2008	2009	2010
N Pig Flows	20	27	24	16
Positive Pig Flows[1]	19	20	15	13
Proportion of positive pig flows (95% CI)	**95.00%** (0.83, 1.07)	**74.07%** (0.558, 0.924)	**62.50%** (0.411, 0.839)	**81.25%** (0.591, 1.034)
N Samples	810	1200	990	680
Positive Samples[2]	209	201	90	44
Proportion of positive samples (95% CI)	**25.80%** (0.227, 0.289)	**16.75%** (0.146, 0.189)	**9.09%** (0.073, 0.109)	**6.47%** (0.046, 0.084)

[1] Pig flow considered positive if 1 or more samples were positive.
[2] Sample considered positive if $>1.00X10^4$ (4 logs) viral genomic equivalents/ml.

Discussion and Conclusions

The analysis of this dataset shows a reduction in PCV2 viremia in individual pigs from 2007 to 2010. The authors speculate that the introduction and widespread application of commercial PCV2 vaccines beginning in 2006 may have reduced the number of viremic pigs and/or the viral load level of viremic pigs in positive herds. A similar reduction in viremia was not observed at the flow level; however, a small sample size was evaluated.

This evaluation calls into question the continued use of qPCR for surveillance of PCV2. The test was initially developed for use differentiating healthy pigs from those with PCVAD, antemortem, but has also been employed for PCV2 surveilance.[3] Today, with a declining proportion of detectable positives, a qualitative PCV2 PCR may be a more appropriate test.

References

[1]Desrosiers R. *Proc.GA Young Swine Conf*. 2006.
[2]Kolb J, et al. *Proc AASV*. 2007.
[3]Brunborg IM, et al. J Virol Methods. 122 (2004) 171-178.