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A comparison of cross-sectional quantitative PCV2 PCR vs. individual animal quantitative PCV2 PCR and associated necropsy findings in 4 cases

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Introduction and Objectives

The clinical picture of porcine circovirus associated disease (PCVAD) in the US industry continues to change, and with it comes a better understanding of the diagnostic tests available to characterize the disease in production systems. This paper describes the findings of 4 diagnostic cases completed in 2007 that used a standardized diagnostic profiling program for pathogens including PRRSV, PCV2, Mycoplasma, Salmonella and Lawsonia and compares only the PCV2 diagnostic results.

Materials and Methods

Each case represents a flow of pigs from wean to market. Cross-sectional serum sampling was performed at 4-5 week intervals with 10 randomly selected animals sampled at each time. The lower detection limit for the quantitative PCV2 PCR (qPCR) test is $1.00X10^4$ (4 logs) viral genomic equivalents/ml. A result reported as $<1.00X10^4$ was entered as $1.00X10^4$ for the purposes of this analysis. Tissue diagnostics were also completed for each case with 3 clinically affected animals selected for complete necropsies at the time of peak disease expression (mortality/clinical signs) which occurred at 17-18 weeks of age (mid finishing) in these cases. Three pigs were also necropsied 4-5 weeks pre-peak disease (early finishing). All tissues were evaluated by the same pathologist. Results reported included PCV2 immunohistochemistry (IHC) findings and the presence/absence of lymphoid depletion.

Results

Figure 1 shows the cross-sectional qPCR results while Table 1 shows individual animal diagnostics including qPCR. Case 2 is only detectable by qPCR at the late finishing sampling point, and the individual animal diagnostics taken at an earlier age, at peak and pre-peak mortality, reflect these findings. Case 4 had mean viral loads of 5 logs and 5.5 logs at the time of pre-peak and peak mortality. The qPCR's of the necropsied pigs are similar to the population results but the tissue diagnostics revealed only 2/6 positive by IHC and one animal with lymphoid depletion meeting the case definition for PCVAD. Cases 1 and 3 have similar wean to market qPCR profiles, although different in magnitude. The individual animal diagnostics for case 1 with 6/6 IHC positives, is in stark contrast to case 3 which had higher qPCR results but 0/6 IHC positives. No lymphoid depletion was identified in either case.

Figure 1. Mean log of PCV2 qPCR

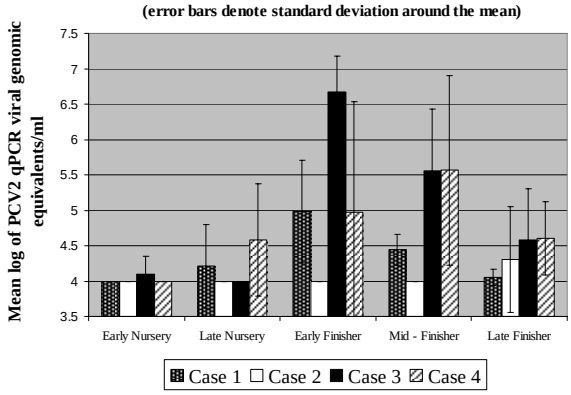

Table 1. Individual animal diagnostics

		4-5 Weeks Prior to Peak Mortality				Peak Mortality			
	Animal ID	PCV2 qPCR Log	PCV2 IHC +/-	Lymphoid Depletion +/-	PCVAD	PCV2 qPCR Log	PCV2 IHC +/-	Lymphoid Depletion +/-	PCVAD
Case 1	1	**7.87**	+	-	No	**4.73**	+	-	No
	2	**6.63**	+	-	No	**5.53**	+	-	No
	3	**6.25**	+	-	No	**5.32**	+	-	No
Case 2	1	4.00	-	-	No	4.00	-	-	No
	2	4.00	-	-	No	4.00	-	-	No
	3	4.00	-	-	No	4.00	-	-	No
Case 3	1	**8.51**	-	-	No	4.00	-	-	No
	2	**6.60**	-	-	No	4.00	-	-	No
	3	**6.85**	-	-	No	4.00	-	-	No
Case 4	1	**6.95**	-	-	No	**5.92**	+	+	**Yes**
	2	**4.89**	-	-	No	**5.03**	-	-	No
	3	**5.48**	-	-	No	**6.17**	+	-	No

Conclusions

PCV2 qPCR is a useful tool to better characterize the viral load of a population. But results, even as high as 8 logs, apparently do not always correlate to positive PCV2 IHC findings, lymphoid depletion, and therefore do not fulfill the case definition of PCVAD.