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Genetic characteristics of porcine circovirus 2 isolates from pigs in farms with or without clinical post-weaning multi-systemic wasting syndrome

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Introduction: PCV2 has been isolated from pigs in farms with or without clinical history of PMWS. The objectives of this study were to isolate PCV2 from swine farms with or without clinical history of PMWS in Minnesota and to analyze genetic characteristics of ORF2 gene of the PCV2 isolates. Attempts were made to correlate the genetic type of PCV2 and the presence of clinical PMWS in the pigs.

Materials and Methods: Serum or tissue samples were collected from pigs of 9 different Minnesota farms with or without clinical PMWS in 2005 and 2006. The samples were examined for the presence of PCV2 by virus isolation and PCR assay (1). Primer pairs were separately designed for sequencings, and purified PCR products were sequenced by the DNA analyzers. The sequence alignment and phylogenic analysis were performed using the CLUSTAL X program. The sequences of PCV2 isolates were compared with PCV2 strains published in GenBank from different countries in N. America, Europe, and Asia.

Results: Of 76 samples examined, 18 showed PCR positive for PCV2. Eight PCV2 were isolated and passed continuously on PK-15 cell line. Two (MN-NP160 and MN-NP162) and 6 isolates (MN-R4, MN-R13, MN-B2, MN-B9, MN-PG34, and MN-H12) were originated from farms with subclinical and clinical PMWS, respectively. Heterogeneity of whole genome between PCV2 isolates from pigs with and without clinical PMWS was 5%. In the phylogenetic analysis, two distinct clusters were identified when ORF 2 genes of the 18 isolates were analyzed. Twelve of the 18 isolates were from clinical PMWS farms in 2005 and 2006 and were categorized within the upper cluster with mainly European strains (Fig. 1). The lower cluster was composed with the 6 isolates from sub-clinical PMWS farms along with the N. American strains reported before 2001.

Discussion: There has been a speculation that the clinical severity before 2005 with the classical US PCV2 strains differed from those after 2005 with recent PCV2 isolates. This is coincided with field observations of dramatic increase of wasting pigs with high mortality in Minnesota from the late 2005. In this study, two different genetic groups were clearly identified. Two PCV2 genotypes of PCV2a and PCV2b were also reported based on a new real time PCR (2). At the same time, they reported that 60 of 63 clinical PMWS cases (95.2%) were caused by infection with PCV2b (2 cases were PCV2a and one case was a dual infection). Our results are similar to these findings (2), identifying PCV2 in the upper cluster (PCV2b) for clinical PMWS. It could be concluded that PCV2 in the upper cluster (PCV2b) is highly associated with clinical PMWS. Further analysis with more isolates and known clinical history may be needed for this conclusion.

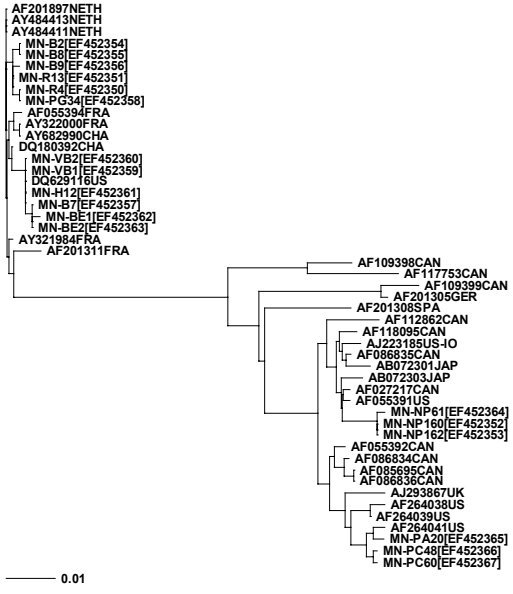

Fig. 1. Phylogenetic analysis of PCV2 isolates. 12 MN isolates in upper cluster (PCV2b) from clinical PMWS.

References

1. Farnham MW et al. (2003), Can J Vet Res 67:108.

2. Gagnon et al. 2007, Proceedings AASV p. 535