Complete genome sequence of a novel porcine circovirus type 2b variant present in cases of vaccine failures in the United States

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Porcine circovirus type 2 (PCV2), a member of Circoviridae family genus Circovirus, is a small nonenveloped circular virus which was initially discovered in 1998 (6). PCV2 is highly prevalent in the domestic pig population. PCV2 is associated with postweaning multisystemic wasting syndrome (PMWS), enteric disease, respiratory disease, porcine dermatitis and nephropathy syndrome (PDNS), and reproductive failure (6). PCV2 isolates are currently further subdivided into three genotypes: PCV2a, PCV2b, and PCV2c (1, 3).

In this study, two PCV2 strains, US22625-33 and US22664-35, were identified by PCR in cases of suspected vaccine failure in PMWS-affected pigs in a production system located in the United States in June 2012. The complete genome was further sequenced using previously described primers (2). The full genome of the two PCV2s is comprised of 1,767 bp with 10 predicted open reading frames (ORFs). The size of ORF1 is 945 bp, encoding a protein of 314 amino acids (aa), and the size of ORF2 is 705 bp, encoding a protein of 234 aa, which is 1 aa longer than that of the common PCV2 (233 aa). Phylogenetic analysis with the nucleotide sequences of ORF2 of the reference strains PCV2a (AF055392), PCV2b (AF055394), PCV2c (EU148503) (1), and representative U.S. PCV2a (DQ397521) and PCV2b strains (GU799576 and HQT713495) suggested that these newly identified strains are closely related to PCV2b. The predicted amino acid sequence of ORF2 showed higher levels of identity to PCV2b strains (93.6% to 94.9%) than to PCV2a (90.6% to 91%). However, the predicted amino acid sequence of ORF1 of the mutant PCV2 strains showed higher levels of identity (99% to 99.4%) with PCV2a than with PCV2b (98%), indicating possible recombination during the origin of the strain US22625-33. Compared with classic PCV2b, a TAA (stop codon) at the end of ORF2 was replaced by an AAG (Lys) at the 3’ end of ORF2 in one novel amino acid in ORF2.

Further sequence BLAST and comparison showed that both U.S. PCV2 strains had a high level of identity (99.9%) with the PCV2 strain BDH, which is sporadically found in China, reported with classical PCV2a/b strain. PLoS One 7:e41463. doi:10.1371/journal.pone.0041463.

The present study is the first to identify a new PCV2b mutant in the United States, where it was discovered in cases of suspected PCV2 vaccine failures in pigs with PMWS, indicating the possible antigen drift of this newly identified PCV2b mutant.

Nucleotide sequence accession numbers. The complete genome sequences of PCV2 strains US22625-33 and US22664-35 have been deposited in GenBank under the accession numbers JX535296 and JX535297.

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REFERENCES