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GENOME ANNOUNCEMENT

Complete Genome Sequence of the Rearranged Porcine Circovirus Type 2

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We first report here the genome sequences of 4 rearranged porcine circovirus type 2 strains, JSTZ, ZJQDH1, ZJQDH2, and JSHM, isolated from porcine sera in China. The complete circular genomes of these isolates are 578, 483, 574, and 772 nucleotides in length, respectively. They are predicted to be defective interfering particles of porcine circovirus type 2. The findings will help us to understand molecular evolution of porcine circovirus type 2 and the relationship between porcine circovirus type 2 and diseases.

Porcine circovirus (PCV), a small, nonenveloped, single-stranded DNA virus with a circular genome from the *Circoviridae* family, was first described as a picornavirus-like contaminant of the continuous porcine kidney cell line PK-15 (ATCC CCL31) in 1974 (3).

The PK-15-derived PCV isolate, designated PCV1, has 1,759 nucleotides (nt) and is considered nonpathogenic (2), while a novel PCV isolate, namely, PCV2, with 1,768 or 1,767 nt, has been considered the primary etiological agent, although not the sole factor, in developing a group of complex multifactorial PCV diseases (PCVD) or PCV-associated diseases (PCVAD), especially postweaning multisystemic wasting syndrome (PMWS). PMWS was first recognized in North America in 1991 (1). Since then, it has caused severe losses in pig production worldwide.

We isolated and identified 4 novel rearranged PCV2 isolates from pigs suffering from PMWS in China. All 4 genomic sequences analyzed here were obtained by PCR analysis and sequenced with an ABI 3730 genome sequencer. Overlapping consensus sequences were assembled and open reading frames (ORFs) were identified using DNAman version 5.2.2.

The complete circular genomes of the four rearranged PCV2 isolates, JSTZ, ZJQDH1, ZJQDH2, and JSHM, are 578, 483, 574, and 772 nt in length, respectively. These DNA molecules are subgenomic rearranged molecules originating from the parental PCV2 genome and display similar structures: they contain the origin of PCV2 genome replication, characterized by a putative stem-loop structure, with a conserved nanonucleotide motif (AA GTATTAC) and 2 to 3 hexamer motifs (CGGCAG) serving as binding sites for the replicases. They include the predicted ORF encoding a whole or truncated capsid protein of PCV2.

Unlike the porcine-circovirus-like agents P1 and P2 (4, 5, 6), the four rearranged PCV2 genomes do not contain the insertion of the exogenous sequence, so they are predicted to be defective interfering particles of PCV2. Of course, it remains to be clarified whether these rearranged components resulting from PCV2 may contribute to PMWS.

Nucleotide sequence accession numbers. The complete genome sequences of the four rearranged PCV2 isolates, JSTZ, ZJQDH1, ZJQDH2, and JSHM, have been deposited in GenBank under the accession numbers JQ690758, JQ690759, JQ690760, and JQ690761, respectively.

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