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Complete Genome Sequence of a Novel Porcine Circovirus-Like Agent

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We report here the genome sequence of a porcine circovirus-like agent. The sequenced genome of this porcine circovirus-like agent is composed of a 648-nucleotide circular DNA that includes three predicted protein-coding genes, which means the agent should be a novel member of the family *Circoviridae*.

Porcine circovirus (PCV), a small, nonenveloped, single-stranded DNA virus with a rather small circular genome (about 1,700 nucleotides [nt]) (2), was first described as a picornavirus-like contaminant of the continuous porcine kidney cell line PK-15 (ATCC-CCL31) in 1974 (4).

The PK-15-derived PCV isolate, designated PCV1, did not produce disease in pigs and was considered a nonpathogenic agent (3), and a novel PCV isolate, designated PCV2, is now considered the primary etiological agent associated with a group of complex multifactorial 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 to pig production worldwide.

We isolated and identified a novel PCV-like agent from pigs suffering from PMWS in China. The whole genome of the PCV-like agent was obtained by reverse PCR analysis and sequenced with an ABI 3730 genome sequencer. Open reading frames (ORFs) were identified by using DNAMAN version 5.2.2.

The circular genome includes 648 nt with a G+C content of 48.4% and is composed of 3 putative ORFs. ORF2 and ORF3 gene products showed a high level of protein similarity, with ORF6 and ORF10 coding for PCV2. Meanwhile, ORF1 protein shared relatively low homology with PCV2 for ORF2 as a nucleotide deletion within ORF1.

Interestingly, we found that the small segment (GGATCCAC TAGTAACGGCCGCC) in the genome of the PCV-like agent is identical to a segment of vector sequence by BLAST search on NCBI.

A more in-depth study of the porcine circovirus-like agent will be reported in a future publication.

Nucleotide sequence accession numbers. The nearly full genome sequences of the porcine circovirus-like agent have been deposited in GenBank under the accession numbers [EF514716](#), [JF803741](#), [JF918541-44](#), [JN040276-79](#), [JN104035-37](#), [JN104039](#), and [JN207908-14](#). The version described in this paper is under accession number [JF803741](#).

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