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# *In Vitro* and *In Vivo* Isolation of a Novel Rearranged Porcine Circovirus Type 2

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Here, we present the first report of a novel rearranged porcine circovirus type 2 (PCV2) strain named BIV, isolated from both *in vitro* and *in vivo* sources. The complete circular genome of BIV is 896 nucleotides in length. The data will help us to update current knowledge of the replication of PCV2 viruses in cell culture and of their molecular evolution, as well as their diagnosis.

Porcine circoviruses (PCVs) are nonenveloped viruses with single-stranded circular DNA genomes in the family *Circoviridae* (6). PCV type 1 (PCV1) was originally discovered as a contaminant of pig kidney cell cultures and is considered to be nonpathogenic (4, 5), while PCV2 is the causative agent of porcine circovirus-associated diseases, especially postweaning multisystemic wasting syndrome (PMWS) (1, 2). The newly discovered PCV-like agents P1 and P2 should also be classified as members of the family *Circoviridae* (10, 11, 12). P1 can cause PMWS-like clinical disease in pigs (9).

As the subgenomic molecules in PCV1 were demonstrated (3), four *in vivo* rearranged PCV2 strains and one *in vitro* rearranged PCV2 strain were also reported (7, 8). Here, we report the complete genomic sequence of a novel rearranged PCV2 strain named BIV isolated both in PCV2-infected PK15 cells and serum of pigs with PMWS. The whole genome of BIV was generated by PCR and sequenced with an ABI 3730 genome sequencer. Open reading frames (ORFs) were determined by using the standard genetic codes in DNAMAN version 5.2.2.

The complete circular genome of the rearranged PCV2 isolate (BIV) is 896 nucleotides in length. It comprises the PCV2 origin of genome replication, characterized by a putative stem-loop structure with nonanucleotide motifs (AAGTATTAC), and 3 repeats of the hexamer motifs (CGGCAG) that serve as binding sites for the replicases adjacent to the stem-loop. Analyses showed that the BIV genome contains six potential ORFs encoding proteins of 29 or more amino acids (aa), two of which are the major ORFs. ORF1 encodes a protein of 15 kDa (134 aa), and ORF2 encodes a 27.5-kDa (231 aa) protein. The N-terminal 41-aa residues of ORF1 and the complete protein sequences of ORF2, respectively, have high identities between BIV and PCV2.

**Nucleotide sequence accession number.** The complete genome sequence of the rearranged PCV2 isolate BIV has been deposited in GenBank under accession number [JX524206](https://www.ncbi.nlm.nih.gov/nuclot/JX524206).

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