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GENOME ANNOUNCEMENT

In Vitro Intragenomic Rearrangement of Porcine Circovirus Type 2

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Institute of Veterinary Medicine, Jiangsu Academy of Agricultural Sciences, Key Laboratory of Veterinary Biological Engineering and Technology, Ministry of Agriculture, National Center for Engineering Research of Veterinary Bio-products, Nanjing, China

We report here for the first time the genome sequence of a rearranged porcine circovirus type 2 (PCV2) strain, CH-IVT1, isolated from PCV2-infected PK-15 cells. The complete circular genome of the CH-IVT1 is 605 nucleotides (nt) in length. The finding will help us to understand the molecular evolution of PCV2 and the relationship between PCV2 and PCV-associated diseases.

Porcine circoviruses (PCVs) belong to the genus *Circovirus* of the family *Circoviridae*. PCV type 1 (PCV1), first described as a picornavirus-like contaminant of the continuous porcine kidney cell line PK-15 in 1974 (4), is considered nonpathogenic (3), while a novel PCV isolate, namely, PCV2, is closely associated with PCV-associated diseases (PCVAD), such as postweaning multisystemic wasting syndrome (PMWS). PMWS was first recognized in North America in 1991 (1). Since then, it has brought great losses to pig production worldwide.

The genome of PCV2 is a single-stranded circular DNA of about 1,770 nucleotides (nt). The existence of subgenomic molecules has already been demonstrated in PCV1 (2), and we have also reported four PCV2 strains rearranged *in vivo* and two other PCV2-like agents (5–8). Here, we report the complete genomic sequence of a novel PCV2 strain (CH-IVT1) rearranged *in vitro*. The whole genome of CH-IVT1 was generated by PCR and sequenced with an ABI 3730 genome sequencer. Identification of open reading frames (ORFs) was carried out by using DNAman version 5.2.2.

The complete circular genome of the rearranged PCV2 isolate (CH-IVT1) is 605 nt in length. It contains the origin of PCV2 genome replication, characterized by a putative stem-loop structure with a nanomer (AAGTATTAC), and 3 hexamer motifs (CGGCAG) that serve as binding sites for the replicases. The genome contains four potential ORFs, two of which are the major ORFs. ORF1 encodes a protein of 18 kDa (174 amino acids), and ORF2 encodes a 24-kDa protein (201 amino acids). Amino acid sequence alignment revealed that a high degree of homology exists between the N-terminal 54 amino acid residues of ORF1 and the N-terminal 119 amino acid residues of ORF2 in CH-IVT1 and PCV2, respectively.

Nucleotide sequence accession number. The complete genome sequence of the rearranged PCV2 isolate CH-IVT1 has been deposited in GenBank under accession number JX094503.

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REFERENCES

1. **Clark EG.** 1997. Post-weaning multisystemic wasting syndrome, p 499–501. *In* Proceedings of the American Association of Swine Practitioners, 28th Annual Meeting, Quebec, Canada.
2. **Mankertz A, Persson F, Mankertz J, Blaess G, Buhk H.** 1997. Mapping and characterization of the origin of DNA replication of porcine circovirus. J. Virol. **71**:2562–2566.
3. **Tischer I, Mields W, Wolff D, Vagt M, Griem W.** 1986. Studies on epidemiology and pathogenicity of porcine circovirus. Arch. Virol. **91**:271–276.
4. **Tischer I, Rasch R, Tochtermann G.** 1974. Characterization of papovavirus-and picornavirus-like particles in permanent pig kidney cell lines. Zentralbl. Bakteriol. Orig. A **226**:153–167.
5. **Wen L, et al.** 2012. Complete genome sequence of the rearranged porcine circovirus type 2. J. Virol. **86**:5963.
6. **Wen L, et al.** 2008. Complete nucleotide sequence of a novel porcine circovirus-like agent and its infectivity in vitro. Sci. China. C Life. Sci. **51**: 453–458.
7. **Wen L, et al.** 2011. Prevalence of porcine circovirus-like agent P1 in Jiangsu, China. Virol. J. **8**:543–547.
8. **Wen L, et al.** 2012. Complete genome sequence of a novel porcine circovirus-like agent. J. Virol. **86**:639.

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Address correspondence to Kongwang He, kwh2003@yeah.net.

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