

Complete Genome Sequence of Recombinant Porcine Circovirus Type 2 Strain SD-3

Jun Li, Shaojian Xu, Xiaoyuan Yuan, Guisheng Wang, Jianli Shi, Jiaqiang Wu, Xiaoyan Cong, Wenbo Sun, Yijun Du, and Jinbao Wang

Shandong Key Laboratory of Animal Disease Control and Breeding, Institute of Animal Science and Veterinary Medicine, Shandong Academy of Agricultural Sciences, Jinan, China

We report here the genome sequence of a recombinant porcine circovirus type 2 strain SD-3, isolated from a commercial swine farm with an outbreak of postweaning multisystemic wasting syndrome (PMWS) in pigs in Shandong Province of China. The complete circular genome of this isolate is 1,767 nucleotides in length. This recombinant isolate has the ORF1 regions from PCV2a viruses and ORF2 regions from PCV2b. The findings will help us to understand the molecular evolution of porcine circovirus type 2 and the relationship between porcine circovirus type 2 and disease.

Porcine circovirus (PCV) is the smallest animal virus known which can be divided into two groups: nonpathogenic viruses, which make up the PCV1 group, and the PCV2 group, whose members are recognized as the causative agents of postweaning multisystemic wasting syndrome (PMWS) (6). PCV2 belongs to the family *Circoviridae* and to the genus *Circovirus*, which has two major open reading frames (ORF1 and ORF2). ORF1 is found to encode the two replication-associated proteins (Rep and Rep') (2), while ORF2 encodes a major structural capsid protein (Cap) (3).

Studies of PCV2 genomic sequences show that the viruses can be further divided into distinct subtypes also known as genotypes (1). PCV2 genotype definition and nomenclature has been proposed (4), with three genotypes identified to date (5), including types a (PCV2a) and b (PCV2b), which are the two main phylogenetic groups, and a third genotype, type c (PCV2c), which has been found only in Denmark.

We isolated a recombinant porcine circovirus type 2 strain, SD-3, from a commercial swine farm with an outbreak of PMWS in Shandong Province of China. Subsequently, nucleotide sequences were amplified by PCR. The PCR product was purified with a QIAquick gel extraction kit (QIAquick) and cloned using the pMD18-T vector (TaKaRa) according to the manufacturer's instructions. Three positive clones for each fragment were sequenced by Sangon Biotech (Shanghai) Co., Ltd., using M13 universal forward and reverse sequencing primers. Genomic analysis was conducted using DNASTAR software (DNASTAR Inc.).

The complete circular genome of this isolate is 1,767 nucleotides in length. The ORF2 nucleotide sequences of this isolate occupy 702 bp. At positions of the ORF2 gene corresponding to amino acids 88 to 89 are PR, which is characteristic of group 1 PCV2.

Comparison of the variable ORF1- and ORF2-encoded amino acids in PCV2 strain SD-3 with those of PCV2a, PCV2b, and PCV2c viruses showed that PCV2 strain SD-3 shared the same variable sites as PCV2a in ORF1 and PCV2b in ORF2. Therefore, we conclude that PCV2 strain SD-3 was derived from a recombination event.

Analysis of ORF1-encoded amino acid sequences showed that three potential glycosylation positions, at amino acids 24 to 26

(NPS), 256 to 258 (NQT), and 286 to 288 (NAT), have no significant differences. Among ORF2-encoded protein sequences, the variation was due mainly to the variability of four major regions observed at amino acid positions 51 to 68, 86 to 91, 121 to 134, and 185 to 191. The potential glycosylation position of the Cap protein, 143 to 145 (NYS), has no variation.

These findings will help us to understand the molecular evolution of porcine circovirus type 2 and the relationship between porcine circovirus type 2 and disease.

Nucleotide sequence accession number. The GenBank accession number for the genome sequence of PCV2 strain SD-3 is [EU366323](https://www.ncbi.nlm.nih.gov/nuclot/EU366323).

ACKNOWLEDGMENTS

The study was partly supported by the National Natural Science Funds (31201889 and 31170146) and Natural Fund of Shandong (ZR2010CQ003 and ZR2010CQ044).

REFERENCES

- Cheung A, et al. 2007. Detection of two porcine circovirus type 2 genotypic groups in United States swine herds. *Arch. Virol.* 152:1035–1044.
- Fenaux M, et al. 2002. Cloned genomic DNA of type 2 porcine circovirus is infectious when injected directly into the liver and lymph nodes of pigs: characterization of clinical disease, virus distribution, and pathologic lesions. *J. Virol.* 76:541–551.
- Morozov I, et al. 1998. Detection of a novel strain of porcine circovirus in pigs with postweaning multisystemic wasting syndrome. *J. Clin. Microbiol.* 36:2535–2541.
- Olvera A, Cortey M, Segales J. 2007. Molecular evolution of porcine circovirus type 2 genomes: phylogeny and clonality. *Virology* 357:175–185.
- Segalés J, et al. 2008. PCV-2 genotype definition and nomenclature. *Vet. Rec.* 162:867–868.
- Tischer I, Gelderblom H, Vettermann W, Koch M. 1982. A very small porcine virus with a circular single-stranded DNA. *Nature* 295:64–66.

Received 28 September 2012 Accepted 30 September 2012

Address correspondence to Jinbao Wang, Wangjb@saas.ac.cn.

J.L., S.X., and X.Y. contributed equally to this work.

Copyright © 2012, American Society for Microbiology. All Rights Reserved.

[doi:10.1128/JVI.02693-12](https://doi.org/10.1128/JVI.02693-12)