

# Complete Genome Sequence of Porcine Circovirus 2b Strain CC1

Xin Yang, Fuwang Chen, Yuhang Cao, Daxing Pang, Hongsheng Ouyang, and Linzhu Ren

Jilin Provincial Key Laboratory of Animal Embryo Engineering, College of Animal Science and Veterinary Medicine, Jilin University, Changchun, Jilin, China

**A porcine circovirus 2 (PCV2) strain, designated CC1, was isolated and purified from tissue samples from pigs with wasting syndromes in China. We report the complete genome sequence of PCV2b strain CC1 with a deletion of C at position 1053 resulting in elongation of open reading frame 2 (ORF2) and formation of ORF5. There were 11 ORFs in the genome.**

Porcine circovirus (PCV) is a member of the *Circovirus* genus of the *Circoviridae* family (6, 7). PCV is the smallest single-stranded DNA virus (class II) that is nonenveloped with an unsegmented circular genome. PCV2 was identified as the etiological agent of postweaning multisystemic wasting syndrome (PMWS) (1, 2, 8). This disease was first confirmed in Canada in 1997 and was subsequently identified in pigs in the United States, France, Japan, South Korea, China, and other countries (3, 8, 9).

A PCV2 strain, designated CC1, was isolated from tissue samples from pigs with postweaning multisystemic wasting syndrome. The full-length genome of the isolated strain was amplified by using primers described by Yi (9). Each PCR product was sequenced at least three times on an ABI 3730 sequencer (Applied Biosystems) using the ABI Prism BigDye terminator v3.0. The result showed that the full-length genome of the PCV2 strain CC1 consists of 1,766 nucleotides (nt). It was reported that there were five genotypes of PCV2 (3). The genotype of the genomic sequence of the CC1 strain was designated by using reference sequences for genotype PCV2a (GenBank accession no. AF055392), PCV2b (accession no. AF055394), PCV2c (accession no. AY181946), PCV2d (accession no. EF524532), and PCV2e (accession no. EU148503) according to the method described by Guo (3) and Zhai (10). The results showed that the PCV2 CC1 strain belonged to the PCV2b genotype.

It was reported that genotype PCV2a strain 1010-Stoon (accession no. AF055392) had 11 open reading frames (ORFs), but genotype PCV2b strain 1011-48285 (accession no. AF055394) had 10 ORFs, except ORF5 (4, 5). The result of sequence analysis showed that there were 11 ORFs in the PCV2 CC1 strain. Compared with reference strain 1011-48285 of the PCV2b genotype, there was a deletion of C at position 1053, resulting in an elongation of the ORF2 gene of 708 nt. Interestingly, although mutation at position 1042 in three genotypes (2b, 2c, and 2d) resulted in deletion of ORF5, the one-base deletion in isolate CC1 at position 1053 led to formation of an ORF5 with 210 nt. Hame predicted that proteins encoded by ORFs 5, 6, 9, 10, and 11 in PCV2 were possibly the contributing factors for the pathogenesis, clinical signs, and lesions associated with PMWS (4). Studies are still going on to identify and characterize the protein encoded by ORF5. Furthermore, five mutations were observed at positions 1077 (T→C), 1166 (T→C), 1320 (A→G), 1559 (G→T), and 1565 (C→T) compared with strain 1011-48285.

**Nucleotide sequence accession number.** The complete genome sequence of PCV2 strain CC1 has been deposited in GenBank and assigned accession no. [JQ955679](https://doi.org/10.1186/1743-422X-7-273).

## ACKNOWLEDGMENT

This study was supported by the Fundamental Research Funds of Jilin University.

## REFERENCES

- Chae C. 2005. A review of porcine circovirus 2-associated syndromes and diseases. *Vet. J.* 169:326–336.
- Finsterbusch T, Mankertz A. 2009. Porcine circoviruses—small but powerful. *Virus Res.* 143:177–183.
- Guo LJ, Lu YH, Wei YW, Huang LP, Liu CM. 2010. Porcine circovirus type 2 (PCV2): genetic variation and newly emerging genotypes in China. *Virology*. doi:10.1186/1743-422X-7-273.
- Hamel AL, Lin LL, Nayar GP. 1998. Nucleotide sequence of porcine circovirus associated with postweaning multisystemic wasting syndrome in pigs. *J. Virol.* 72:5262–5267.
- Meehan BM, et al. 1998. Characterization of novel circovirus DNAs associated with wasting syndromes in pigs. *J. Gen. Virol.* 79:2171–2179.
- Misinzio G, Delputte PL, Meerts P, Lefebvre DJ, Nauwynck HJ. 2006. Porcine circovirus 2 uses heparan sulfate and chondroitin sulfate B glycosaminoglycans as receptors for its attachment to host cells. *J. Virol.* 80:3487–3494.
- Segalés J, Allan GM, Domingo M. 2005. Porcine circovirus diseases. *Anim. Health Res. Rev.* 6:119–142.
- Shuai J, et al. 2007. Genetic characterization of porcine circovirus type 2 (PCV2) from pigs in high-seroprevalence areas in southeastern China. *Virus Genes* 35:619–627.
- Yi J, Liu C. 2010. Molecular characterization of porcine circovirus 2 isolated from diseased pigs co-infected with porcine reproductive and respiratory syndrome virus. *Virology*. doi:10.1186/1743-422X-7-286.
- Zhai SL, et al. 2011. Co-existence of multiple strains of porcine circovirus type 2 in the same pig from China. *Virology*. doi:10.1186/1743-422X-8-517.

Received 6 June 2012 Accepted 11 June 2012

Address correspondence to Linzhu Ren, renlz@jlu.edu.cn, or Hongsheng Ouyang, ouyh@jlu.edu.cn.

X.Y., F.C., and Y.C. contributed equally to this article.

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

doi:10.1128/JVI.01406-12