

Complete Genome Sequence of a Novel Porcine Circovirus-Like Agent

LiBin Wen, KongWang He, ZhengYu Yu, AiHua Mao, YanXiu Ni, XueHan Zhang, RongLi Guo, Bin Li, XiaoMin Wang, JunMing Zhou and LiXin Lv
J. Virol. 2012, 86(1):639. DOI: 10.1128/JVI.06469-11.

Updated information and services can be found at:
<http://jvi.asm.org/content/86/1/639>

	<i>These include:</i>
REFERENCES	This article cites 3 articles, 0 of which can be accessed free at: http://jvi.asm.org/content/86/1/639#ref-list-1
CONTENT ALERTS	Receive: RSS Feeds, eTOCs, free email alerts (when new articles cite this article), more»

Information about commercial reprint orders: <http://jvi.asm.org/site/misc/reprints.xhtml>
To subscribe to to another ASM Journal go to: <http://journals.asm.org/site/subscriptions/>

Complete Genome Sequence of a Novel Porcine Circovirus-Like Agent

LiBin Wen, KongWang He, ZhengYu Yu, AiHua Mao, YanXiu Ni, XueHan Zhang, RongLi Guo, Bin Li, XiaoMin Wang, JunMing Zhou, and LiXin Lv

Jiangsu Academy of Agricultural Sciences, Nanjing 210014, People's Republic of China

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](#).

ACKNOWLEDGMENTS

This work was supported by grants from the National Natural Science Foundation of China (30972184) and the Jiangsu Provincial Natural Science Foundation (BK2008351).

REFERENCES

1. Clark EG. 1997. Post-weaning multisystemic wasting syndrome, p 499–501. *In* Proceedings of the 28th American Association of Swine Practitioners, Quebec, Canada.
2. Tischer I, et al. 1982. A very small porcine virus with circular single-stranded DNA. *Nature* 295:64–66.
3. Tischer I, et al. 1986. Studies on epidemiology and pathogenicity of porcine circovirus. *Arch. Virol.* 91:271–276.
4. Tischer I, et al. 1974. Characterization of papovavirus- and picornavirus-like particles in permanent pig kidney cell lines. *Zentralbl. Bakteriol.* 226: 153–167.

Received 3 October 2011 Accepted 6 October 2011

Address correspondence to KongWang He, kwh2003@263.net.

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

doi:10.1128/JVI.06469-11