

# Complete Genome Sequence of a Novel Porcine Sapelovirus Strain YC2011 Isolated from Piglets with Diarrhea

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**Sapelovirus is a member of the family *Picornaviridae* and is emerging as an enteric porcine, simian, and avian pathogen. Here, we report the genome sequence of a novel porcine sapelovirus strain YC2011 isolated from piglets with severe diarrhea. The availability of the genome sequence is helpful to further investigations of molecular characteristics and epidemiology of porcine sapelovirus.**

*Sapelovirus*, a new genus in the family *Picornaviridae*, is a single-stranded, positive-sense genomic RNA virus. To date, the genus *Sapelovirus* consists of three species, porcine, simian, and avian (9). Porcine sapelovirus (PSV) is confirmed to replicate in the gastrointestinal epithelia that causes acute diarrhea, pneumonia, and polioencephalomyelitis in swine (3).

Since December 2010, outbreaks of severe diarrhea in suckling piglets have been observed in China. The causative agent has not been identified until now (7). Various pathogens have been detected in the fecal samples, such as the porcine epidemic diarrhea virus (PEDV), porcine bocavirus (PBoV), transmissible gastroenteritis virus (TGEV), porcine kobuvirus, porcine circovirus 2 (PCV2), porcine rotavirus (PRV), and so on (2, 4–8). Although PSV infection is most frequently asymptomatic (1), some strains have been associated with a wide variety of clinical conditions. Here, we determined the complete genome sequence of porcine sapelovirus strain YC2011, which was isolated from fecal samples in this outbreak.

Eleven pairs of oligonucleotide primers to amplify the different regions of the YC2011 genome were designed according to the published genomic sequences of PSV strains V13 and csh (AF406813.1 and HQ875059.1). The PCR products were purified, cloned into the pMD18-T vector (TaKaRa, Japan), and sequenced with an automated genome sequencer (Genetic Analyzer 3730XL; Applied Biosystems). The terminal sequences were acquired by using a kit for rapid amplification of cDNA ends (RACE) (Clontech, Japan). All fragments were sequenced in both directions in triplicate.

The complete genome of the YC2011 strain is 7,540 nucleotides (nt) in length, excluding the poly(A) tail. Analysis of the genome sequence demonstrated the presence of a 465-nt 5' untranslated region (UTR), a 111-nt 3' UTR, and an open reading frame (ORF) that maps between positions 466 and 7461 and encodes a 2,331-amino-acid polypeptide. The polypeptide is encoded by a single ORF comprising a leader protein, four structural proteins (VP4, VP3, VP2, and VP1), and seven nonstructural proteins (2A, 2B, 2C, 3A, 3B, 3C, and 3D). A phylogenetic tree based on the entire genome sequence of representative sapeloviruses indicated that YC2011 was more closely related to porcine sapelovirus than to other sapeloviruses. The genome sequence of YC2011 shared 90.2% and 84.9% at the nucleotide level identity with porcine sapelovirus strains csh and V13, respectively. Inter-

estingly, a continuous insertion of 22 nucleotides was found in the 5' UTR (at positions 1 to 22), and the insertion shows no homology with any known strains. The role of the inserted nucleotides needs further investigation. The genome data for YC2011 will facilitate future investigations of the molecular pathogenesis and evolutionary characteristics of PSV.

**Nucleotide sequence accession number.** The complete genome sequence of PSV strain YC2011 has been deposited in GenBank under accession number JX286666.

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## REFERENCES

1. Abe M, et al. 2011. A novel sapelovirus-like virus isolation from wild boar. *Virus Genes* 43:243–248.
2. Chen J, et al. 2011. Complete genome sequence of a Chinese virulent porcine epidemic diarrhea virus strain. *J. Virol.* 85:11538–11539.
3. Lan D, et al. 2011. Isolation and characterization of the first Chinese porcine sapelovirus strain. *Arch. Virol.* 156:1567–1574.
4. Li B, et al. 2012. Complete genome sequence of a highly prevalent porcine circovirus 2 isolated from piglet stool samples in China. *J. Virol.* 86:4716.
5. Li B, et al. 2012. Complete genome sequence of a novel species of porcine bocavirus, PBoV5. *J. Virol.* 86:1286–1287.
6. Li B, et al. 2012. Genome sequence of a highly prevalent porcine partetetravirus in mainland China. *J. Virol.* 86:1899.
7. Lin Y, et al. 2012. Complete genome sequence of porcine kobuvirus strain WUH1. *J. Virol.* 86:7010.
8. Sun R-Q, et al. 2012. Outbreak of porcine epidemic diarrhea in suckling piglets, China. *Emerg. Infect. Dis.* 18:161–163.
9. Tseng C-H, Tsai H-J. 2007. Sequence analysis of a duck picornavirus isolate indicates that it together with porcine enterovirus type 8 and simian picornavirus type 2 should be assigned to a new picornavirus genus. *Virus Res.* 129:104–114.

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