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Complete Genome Sequence of Porcine Kobuvirus Strain WUH1

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Porcine kobuvirus, an emerging virus, was first identified in Hungary in 2007. We report here the complete genome sequence of porcine kobuvirus strain WUH1 isolated from piglets with severe diarrhea, which will help toward understanding the molecular and evolutionary characteristics of the porcine kobuvirus.

Kobuvirus is a new genus in the family *Picornaviridae*. To date, the genus *Kobuvirus* consists of only two established species, Aichi virus and bovine kobuvirus, and the tentative species porcine kobuvirus (10). More recently, kobuviruses or koku-like viruses have also been detected in sheep, bats, and dogs (6, 11). Porcine kobuvirus was first identified in 2007 in Hungary (8). Since then, porcine kobuvirus was reported in many countries, including Japan, South Korea, Thailand, China, Brazil, Germany, and the Netherlands (2–4, 7, 14). Notably, a very high prevalence of this virus could be detected in piglets less than 6 weeks old, especially in piglets with diarrhea (13). As an emerging virus, the pathogenicity of porcine kobuvirus is unknown. Because Aichi virus and bovine kobuvirus are associated with diarrhea (1, 5), porcine kobuvirus might be an emerging virus for swine diarrhea (7).

Since December 2010, a large-scale outbreak of diarrhea, characterized by watery diarrhea, dehydration, and vomiting, with 80 to 100% morbidity and 50 to 90% mortality in suckling piglets, has been observed in swine farms in China. The causative agent has not been identified until now. Considering the possible association of porcine kobuvirus with diarrhea, we determined the complete genome sequence of porcine kobuvirus strain WUH1, which was isolated in this outbreak.

Based on the sequences of porcine kobuvirus strains S-1-HUN (HUN stands for Hungary) (EU787450) and Y-1-CHI (CHI stands for China) (GU292559.1), nine pairs of oligonucleotide primers were designed to amplify the different regions of the WUH1 genome. The PCR products were cloned into pGEM-T Easy vector (Promega) and sequenced with an ABI3730XL genome sequencer. The 5'-terminal sequences were determined by 5' rapid amplification of cDNA ends (RACE) as described previously (9). All fragments were sequenced in both directions in triplicate. The complete genome sequence of WUH1 is 8,210 nucleotides (nt) in length excluding the poly(A) tail. The predicted polyprotein encoded by a single open reading frame (7,467 nt), flanked by a 577-nt-long 5' untranslated region (5' UTR) and a 166-nt-long 3' UTR, comprise a leader protein, three structural proteins (VP0, VP3, and VP1), and seven nonstructural proteins (2A to 2C and 3A to 3D).

A phylogenetic tree based on the entire genome sequence of representative kobuviruses showed that WUH1 was more closely related to porcine kobuvirus than to other kobuviruses. The genome sequence of WUH1 shared 89.2%, 87.4%, and 89.4% identity at the nucleotide level to those of porcine kobuvirus strain S-1-HUN (9), K-30-HUN (12), and Y1-CHI (15), respectively. Interestingly, although they showed lower identity at the nucleotide level, all isolates possess higher amino acid identity (over 96.3%). Compared to previous porcine kobuvirus isolates, there was one-nucleotide deletion in its 3' UTR and one-nucleotide insertion in the 5' UTR. The role of the inserted or deleted nucleotide needs further investigation.

The availability of the genome sequence of WUH1 will not only facilitate future investigations of the epidemiology and evolution of porcine kobuvirus but also contribute to knowledge of its pathogenicity.

Nucleotide sequence accession number. The genome sequence of porcine kobuvirus strain WUH1 has been deposited in GenBank under accession number [JQ692069](http://www.ncbi.nlm.nih.gov/nuccore/JQ692069).

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REFERENCES

- Ambert-Balay K, et al. 2008. Prevalence and genetic diversity of Aichi virus strains in stool samples from community and hospitalized patients. *J. Clin. Microbiol.* 46:1252–1258.
- Barry AF, Ribeiro J, Alfieri AF, van der Poel WH, Alfieri AA. 2011. First detection of kobuvirus in farm animals in Brazil and the Netherlands. *Infect. Genet. Evol.* 11:1811–1814.
- Khamrin P, et al. 2010. Molecular detection of kobuvirus sequences in stool samples collected from healthy pigs in Japan. *Infect. Genet. Evol.* 10:950–954.
- Khamrin P, et al. 2009. Porcine kobuvirus in piglets, Thailand. *Emerg. Infect. Dis.* 15:2075–2076.
- Khamrin P, et al. 2008. Bovine kobuviruses from cattle with diarrhea. *Emerg. Infect. Dis.* 14:985–986.
- Li L, et al. 2011. Viruses in diarrhoeic dogs include novel kobuviruses and sapoviruses. *J. Gen. Virol.* 92:2534–2541.
- Park SJ, et al. 2010. Molecular detection of porcine kobuviruses in pigs in Korea and their association with diarrhea. *Arch. Virol.* 155:1803–1811.
- Reuter G, Boldizsar A, Kiss I, Pankovics P. 2008. Candidate new species of Kobuvirus in porcine hosts. *Emerg. Infect. Dis.* 14:1968–1970.
- Reuter G, Boldizsar A, Pankovics P. 2009. Complete nucleotide and amino acid sequences and genetic organization of porcine kobuvirus, a member of a new species in the genus *Kobuvirus*, family *Picornaviridae*. *Arch. Virol.* 154:101–108.
- Reuter G, Boros A, Pankovics P. 2011. Kobuviruses - a comprehensive review. *Rev. Med. Virol.* 21:32–41.
- Reuter G, Boros A, Pankovics P, Egyed L. 2010. Kobuvirus in domestic sheep, Hungary. *Emerg. Infect. Dis.* 16:869–870.
- Reuter G, Kecskemeti S, Pankovics P. 2010. Evolution of porcine kobuvirus infection, Hungary. *Emerg. Infect. Dis.* 16:696–698.
- Wang C, Lan D, Hua X. 2011. Porcine kobuvirus from pig stool specimens in Shanghai, China. *Virus Genes* 43:350–352.
- Yu JM, et al. 2009. Candidate porcine Kobuvirus, China. *Emerg. Infect. Dis.* 15:823–825.
- Yu JM, et al. 2011. Analysis and characterization of the complete genome of a member of a new species of kobuvirus associated with swine. *Arch. Virol.* 156:747–751.

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