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VIRUSES

Complete Genome Sequence of a Porcine Kobuvirus Variant Strain from Jiangxi, China

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ABSTRACT The complete genome sequence of a porcine kobuvirus (PKoV) variant strain, CH/KB-1/2014 from Jiangxi, China, with a 90-nucleotide deletion in the 2B gene, was determined and characterized. This study provides a better understanding of the molecular characteristics and evolution of PKoV in Jiangxi, China.

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Porcine kobuvirus (PkoV) is a small, round, nonenveloped, single-stranded, and positive-sense genomic RNA virus in the genus *Kobuvirus*, family *Picornaviridae* (1, 2). The genus *Kobuvirus* comprises three officially recognized species: aichivirus A, aichivirus B, and aichivirus C (1). The genome of PKoV contains a 5′ untranslated region (UTR), a leader (L) protein gene, three structural protein genes (VP0, VP3, and VP1), seven nonstructural protein genes (2A, 2B, 2C, 3A, 3B, 3C, and 3D), and a 3′ UTR (3). A high PKoV infection rate was detected in both diarrheal and asymptomatic piglets in China (4–9).

Small intestinal samples ($n = 12$) were collected from nursing diarrheal piglets in Jiangxi, China, in 2014 to screen for the presence of PKoV with the primer set PKV-S1 and PKV-R1 (10). One of the PKoV-positive samples, designated CH/KB-1/2014, served as the template for amplification of the complete genome with 10 sets of overlapping primers. RNA was extracted from the sample using the TRIzol reagent (TaKaRa, Dalian, China), according to the manufacturer's instructions. The reverse transcription-PCR (RT-PCR) was carried out based on the standard protocol, and the amplicons were purified using a gel purification kit (TaKaRa) and then cloned into pMD18-T vectors (TaKaRa) for sequencing at both directions. Rapid amplification of 5′ and 3′ cDNA ends (RACE) was performed using a SMARTer RACE 5′/3′ kit (Clontech, Beijing, China) to obtain the extreme ends of PKoV genome. The sequences obtained were assembled and annotated using the SeqMan software (Lasergene 8; DNAStar, Madison, WI).

The full-length genome of CH/KB-1/2014 determined was 8,145 nucleotides (nt) in length, excluding the poly(A) tail, and contained a single open reading frame encoding a polyprotein of 2,459 amino acids (aa), which was slightly shorter than other reference PKoV strains. The genome organization of CH/KB-1/2014 was composed of three structural proteins (VP0, VP3, and VP1) and seven nonstructural proteins (2A, 2B, 2C, 3A, 3B, 3C, and 3D). Notably, CH/KB-1/2014 had a 90-nt deletion in 2B protein region compared with the prototype strain S-1-HUN/2007 (GenBank accession no. EU787450). Phylogenetic analysis of the complete genome sequences revealed that all the Chinese PKoVs were divided into two groups, Chinese group I and Chinese group II. CH/KB-1/2014, along with other 10 Chinese PKoV strains, fell into Chinese group I. Three PKoVs, GS-1/2012/CH (GenBank accession no. KC424639), GS-2/2012/CH (GenBank accession no. KC424640), and K-4/2012/CH (GenBank accession no. KC424638), from Gansu Province in China formed Chinese group II. CH/KB-1/2014 strain had a close phylogenetic relationship with swKoV_CH441, which was isolated from Gansu as well.

A sequence analysis of the VP1 gene of PKoVs indicated that CH/KB-1/2014 shared 81.7 to 87.9% nucleotide (nt) identity and 86.2 to 96.5% amino acid (aa) similarity with other reference PKoVs, respectively. However, CH/KB-1/2014 had low nucleotide and amino acid similarities with both aichivirus A and aichivirus B. CH/KB-1/2014 only showed 59%/50.8% and 51.3%/38.9% nt/aa identities with bovine_kobuvirus (GenBank accession no. NC_004421) and Aichi_virus (GenBank accession no. AB040749), respectively.

In conclusion, the full-length genome sequence of CH/KB-1/2014 was determined and characterized. The study will help understand the epidemiology and evolution of PKoV in Jiangxi, China.

Accession number(s). The complete genome sequence of CH/KB-1/2014 was deposited in GenBank under accession number KM051987.

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