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GENOME ANNOUNCEMENT

Complete Genome Sequence of a Porcine Epidemic Diarrhea Virus Variant

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In 2011, outbreaks of viral diarrhea were observed on most swine-breeding farms in most of the provinces of China. The disease is characterized by vomiting, severe diarrhea, and a high mortality rate (82.3%) in newborn piglets. The clinical appearance was similar to that of porcine epidemic diarrhea virus (PEDV) infection. PEDVs were detected in samples (feces or small intestines) from most farms. In order to investigate whether there is a PEDV variant circulating in China, we sequenced and analyzed the complete genome of the recently identified field strain, CH/FJND-3/2011. The sequence data indicate that this PEDV variant prevails in China.

Porcine epidemic diarrhea virus (PEDV), a member of the genus *Alphacoronavirus* (family *Coronaviridae*, order *Nidovirales*), is a single-stranded, positive-sense RNA virus that causes an acute and highly contagious enteric disease characterized by severe enteritis, vomiting, and watery diarrhea in swine. To date, the complete genome sequences of Belgian strain CV777 and Chinese strain CH/S have been reported (2, 1). Since December 2010, outbreaks of viral diarrhea have been observed on most swine-breeding farms in most of the provinces of China. The clinical appearance is similar to that of PEDV infection. In order to investigate whether there is a PEDV variant circulating in China, we sequenced the complete genome of CH/FJND-3/2011.

The 5′ and 3′ ends of the genome of CH/FJND-3/2011 were confirmed by a SMARTer rapid amplification of cDNA ends (RACE) cDNA amplification kit (Clontech, Japan). The other parts were generated by 20 overlapping cDNA fragments to encompass the entire genome and were determined by genome-walking sequencing. The complete genome sequence of CH/FJND-3/2011 is 28,038 nucleotides (nt) in length [excluding the poly(A) tail]. The 5′ untranslated region (UTR) has 292 nt. The Rep gene is 20,345 nt in length, 3 nt longer than that of CH/S. The S gene contains 4,161 nt, ORF3 contains 675 nt, the E gene contains 231 nt, the M gene consists of 681 nt, the N gene consists of 1,326 nt, and the 3′ UTR is 334 nt in length.

CH/FJND-3/2011 has 738 different nt, of which 3 are in the 5′ UTR, 397 in ORF1, 254 in the S gene, 8 in ORF3, 9 in the E gene, 12 in the M gene, 48 in the N gene, and 7 in the 3′ UTR. The complete genome sequence of CH/FJND-3/2011 has 97.34% nucleotide sequence identity with that of CH/S. Among the six genes of CH/FJND-3/2011, the S gene has the lowest sequence identity (93.75%) with that of CH/S and is 9 nt longer than those of CV777 and CH/S. The PEDV S gene plays an important role in the molecular epidemiology of PEDV in the field and in the genetic variation of PEDV field isolates (3, 4, 5). The alignment in the S1 region (nt 1 to 2217) of the S gene reveals two domains exhibiting increased divergence compared to the remaining part of the sequence. The first domain is composed of the 1,100 N-terminal nucleotides. In this domain, the CH/FJND-3/2011 S gene has three insertion regions (nt 162, nt 170 to 180, and nt 413 to 415) and one deletion region (nt 470 to 475). Furthermore, the largest number of nucleotide differences is clustered in the N-terminal region of the S1 gene. The second domain is located at positions 1428 to 1914. These regions are also found in the S genes of Korean PEDV isolates (3).

The sequence data indicate that a PEDV variant prevails in China. Knowledge of its sequence will not only facilitate future investigations on the molecular pathogenesis of PEDV but also contribute to elucidation of the genetic variations of PEDV field strains in China.

Nucleotide sequence accession number. The complete genome sequence of PEDV variant CH/FJND-3/2011 was deposited in GenBank under accession no. JQ282909.

ACKNOWLEDGMENTS

This work was supported by grants from the National Natural Science Foundation of China (30901081 and 31172350), the State Key Laboratory of Veterinary Biotechnology (SKLVBP201028), the Natural Science Foundation for Distinguished Young Scholars of Heilongjiang Province (JC201118), and the Technology Research and Development Program of Harbin (2009AA6AN029).

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Received 19 December 2011 **Accepted** 22 December 2011

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doi:10.1128/JVI.07150-11