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J. Virol. 2012, 86(19):10910. DOI: 10.1128/JVI.01919-12.

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Complete Genome Sequence of Porcine Epidemic Diarrhea Virus Strain AJ1102 Isolated from a Suckling Piglet with Acute Diarrhea in China

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A diarrhea outbreak caused by porcine epidemic diarrhea virus (PEDV) has been observed in China since December 2010. We report here the complete genome sequence of PEDV strain AJ1102 isolated from a suckling piglet with acute diarrhea, which will help toward understanding the molecular and evolutionary characteristics of the epidemic PEDV in China.

Porcine epidemic diarrhea virus (PEDV), a member of the family *Coronaviridae*, is an enveloped virus with a single-stranded, positive-sense RNA genome of about 30 kb (10, 12). PEDV infection causes porcine epidemic diarrhea, an enteric disease characterized by acute watery diarrhea, dehydration, vomiting, and high mortality in nursery piglets (9, 10), resulting in severe economic losses. Outbreaks of PEDV infections have been reported in many swine-producing countries, especially in Europe and Asia (2, 5, 7, 8, 11, 13, 14).

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. Although the causative agent has not been identified until now, accumulative evidences indicate that this large-scale outbreak of diarrhea may be caused by a PEDV variant (1, 13). PEDV strain AJ1102 was isolated from a suckling piglet with acute diarrhea in 2011. Obvious cytopathic effect, characterized by cell fusion, syncytium formation, and eventual detachment, could be observed in AJ1102-infected Vero cells. To understand the diversity and the evolutionary characteristics of AJ1102, we determined its complete genomic sequence.

Based on the sequences of PEDV strains CH/FJND-3/2011 (JQ282909) and CV777 (AF353511) (1, 6), 16 pairs of oligonucleotide primers were designed to amplify the different regions of the AJ1102 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 (6). All fragments were sequenced in both directions in triplicate. The complete genome sequence of AJ1102 is 28,035 nucleotides (nt) in length, excluding the poly(A) tail. The organization of the genome of AJ1102 is similar to that of other reported PEDV genomes, with the characteristic gene order 5'-ORF1a/1b-S-ORF3-E-M-N-3' (1, 3, 4, 6). The ORF1a/1b gene is 20,345 nt in length. The sizes of the other six genes, S, ORF3, E, M, and N, are 4,158 nt, 675 nt, 231 nt, 681 nt, and 1,326 nt, respectively. Compared to CH/S (a Chinese virulent PEDV strain isolated in 1986 in China) and the classical strain CV777 (3, 6), the AJ1102 S gene has a 6-nt insertion. Interestingly, similar insertions could be observed in the S gene of three field strains (GenBank accession numbers JN980698, JQ239429, and JQ638915) which were recently isolated in China. It is possible that the 6-nt insertion can be

used as an epidemiological genetic marker of PEDV in this outbreak in China.

A phylogenetic tree based on the entire genome sequence of representative PEDVs showed that Chinese PEDVs could be divided into three subgroups. AJ1102, together with three field strains isolated in 2011 (WUH1-2011, BJ-2011-1, CH/FJND-3/2011), forms a separate branch, supporting the concept that AJ1102 is the epidemic PEDV in China. The availability of the genome sequence of AJ1102 will facilitate future investigations of the epidemiology and evolution of PEDV.

Nucleotide sequence accession number. The genome sequence of PEDV strain AJ1102 has been deposited in GenBank under the accession number JX188454.

ACKNOWLEDGMENT

This work was supported by the Key Technology R&D Programme of China to L.F.

REFERENCES

- Chen J, et al. 2012. Complete genome sequence of a porcine epidemic diarrhea virus variant. *J. Virol.* 86:3408.
- Chen J, et al. 2010. Molecular epidemiology of porcine epidemic diarrhea virus in China. *Arch. Virol.* 155:1471–1476.
- Chen J, et al. 2011. Complete genome sequence of a Chinese virulent porcine epidemic diarrhea virus strain. *J. Virol.* 85:11538–11539.
- Duarte M, Gelfi J, Lambert P, Rasschaert D, Laude H. 1993. Genome organization of porcine epidemic diarrhoea virus. *Adv. Exp. Med. Biol.* 342:55–60.
- Kim O, Chae C. 2000. In situ hybridization for the detection and localization of porcine epidemic diarrhea virus in the intestinal tissues from naturally infected piglets. *Vet. Pathol.* 37:62–67.
- Kocherhans R, Bridgen A, Ackermann M, Tobler K. 2001. Completion of the porcine epidemic diarrhoea coronavirus (PEDV) genome sequence. *Virus Genes* 23:137–144.
- Li ZL, et al. 2012. Molecular characterization and phylogenetic analysis of porcine epidemic diarrhea virus (PEDV) field strains in south China. *Virus Genes* 45:181–185.
- Martelli P, et al. 2008. Epidemic of diarrhoea caused by porcine epidemic diarrhoea virus in Italy. *Vet. Rec.* 162:307–310.

Received 22 July 2012 Accepted 23 July 2012

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doi:10.1128/JVI.01919-12

9. Pensaert MB, de Bouck P. 1978. A new coronavirus-like particle associated with diarrhea in swine. *Arch. Virol.* **58**:243–247.
10. Pensaert MB, Yeo SG. 2006. Porcine epidemic diarrhea, p 367–372. *In* Straw BE, Zimmerman JJ, D’Allaire S, Taylor DJ (ed), *Disease of swine*. Blackwell Publishing Professional, Ames, IA.
11. Puranaveja S, et al. 2009. Chinese-like strain of porcine epidemic diarrhea virus, Thailand. *Emerg. Infect. Dis.* **15**:1112–1115.
12. Song D, Park B. 2012. Porcine epidemic diarrhoea virus: a comprehensive review of molecular epidemiology, diagnosis, and vaccines. *Virus Genes* **44**:167–175.
13. Sun RQ, et al. 2012. Outbreak of porcine epidemic diarrhea in suckling piglets, China. *Emerg. Infect. Dis.* **18**:161–163.
14. Van Reeth K, Pensaert M. 1994. Prevalence of infections with enzootic respiratory and enteric viruses in feeder pigs entering fattening herds. *Vet. Rec.* **135**:594–597.