

Complete Genome Sequence of Novel Porcine Epidemic Diarrhea Virus Strain GD-1 in China

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Porcine epidemic diarrhea virus (PEDV) infection, which causes acute diarrhea and dehydration in suckling piglets, has become a serious problem for the swine industry of China in recent years. In this study, a virulent PEDV strain, GD-1, was obtained from fecal samples from suckling piglets that suffered from severe diarrhea in 2011 in Guangdong, China. Here we describe the complete genome sequence of strain GD-1, which may be helpful in further understanding the molecular epidemiology and genetic diversity of PEDV field isolates in China.

Porcine epidemic diarrhea virus (PEDV) is an enveloped, positive-sense, single-stranded RNA virus that belongs to the family of *Coronaviridae*. PEDV infection causes acute diarrhea, dehydration, and even death in suckling piglets (10). Since 2010, PEDV had re-emerged in vaccinated swine herds and caused great economic losses to the swine industry in China (3, 5, 7). Here we report the complete genome sequence of a PEDV isolate, GD-1, that was recently obtained from suckling piglets.

The 3'-terminal sequence of the viral genome was confirmed by using a kit for rapid amplification of cDNA ends (RACE kit; TaKaRa). The other parts of the genome were generated by 28 overlapping cDNA fragments and were determined by primer-walking sequencing. DNASTar version 7.1 and ClustalX were applied to the genomic analysis. The complete genome sequence of GD-1 was 28,035 nucleotides (nt) in length [excluding the poly(A) tail], with 5' (292-nt) and 3' (334-nt) ends including untranslated regions. The genomic organization of GD-1 was similar to that of other reported PEDVs, with the characteristic gene order of 5'-replicase (1a/1b)-S-open reading frame 3 (ORF3)-E-M-N-3' (1, 2, 4, 8, 9). The Rep-encoding gene was 20,345 nt in length and contained two large ORFs (ORF1a and ORF1b) that encoded two large nonstructural precursor polyproteins, replicase 1a (nt 293 to 12,601) and replicase 1b (nt 12,601 to 20,637). There were five coding regions downstream of the replicase gene, which translated four structural proteins, S (nt 20,634 to 24,791), E (nt 25,446 to 25,676), M (nt 25,684 to 26,364), and N (nt 26,376 to 27,701). ORF3, which encoded the only accessory protein, was located at nt 24,791 to 25,465.

The complete genome sequence of GD-1 shared 98.3%, 98.1%, 97.6%, and 96.8% nucleotide sequence identity with those of GD-B, CH/FJND-3/2011, DR13, and CV777, respectively (2, 6, 8, 9). Comparative genomic analysis of the S gene revealed that GD-1 had 94.1% to 98.0% nucleotide sequence identity with those of the reference strains reported previously. Compared to DR13 (a Korean virulent PEDV strain isolated in 1999 in South Korea) and classical strain CV777 (6, 9), there was a 3-nt deletion (nt 24,220 to 24,222) found in the S gene of GD-1. Intriguingly, similar deletions could be observed in the S gene of PEDV strains GD-A and AJ1102 (1, 4), which were recently isolated in China. This deletion could be responsible for the unique character of the novel PEDV variants that have circulated in China.

Phylogenetic analysis of the complete genome revealed that Chinese PEDVs could be divided into three subgroups, among which GD-1 and other recent isolates, such as GD-A and AJ1102, belong to the same subgroup, which was distant from the CV777 vaccine strain and other foreign PEDV strains. The data indicate that GD-1 is a novel PEDV variant. The genome sequence analysis of GD-1 will promote further investigations of the molecular epidemiology and genetic diversity of PEDV field isolates in China.

Nucleotide sequence accession number. The complete genome sequence of PEDV strain GD-1 has been deposited in GenBank under accession no. [JX647847](https://www.ncbi.nlm.nih.gov/nuccore/JX647847).

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