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.

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.

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