Porcine epidemic diarrhea virus (PEDV), a member of the family Coronavirus, was first reported in 1978. The virus is an enveloped, single-stranded, positive-sense RNA virus and causes diarrhea in swine of all ages, with high mortality in piglets (3,7). In recent years, acute outbreaks of epizootic diarrhea, clinically similar to porcine epidemic diarrhea (PED), occurred in most of the provinces in China. Attempts to isolate PEDV from diseased pigs failed, but genomic sequences of PEDV were consistently detected from feces of pigs by reverse transcription-PCR (RT-PCR). Here we report a complete genome sequence of PEDV which is apparently different from those of early PEDV circulated in Chinese swine herds.

In our study, 18 sets of primers to amplify the different regions of the ZJCZ4 genome were designed based on the sequences of PEDV strain CV777. The PCR products were purified, cloned into the pMD18-T vector, and subsequently sequenced. The Lasergene sequence analysis software package (DNASTAR Inc., Madison, WI) was used to compile and edit the sequence data. The complete genome sequence of Chinese strain CH/FJND-3/2011 has been reported (1). In order to provide more information on the molecular basis of PEDV isolates in China, we sequenced the complete genome of ZJCZ4.

In our study, 18 sets of primers to amplify the different regions of the ZJCZ4 genome were designed based on the sequences of PEDV strain CV777. The PCR products were purified, cloned into the pMD18-T vector, and subsequently sequenced. The Lasergene sequence analysis software package (DNASTAR Inc., Madison, WI) was used to compile and edit the sequence data. The complete genome of ZJCZ4 strain is 28,038 nucleotides (nt) in length, excluding the poly(A) tail. Its genome organization is similar to those of other reference PEDV isolates. The 5′ untranslated region (UTR) has 292 nt (nt 1 to 292). The ORF1ab gene is 20,345 nt (nt 293 to 20637) in length. The S gene contains 4,160 nt (nt 20634 to 20793), the M gene consists of 681 nt (nt 20794 to 21474), and the N gene consists of 1,326 nt (nt 21475 to 22800). The 3′ UTR is 334 nt (nt 27705 to 28038) in length.

Although it is known that PEDV has only one serotype at present, the genome of PEDV is well documented, and both the S gene and the ORF3 gene have high levels of genetic diversity (4, 6, 8). The complete genome of ZJCZ4 exhibited 98.1%, 97.3%, and 96.9% sequence identity with CH/S, CV777, and attenuated strain DR13, respectively (2, 5). Among the genes, the S gene of ZJCZ4 encoding the amino acid sequence shows 93.2% to 97.0% homology, which is a lower level of homology than those found in other strains. It is important to note that a discontinuous 5-amino-acid insertion (59QGVN62 and 140N) exists in the S1 domain of the S protein of ZJCZ4 compared with CH/S, CV777, and attenuated strain DR13. At the same time, there are two continuity amino acid deletions (162GK162 or 164NI164). In addition, comparing the amino acids encoded by the ORF3 gene of ZJCZ4 with those of CV777, CH/S, and CH/FJND-3/2011, the homologies are between 43.3% and ~96.0%.

It is hoped that the genome data of ZJCZ4 will facilitate future investigations of the evolutionary characteristics and molecular pathogenesis of PEDV.

**Nucleotide sequence accession number.** The genome sequence of PEDV strain ZJCZ4 has been deposited in GenBank under accession number JX524137.

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**REFERENCES**