Transmissible gastroenteritis virus strain AYU was isolated in Shanghai. The complete genome has a length of 28,582 bp and contains seven open reading frames. Sequence analysis suggested that Shanghai strain AYU and U.S. strain Purdue P115 are derived from a common ancestor, as they have 99.6% similarity at the nucleotide level.

Transmissible gastroenteritis (TGE), a highly contagious disease of pigs, is caused by the TGE virus (TGEV) and is characterized by vomiting, watery diarrhea, and dehydration (3, 4). TGEV, a member of Alphacoronavirus genus (family Coronaviridae, order Nidovirales), is a single-stranded, positive-sense RNA virus (2). It has eight functional genes that code for four structural proteins (spike protein S, outer membrane protein Sm, membrane protein M, and nucleocapsid protein N) and four nonstructural genes (replicase polyprotein PPla/PP1ab, nsp3a, nsp3b, and nsp7) (5).

Here we report the complete genomic sequence of a novel strain of TGEV, Shanghai strain AYU, which was isolated from stool samples from a piglet with diarrhea symptoms in Shanghai. The stool samples were tested by reverse transcription-PCR. To amplify different regions of the viral genome, 17 pairs of primers were designed by using the genomes of TGEV strains TS and WH-1 as the template (reference for these two viruses). By using these primers, 17 TGEV fragments were successfully amplified with an overlap between every two adjacent fragments. These PCR products were purified, cloned into the pMD18-T vector (TaKaRa Bio, Tokyo, Japan), and sequenced by the methods of Shanghai Jieli Technologies Co., Ltd. Sequence splicing was performed using Bioline (SKLVBF201209). Sequence alignment was analyzed using ClustalX 2.1. A phylogenetic tree was constructed using MEGA4.

We found that the complete genome of strain AYU is 28,582 bp in length, excluding the poly(A) nucleotides. The G+C content of the whole genome is 39.1%. The genomic structure of the AYU strain is similar to that of the reported TGEV genomes that have the following segment order: 5′-ORF1a-ORF1b-S-ORF3a-ORF3b-E-M-N-ORF7-3′ (1). The 5′-end untranslated region (UTR) has 317 nucleotides (nt), and the 3′-end UTR contains 277 nt. There is a conserved sequence (CS), CUAAAC, between every two adjacent genes. Interestingly, the sixth nucleotide, C, in the CS of ORF3b is changed to U (CUAAAU). A small reading frame (AUGAAUAUC) consisting of three codons lies in the 5′ end, stretching from nt 117 to nt 125.

In comparison with TGEV strains Purdue, Purdue P115, PUR46-MAD, Miller M6, Miller M60, TS, and porcine respiratory coronavirus ISU-1, the nucleotide sequence of strain AYU has 99.1%, 99.2%, 99.6%, 98.3%, 98.2%, 98.5%, and 97.8% homology, respectively. Phylogenetic analysis indicated that strain AYU and TGEV strains Purdue, PUR46-MAD, and Purdue P115 are in the same subgroup (2).

**Nucleotide sequence accession number.** The complete genome sequence of TGEV strain AYU was deposited in GenBank under accession no. HM776941.

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**REFERENCES**


