

Complete Genome Sequence of the Genotype 4 Hepatitis E Virus Strain Prevalent in Swine in Jiangsu Province, China, Reveals a Close Relationship with That from the Human Population in This Area

Hua Wang,^a Yilin He,^b Quan Shen,^a Xiaochun Wang,^a Shixing Yang,^c Li Cui,^d Liping Ren,^e Guangming Sun,^f Xiuguo Hua,^d Shihe Shao,^a and Wen Zhang^a

Department of Microbiology, School of Medical Science and Laboratory Medicine, Jiangsu University, Zhenjiang, People's Republic of China^a; Division of Acute Infectious Disease Prevention and Control, Taizhou Center for Disease Control and Prevention, Taizhou, People's Republic of China^b; Translational Medicine Center, Shanghai Pulmonary Hospital, Tongji University School of Medicine, Shanghai, People's Republic of China^c; Group of Zoonotic Diseases and Comparative Medicine, School of Agriculture and Biology, Shanghai JiaoTong University, Shanghai, People's Republic of China^d; School of Life Sciences, Fuyang Teachers College, Fuyang, People's Republic of China^e; and Department of Clinical Laboratory, Fourth Affiliated Hospital of Jiangsu University, Zhenjiang, People's Republic of China^f

Hepatitis E virus (HEV) is a zoonotic pathogen of which several species of animal were reported as reservoirs. Swine stands out as the major reservoir for HEV infection in humans, as suggested by the close genetic relationship of swine and human viruses. In a previous study, we sequenced the complete genome of a human genotype 4 HEV strain (HM439284) that is prevalent in Jiangsu Province, China. Here we report the complete genome of one genotype 4 HEV strain which is prevalent in swine herds in Jiangsu Province. Phylogenetic analysis indicated that the swine HEV strain in the present study has high sequence homology (>92%) with the genotype 4 HEV strains prevalent in the human population of Jiangsu Province. These results suggested that the genotype 4 HEV strain in the present study is involved in cross-species transmission between swine and humans in this area.

Hepatitis E virus (HEV) is a nonenveloped virus with a positive-stranded RNA genome of approximately 7.2 kb (13). HEV has been a major cause of sporadic hepatitis in Asia and Africa (1, 3, 11, 16). HEV and antibodies to HEV have been found in a wide variety of animals (6, 14, 15, 18). It has been hypothesized that zoonosis is involved in the transmission of HEV. Swine stands out as a reservoir for HEV infection in humans (2, 5, 9, 10, 17, 19). HEV isolates were divided into four distinct genotypes. Genotypes 1 and 2 have been identified exclusively in humans, while genotypes 3 and 4 have been found in humans and animals (4, 12, 20).

In a previous report, we sequenced the complete genome of a human genotype 4 HEV strain (HM439284) that is prevalent in Jiangsu Province, China (19). Phylogenetic analysis revealed that this strain closely clustered with some swine HEV strains from other provinces in China. In order to elucidate the relationship of HEVs prevalent in swine and humans in Jiangsu Province, 96 swine fecal samples were collected from general pigs aged 6 to 12 weeks in Zhenjiang City, Jiangsu Province, and HEV RNA was detected (19). Results indicated that seven samples were positive for HEV RNA. Sequence analysis based on the 348-bp partial capsid genes indicated that they all belonged to genotype 4, with >97% sequence identity.

Here we report the complete genome sequence of the virus from one HEV RNA-positive fecal sample, which was determined using 17 sets of primers designed according to HEV strains (DQ450072, EF570133, HM439284, and AB369690). The 3'-end fragment was determined by reverse transcription (RT)-PCR using 3' rapid amplification of cDNA ends, and the 5'-end fragment was determined using a forward primer designed according to the 5'-most end sequences of genotype 4 HEV strains and a reverse primer designed according to the sequence we determined. RT-PCR-amplified DNA fragments of the expected sizes were sequenced in a DNA analyzer (Applied Biosystems 3730 DNA Analyzer; Invitrogen) and assembled using Phred software (8).

The complete genome comprises 7,225 nucleotides (nt), excluding the 3' poly(A) tail. Open reading frame 1 (ORF1) begins at nt 27 and ends at nt 5135 (5,109 nt in length), ORF2 (nt 5141 to 7156) comprises 2,016 nt and encodes 671 amino acids (aa), and ORF3 (nt 5160 to 5504) comprises 345 nt and encodes 114 aa. A phylogenetic tree obtained for the complete genome of this strain and other genotype 4 strains available in GenBank indicates that it belongs to subtype 4b and closely clusters with AB369690 and HM439284, showing 94.6% and 92.6% sequence identity with them, respectively. HM439284 is one representative genotype 4 strain prevalent in humans in Jiangsu Province, China (19). AB369690 was isolated from a Japanese patient who had traveled to eastern China before the onset of acute hepatitis E (7). These results suggest that the HEV strain in the present study was involved in cross-species transmission between swine and humans in Jiangsu Province, China.

Nucleotide sequence accession number. The virus genome sequence described here has been deposited in the GenBank database under the strain name HEV-ZJ1 and assigned accession no. [JQ993308](https://doi.org/10.1128/JQ993308).

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Address correspondence to Wen Zhang, z0216wen@yahoo.com.

H.W. and Y.H. contributed equally to this work.

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