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

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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.

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.

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