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GENOME ANNOUNCEMENT

Complete Genome Sequence of a Novel Type of Human Parechovirus Strain Reveals Natural Recombination Events

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Human parechoviruses (HPeVs) are a species in the *Parechovirus* genus of the *Picornaviridae* family. We report a complete genome sequence of a novel HPeV strain, CH-ZJ1, that was found in an infant with gastroenteritis in Zhenjiang City, China. The complete genome consists of 7,298 nucleotides (nt), excluding the 3′ poly(A) tail; the open reading frame is mapped between nucleotide positions 654 and 7211 and encodes a 2,185-amino acid (aa) polyprotein. The phylogenetic tree obtained for the complete genome of this HPeV strain and the other HpeV strains available in GenBank indicated that CH-ZJ1 is intervenient between HpeV type 4 (HpeV4) and HpeV5. Phylogenetic analysis based on the 3D and VP1 genes reveals two incongruent trees. Recombination detection indicated that CH-ZJ1 might be a recombinant which was produced by more than one genomic recombination event that occurred among HPeV1, HPeV4, and HPeV3 strains.

Human parechoviruses (HPeVs) are a species in the *Parechovirus* genus of the *Picornaviridae* family, which are nonenveloped, positive-sense RNA viruses with icosahedral capsids (2). They have a genome of around 7,000 to 8,000 nucleotides (nt) encoding one polyprotein, which is cleaved by virus proteases to give the structural and nonstructural (2A to -C and 3A to -D) proteins. The open reading frame (ORF) is flanked by untranslated regions (UTRs) that are involved in RNA translation and replication (8). The *Human parechovirus* species is subdivided into 16 different types (1, 3, 4, 6, 16). HPeVs are frequent infectious agents, and although they usually cause mild gastroenteritis and respiratory disease in young children, more serious cases, such as flaccid paralysis, encephalitis, and myocarditis, have also been reported, particularly associated with HPeV type 3 (HPeV3) infection (5, 12–15).

We report an HPeV strain, CH-ZJ1, found in an infant in Zhenjiang City, China, in 2011. The stool sample was collected from a male infant with gastroenteritis and was determined to be positive for enterovirus by the reverse transcription-PCR (RT-PCR) method using primers as described elsewhere (10). Complete genome sequencing was performed by using 9 sets of primers designed according to the HPeV strains available in GenBank. The 3′-end fragment was determined by RT-PCR using 3′ rapid amplification of cDNA ends (RACE), the 5′-end fragment was determined using the forward primer designed according to the 5′-most sequences of HPeV strains in GenBank, and the reverse primer was designed according to the sequence we determined. RT-PCR-amplified DNA fragments of the expected sizes were sequenced with a DNA analyzer (Applied Biosystems 3730 DNA analyzer; Invitrogen) and assembled using Phred software.

The complete genome comprises 7,298 nt, excluding the 3′ poly(A) tail. The ORF begins at nt 654, ends at nt 7211 (6,558 nt in length), and encodes 2,185 amino acids (aa). When we performed a BLAST search, CH-ZJ1 showed the highest sequence homology (82%) with two HPeV strains (AF055846 and AM235750), of which AF055846 belongs to HpeV5 (11) while AM235750 belongs to HpeV4 (1). The phylogenetic tree obtained for the complete genome of this HPeV strain and the other HpeV strains available in GenBank indicated that CH-ZJ1 is intervenient between HpeV4 and HpeV5. In order to further identify this HPeV strain, two phylogenetic trees, based on the VP1 gene and the 3D gene regions, were constructed. VP1 sequence analysis shows that CH-ZJ1 shares highest sequence identity (75%) with DQ315670 and belongs to HpeV4, while 3D sequence analysis indicates that CH-ZJ1 shows the highest sequence homology (>92%) with AB668033, which is an HpeV3 strain. The incongruence between the VP1 and 3D trees is indicative of recombination during HPeV evolution. To look at this further, RDP3.0 software was used to analyze the relationship between the other 51 complete HPeV genomes and CH-ZJ1. The results indicated that CH-ZJ1 might be a recombinant which was produced by more than one genomic recombination event that occurred among HPeV1, HPeV4, and HPeV3 strains, which is a relatively common phenomenon in RNA viruses (7, 9, 17, 18).

Nucleotide sequence accession number. The virus genome sequence was deposited in GenBank with the strain name CH-ZJ1 under GenBank accession no. JX050181.

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