

# Complete Genome Sequence of a Novel Human Parechovirus

Chunmei Wang,<sup>a,b</sup> Tongling Shan,<sup>b</sup> Hao Zheng,<sup>b</sup> Wu Tong,<sup>b</sup> Fangzhou Chen,<sup>a</sup> Han Hu,<sup>a</sup> Qigai He,<sup>a</sup> and Guangzhi Tong<sup>b</sup>

State Key Laboratory of Agricultural Microbiology, Division of Animal Infectious Disease, Huazhong Agricultural University, Wuhan, Hubei, China,<sup>a</sup> and Department of Swine Infectious Disease, Shanghai Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Shanghai, China<sup>b</sup>

**Human parechoviruses (HPEVs) belonging to the family *Picornaviridae* are widely spread pathogens among young children. We report the complete genome sequence of a novel HPEV isolated from the stool sample of a hospitalized child with diarrhea in China. The genome consists of 7,305 nucleotides, excluding the 3' poly(A) tail, and has an open reading frame that maps between nucleotide positions 675 and 7217 and encodes a 2,180-amino-acid polyprotein. The genome sequence of the virus was sufficiently distinct from the 8 known HPEV types. Phylogenetic analysis based on the complete genome indicated that the HPEV strain represents a new genotype.**

Human parechoviruses (HPEVs) are small, nonenveloped RNA viruses with icosahedral capsids that are members of the recently identified genus *Parechovirus*, belonging to the family *Picornaviridae* (3). Genetic analyses have shown that HPEVs are classified into at least eight genotypes on the basis of the sequence similarity of their capsid protein (HPEV1 to -8) (1, 2, 4, 6, 7, 10, 13). HPEV1 and HPEV2, previously known as the enteroviruses echo22 and echo23 isolated in 1956, were reclassified as members of a new genus, *Parechovirus*, in the family *Picornaviridae* in 1999 (11, 15). At present, at least 8 genotypes of HPEVs isolated from young children were reported (1, 2, 4, 6, 7, 10, 11, 13). Other new sequences of HPEV genotypes continue to be characterized (<http://www.picornaviridae.com/parechovirus/hpev/hpev.htm>). HPEVs are widely spread infectious pathogens which usually cause mild gastroenteritis, respiratory disease, flaccid paralysis, encephalitis, and myocarditis in young children (5, 8, 9, 12, 16). HPEVs were also detected in monkeys with diarrhea in 2010 (14). HPEV strain SH401 was accidentally isolated from the stool sample of a child in China in 2009. To understand the diversity and evolutionary characteristics of SH401, the complete genome was cloned and sequenced.

Based on the complete genome sequences of HPEV1 available in GenBank (GenBank accession no. L02971, FM178558, GQ183022, GQ183035, FJ840477, and GQ183034), 8 pairs of primers were designed to amplify the different regions of the SH401 genome. The 3'-end fragment was determined by reverse transcription (RT)-PCR using 3' rapid amplification of cDNA ends (3' RACE). The 5'-end fragment was determined using a forward primer designed according to the most 5'-end sequences of HPEV1 to -8 and a reverse primer designed according to the sequence we determined. The PCR products were cloned into pMD18-T vector (TaKaRa, Dalian, China), sequenced (Applied Biosystems 3730 DNA analyzer), and assembled using DNASTar.

The nearly complete genome of SH401 consists of 7,305 nucleotides (nt), excluding the 3' poly(A) tail, which contains a 674-nt region of the 5' untranslated region (UTR), an open reading frame (ORF) encoding a polyprotein precursor of 2,179 amino acids, and a 3' UTR of 88 nt. The nearly complete genome of SH401 showed a lower nucleotide identity (77.7 to 82.8%) with the complete genomes of HPEV1 to -8 available in GenBank (HPEV1, FJ840477; HPEV2, NC001897; HPEV3, AB084913; HPEV4, AM235750; HPEV5, AM235749; HPEV6, AB252582; HPEV7, EU556224; and HPEV8, EU716175) and was sufficiently distinct from the 8 known HPEV types. Phylogenetic analysis obtained for

the complete genome of HPEV strain SH401 and the other 24 HPEVs and related genomes available in GenBank showed that SH401 was separate from the known HPEV types and formed a novel branch, which suggests that this strain may represent a novel genotype of HPEVs.

**Nucleotide sequence accession number.** The virus genome sequence described here has been deposited in the GenBank database under the strain name SH-1 and assigned the accession no. JX441355.

## ACKNOWLEDGMENTS

This work was supported by the Ministry of Agriculture of China (grant CARS-36) and the National Natural Science Foundation of China (grants 31201953 and 31201915).

## REFERENCES

1. Abed Y, Boivin G. 2005. Molecular characterization of a Canadian human parechovirus (HPEV)-3 isolate and its relationship to other HPEVs. *J. Med. Virol.* 77:566–570.
2. Baumgarte S, et al. 2008. Prevalence, types, and RNA concentrations of human parechoviruses, including a sixth parechovirus type, in stool samples from patients with acute enteritis. *J. Clin. Microbiol.* 46:242–248.
3. Bedard KM, Semler BL. 2004. Regulation of picornavirus gene expression. *Microbes Infect.* 6:702–713.
4. Benschop KS, et al. 2006. Fourth human parechovirus serotype. *Emerg. Infect. Dis.* 12:1572–1575.
5. Boivin G, Abed Y, Boucher FD. 2005. Human parechovirus 3 and neonatal infections. *Emerg. Infect. Dis.* 11:103–105.
6. Drexler JF, et al. 2009. Novel human parechovirus from Brazil. *Emerg. Infect. Dis.* 15:310–313.
7. Ghazi F, Hughes PJ, Hyypia T, Stanway G. 1998. Molecular analysis of human parechovirus type 2 (formerly echovirus 23). *J. Gen. Virol.* 79(Pt 11):2641–2650.
8. Harvala H, et al. 2009. Specific association of human parechovirus type 3 with sepsis and fever in young infants, as identified by direct typing of cerebrospinal fluid samples. *J. Infect. Dis.* 199:1753–1760.
9. Harvala H, et al. 2008. Epidemiology and clinical associations of human parechovirus respiratory infections. *J. Clin. Microbiol.* 46:3446–3453.
10. Ito M, Yamashita T, Tsuzuki H, Takeda N, Sakae K. 2004. Isolation

Received 13 August 2012 Accepted 13 August 2012

Address correspondence to Qigai He, heqigai@yahoo.com.

Copyright © 2012, American Society for Microbiology. All Rights Reserved.

doi:10.1128/JVI.02099-12

- and identification of a novel human parechovirus. *J. Gen. Virol.* **85**: 391–398.
11. Joki-Korpela P, Hyypia T. 2001. Parechoviruses, a novel group of human picornaviruses. *Ann. Med.* **33**:466–471.
  12. Levorson RE, Jantusch BA, Wiedermann BL, Spiegel HM, Campos JM. 2009. Human parechovirus-3 infection: emerging pathogen in neonatal sepsis. *Pediatr. Infect. Dis. J.* **28**:545–547.
  13. Li L, et al. 2009. Genomic characterization of novel human parechovirus type. *Emerg. Infect. Dis.* **15**:288–291.
  14. Shan TL, et al. 2010. Human parechovirus infections in monkeys with diarrhea, China. *Emerg. Infect. Dis.* **16**:1168–1169.
  15. Stanway G, Hyypia T. 1999. Parechoviruses. *J. Virol.* **73**:5249–5254.
  16. Verboon-Maciolet MA, et al. 2008. Human parechovirus causes encephalitis with white matter injury in neonates. *Ann. Neurol.* **64**:266–273.