Complete Genome Sequence of a Novel Human Parechovirus

Chunmei Wang, Tongling Shan, Hao Zheng, Wu Tong, Fangzhou Chen, Han Hu, Qigai He and Guangzhi Tong
State Key Laboratory of Agricultural Microbiology, Division of Animal Infectious Disease, Huazhong Agricultural University, Wuhan, Hubei, China, and Department of Swine Infectious Disease, Shanghai Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Shanghai, China

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.

REFERENCES