Complete Genome Sequence of Human Enterovirus Strain 71 (EV71/Taipei/3118/2011), Isolated from a Patient in Taiwan

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This full-length genome sequence of human enterovirus strain 71 (EV71/Taipei/3118/2011) was isolated from a clinical patient in Taiwan in 2011. According to the phylogenetic analysis, the complete genome sequence in this study is part of the subgenotype C4.

H uman enterovirus strain 71 (EV71) has been determined to be part of the Picornaviridae, which cause mild and self-limiting hand, foot, and mouth disease (HFMD) in young children and infants under the age of 5 years. EV71 has caused epidemic HFMD predominantly in the Asia-Pacific region, such as Taiwan, China, Japan, Malaysia, Singapore, and even Australia. This virus has been associated with more severe cases such as aseptic meningitis, encephalitis, or even death (1). The genome of EV71 is about 7.4 kb, consisting of a 5'-untranslated region (UTR), P1 structure protein region, P2 and P3 functional protein regions, and a 3'-untranslated region containing a long poly-A tail. This virus can be further classified into three main genotypes (A, B, and C) and 11 subgenotypes (A1 to C5) (2). Understanding of the genotypes and subgenotypes played a fundamental role in the development of novel strategies for the prevention and treatment of the diseases associated with EV71.

In this study, we obtained a human EV71 (EV71/Taipei/3118/2011) that was isolated at the Taiwan Centers for Disease Control (Taiwan CDC) in 2011. The clinical isolate was collected from a patient with a clinical diagnosis of a severe case of HFMD in Taiwan, and we are grateful for technical support from C.H. Huang from the Institute of Biochemical and Biomedical Engineering, National Taipei University of Technology, and C.I. Lee from the Department of Life Science, National Chung Cheng University.

R eferences