

# Full Genome Sequence of a Novel Coxsackievirus B5 Strain Isolated from Neurological Hand, Foot, and Mouth Disease Patients in China

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**Coxsackievirus B5 (CVB5) belongs to the human enterovirus B species within the family *Picornaviridae*. We report the complete genome sequence of a novel CVB5 strain, CVB5/SD/09, that is associated with neurological hand, foot, and mouth disease in China. The complete genome consists of 7,399 nucleotides, excluding the 3' poly(A) tail, and has an open reading frame that maps between nucleotide positions 744 and 7301 and encodes a 2,185-amino-acid polyprotein. Phylogenetic analysis based on different genome region regions reveals that CVB5/SD/09 belongs to a novel CVB5 lineage, and similarity plotting and bootscanning analysis based on the whole genome of CVB5 in the present study and those available in GenBank indicate that the genome of CVB5/SD/09 has a mosaic-like structure, suggesting that recombination between different CVB5 strains may occur.**

The coxsackieviruses are subdivided into two serogroups, A and B, comprising 23 (1 to 22 and 24) and 6 (1 to 6) serotypes, respectively. Among the coxsackie B viruses, coxsackievirus B5 (CVB5) is one of the most predominant serotypes in humans; it is a common cause of viral myocarditis and may be detected in more than 25% of sporadic acute-onset cases of dilated cardiomyopathy. CVB5 is also frequently associated with sporadic cases of neurological diseases and epidemics of meningitis (1, 8, 13).

During our enterovirus screening of throat swabs and serum specimens from children with hand, foot, and mouth disease (HFMD) as previously described (3), we unexpectedly found that 12.7% of the HFMD patients tested had a novel CVB5 infection and most of these patients showed certain neurological manifestations. Further, phylogenetic analysis based on the VP1 sequences of these CVB5 strains showed that they represent a novel lineage of CVB5 in the phylogenetic tree (3).

Here we report the complete genome of this virus, CVB5/SD/09, obtained from one throat swab specimen by using 8 sets of overlapping primers. Genome extremities were acquired with a rapid amplification of cDNA ends kit (Invitrogen). PCR products of the expected sizes were sequenced with an Applied Biosystems 3730 Sanger-based DNA analyzer, and contigs with high-quality trace files were assembled by using vNTI (Invitrogen).

The complete genome of this virus consists of 7,301 nucleotides (nt), excluding the 3' poly(A) tail. Analysis of the sequence demonstrated the presence of a 743-nt 5' untranslated region (UTR), a 98-nt 3' UTR, and an open reading frame that maps between positions 744 and 7301 and encodes a 2,185-amino-acid polyprotein. The genome organization of this virus is identical to that of previously published CVB5 strains (5, 9). Over the whole genome, the virus shows the highest nucleic acid sequence homology, 89.4%, with CVB5/CC10 strains (GenBank accession no. JN580070.1) (2) and shows 98.2% protein sequence identity with strain CVB5/CC10. In order to identify the serotype/genotype and species that this Chinese sequence belongs to, phylogenetic trees based on different genome regions, such as the VP1 gene and the 3C and 3D gene regions, respectively, were constructed (10). The results indicated that though CVB5/SD/09 is closest to CVB5/CC10 on the basis of the phylogenetic tree of the P1 gene, on the basis of the phylogenetic tree of the 3C gene, it is closer to a Korean strain, CVB5/2000/CSF/KOR (GenBank accession no.

AY875692.1), and in the 3D region, it is closer to an Australian echovirus 4 strain, AUS250G (GenBank accession no. FJ172447.1). Further, similarity plotting and bootscanning analysis (6) based on genomes available in the GenBank database, i.e., those of CVB5/CC10/10 (GenBank accession no. JN580070.1), COXB5/Henan/2010 (GenBank accession no. HQ998851.1), CVB5/Faulkner (GenBank accession no. AF114383.1), CVB5/2000/CSF/KOR (GenBank accession no. AY875692.1), 1954/85/UK (GenBank accession no. X67706.1), Echo4/AUS250G (GenBank accession no. FJ172447.1), and Echo30/Zhejiang/03 (GenBank accession no. DQ246620.1), indicate that the genome of CVB5/SD/09 shows a mosaic-like structure, suggesting that recombination between different CVB5 strains may occur, which is a relatively common phenomenon among enteroviruses (2, 4, 7, 11, 12).

**Nucleotide sequence accession number.** The genome sequence reported here was deposited in the NCBI GenBank database under accession number JX276378.

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