Coxsackievirus B3 (CVB3) is one of six serotypes of group B coxsackieviruses that belong to the enterovirus family Picornaviridae (8). It is associated with a wide spectrum of human illness that ranges in severity from subclinical infection to rapidly fatal disease, with symptoms as diverse as acute myocarditis, aseptic meningitis, and pancreatitis, among others (1–3, 6, 7, 9–13).

In addition to humans, Sichuan snub-nosed monkeys can be infected and killed by CVB3. Such infections have been confirmed through microbiological detection and immunofluorescence staining (5). This study is the first report of a Sichuan snub-nosed monkey dying from a virus (5). This novel virus strain was isolated from the deceased monkey and was designated SSM-CVB3. Macaques could also be infected with SSM-CVB3 experimentally and showed serious hepatic and renal damage besides myocarditis (4). However, little is known about the biological properties of SSM-CVB3.

The 5' and 3' ends of the SSM-CVB3 genome were confirmed using rapid amplification of cDNA ends (RACE) kits (TaKaRa, Japan), and other sections were generated using 6 overlapping cDNA fragments to encompass the entire genome. The genome sequence was determined through primer walking. The complete genome sequence of SSM-CVB3 was 7,397 nucleotides (nt) in length, excluding the poly(A) tract. Following a 5' untranslated region (UTR) of 742 nt, a large open reading frame (ORF) was found, which consisted of 6,555 nt encoding a potential polyprotein precursor that was 2,185 amino acids in length, excluding the poly(A) tail.

A phylogenetic tree based on the entire genome sequence of representative CVB3 isolates showed that SSM-CVB3 was more closely related to human CVB3 than to other coxsackieviruses. Over the entire SSM-CVB3 genome, the highest nucleotide sequence homology (93.5%) was shared with CVB3-GZ803 (GenBank accession no. FJ357838). Additionally, there was 83.6%, 97.2%, and 98% nucleotide identity in the 5'-UTR, ORF, and 3'-UTR, respectively, of CVB3-GZ803. However, the genome sequence of SSM-CVB3 also shared 93.5%, 80.8%, and 86.1% identity with the 5'-UTR, ORF, and 3'-UTR, respectively, of CVB3-Fuyang19 (GenBank accession no. FJ000001). These results suggest that recombination may have occurred between different CVB3s and SSM-CVB3 may be a recombination product of CVB3-Fuyang19 and CVB3-GZ803. This phenomenon has been known to occur in other coxsackieviruses (14). Compared with the genome of the standard strain CVB3-Nancy (GenBank nucleotide no. M3854), SSM-CVB3 showed only 78.5%, 80.6%, and 85.1% sequence identity in the 5'-UTR, ORF, and 3'-UTR, respectively. Compared with the other CVB3 isolates deposited in GenBank, there were three nucleotide deletions at 508 (T), 509 (G), and 521 (A) of the ORF, which caused an amino acid deletion at position 172 in the VP2 region of the capsid protein, and the corresponding amino acid sequences were changed from LGRTG to WS-DW. The impact of the deleted nucleotides requires further investigation. This genome data for SSM-CVB3 will facilitate future investigations of the evolutionary characteristics and molecular pathogenesis of this virus.

Nucleotide sequence accession number. The genome sequence of SSM-CVB3 has been deposited in GenBank under accession number GU109481.

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Complete Genome Sequence of a Coxsackievirus B3 Isolated from a Sichuan Snub-Nosed Monkey

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Coxsackievirus B3 (CVB3) is an enterovirus in the family Picornaviridae that is significant to human health, being associated with myocarditis, aseptic meningitis, and pancreatitis, among other conditions. In addition to humans, Sichuan snub-nosed monkeys can be infected and killed by CVB3. Here, we report the first complete genome sequence of a novel coxsackievirus B3 strain, SSM-CVB3, which was isolated from a deceased Sichuan snub-nosed monkey with severe myocarditis. Our findings may aid in understanding the evolutionary characteristics and molecular pathogenesis of this virus.