



# Genomic characterization and phylogenetic analysis of Chinese sacbrood virus isolated from Loess Plateau, China

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**ABSTRACT.** The complete genomic RNA of the Chinese sacbrood virus (CSBV) strain, which infects the honeybees in the Loess plateau, was sequenced and analyzed. The CSBV-SX strain contains 8705 nucleotides, which includes a single large open reading frame (99-8681 nucleotides) encoding 2860 amino acids. A novel efficient identification method was used to investigate the samples infected by CSBV. The putative amino acid sequence alignment analysis showed that, except for some normal well characterized domains such as RNA helicase, RNA protease, and RNA-dependent RNA polymerase domains, a calicivirus coat protein domain was identified at amino acids 493-564. Phylogenetic analysis indicated that CSBV-SX was closely related to CSBV-BJ, and this result was supported by nucleotide multiple sequence alignment and protein multiple

sequence alignment analysis results. These differences in the CSBV-SX strain may be related to virus adaptation to the xerothermic, low relative humidity, and strong ultraviolet radiation conditions in the Loess Plateau.

**Key words:** *Apis cerana*; Chinese sacbrood virus; Genome sequence; Honeybee