

Genome sequence determination and analysis of YM2019, an Equine herpesvirus 1 Chinese strain

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August 3, 2020

Abstract

Equine herpesvirus 1 (EHV-1) is prevalent in China, and this has had negative consequences for horse breeding. However, this is no date about the genome sequence and genetic characterization of the strains from China. This study aimed to determine the character of the strain that was isolated in China and to serve as a key reference for the development of specific assays for diagnosis and epidemiological research. EHV-1 YM2019 was isolated from the lung tissue of an aborted horse fetus in Xinjiang, China, and the YM2019 genome was sequenced and analysed. The amino acid sequences of 76 EHV-1, EHV-3, EHV-4, EHV-8 and EHV-9 proteins were compared and analysed, and the amino acid sequences of the ORF30 and ORF42 proteins were analysed through bioinformatics. The genome sequence (GenBank accession number: MT063054) is 150,267 bp in length. It shared the highest similarity with Ab4 strain (92.26% nucleotide identity), which was isolated in the United Kingdom and belonged to the same monophyletic group. Amino acid analysis showed that the YM2019 strain is of the ORF30 A2254/N752 genotype. Multiple sequence alignments of the 76 proteins indicated that the ORF42 protein had the highest sequence identity and the ORF68 protein had the lowest identity. This could facilitate the tracking of EHV-1 in the outbreak situation and allow for the differentiation of the outbreak virus from the other EHV strains. In conclusions, this study provides the genome sequence for EHV-1 YM2019 in China and the strain shared high nucleotide homology with Ab4 strain. In addition, Analysis suggests that EHV-8 and EHV-9 are more closely related to EHV-1 than to EHV-3 and EHV-4, the prevalence of EHV-8 and EHV-9 in China and the potential threat to horse breeding deserve further investigation.

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