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Analysis of codon usage bias of Crimean-Congo Hemorrhagic fever virus and its adaptation to hosts

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Abstract

Crimean-Congo hemorrhagic fever virus (CCHFV) is a negative-sense, single stranded RNA virus with a three-segmented genome that belongs to the genus *Nairovirus* within the family *Bunyaviridae*. CCHFV uses *Hyalomma* ticks as a vector to infect humans with a wide range of clinical signs, from asymptomatic to Zika-like syndrome. Despite significant progress in genomic analyses, the influences of viral relationships with different hosts on overall viral fitness, survival, and evading the host's immune systems remain unknown. To better understand the evolutionary characteristics of CCHFV, we performed a comprehensive analysis of the codon usage pattern in 179 CCHFV strains by calculating the relative synonymous codon usage (RSCU), effective number of codons (ENC), codon adaptation index (CAI), and other indicators. The results indicate that the codon usage bias of CCHFV is relatively low. Several lines of evidence support the hypothesis that a translation selection factor is shaping codon usage pattern in this virus. A correspondence analysis (CA) showed that other factors, such as base composition, aromaticity, and hydrophobicity may also be involved in shaping the codon usage pattern of CCHFV. Additionally, the results from a comparative analysis of RSCU between CCHFV and its hosts suggest that CCHFV

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