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Abstract

The First Complete Genome Sequences of Hepatitis C Virus Subtype 2b from Latin America: Molecular Characterization and Phylogeographic Analysis †

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Abstract: The hepatitis C virus (HCV) has remarkable genetic diversity and exists as eight genotypes (1 to 8) with distinct geographic distributions. No complete genome sequence of HCV subtype 2b (HCV-2b) is available from Latin American countries, and the factors underlying its emergence and spread within the continent remain unknown. The present study was conducted to determine the first full-length genomic sequences of HCV-2b isolates from Latin America and reconstruct the spatial and temporal diversification of this subtype in Brazil. Nearly complete HCV-2b genomes isolated from two Brazilian patients were obtained by direct sequencing of long PCR fragments and analyzed together with reference sequences using the Bayesian coalescent and phylogeographic framework approaches. The two HCV-2b genomes were 9318 nucleotides (nt) in length (nt 37–9354). Interestingly, the long RT-PCR technique was able to detect the co-circulation of viral variants that contained an in-frame deletion of 2022 nt, encompassing E1, E2, and p7 proteins. Spatiotemporal reconstruction analyses suggest that HCV-2b had a single introduction in Brazil during the early 1980s, displaying an epidemic history characterized by a low and virtually constant population size to date. These results coincide with epidemiological data in Brazil and may explain the low national prevalence of this subtype.

Keywords: hepatitis C virus; HCV subtypes; Latin America; RT-PCR; full-length genome; Bayesian framework; phylogeography