Complete Genome Sequence of Hepatitis B Virus Genotype E, the First Molecular Characterization from an Imported Case in Mexico

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Hepatitis B virus infection is currently a global public health problem. Here, we present the first characterization and complete genome sequence of a strain belonging to genotype E in Mexico, obtained from a foreign carrier with chronic infection.

In a retrospective study on molecular characterization of different genotypes in a Mexican population (not published), we identified one sample belonging to HBV/E, which was obtained from an African traveler of temporary residence in 2011. Initially, DNA was extracted from plasma, and a fragment (429 bp) of the HBV S gene was amplified by PCR to perform direct Sanger sequencing. The identity of the partial sequence was established using the NCBI BankIt tool. Phylogenetic analysis at the full-genome scale using 118 HBV/E sequences revealed that the identified strain is closely related to isolates from South Africa and Japan and belongs to the recently described Southwest African lineage (7). Additionally, the nonsynonymous A1762T and G1764A mutations in the basal core promoter region were found in the characterized strain. These nucleotide changes have been associated with increased viral replication levels (2) and proposed as predictive biomarkers for hepatocellular carcinoma development (8).

Public policies for handling infected patients and disease control include treatment and prevention schedules, which are related to viral factors. For that reason, the surveillance of circulating HBV genotypes in the Mexican population and the screening of molecular markers associated with disease progression and prognosis will be helpful to understand the HBV molecular epidemiology and its relationship with the pattern of disease spread.

Nucleotide sequence accession number. The complete genome sequence of hepatitis B virus strain InDRE 1109 has been deposited in GenBank under the accession number KT192626.

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REFERENCES