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GENOME ANNOUNCEMENT

Complete Genome Sequence of Central Africa Human T-Cell Lymphotropic Virus Subtype 1b

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Human T-lymphotropic virus type 1 (HTLV-1) has a global spread, and it is estimated that around 20 million persons are infected. Seven major genetic subtypes are recognized. However, there are complete genomes only from the HTLV-1a (cosmopolitan) and HTLV-1c (Melanesian) subtypes. Here, the first full-length genome of an HTLV-1b strain, a subtype so far restricted to Central African countries, is revealed. The genome size of HTLV-1b SF26, a strain isolated in Brazil, was determined to be 8,267 bp. The genomic analysis showed that all characteristic regions and genes of a prototypic HTLV-1 virus are conserved. This genome can provide information for further studies on the evolutionary history and pathogenic potential of this human oncovirus.

Human T-cell lymphotropic virus type 1 (HTLV-1) is a member of the *Deltaretrovirus* genus of the *Retroviridae* family. It was the first oncogenic human retrovirus discovered, in 1980 (5). This human virus originated in Africa through zoonotic infections from lineages of simian T-lymphotropic virus type 1 (4). HTLV-1 is the etiological agent of adult T-cell leukemia/lymphoma (ATL), tropical spastic paraparesis/HTLV-1-associated myelopathy (TSP/HAM), and other inflammatory diseases.

HTLV-1 has a remarkably low genetic variability and, based on the nucleotide diversity of its long terminal repeat (LTR) region, is segregated into seven major genetic subtypes (a to g) (6), some of them with restricted geographic distribution. HTLV-1b, the so called Central Africa subtype, has so far been identified in Gabon, Congo, and Cameroon. This HTLV-1 subtype was first identified and characterized (1984) in an African patient with ATL. The analysis revealed that, despite its polymorphisms when compared with the cosmopolitan and widespread subtype HTLV-1a, HTLV-1b also showed the ability to transform T-lymphocytes (3).

Due to the prevalence rates of HTLV infection, blood donor screening is mandatory in several countries, including in Brazil since the 1990s. In a clinical laboratory diagnosis routine in Rio de Janeiro, Brazil, samples were screened for HTLV by immunoassays. The HTLV strains from the reactive samples were typed by using an in-house PCR and sequencing of the HTLV *tax* region. The *tax* sequence of the SF26 sample showed high identity with the rare HTLV-1b subtype, the Central Africa subtype. So far, there is not a complete genome sequence of this HTLV subtype.

Here, the entire genome sequence of HTLV-1b has been determined by using nested PCR with degenerate HTLV primers and a PCR-based genome-walking strategy using DNA extracted from whole peripheral blood. The complete genome of HTLV SF26 was determined to be 8,267 bp in length. Phylogenetic analysis based on the LTR region revealed that it belongs to the Central African subtype 1b cluster. The HTLV-1b GC content is 53%, contrasting with the GC content of another human retrovirus, human immunodeficiency virus type 1 (42%). The overall percentages of sequence identity of HTLV-1b SF26 with HTLV-1a L36905 (1) and HTLV-1c L02534 (2) are 96% and 92%, respectively. The genomic structure of HTLV-1b SF26 provirus had a similar gene content, and the genes were syntenic to those of other HTLV-1 subtypes; their products included the structural, enzymatic, regulatory, and accessory proteins, all flanked by LTRs. A nuclear basic leucine zipper (b-ZIP) gene that is encoded in the antisense strand of HTLV-1a was also found in the complementary strand of HTLV-1b SF26.

Nucleotide sequence accession number. The complete genome sequence of HTLV-1b SF26 was deposited in GenBank under accession number JX507077.

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