HTLV-1 ORIGIN, EPIDEMIOLOGY AND MOLECULAR CHARACTERIZATION AT BAHIA STATE.

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Human T cell leukemia virus type 1 (HTLV-1) is associated with a few clinical status, like a neurological syndrome named tropical spastic paraparesis/HTLV-associated myelopathy (TSP/HAM) and the Adult T-cell Leukemia/Lymphoma (ATL). This viral infection has prevalence rates of more than 30% in Southern Japan, in the Caribbean Basin and some African regions, and to a lesser extent in Latin America. In Brazil, whose population is a mixture of Amerindians, Africans and Europeans, about 2.5 million of individuals are HTLV-1 infected. One of the greatest prevalence into general population is registered in Salvador city, Bahia state. The aim of this report is to investigate the origin, epidemiology and genotypic characterization of HTLV-1 at Bahia State. So that, nested PCR and sequencing, for viral genomic data, were performed on the HTLV-1 positive samples, identified in this serologic screening, originated from five different geographic regions at Bahia State. Bioinformatics tools, like phylogenetic analyses will be performed using the new viral generated sequences. Since the distribution of the virus is considered to be related to the anthropological background and past human movements, a host polymorphism characterization will be also carried out. So far, only three viral sequences were generated while others 20 samples are at sequencing stage. We thank to CHTLV (Escola Bahiana de Medicina e Saúde Pública), which is the health unit where the infected individuals are followed, and the Instituto de Ciências da Saúde (Universidade Federal da Bahia) for all the academic support.

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