



HTLV-1 Origin, Epidemiology and Molecular Characterization at Bahia State.

Dos Santos, J. L. A.¹; Araújo, T. H. A.²; Santos, L. A.^{3,4} Galvão-Castro, B.²; Mota-Miranda, A. C. A.¹;

¹ Universidade Federal da Bahia, Instituto de Ciências da Saúde, Salvador, Bahia, Brasil; ² Escola Bahiana de Medicina e Saúde Pública, Salvador, Bahia, Brasil. ³ Escola Bahiana de Medicina e Saúde Pública, Salvador, Bahia, Brasil; ⁴ Laboratório de Imunoparasitologia, Centro de Pesquisa Gonçalo Moniz, Fundação Oswaldo Cruz, Salvador, Bahia, Brasil

Introduction - Human T-type virus-cell leukemia 1 (HTLV-1) is associated with a few clinical conditions, such as a neurological syndrome called tropical spastic paraparesis / HTLV-associated myelopathy (HAM / TSP) and T cell Adult leukemia / lymphoma (ATL). This viral infection has prevalence rates of over 30% in southern Japan, the Caribbean and Africa, and to a lesser extent in Latin America. In Brazil, whose population is a mixture of Amerindians, Africans and Europeans, about 2.5 million people are infected with HTLV-1, with the highest prevalence in the city of Salvador, Bahia. **Objective** - The aim of this report is to investigate the origin, epidemiology and genotypic characterization of HTLV-1 at Bahia State. **Material and Methods** - 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. **Results** and **Discussion** - Fourteen new viral sequences were generated in this study and other sixty two already submitted to GenBank, from HTLV-1 infection at Bahia State, were analyzed using the Bioinformatics tools. All new LTR sequences were subtyped as Cosmopolita Subtype and Transcontinental subgroup. The phylogenetic analysis using only Brazilian HTLV-1 LTR sequences, suggests different introductions of HTLV-1 in the Bahia State, possible through Salvador Metropolitan Region. Estimated mean value of the HTLV-1 evolutionary rate was 1.3874E-4 substitution/site/year (95% HPD: 5.10006E-7, 3.3916E-4). **Conclusions** – We can conclude that this preliminary study suggest a possible route of introduction of HTLV-1 at Bahia state, however, a great number of sequences from different mesoregions must be necessary to confirm these findings.

We Acknowledgements to CHTLV (Bahia School of Medicine 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.

Palavras-chave: Origin, HTLV-1 e Bahia.

