

TITLE: MOLECULAR CHARACTERIZATION OF GLYCOPROTEIN 46 (gp46) GENE OF *HUMAN T LYMPHOTROPIC VIRUS TYPE 1* (HTLV-1) IN ENDEMIC REGION IN THE BRAZILIAN AMAZON

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ABSTRACT:

Human T lymphotropic virus type 1 (HTLV-1) affects about 2-5 million people worldwide, is associated to degenerative and infectious diseases. Because envelope glycoproteins are highly conserved among HTLV-1 isolates nucleotide substitutions in the gene region encoding these proteins can influence both viral infectivity and virus replication. The gp46 has functional domains already associated with inhibition of syncytium formation, cell-cell transmission and antibody production. Therefore, the main objective of the study was to determine the genetic stability of the HTLV-1 gp46 region in the metropolitan region of Belém. We used samples from patients served by NMT/UFGA from January 2010 to December 2015. Our results showed That 223 samples were confirmed for HTLV-1, with 62.5% of women and 37.5% of men, with 45.2 years of mean age; 30% asymptomatic and 70% presenting diverse symptomatology, with predominance of painful or sensory, dysautonomic and motor inability. The molecular characterization revealed a 100% frequency of the HTLV-1aA (Cosmopolitan subtype, Transcontinental subgroup) between investigated samples and a very low and very characteristic evolutionary rate of this coding region (aA - 1.83.10⁻⁴ mutations per site per year). We identified 3 mutations (N93D, G72S, S192P) with frequency above 19% between the samples. Only the G72S mutation is present in a previously identified functional domain (53-75aa). Such change, along with N93D were as frequent among individuals. When we correlated with the presence of symptoms, 33.3% were asymptomatic, and 66.6% had a symptom/disease or disease signal associated with the presence of HTLV-1, a significant difference with $p = 0, 0091$. Samples that did not show any aminoacid changes, 68.4% were asymptomatic and 31.5% had some sign/symptom or disease associated with the virus. We concluded that there was no variation of the HTLV-1 subtype in the metropolitan area of Belém, only the viral subtype aA was detected, circulating during the investigation period, with an economic evolution rate between HTLV-1 positive samples very low, revealing high genetic stability of the coding region for gp46, with a diversity of symptoms predominant in adults, female, low income and educational level; with predominance of HAM/TSP among individuals. However, it is suggested that new studies are conducted to expand understanding of the molecular diversity of this protein, especially in its modeling, after all we believe the potential of this coding region with its stability to be a candidate vaccine against HTLV-1.

Key words: HTLV-1, symptom, gp46, stability.

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