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**STUDY ON THE GENETIC POLYMORPHISM OF THE HTLV- 1 U3-LTR REGION ISOLATED FROM ASYMPTOMATIC AND SYMPTOMATIC (TSP/HAM) INFECTED INDIVIDUALS FROM SALVADOR-BRAZIL.**

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The mechanism of HTLV-1 proviral sequence transcription depends of the Tax viral protein that trans-acts the three 21 bp repeat sequences on the U3-LTR proviral region. Deletions in this region result in lower trans-acting transcriptional activation. We sequenced these regions of the HTLV-1 isolates obtained from 88 patients from Salvador-Bahia: 52 asymptomatic (asym) and 36 symptomatic (TSP/HAM) (sym). The ATK1 prototype was used as standard sequence. It was detected a -632C>T mutation that were more frequent in the asymptomatic group (19,2%; p=0.024). In addition, when we split the asym patients by age (up and down 45), the -631C insertion was detected only in younger asym patients (25%, p=0.017). When we correlated the phylogenetic analysis with the punctual mutations, we have found that all new isolates into the Latin American cluster had the -632 and -452 mutations. Besides, the -595, -471 and -631 mutations was found out of Latin American cluster. The mutations detected in HTLV-1 U3-LTR region may have impact in the viral transcription and TSP/HAM development.

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