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SEROPREVALENCE AND MOLECULAR EPIDEMIOLOGY STUDY OF THE HTLV-1 ISOLATES FROM THREE VILLAGES OF THE SÃO FRANCISCO VALLEY, BAHIA, BRAZIL.

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Bahia state has sociodemographic characteristics similar to some African places, and Salvador, the capital city of Bahia, has the highest prevalence of HTLV-1 (1.74%) in Brazil. To investigate the prevalence of HTLV-1 in the neighborhoods of Salvador, and the molecular epidemiology of this virus, we studied 249 individuals from three villages of São Francisco Valley (104 from Taquarendi, 81 from Junco and 64 from Alegre). The HTLV-1 seroprevalences were 3.85%, 1.23% and 1.56% in these villages, respectively. These results demonstrate that the high prevalence of this virus can not only exist in Salvador, but also in other localities of Bahia state. Phylogenetic analysis of the LTR region from five positive samples showed that all the isolates belong to the A subgroup of HTLV-1a. Only one isolate clustered inside the main Latin American cluster. The other ones grouped in a new Latin American cluster, with the majority of the isolates are from Salvador. We obtained in this cluster one isolate from South Africa, suggesting that this virus could be probably brought from South Africa to Bahia state during the slave trade. Phylogenetic analysis confirmed the horizontal transmission among two individuals in Taquarendi. The presence of Bahia sequences in different clusters in the phylogenetic tree suggests multiple introductions of HTLV-1 in our population. Furthermore, the comment of the low level of diversity in the LTR region suggests a recent introduction of this virus lineage in Bahia state. In order to establish the origin of the isolates, the B^A-globin haplotypes will be analyzing.