

P-20

MOLECULAR EPIDEMIOLOGY STUDY OF THE HTLV-1 ISOLATES FROM A BLOOD DONOR COHORT TO INVESTIGATE THE ORIGIN OF THIS VIRUS IN BRAZIL.

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Objective: It has been difficult to explain why all HTLV-1 isolates in Salvador, a city in northeast Brazil, are of the transcontinental (A) subgroup of the Cosmopolitan (a) subtype, since according to historical data the vast majority of slaves brought to Brazil (through Salvador) came for western Africa, where only the western African subgroup (C) has been found. To shed more light on this subject we conducted a phylogenetic analysis of 23 isolates from blood donors.

Methods: DNA was extracted and submitted to a nested PCR for amplification of the entire long terminal repeat (LTR) region. The PCR products were purified and sequenced on a automated sequencer. Neighbor-joining and maximum likelihood phylogenetic analysis were performed.

Results: All isolates belonged to the transcontinental subgroup (A) of the Cosmopolitan subtype, and clustered in two Latin American clusters. For the first time we showed isolates from southern Africa clustering in both Latin American clusters. One of our new isolates diverged before the larger Latin American cluster, due to a duplication of a 12 base pair long fragment, a finding that has not been previously described.

Conclusions: These findings further support the hypothesis that HTLV-1 isolates circulating in Salvador were introduced by individuals from southern Africa. It is unclear the reason for the absence of western African isolates in our city, a finding that contrasts with historical data. The 12-bp long duplication in one of the isolates has no obvious clinical or biological implication as of yet.

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