

Poster presentation

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Phylogeny of HTLV-I isolates from groups with risk antecedents for human retrovirus infections in Argentina

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Background

HTLV-I infection shows an ethnic-geographic restriction being naturally endemic among aborigines from the Northwest. At-risk populations are also infected with HTLV-I. Cosmopolitan subtype (a) including subgroups A, B and C has been described previously in our country.

Materials and methods

35 HTLV-I samples were analyzed including 3 MSM, 6 FSW (1 from Peru and 3 from Salta), 13 BD (1 Japanese descendent), 5 HAM/TSP (3 from Peru) and 8 HIV positive individuals. The rest were from Buenos Aires (BA) city. LTR regions were amplified by n-PCR. Neighbor-joining and Parsimony trees were performed using Phylip package program.

Results

32 samples were identified as the Cosmopolitan subtype a, subgroup A. One HAM/TSP aA sample from BA was more distantly related to the rest of the aA samples. Furthermore, 2 samples (1 Peruvian HAM/TSP and 1 Japanese BD from BA) clustered with the previously described Br4, Br9 (from Brazil) and B13.Peru.

Conclusion

The majority of the circulating HTLV-I strains in Argentina belonged to the subgroup A. The finding of these 2 samples, clustering separately from any other known HTLV-I subgroup, agrees with previous suggestions of a possible divergent subgroup within subtype a.