

Poster presentation

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P20-11. Subtype B/BF recombinants multiple infection in patients with dual-transmission risks by means of Heteroduplex assay

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Background

The HIV-1 epidemics in Argentina presents a higher prevalence of subtype B in men having sex with men and of BF recombinant forms in injecting drug users and heterosexuals. Since little is known about HIV-1 dual infections in a population with double transmission risk, the aim of this study was to analyze the frequency of multiple infections in HIV (+) individuals from this at-risk group, by implementing the Heteroduplex assay (HAD) as a screening methodology.

Methods

Informed consents and sequential blood samples were obtained from 10 HIV+ patients (P) from Buenos Aires. Partial gag and pol proviral coding regions were amplified by Nested-PCR and the amplicons were used to perform the HDA as described by Powell et al. (2008). Dual infections were confirmed by cloning and sequencing. Phylogenetic and bootscanning analysis were performed by Neighbor-joining and Simplot. CD4 cell count, viral load (VL) and antiretroviral (ARV) treatment were evaluated.

Results

Gag and pol PCR products were obtained from 6 out of 10 patients. Heteroduplex formation was observed for 3 of them. Gag analysis showed that in 2 patients (P1, P2) sequences from samples 1 and 2 clustered with B and F references, respectively. In both cases, BF recombinant sequences were detected. In P3, sequences from samples 1

and 2 clustered with B references, but the genetic divergence between the two groups of sequences suggested that intrasubtype dual infection may have occurred. pol sequences analysis showed that all of them clustered together. No significant changes were observed in CD4 and viral load values.

Conclusion

The HDA allowed us to identify the coexistence of different sequences in this population. Further, it was possible to detect subtype B/BF recombinant multiple infections. These results suggest that multiple infections could be driving viral evolution in our country, possibly complicating vaccine strategies.