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HIV-1 pol gene diversity and antiretroviral drug resistance mutations in Itanhaém city, Brazil

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Background

Itanhaém city has shown a pivotal role in the epidemiology of HIV-1 due to its geographic location near the city of Sao Paulo, the epicenter of Brazilian AIDS epidemic, and between the southern region where there is a high level of Brazilian subtype C and Santos city where were identified two HIV-1 circulating recombinants forms classified as CRF28_BF and CRF29_BF. In this work, we describe the viral genetic diversity and drug resistance mutations in different subtypes of random samples.

Methods

We studied 23 samples from 255 HIV-1 infected patients enrolled in the Itanhaém AIDS program. Samples were collected in 2006, 2007 and 2008 after informed consent. DNA was extracted from buffy coat and used as target to amplify 1200 bp of pol gene (protease and reverse transcriptase) of HIV-1. PCR products were sequenced, phylogenetic analyses were performed by neighbor-joining, and recombination was evaluated by Bootscan.

Summary of results

Pol gene sequencing of the samples revealed that 15 strains belonged to subtype B, two to subtype F, two to subtype C, and four were B/F recombinants. Recombinants break-points in three samples were the same identified in CRF28_BF and CRF29_BF; one sample was unique recombinant forms B/F. Subtype B and the recombinant B/F were identified with two drug resistance mutations in common, the M184V which confers high level resistance to lamivudine (3TC), and the K103N which confers high level resistance to delavirdine (DLV), efavirenz (EFV) and nevirapine (NVP).

Conclusion

Our results suggest that the same amino acids are emerging in subtype B and recombinants B/F due to the selective pressure of antiretrovirals.