SESSIONS OF THE COMPLETE GENOME OF RECOMBINANT HIV-1 STRAINS CIRCULATING IN BAHIA-BRAZIL
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Introduction: Numerous efforts have been made in the combat against HIV since the beginning of the AIDS epidemic, but a vaccine to prevent infection or drugs that can eliminate the virus are still not available. The large genetic variability of HIV-1 is reflected in the emergence of viral isolates with different biological behaviors and this is the main obstacle to the efficient functioning of the human immune system and development of universal vaccines and therapies. Previous studies from our group have indicated a wide range of HIV-1 genotype prevalence in Bahia and a recombinant strain not yet identified, having the same gene pattern in approximately 6% of the infected population. Objectives: The objective of this study is to perform the sequencing of the complete genome of recombinant strains of HIV-1 circulating in Bahia to investigate the existence of a new circulating recombinant form (CRF) of HIV-1 in Bahia. Thus, the sequencing of the total genome of samples previously characterized as BF recombinants in viral genes gag and pol will be held. Material and methods: These DNA sequences will be subjected to phylogenetic and recombination analysis through bioinformatics tools. Discussion and results: We expect to identify new HIV-1 CRF suggested by previous studies developed by our research group. Then define the source and the period of recombination event occurrence that gave rise to this CRF, and identification of preferred genomic regions for the occurrence of genetic recombination ("hotspots"); identification of molecular features that can be related to the greater dispersion and adaptation of recombinant B/F compared with the pure form of the subtype. Conclusion: This study may contribute to a better understanding of the evolutionary properties of HIV, to AIDS of local epidemic surveillance and the appropriate choice of control measures.

Key words: sequencing; HIV-1; recombinants.