Identification of Recombinant HIV-1 Strains Circulating in Bahia-Brazil

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INTRODUCTION: Numerous efforts have been made in the combat against HIV. 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. **MATERIALS AND METHODS:** The blood sample are collected, the DNA are extracted and then a Nested PCR are performed for four overlapping regions of viral integrated genome. These regions are submitted to sequencing and then through bioinformatics tools make phylogenetic and recombination analysis. **DISCUSSION AND RESULTS**: A successful standardization was performed for three of the four regions. Until the time we identified four recombinants in *gag* that are possible BF recombinants. The standardization of the fourth region is currently being held and the sample collection will be intensified to identify a new HIV-1 CRF suggested by previous studies developed by our research group. After that, the origin and the occurrence period of recombination event as well as the identification of preferred genomic regions for the occurrence of genetic recombination ("hotspots") will be identified. **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.
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