

Phylogenetic Characterization and Therapeutic Resistance Profile of Human Immunodeficiency Virus Type 1 (HIV-1) Circulating in Populations of Northeastern Brazil.

Melo, É. L. S.^{1,2}, Monteiro, J. P.²

¹ Programa de Pós-graduação Multicêntrico em Bioquímica e Biologia Molecular, Departamento de Biofunção, UFBA, Salvador, Brasil.

² Núcleo de Bioinformática em Vigilância Molecular, Epidemiológica e Clínica de Agentes Infecciosos, Instituto de Ciências da Saúde, UFBA, Salvador, Brasil.

Introduction: By the end of 2011, 34.0 million people were living with HIV worldwide. The latest records show that Brazil has 656,701 cases of AIDS and that despite the drop in the incidence rate in the Southeast, there was an increase in other regions of Brazil. The high genetic variability of HIV is a major obstacle both to infection control by the host immune system and to the development of efficient drugs and vaccines.

Objective: This study aims to characterize the profile of mutations associated with resistance to different classes of antiretroviral drugs and the phylogenetic relationship of circulating HIV-1 strains in Northeastern Brazil.

Material and Methods: Genomic sequences of HIV previously published in GenBank are being collected and organized at a local database. Bioinformatics tools are being used to interpret the data. Associations with epidemiological and clinical characteristics will be investigated through statistical analysis.

Results and Discussion: To date approximately 200 nucleotide sequences of the *pol* and *env* genes of HIV-1 circulating in Northeast Brazil (Bahia, Pernambuco, Piauí, Alagoas, Maranhão) were obtained. The Los Alamos - Sequence Locator Tool were used to identify the genomic position and the REGA HIV Subtyping Tool were used to identify the sequence subtype. Moreover, a database with socio-epidemiological patient information were created and categorized.

Conclusions: This study may contribute to the generation of relevant information for better understanding of the evolutionary properties of the virus to AIDS local epidemic surveillance and the appropriate choice of control measures.

Keywords: HIV-1, resistance, mutations.