PHYLOGENETIC CHARACTERIZATION AND THERAPEUTIC RESISTANCE PROFILE OF HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1) CIRCULATING IN POPULATIONS OF NORTHEASTERN BRAZIL.

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By the end of 2011, there were in the world about 34.0 million people living with HIV. The high genetic variability of HIV is a major obstacle both to control infection by the host immune system and for the development of efficient drugs and vaccines. The monitoring of the dispersion of the different genotypes as well as the emergence of new virulent HIV-1 is of great importance for the control of epidemic and to assist in the further understanding of the many shortcomings concerning the biology of HIV-1. Furthermore, the identification of mutations in the viral genome that are related to antiretroviral drugs resistance and therapeutic failure may contribute for proper handling and life improvement of patients. The aim of this study is to characterize the profile of mutations associated with resistance to different classes of antiretroviral drugs and the phylogenetic relationship of HIV-1 strains circulating in the Northeast of Brazil. Therefore, genomic sequences of HIV previously published in GenBank will be collected, organized in a local database and analyzed by computer programs. We expected to identify associated mutations with therapeutic resistance; to characterization the epidemiological profile and its relationship to genetic subtypes of HIV-1 circulating in the region the Northeast; to identify the phylogenetic and phylogeographic relationship of HIV-1 isolates in the Northeast region of the country; In general, it is expected that the results obtained in this study contribute to a better understanding of the mechanisms involved in the prevalence of the resistance process mutations and the different therapeutic antiretroviral class. Associations with epidemiological and clinical characteristics will be investigated through statistical analysis. This study may contribute to the generation of relevant information for better understanding of the evolutionary properties of the virus, to the AIDS epidemic site surveillance and the appropriate choice of control measures.

Keywords: HIV-1, resistance, mutations.