GENOTYPIC AND FENOTYPIC CHARACTERIZATION OF HIV-1 ISOLATES CIRCULATING IN BAHIA: CLINICAL AND EPIDEMIOLOGICAL IMPLICATIONS

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Introduction: After 30 years of epidemic, HIV infection is still a disease with no cure and no effective vaccine. Nevertheless, the Highly Active Antiretroviral Therapy (HAART) significantly improved the quality and life expectancy of infected patients. However, due to HIV intense genetic variability and high rate of mutation, resistant variants are often emerging, which decreases clinical management options. Thus, new classes of drugs are constantly being developed and the more recent fusion inhibitors prevent viral entry into the cell. The administration of these drugs requires viral tropism determination and monitoring mutations that may lead to resistance. Objectives: To characterize the genotypic and phenotypic variability of HIV circulating in Bahia and the prevalence of fusion inhibitors resistance mutations. Materials and Methods: Viral envelope genomic sequences of HIV-1 isolates circulating in Bahia obtained between 2002 and 2012 were collected and analyzed via bioinformatics tools to determine genetic subtype, viral tropism and presence of mutations associated with resistance to fusion inhibitors. Patients clinical and epidemiological data were obtained from consultation of medical records and questionnaires answered by patients. Results and conclusions: It was observed prevalence of subtype B, a higher prevalence of infection among heterosexual individuals, with significant numbers of infected women and prevalent age group of 31-50 years, coinciding with the Brazilian Ministry of Health data. As for viral tropism, which is related to clinical outcome, most strains had R5 phenotype prediction. Therefore, most of the patients is candidate to treatment with fusion inhibitors, CCR5 antagonists, such as Maraviroc and Vicriviroc. Despite of this, it was found a significative prevalence of mutations in this population, such as A316T and I323V, that are associated with resistance to these drugs. This study demonstrates the importance of the molecular characterization of HIV-1 strains in infected patients for adequate therapeutic management and for epidemic surveillance.

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