

Genetic diversity and drug resistance profiles in HIV type 1- and HIV type 2-infected patients from Cape Verde Islands.

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Abstract

Our aim was to characterize for the first time the genetic diversity of HIV in Cape Verde Islands as well as the drug resistance profiles in treated and untreated patients. Blood specimens were collected from 41 HIV-1 and 14 HIV-2 patients living in Santiago Island. Half of the patients were on antiretroviral treatment (ART). Pol and env gene sequences were obtained using in-house methods. Phylogenetic analysis was used for viral subtyping and the Stanford Algorithm was used for resistance genotyping. For HIV-1, the amplification of pol and env was possible in 27 patients (66%). HIV-1 patients were infected with subtypes G (13, 48%), B (2, 7%), F1 (2, 7%), and CRF02_AG (2, 7%), and complex recombinant forms including a new C/G variant (n=8, 30%). Drug resistance mutations were detected in the PR and RT of three (10%) treated patients. M41L and K103N transmitted drug resistance mutations were found in 2 of 17 (12%) untreated patients. All 14 HIV-2 isolates belonged to group A. The origin of 12 strains was impossible to determine whereas two strains were closely related to the historic ROD strain. In conclusion, in Cape Verde there is a long-standing HIV-2 epidemic rooted in ROD-like strains and a more recent epidemic of unknown origin. The HIV-1 epidemic is caused by multiple subtypes and complex recombinant forms. Drug resistance HIV-1 strains are present at moderate levels in both treated and untreated patients. Close surveillance in these two populations is crucial to prevent further transmission of drug-resistant strains.

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