

HIV-1 drug resistance and genetic diversity in people with HIV-1 in Cape Verde, 2019-2021

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October 3, 2023

Abstract

The aim of this study was to characterize the genetic diversity and drug resistance profiles of people with HIV-1 failing ART in Cape Verde (CV). This cross-sectional study was conducted between January 2019 and December 2021 in 24 health centres on the islands of Santiago and São Vicente. The HIV-1 *pol* gene was sequenced in individuals with a detectable viral load (VL). Phylogenetic analysis was used to determine HIV-1 genetic diversity. Drug resistance mutation patterns and resistance phenotypes were estimated using the Stanford algorithm. VL was detected in 73 of 252 (29%) enrolled participants and sequencing data were produced for 58 (79%) participants. CRF02_AG strains predominated (46.5%), followed by subtype G (22.4%). Most patients (80%) had mutations conferring resistance to non-nucleoside reverse transcriptase inhibitors (NNRTIs) (67%), nucleoside reverse transcriptase inhibitors (55%), integrase inhibitors (10%) and/or protease inhibitors (7%) used in CV, a significant increase compared to a study conducted in 2010-2011. The most common mutations were M184V/I (43%), K103N/S (36%) and G190A/S (19%). NNRTI resistance was associated with younger age and exposure to two or more drug regimens. These results provide valuable information to guide appropriate treatment for people failing antiretroviral therapy in CV.

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