Correlation of HIV-1 drug resistant mutations and virologic failure

Abstract

Introduction: mutations are important by ensuring that the HIV-1 agent remains fit in the environment and evades drugs that are developed purposely to kill them. In Kenya, mutations conferring resistance to available ARVs have been reported in previous studies. However, there is a paucity of information on whether these previous studies have reported all mutations conclusively that confer resistance to available drugs leading to virologic failure. Therefore, this study was sought to identify the current HIV-1 drug-resistant mutations attributable to virologic failure among adults on various ARV regimens.

Methods: the samples were collected in March to June 2020. Analysis of viral loads and HIV-1 drug-resistant mutations through sequencing of the pol region of HIV-1 were done. Alignment of the cDNA sequences was done by Recall (beta version 3.05) software. HIV-1 resistant mutations were identified by Stanford University HIV drug resistance database.

Results: most of the participants had viral loads of more than 1000 copies/ml during all the three visits. Out of 125 mutations identified, 83 mutations resulted in virologic failure. Out of 17 new mutations, 14 resulted in virologic failure and included NRTIs (L74I, L74V, T69D, V65R); NNRTIs (A98G, V179E, V179F, V179D, 179F); PIs (I54V3, F53L2, L89T, G48A).

Conclusion: the study reveals new HIV-1 drug-resistant mutations which have never been reported in Kenya as well as old and both resulted in virologic failure. This calls for frequent monitoring and profiling of mutations that will enable decision-making in the drugs and vaccine design and development.

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