

Abstract

Introduction: antiretroviral therapy plays a major role in reducing the impact of Human Immunodeficiency Virus/Acquired Immune Disease Syndrome, especially in resource-limited settings. However, without proper infrastructure, it has resulted in emergence of drug resistance mutations in infected populations. To determine drug resistance mutations among patients attending a comprehensive care facility in Nairobi, 65 blood samples were successfully sequenced.

Methods: whole blood samples were also tested for CD4+T-cell count and plasma HIV-1 RNA Viral load. Drug-resistance testing targeting the HIV-1 RT gene was determined. Patients were on first line ART that consisted of two NRTIs, and one NNRTI.

Results: females were younger (mean 42) than males (mean 45) and lower median CD4+ counts (139 cells/ μ l) than males (152 cells/ μ l). The prevalence of drug resistance mutations (any major mutation) in this population was 23.1% (15/65). Major NRTI mutations were detected in 11 patient samples, which included M184V (n = 6), M41L (n=3), D67N (n=2), K219Q (n=3) and T215F (n=2). Major NNRTI mutations were detected in 14 patient samples. They included K103N (n = 10), G190A (n = 1), Y181C (n = 1) and Y188L (n = 1).

Conclusion: presence of major mutations in this study calls for proper laboratory infrastructure to monitor treatment as well as regular appraisals of available regimens.