

## Abstract

Circulating strains of human immunodeficiency virus (HIV) exhibit an extraordinary degree of genetic diversity and have been classified on the basis of relationships into distinct lineages called groups, types, subtypes, and subsubtypes. Sexually transmitted infections (STIs) are known to be a risk factor for HIV infection. To establish HIV-1 subtype diversity among STI patients in Nairobi, 140 samples were collected and partial *pol* gene sequencing done. From the analysis it was established that subtype A1 was the major subtype (64%) followed by D (17%), C (9%), G (1%), and recombinants AD (4%), AC (3%), CRF02\_AG (1%), and CRF16\_A2D (1%). These results suggest that the HIV-1 epidemic may be evolving toward more virulent and complex subtypes through transmission of complex recombinants due to viral mixing. Any use of ARVs may therefore require initial testing for *de novo* resistance before commencement of treatment and/or management.