

Poster presentation

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## P20-01. HIV-1 genetic diversity among HIV drug naive populations of Nairobi, Kenya

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### Background

In sub-Saharan Africa, where the effects of human immunodeficiency virus type 1 (HIV-1) have been most devastating, there are multiple subtypes of this virus. The distribution of different subtypes within African populations is generally not linked to particular risk behaviours. Thus, Africa is an ideal setting in which to examine the diversity and mixing of viruses from different subtypes on a population basis. Objectives: To determine the subtypes of human immunodeficiency virus -1 (HIV-1) circulating in a HIV-positive drug naive populations Nairobi, Kenya.

### Methods

In this study, 78 blood samples were sampled randomly and peripheral mononuclear cells (PBMCs) separated. Total proviral DNA was used in nested polymerase chain reaction to amplify 697 bp HIV Pol region. The PCR amplicons were cloned and partially sequenced. Generated sequences were aligned and phylogenetically analysed using known reference subtypes sequences.

### Results

The distribution of subtypes in this population was as follows: subtype A, 39(50%); subtype D, 8(10.25%); subtype C, 28(35.9%); and CRF A1D, 3(3.0%). Based on the small sample size analysed, the 3.0% intersubtype recombinants detected suggested, there is a higher levels in Kenya and in other parts of Africa where are multiple subtypes.

### Conclusion

Our analysis indicated that HIV subtypes in Nairobi province of Kenya are predominated by subtypes A1. Additionally, the detection of high prevalence of recombinant forms indicates viral mixing in among the population, possibly as a result of dual infections.