

Abstract

Phylogenetic analysis of the envelope HIV-1 type 1 isolates among Kenyan cohort

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Background: As the AIDS pandemic progresses, an increasingly broad range of genetic diversity continues to be reported within the main (M) group of HIV-1 viruses with viral subtype predominating in specific geographical areas.

Objective: Determine the genetic diversity and trends of HIV-1 subtypes among Kenyan individuals.

Methodology: One hundred and seventy six subjects (176) were recruited from five study sites in Nairobi and its environs. The viral DNA was extracted using Qiagen® MiniViral DNA isolation kit and target *env*-C2-V3 gene amplified by nested PCR. The amplified products were analysed by gel electrophoresis and visualized under UV light. The successfully amplified products were then labeled with a sequence dye in sequence PCR reaction using the Big Dye® sequence terminator kit (Applied Biosystem®) and the products purified by use of Qiagen purification kit before directly sequenced using an automated ABI 310 sequencer (Applied Biosystem, Foster City CA). In RT gene (288bp) of viruses sequenced.

Results: Analysis of the sequences showed that a majority of them belonged to subtype A1: 73.9% (130/176), followed by C: 10.8% (19/176), D: 9.7% (17/176), G, A1C and A2 1.1% (2/176) each and 2.3% (4/176) were unique recombinants forms. As from previous studies conducted in other parts of Kenya, HIV-1 subtype A1 still remains the most predominant subtype while subtype C continues to show an increasing prevalence.

Conclusion: Continued surveillance of circulating subtypes of HIV-1 in Kenya is important in determining the evolution of the HIV/AIDS epidemic in Kenya.

Key words: HIV-1, genetic diversity, subtypes, sequencing

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