Circulating trends of non-B HIV type 1 subtypes among Kenyan individuals.

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Abstract

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 geographic areas. To determine the genetic diversity of HIV-1 subtypes among Kenyan individuals, the env-C2-V3 gene was successfully sequenced in samples from 176 patients. 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: 10.2% (18/176), and 0.6% (1/176) for G and A2 as pure subtypes while the rest were recombinants of A1/U: 2.3% (4/176) and 0.6% (1/176) each for D/U, A/C/U, and AC. Similar to 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. Continued surveillance of circulating subtypes of HIV-1 in Kenya is important in determining the evolution of the HIV/AIDS epidemic in Kenya.