

**Genetic diversity of HIV-1 in Central province, Kenya-Pilot study**

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## ABSTRACT

Reports on emergence of new strains characterize HIV epidemic in Sub-Saharan African countries. The distribution of these diversified strains is thought to follow geographic and population dynamics. These HIV variants have been reported to have distinctively regionalized endemicity. In Kenya, studies on subtype distribution have been done in Western, Nyanza, North-Eastern, Rift Valley, Nairobi and Coastal Provinces. However, this information in Central Province is lacking. This work reports genetic diversities of HIV-1 circulating in the Central Province of Kenya. HIV positive blood samples were collected from 8 health facilities in the province namely Nyeri, Maragua, Kiambu, Thika, Kerugoya, Kikuyu, Tumutumu and Kieni Mission hospital. A total of 96 samples were collected, 12 from each health facility. Part of the proviral HIV-1 *env* gene (*gp41*) was PCR amplified and directly sequenced. Subtypes were determined by sequence analysis using geographically diverse subtype reference sequences as well as sequences of known subtypes from Kenya. Sixty eight percent (68 %) of the samples analysed were subtype A-1, 10% were subtype C, 12% subtype D, while the rest were circulating recombinant forms (CRFs) mainly between C, D, G and A. This analysis of HIV-1 strains demonstrated the predominance of HIV-1 subtype A-1. Understanding the genetic diversity of HIV-1 in this region is important in monitoring the spread of infection and developing effective control strategies. This pilot study provides the basis for more expansive studies in determining HIV genetic diversity in Central province of Kenya. It also sets the benchmark for future studies in viral phylogeography.