

Abstract

As part of a program to determine the genetic diversity of human immunodeficiency virus in rural Kenya, we carried out a molecular analysis of the C2–V3 region of HIV-infected blood samples obtained from 30 antenatal clinic attendees of seven health centers in western Kenya. Direct sequencing was carried out on the envelope C2–V3 region of proviral DNA. On phylogenetic analysis with reference strains, 20 were subtype A1, 2 were subtype D, 1 was subtype C, 1 was subtype G, 1 was CRF-10, 2A/D, 2A/C, and 2 were unclassified. The presence of CRF-10 and the great variety of subtypes and recombinants in such a limited sample size suggest that western Kenya may be a potential hotspot for HIV recombination in the country.