

A switch of HIV coreceptor usage from CCR5 to CXCR4 occurs in AIDS pathogenesis and may play a critical role in the use of entry inhibitors. To determine the potential usefulness of maraviroc and other CCR5 antagonists among drug-naïve and experienced patients in Kenya, the env-C2-V3 gene was successfully sequenced in samples from 176 (98 men and 78 female) consenting subjects between January 2009 and December 2012. In silico CPSSM, webPSSM/, and (ds) Kernel tools were used in predicting coreceptor usage. On the basis of the env V3 loop sequences, 84.1% (148) were reported with R-5 tropism, 4.5% (5) were dual tropic, while 13.4% (23) were of X4 tropism. However, similar to previous studies conducted in Kenya on genetic diversity, HIV-1 subtype A1 (73.9%; 130/176) still remains the most dominant subtype. The high levels of R5 tropism among the studied Kenyan infected populations suggested the potential use of CCR5 antagonists as new therapeutic options in Kenya.