Abstract:

Kenya is one of the sub-Saharan African countries affected by HIV-1 infection and AIDS. We investigated HIV-1 genetic diversity in 130 individuals from Busia, Bungoma, and Kakamega in western Kenya as part of an HIV-1 vaccine feasibility study in preparation for Phase III efficacy clinical trials. After RNA extraction the partial gag (484 bp) and env (1297 bp) regions were amplified and directly sequenced. Phylogenetic analysis was done using MEGA version 4 and recombinants were identified using the jpHMM tool and phylogenetic analysis. HIV-1 sequences were amplified from 122 of the 130 samples, 118 (90.8%) from the gag region and 78 (60 %) from the env region and 74 samples (56.9%) from both the gag and env regions. Of these sequenced on both regions, 51.4% were subtype A, 9.4% subtype D, 1.4% subtype C, 4.1% subtype G, and 33.7% were discordant and thus possible recombinants, including A1/C, A1/D, A1/A2, and A2/C. The jpHMM tool indicated a further two samples with CD and BD breakpoints within the env gene and one within the gag gene (A1C). An additional sample had an A1D breakpoint in the gag gene, but the envelope was not amplified. HIV-1 subtype diversity in western Kenya should be considered in vaccines designed for clinical trials in this region and this genetic diversity should be continuously monitored.