

ABSTRACT

We performed a molecular phylogenetic study on HIV-1 polymerase sequences of men who have sex with men (MSM) and heterosexual patient samples in Kenya to characterize any observed HIV-1 transmission networks. HIV-1 polymerase sequences were obtained from samples in Nairobi and coastal Kenya from 84 MSM, 226 other men, and 364 women from 2005 to 2010. Using Bayesian phylogenetics, we tested whether sequences clustered by sexual orientation and geographic location. In addition, we used trait diffusion analyses to identify significant epidemiological links and to quantify the number of transmissions between risk groups. Finally, we compared 84 MSM sequences with all HIV-1 sequences available online at GenBank. Significant clustering of sequences from MSM at both coastal Kenya and Nairobi was found, with evidence of HIV-1 transmission between both locations. Although a transmission pair between a coastal MSM and woman was confirmed, no significant HIV-1 transmission was evident between MSM and the comparison population for the predominant subtype A (60%). However, a weak but significant link was evident when studying all subtypes together. GenBank comparison did not reveal other important transmission links. Our data suggest infrequent intermingling of MSM and heterosexual HIV-1 epidemics in Kenya.