Identification of modifiable factors that affect the genetic diversity of the transmitted HIV-1 population

Abstract:

BACKGROUND: Our previous studies have shown that the majority of African women were infected with multiple HIV-1 genetic variants, while in the remaining women only a single viral genotype was detected early in infection. Infection with multiple viral variants was associated with higher plasma HIV-1 RNA levels and faster CD4 T-cell decline. METHOD: Sociobehavioral characteristics, use of hormonal contraceptives, and the presence of sexually transmitted diseases were prospectively assessed at approximately monthly intervals around the time of HIV-1 acquisition in female sex workers in Kenya. We assessed the relationship between these factors and HIV-1 genetic complexity early in infection. RESULTS: One hundred and fifty-six women were included in this analysis, of whom 89 had multiple viral genotypes and 67 had a single genotype at primary infection. Women with multiple variants were more likely to have a genital tract infection [odds ratio (OR), 4.7; 95% confidence interval (CI), 1.4-18.1] or to be using hormonal contraceptives (OR, 2.7; 95% CI, 1.3-5.6) at the time of their infection than those with a single variant. In multivariate analyses, these factors were independent predictors of early HIV-1 genetic complexity, and the presence of multiple viral variants early in infection remained significantly associated with a higher steady state plasma HIV-1 RNA level. CONCLUSION: The presence of genital tract infections and hormonal contraceptive use at the time of transmission were associated with the acquisition of multiple HIV-1 variants.