

Abstract:

Background: There is increasing recognition of recombinant HIV-1 strains globally, but it has been unclear whether recombination results from superinfection during untreated, chronic infection. Objective: To search for evidence of recombination and superinfection in Africa, where multiple HIV-1 subtypes facilitate identification of strains. Methods: Serial blood samples from highly exposed, chronically infected women in Nairobi's Pumwani sex workers cohort were examined. Serial, complete HIV-1 RNA sequence analyses were performed for seven untreated long-term survivors. Sequences were subjected to computational analysis. Results: One woman had evidence of both superinfection and recombination. Complete HIV-1 RNA sequences were first derived from plasma obtained in 1986, when the woman had been HIV seropositive for at least 21 months; this sequence was entirely subtype A. The sequences obtained from plasma in 1995 and 1997, however, were subtype A/C recombinants with a SimPlot demonstrating that the subtype A fragment in 1995 and 1997 was derived from the original 1986 A sequence. Heteroduplex tracking assays demonstrated that the subtype C sequences were not detectable as minor species in 1986. Conclusion: Intersubtype recombination took place between the original non-recombinant subtype A strain and the superinfecting subtype C strain in an untreated, chronically infected woman. This finding helps to explain the rising prevalence of recombinant HIV-1 worldwide. Recombination resulting from superinfection with diverse strains may pose problems for eliciting broad immune responses necessary for an effective vaccine.