

## ABSTRACT

HIV-1, a highly diverse infectious agent, shows the greatest sequence diversity in highly exposed individuals, including greater levels of recombination. HIV-1 diversity in Nairobi, Kenya was examined in 240 individuals, including both those with high and low exposure to HIV. Sequence analysis of a 590 nucleotide proviral region encompassing *vpu* and part of *env* revealed that most viruses were clade A1 (70%), while both clade D (9%) and clade C (6%) virus were also observed, as was recombinant virus (15%). Participation in sex work was significantly associated with clade: these subjects had a lower likelihood of infection with clade C virus and a higher likelihood of infection with a recombinant isolate ( $p = 0.038$ ). Interestingly, most of the recombinants formed distinct groups based on shared recombination breakpoints between common clades ( $n = 33/37$ ). This study shows the value of continued HIV sequence analysis to examine and monitor viral genetic variability.