Abstract

The genetic subtypes of HIV-1 circulating in northern Kenya have not been characterized. Here we report the partial sequencing and analysis of samples collected in the years 2003 and 2004 from 72 HIV-1-positive patients in northern Kenya, which borders Ethiopia, Somalia, and Sudan. From the analysis of partial *env* sequences, it was determined that 50% were subtype A, 39% subtype C, and 11% subtype D. This shows that in the northern border region of Kenya subtypes A and C are the dominant HIV-1 subtypes in circulation. Ethiopia is dominated mainly by HIV-1 subtype C, which incidentally is the dominant subtype in the town of Moyale, which borders Ethiopia. These results show that cross-border movements play an important role in the circulation of subtypes in Northern Kenya.