Phylogenetic evaluation of Kenyan HIV type 1 isolates.AIDS Res Hum Retroviruses

Abstract:

Diversity among global isolates of HIV-1 presents a formidable challenge for vaccine development. As distinct clades of the virus are recognized, it will be important to monitor their geographic distribution and divergence. In this study, we characterized HIV-1 subtypes from 17 seropositive individuals in Nairobi and Mombasa, Kenya. Seventy-one percent of viruses were clade A and 29% were clade D. The most divergent clade A isolate in our survey, Q45-CxA, grouped closely with two other taxa that were previously reported as having no distinct clade affiliation. Thus, these data may suggest the emergence of an outlier group of clade A variants or a new subtype of HIV-1. Phylogenetic relatedness of the 17 Kenyan isolates was determined separately for C2-V3 and V2 sequences of envelope and subtype designation for these isolates was independent of the region analyzed. However, evaluation of transitions, transversions, and specific character state changes indicated that mutations characterizing V2 differed from those in V3 for clade A and clade D isolates. Comparison of secondary structural characteristics of the V1-V3 region between a clade A and a clade D virus revealed conservation of motifs. PIP: The authors characterized HIV-1 subtypes from 17 seropositive individuals in Nairobi and Mombasa, Kenya. 71% of the viruses were clade A and 29% were clade D. The most divergent clade A isolate identified in the study, Q45-CxA, grouped closely with two other taxa previously reported as having no distinct clade affiliation. These findings may therefore signal the emergence of an outlier group of clade A variants or a new subtype of HIV-1. The evaluation of transitions, transversions, and specific character state changes indicated that mutations characterizing V2 differed from those in V3 for clade A and clade D isolates. Comparison of the secondary structural characteristics of the V1-V3 region between a clade A and a clade D virus revealed conservation of motifs.