ABSTRACT

Human immunodeficiency virus type 1 (HIV-1) non-B clade viral infections of the brain have not been studied to date. Among nine AIDS patients from Nairobi, Kenya, infected with HIV-1 A (N = 5) or D (N = 4) clade strains, brain-derived HIV-1 env sequences displayed greater evolutionary distance than B clade brain-derived viruses ($P < 0.001$). Similarly, molecular diversity between matched brain and spleen env clones was clade-dependent and concentrated in the hypervariable V4 region ($P < 0.001$), with phylogenetic clustering of sequences derived from the same organ. Brain-derived A and D clade sequences displayed significantly lower ratios of nonsynonymous/synonymous substitution rates (dN/dS) compared to matched spleen-derived clones and brain-derived B clade viruses. Interclade recombination events were infrequently observed among the present env sequences. A chimeric virus containing the C2V3 region from an A clade brain-derived sequence preferentially used CD4 and CCR5 for infection. These findings demonstrate that differences in molecular diversity in brain-derived sequences were dependent on the individual clade and domain within the env gene, but both B and non-B clade brain-derived viruses exhibit a preference for CCR5 as a coreceptor.