

Abstract

Human immunodeficiency virus (HIV) genetic diversity is a major impediment to the design of a successful vaccine. Even if an HIV vaccine is proven effective, it remains to be seen whether this protection will extend to inter-clade, intra-clade, and recombinant strains. We used recombinant vaccinia-based interferon gamma (IFN) Elispot assays to test the inter-clade crossreactivity of clades A, B, C, and D HIV Env in two cohorts of HIV-infected Kenyans. Despite the tremendous diversity in this HIV protein, a substantial proportion of multi-clade responses were observed. Although these multi-clade responses correlated well with each other in regression analyses, clade A responses were seen at a higher frequency and at greater relative magnitudes in a proportion of these patients, when compared to the other three clades. Epitope mapping indicates CD8(+) T cell recognition of conserved regions of Env, accounting for the high degree of cross-reactivity but not the clade A preference. A better understanding of cross-clade CD8(+) T cell responses to HIV may help to predict whether a successful vaccine could be used to stop geographically and genetically distinct HIV epidemics.