Retrovirology

Poster presentation

P20-19 LB. Extensive HLA-driven viral diversity following a single-source HIV-1 outbreak in rural China

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Background

High rates of mutation in HIV infected individual allow the virus to adapt rapidly in vivo to selective forces such as anti-retroviral therapy (ART) and host immune pressure. This provides an opportunity to determine the relative contribution of different components of the immune response to HIV-1 infection in driving viral diversity, which may also facilitate assessment of their role in controlling viral replication. It is accepted that HIV-1-specific cytotoxic T-lymphocytes (CTL) may drive the selection of viral variants that can escape T-cell recognition but the extent of this selective pressure has been controversial.

Methods

Two digit HLA typing; ELISPOT assay; HIV-1 sequence analysis; HIV sequence clustering and phylogenetic analysis of HLA associations using the neighbour-joining method, S-Plus 8.0, "Partitioning around medoids" (PAM) method and Stratification analysis by Mantel-Haenszel tests.

Results

Here we describe the consequences of HLA-associated selection on viral diversity in the main targets of T-cell recognition following an outbreak of HIV-1 in a cohort of 258 former plasma donors in rural China. The surprising finding that all the donors appear to have been infected with the same strain of clade B HIV-1 ensured that the analysis was not confounded by "founder effect". At least 32.63% (232/711) of the mutations in the gag, pol and nef genes leading to amino acid substitutions were associated with class I HLA molecules: of these, 27.16% (63/232) were found within or close to known CD8+ T-cell epitopes.

Conclusion

Taken together our data confirm that CD8+ T-cell pressure has a major impact on HIV-1 viral diversity and represent an important element of viral control in the infected host.