Epidemiological consequences of HIV immune escape

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During each infection HIV evolves to escape the immune responses of its individual host.
Cytotoxic T-Lymphocyte (CTL) responses play a major role in limiting the HIV virus load, and depend on the host's Human Leukocyte Antigen (HLA) molecules that are used by infected cells to present small peptides samples from HIV's proteins. HIV evolves mutations that prevent the presentation of these peptides by the HLA of the host.

HLA is highly polymorphic in the human population. Hence most adaptive mutations in one host are likely be deleterious in the next infected host. We use a computational model to study this effect of host heterogeneity on HIV evolution. Escape mutations and deleterious mutations alter the set-point virus load, and affect both infectiousness and virulence. This relates the heterogeneous within-host immune escapes with the between-host epidemiology.

We find that for realistic mutation rates, the within-host evolutionary dynamics are more important than the virulence effects on transmission for the population-wide evolution of HIV. Despite the dominance of the within-host evolution, we do find the positive heritability of the set-point virus load that has been observed in epidemiological studies, and we suggest that immune escapes can explain this observation.

Other epidemiological studies have suggested that HIV has evolved a virulence that is optimal for transmission. We propose a novel mechanism that is dependent on clonal interference and HLA-heterogeneity that can also explain these observations.