Genetic Evolution of HIV in the host during course of disease: influence of co-morbid conditions

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Faster disease progression and increased mortality is observed in the HIV-1 infected individuals with comorbidities of either co-infected with *Mycobacterium tuberculosis* (Mtb) or are concomitantly on intravenous drug use (IDU). The mechanism involved in the breakdown of host immune defense and the synergistic effect in both the two conditions is still not well understood. Recent studies indicate the emergence of genetically diversified variants of virus in comorbid human host among HIV-1 subtype-C infected population.

Studies performed on HIV-1 subtype-C infected individuals constituting cohorts of HIV-1 mono-infected, HIV-1-*M. tuberculosis* (HIV-TB) co-infected and HIV-1 infected individuals on substance abuse (HIV-IDU) for acquisition of genetic alterations reveal a significantly higher viral load, higher death rate and higher frequency of major DR mutations in the RT region and additional NF-kB binding sites in the LTR region of viral genome from HIV-TB and HIV-IDU cohorts as compared to HIV mono-infected. Majority of the mutations found in the HIV-TB co-infected and HIV-IDU cohorts conferred high level of resistance to the first line treatment regimen (Lamivudine with Tenofovir or zidovudine or Abacavir and Nevirapine or Efavirenz). The findings support the hypothesis that the HIV-1 evolve while replicating in the host with Mtb co-infection or substance abuse, with the emergence and accumulation of genetically diversified quasi-species. These observations help us to understand the association of such genetic variations with increased replication competence and faster rate of disease progression in such individuals.