Retrovirology

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Oral presentation

Genetic variation in HIV-1C: implications for prevention and treatment

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HIV-1C of southern Africa shows higher rates of genomic variation than does HIV-1B. Prevalence rates are far higher in this region as compared to elsewhere in sub-Saharan Africa or in the world. Enhanced rates of transcriptional activation, presumably related to duplication in the LTR NF-kB enhancer region of the genome, have been well documented. This may in turn be associated with better replication in vaginal and GALT tissues, different patterns of mother/infant transmission, and elevated transmission rates. HIV-1C has also been shown to have higher rates of nevirapine resistance in mothers given labor nevirapine, higher rates of K65R resistance to tenofovir after in vitro selection, different patterns of accumulation of thymide analogue mutations to the nucleoside analogue drugs, and different patterns of mutations to the protease inhibitor drugs. HIV-1C also shows different patterns of immunoselection for immunodominant epitopes to both CTL and antibody responses. With the gag gene epitopes, for example, the p17 region is immunodominant in HIV-1B while the p24 region is immunodominant for HIV-1C. How these responses may be related to differences in major histocompatibility alleles in the people of southern Africa is unclear.