Molecular Characterization of the RANTES Gene Polymorphisms in Nairobi Province, Kenya

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ABSTRACT

Expression of CC chemokine receptor 5 (CCR5), the major co-receptor for HIV-1 cell entry, and its ligands (RANTES, MIP-1α & MIP-1β) are widely regarded as central to the pathogenesis of HIV-1 infection. RANTES (regulated on activation normal T cell expressed and secreted) potently suppresses *in vitro* replication of the R5 strains of HIV-1, which use CCR5 as a co-receptor. Previous studies have shown that RANTES gene polymorphisms lead to altered gene expression and influence the natural course of HIV infection. In this study, existence and frequencies of RANTES-28 (C→G) alleles polymorphisms in persons in Nairobi were determined using PCR-RFLP. Allele frequencies for RANTES-403 (G→A) were estimated by use of haplotype model. Forty four percent of HIV positive persons had the RANTES-403 & -28 G-C Haplotype compared to fifty percent of HIV negative blood donors. There was no significant difference ($P>0.05$) in the frequencies of each RANTES genotypes and haplotypes single nucleotide polymorphisms (SNPs). The distribution of these haplotypes is in Hardy–Weinberg equilibrium, indicating a lack of selection for or against each SNP. RANTES mutant frequency was one percent for both categories indicating low frequency of gene responsible for high RANTES secretion. This suggests that the Nairobi population lacks the beneficial high RANTES levels.