

Poster presentation

Open Access

P08-03. Genetic complexity of TRIM5 and APOBEC in East Africa

AM Walsh⁵, K Perret⁵, R Koehler⁵, N Moqueet⁵, C Bautista⁵, L Eller¹, M Eller¹, H Kibuuka¹, M Hoelscher², L Maboko³, F Wabwire-Mangen¹, ML Robb⁵, NL Michael⁴, F McCutchan⁵, J Kim⁴ and GH Kijak^{*5}

Address: ¹Makerere University Walter Reed Project, Kampala, Uganda, ²Dept. of Infectious Diseases & Tropical Medicine, Univ. of Munich, Munich, Germany, ³Mbeya Medical Research Program, Mbeya, Tanzania, ⁴US Military HIV Research Program/WRAIR, Rockville, MD, USA and ⁵US Military HIV Research Program/Henry M. Jackson Foundation, Rockville, MD, USA

* Corresponding author

from AIDS Vaccine 2009
Paris, France. 19–22 October 2009

Published: 22 October 2009

Retrovirology 2009, 6(Suppl 3):P111 doi:10.1186/1742-4690-6-S3-P111

This abstract is available from: <http://www.retrovirology.com/content/6/S3/P111>

© 2009 Walsh et al; licensee BioMed Central Ltd.

Background

Host restriction factors (HRFs) TRIM5alpha and APOBECs effect post-entry inhibition of HIV-1 replication *in vitro* but *in vivo* significance remains unclear. By acting as a first line of defense, HRFs could potentially act synergistically with adaptive/vaccine-induced immunity. HRFs are polymorphic in world populations, but little is known about their variation in East Africa, despite its high rate of HIV-1 infection. This study describes trim5 and apobec polymorphisms in East African populations.

Methods

East African HIV-negative adults from Mbeya, Tanzania (n = 174) and Kampala, Uganda (n = 160) were studied. Putative polymorphic loci in trim5 (n = 10), apobec3b (n = 6), apobec3f (n = 7), and apobec3g (n = 11) were genotyped from gDNA using real-time PCR. Genetic analyses were conducted (Pypop/Arlequin/Genepop/Haploview).

Results

Genotyping data was obtained in 11244/11356 (99.0%) reactions. Extensive genetic polymorphism was observed: 8/10 trim5 and 14/24 apobec loci exhibited minor allele frequencies (MAFs) >0.05 (range: 0.070–0.475), without significant deviations from Hardy-Weinberg equilibrium. Genic/genotypic differentiation tests failed to reject the null hypothesis that alleles and genotypes were drawn from the same distribution in the two populations. TRIM5alpha 136Q (coiled-coil domain) was represented

at frequencies of 0.075 and 0.073 in Uganda and Tanzania, respectively. Variation at TRIM5alpha codon 419 (SPRY domain) was low (MAF<0.01). Genotype frequencies of 186R/R in APOBEC3G were 10.8% in Uganda and 14.8% in Tanzania. Among apobec, strong intragenic linkage disequilibrium was observed but was weaker between loci in different genes. No trim5 or apobec haplotype predominated, and there was congruence in the most common haplotypes in Uganda and Tanzania.

Conclusion

This initial description of trim5 and apobec in East Africa reveals extensive genetic diversity, with similarity in the distribution of alleles and haplotypes in HRFs among Ugandan and Tanzanian populations, making this a preferred setting to define the impact of HRF variation on HIV acquisition, disease progression, and vaccine efficacy.