
Poster presentation

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Abstract

Background
Differences in HLA allele and haplotype frequency across different populations worldwide might translate into differences in viral imprinting at a population level. Here we characterized the HLA genotypes and associated HIV polymorphism in a cohort of Ethiopian patients.

Methods
356 antiretroviral naïve patients of Ethiopian origin participated in the study. 299 were recruited in Israel (Jewish immigrants from Ethiopia living in the Jerusalem area). Genotypes at HLA-A, -B, -C and DRB1 loci were determined based on locus-specific PCR amplification of exons 2-3. The consensus sequence was determined for the population by applying the most common amino acid at each position. Full-length viral sequencing was performed using both Sanger and 454 deep pyrosequencing techniques. HLA-HIV sequence associations have been corrected for viral phylogenetic relatedness and multiple comparisons (q ≤ 0.2).

Results
There were 36 different HLA-A, 49 HLA-B and 24 HLA-C alleles detected in this cohort. Significant differences in HLA class I allele frequencies were found between these patients and a cohort of clade C infected patients from South Africa. In this regard, alleles uniquely described in the past among Africans were much more frequent among South Africans compared with Ethiopians. High rates of HLA-B57 and HLA-B13, which are associated with disease control were found among this Ethiopian cohort. The analysis reproduced many previously described HLA-associated HIV polymorphisms both in African and Caucasian cohorts, but new targets for selective pressure were found.

Conclusions
This is the first work to characterize comprehensively and at a large scale an African cohort from Ethiopia, and the first to apply deep pyrosequencing to HLA-HIV association analysis. We found the unique HLA background of the Ethiopian cohort to be associated with unique viral imprinting.

Methods

Results

Fig 1: HLA-B Alleles Frequency in Ethiopians, Compared to a Cohort from Durban, SA

Fig 2: Associations Density (corrected for protein length)

HIV-1 adaptation to HLA:
We identified 196 significant associations of unique amino acid polymorphisms and HLA-A (28%), HLA-B (45%), or HLA-C (27%) alleles (q values ≤ 0.2).

Conclusions

References

1. Leslie A et al. 2015. Additive contribution of HLA class I alleles in the immune control of HIV-1 infection. J Virol
2. Philip Goulder, Oxford, UK, personal communication