

Poster presentation

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Differential HLA-dependent HIV evolution among subtypes

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Introduction

Population HLA-dependent evolution has been documented over the principal HIV proteins. Effect of subtype variability is uncertain. In Argentina, B subtype and recombinant BF variants circulate in equal proportions.

Methods

Blood samples were collected from 94 drug-naive HIV infected individuals. DNA and RNA extraction were performed from PBMC and plasma, respectively. HLA-A and B genes were genotyped by PCR-SSOP. Pol and vpu genes were amplified by RT-PCR and sequenced. Aminoacidic positions were codified as 0 = "equal state" (to consensus sequence) and 1 = "variated state" (polymorphism). Phylogenetic analyses were performed by BootScanning. Statistical analysis was performed by ODDS-ratio/power calculations, Fischer exact test, Logistic regression and randomization tests. Potential new epitopes and affinities with HLA were assessed by using BIMAS software.

Results

We found 95 polymorphisms associated with different HLA alleles. 44 out of them were inside predicted epitopes for the associated HLA allele. 13 out of them reduced the affinity for the HLA allele in the "variated" state. 5 out of them were associated with viral subtype.

Conclusion

Our results suggest that vpu could be undergoing adaptation to the immune response at the population level, as previously reported for pol gen. Associations with viral subtype suggest that this evolution is different among sub-

types and that variants from subtype B and BF could respond differently to both natural and vaccine-induced immune response.