



POSTER PRESENTATION

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HLA-associated viral polymorphism in chronically HIV-1-infected Japanese cohort: analysis of four-digit HLA allele level

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Background

It is assumed that the difference of HLA class I distribution among ethnic populations influences HIV evolution because HLA-restricted immune pressure selects escape mutations. Approximately 50% of HLA class I alleles are shared between Japanese and Caucasians. The analysis of HLA-associated polymorphism (HLA-AP) in both Japanese and Caucasian infected with clade B virus is expected to clarify the difference of HIV-1 evolution between both populations.

Methods

We sequenced Gag, Pol, and Nef genes in 430 treatment-naïve Japanese chronically infected with HIV-1 clade B and then identified HLA-associated amino acids at each codon using a phylogenetically corrected logistic regression model and false discovery rates to correct for multiple tests.

Results

We completely determined 400, 366, and 309 sequences of Gag, Pol, and Nef, respectively, and then analyzed polymorphisms associated with 78 four-digit HLA alleles (21 HLA-A, 38 HLA-B, and 19 HLA-C alleles). At the threshold of $q < 0.2$, we found 195 HLA-APs (67 in Gag, 61 in Pol, and 67 in Nef). These polymorphisms were observed at 39 of 501 (7.8%) Gag, 42 of 1004 (4.2%) Pol, and 33 of 207 (16.0%) Nef codons. Ninety-six HLA-APs associated with more than one HLA subtype allele were detected in 4-digital HLA allele analysis. Approximately 40% of HLA-APs were associated with HLA alleles

predominantly found in Asia. Out of HLA-APs associated with common HLA alleles, approximately 50% were found in Caucasian population (IHAC cohort).

Conclusion

This study demonstrated that only 30% of HLA-APs were shared between Caucasians and Japanese, indicating that the difference in HLA allele distributions resulted in distinct HIV-1 evolution.

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