# **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.

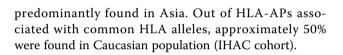
## Methods

We sequenced Gag, Pol, and Nef genes in 430 treatmentnaïve 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

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#### 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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