

Poster presentation

Site Specific Codon Bias in HIV-1 pol Gene

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Background

There is increasing concern that synonymous genetic polymorphisms in HIV can influence drug resistance and molecular evolution. This study investigated the distribution of synonymous codons in HIV-1 and SIV reverse transcriptase enzymes.

Materials and methods

HIV-1 and SIV pol gene sequences were translated and the resulting protein sequences used as a scaffold to align the corresponding nucleic acid sequences. Synonymous codon usage was assessed in order to find out whether the use of unfavoured codons at a given site is conserved.

Results

Some aligned positions contained unfavoured codons in most or all of the sequences analysed. Some of these positions are involved in drug resistance, CTL responses and enzymatic activity of RT.

Conclusion

Synonymous codons are differentially preferred at various sites and undergo positive selection. Thus, sites at which unfavoured codons are conserved could be important in adaptive evolution of HIV. Knowledge on these sites can be applied in drug and vaccine design.