Title:	Differential trends in the codon usage patterns in HIV-1 genes
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Abstract:	Host-pathogen interactions underlie one of the most complex evolutionary phenomena resulting in continual adaptive genetic changes, where pathogens exploit the host's molecular resources for growth and survival, while hosts try to eliminate the pathogen. Deciphering the molecular basis of host–pathogen interactions is useful in understanding the factors governing pathogen evolution and disease propagation. In host-pathogen context, a balance between mutation, selection, and genetic drift is known to maintain codon bias in both organisms. Studies revealing determinants of the bias and its dynamics are central to the understanding of host-pathogen evolution. We considered the Human Immunodeficiency Virus (HIV) type 1 and its human host to search for evolutionary signatures in the viral genome. Positive selection is known to dominate intra-host evolution of HIV-1, whereas high genetic variability underlies the belief that neutral processes drive inter-host differences. In this study, we analyze the codon usage patterns of HIV-1 genomes across all subtypes and clades sequenced over a period of 23 years. We show presence of unique temporal correlations in the codon bias of three HIV-1 genes illustrating differential adaptation of the HIV-1 genes towards the host preferred codons. Our results point towards gene-specific translational selection to be an important force driving the evolution of HIV-1 at the population level.
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