Sequence Analysis of the Human Immunodeficiency Virus Type 1 Genome

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Human Immunodeficiency Virus Type 1 is known for its ability to evolve very quickly, which leads to increased studies in its evolution. Using its genomic sequence, a comparison in observed and theoretical synonymous sites was used to determine whether or not each gene is undergoing differential selective pressure (Kreitman and Hudson, 1991). The HIV-1 genome was also compared to genomes of similar species (HIV-2, SIV-1, and SIV-2) in order to test if the differences between species are neutral (McDonald and Kreitman (1991). HIV-1's regulatory region (U3/R) was also analyzed to test the levels of polymorphisms present within this region. This data was then used to predict potential transcription fact binding sites within the promoter region. These tests provide us with information about any evolutionary constraints within the HIV-1 virus potentially helping us understand the structure of the regulatory regions as well as determining which areas of the virus are most essential.