

A QUANTITATIVE ANALYSIS OF THE SIMILARITIES AND DIFFERENCES OF THE HIV/FIV GAG GENOME

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ABSTRACT

Among viruses, human immunodeficiency virus (HIV) presents the greatest challenge to humans. Here, we retrieved genome sequences from NCBI and were then run through LALIGN bioinformatics software to compute the E value, bit score, Waterman eggert score, and percent identity, which are four important indicators of how similar the sequences are. These 4 values are 3.1×10^{-9} , 51.9, 241 and 55.4%. Bases 1600 to 1990 in HIV and bases 800 to 910 in FIV have a higher-than-normal similarity. This reflects that while the DNA sequences of the gag region of both the HIV and FIV genomes are rather similar, it is unlikely that this similarity is due to random chance; therefore, there are a noticeable number of differences. A better understanding of the level of similarity and differences in the gag region of the genome sequence would facilitate our understanding of structural and cellular behavioral differences between FIV and HIV, and in the long term, it will provide new insights into the differences observed in previous studies or even facilitate the development of an effective HIV treatment.

Keywords: HIV, FIV, gag.