

In-silico analysis of nucleic acid and amino acids (Env, Pol,Gag,Vif,Tat) of the HIV-1 virus (human immunodeficiency virus) for evaluating of the genetic evolutionary and signature pattern of Iran strains

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Abstract:One of the important management concerns in front of health authorities are transmission ways and molecular epidemiology for prevention and informing of the patients in each country. In this research, bioinformatics analyzes were performed in order to determine the genetic signature pattern and genetic evolution in conserved and none conserved genetic regions of (Env, Pol) protein. Ten complete sequences from Iran and 40 complete sequences from other countries were obtained from the gene bank, along with reference (K03455 HXB2). The (Env, Pol,Gag,Vif,Tat) genes were aligned and then selected for analyzing by bioinformatics software (CLC Main Workbench 5.5, MEGA7. 0.26, DnaSP 5.10) according to the HIV Genome Analysis Data Center (www.hiv.lanl.gov).The molecular phylogenetic analysis in the new codification by comparison of the amino acid and nucleic acid methods showed that the CRF-AE strain was evolutionally and species isolated from CRF-AD strains.The average rate of genetic identiti in the straw is 95.71. The CRF-AD strains of Iran are most closely related to Ugandan strains (AF075702) and Pakistan (KX232613) and have the least identitie with strains of France (KU168218) and Cameroon (KU168297) and the CRF-AE strain is most closely related to Thai strains KC522034) and Malaysia (GQ366662). The percentage of informative areas in the genes (gag, pol, env) is 85%, 80% and 83%, most of which are two variants. Based on the comparison of dN to dS, the most important amino acid changes were gag 76% and the least changes were related to the env gene 31%, but the Tajima's D (NonSyn / Syn) ratio showed that every 5 genes The highest rate of Tajima's D is related to the env gene (89.34) and the lowest rate is related to the TAT gene, which indicates a change in the positive direction of amino acid selection. Based on the findings, the pol gene (Tajima's D: -0.974) has evolved negatively, while other genes have created a progressive evolutionary process (positive). For the Signature Pattern 114 amino acid analysis form the CRF-AE strain V3, along with the reference with 9 strains of CRF-AD, showed that 29 to 33 amino acids were different from 42 amino acids. Similarly, when analyzing the CRF-AE strain with Thailand strain THR48F, 28 amino acid changes were observed in two strains of the total (28), indicating the presence of these two strains with each other and confirming the accuracy of the phylogenetic analyzes.

Keywords: HIV-1; Signature pattern; Insilico; identities