

عنوان مقاله:

HIV Iranian sequences subtyping by using Bioinformatics tools

محل انتشار:

هشتمین همایش بیوانفورماتیک ایران (سال: 1397)

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خلاصه مقاله:

Abstract Background: Patients with human immunodeficiency virus (HIV) are increasingly susceptible to liver disease. The rate of human immunodeficiency virus type 1 (HIV-1) infection in Iran has increased dramatically in the last few years. **Methods:** In this study, 315 sequences of protease, reverse transcriptase genes, integrase, and gag of HIV-1 were obtained from NCBI. HIV-1 subtyping was done by 8 reliable software and phylogenetic analysis was done by CLC sequence bench. **Results:** The phylogenetic tree results did not confirm any specific subtype for selected sequences. However, the final results of 8 online tools indicated that the majority of sequences were HIV-1 subtype CRF35 AD. However, it seemed in some genes that a minority of programs could not determine specific subtypes and in some cases, they described different subtypes. **Conclusion:** By considering the diagram of CRF35 AD, it was clear that integrase was not an appropriate region to define this subtype; also the full length of gag gene should be used for subtyping. For CRF1, AE envelop gene is the reliable region to define this subtype. Stanford software was used to determine the drug resistance prevalence and in 5.7% of the sequences drug resistance mutations were found.

کلمات کلیدی:

HIV subtyping, Bioinformatics, Iran

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