

عنوان مقاله:

Multilocus Sequence Analysis (MLSA) of Mycobacterium tuberculosis from Clinical Isolates in Northeast of Iran

محل انتشار:

بیستمین کنگره بین المللی میکروب شناسی ایران (سال: 1398)

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خلاصه مقاله:

Introduction and Objectives: Mycobacterium tuberculosis is still one of the most dangerous human pathogens. Identification of the relationships between different clinical strains has remained a high priority for epidemiology research. In this study, we used MLSA (Multilocus sequence analysis) to generate a highly robust phylogeny of M. tuberculosis. MLSA, based on single nucleotide polymorphism (SNP) was performed on five genes fragments from the Rpsl (302 bp), MprA (559 bp), LipR (322 bp), KatG (488 bp) and Fgd1 (266 bp), in order to identify polymorphic nucleotide sites, and the discriminatory power of each locus for all genes was measured with Hunter-Gaston Index (HGI). **Materials and Methods:** Twenty M. tuberculosis isolates were selected from pulmonary tuberculosis patients, during 2017 in the Regional Reference Tuberculosis Laboratory, in north-east of Iran. H37RV (ATCC27294) was also included as a reference strain in this study. These genes were amplified with the primers designed, using Primer3 software and DNA sequencing was performed on the ABI 3730XL DNA Analyzer. SNP data analysis including sSNPs (synonymous) and nsSNPs (non-synonymous) were analyzed, using the Vector NTI software. **Results:** The sequencing results were multiple aligned, using MEGA Software, and compared with the reference sequence H37Rv. In final analysis of the sequencing data and phylogeny, two models have been compared: the first model was character-based and the second model was distance-based. There are 31 SNP among 20 isolates, these polymorphisms comprised of 6 nsSNPs, 25 sSNPs. In Rpsl, three nsSNP, in KatG three nsSNP and 1 sSNP, in MprA five sSNP, in LipR ten sSNP and in Fgd1 nine sSNP were found. In our study, sSNPs were much more abundant than nsSNPs. The mutation in codon 128 of rpsl led to changes of lysine to arginine, and the mutation in codon 1280 of katG led to changes of alanine to glycine. Finally, sequence type (ST) number was assigned to each unique allelic profile, and 9 sequence types were identified from 20 strains, these imply that there is a high diversity of strains in this area of country. **Conclusion:** Our study implies that there is a high diversity of strains in this area of the country. SNPs can also be used to measure evolutionary distances between strains, to estimate the time of divergence of strains from their genetic distance if a mutation rate is known. Analysis of partial gene sequences of rpsl, lipR, katG, .fgd1, mprA, revealed that M. tuberculosis strains showed that rpsl phylogeny power is weaker than others

کلمات کلیدی:

Mycobacterium tuberculosis, MLSA, Molecular study

