

عنوان مقاله:

Genetic diversity of clinical isolates of Mycobacterium tuberculosis in Northeast of Iran

محل انتشار:

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خلاصه مقاله:

Abstract Background: 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. Methods: 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 (۳۰۲ bp), MprA (۵۵۹ bp), LipR (۳۲۲ bp), KatG (۴۸۸ bp) and Fgd۱ (۲۶۶ 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). Results: In this study, a sequence type (ST) number was assigned to each unique allelic profile, and ۹ sequence types were identified from ۲۰ strains, these imply that there is a high diversity of strains in this area. Conclusion: Our results showed that the presence of high genetic diversity among clinical isolates of M. tuberculosis in Northeast of Iran. There is no evidence for recent transmission. Keywords: Mycobacterium tuberculosis, Multi-locus sequence analysis; Molecular epidemiology; Tuberculosis; KatG; Rpsl. Introduction Mycobacterium tuberculosis (M. tuberculosis), the causative agents of tuberculosis (TB), is one of the most successful human pathogens, infecting nearly one-third of the people all around the world, causing over ۹ million new cases and ۱.۷ million deaths each year [۱-۲]. Identification of the [relationships between different clinical strains of M. tuberculosis has great significance to the public health [۳

کلمات کلیدی:

Mycobacterium tuberculosis, Multi-locus sequence analysis, Molecular epidemiology, Tuberculosis, KatG, Rpsl

