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Determination of trend of *Mycobacterium tuberculosis* genetic diversity in Iranian population with tuberculosis by MIRU-VNTR from 2011 to 2013

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Tuberculosis (TB) is an important public health. *Mycobacterium tuberculosis* the etiological agent of tuberculosis is responsible for maximum mortality by infection diseases globally. Tuberculosis molecular diagnostics is a useful for epidemiology control of TB. We evaluated the performances of 24-loci mycobacterial interspersed repetitive units-variable number of tandem repeats (MIRU-VNTR) for detection of transmission in Iran. During 2011-2013, a total of 67 *Mycobacterium tuberculosis* isolates were collected from microbial bank Pasteur Institute. Drug susceptibility testing for Isoniazid, Rifampin, Kanamycin, ethambutol and Streptomycin was performed using the agar proportion method. These isolates were genotyped by using 24-locus based MIRU-VNTR typing. Sixty seven strains were classified into 34 MIRU patterns of which 10 were Clusters and 24 unique strains. HGDI was calculated to measure the discriminatory power of each of MIRU-VNTR loci. Mtub21 and QUB26 were highly discriminant. The result also underlined the usefulness of MIRU-VNTR to detect mixed infection among certain of Iranian patient. Association between genotype and patients was with INH-resistant was found (p-Value=0.44). Genotyping based on Mycobacterial interspersed repetitive unit is rapid, high discrimination power, portable and suitable method for the detection of mixed infection therefore this method is useful genotyping tool to be applied to *Mycobacterium tuberculosis* isolates. The high proportion of molecular clusters suggests a high permeability of tuberculosis transmission between Iranian populations. These results prompt for the need to strengthen the current tuberculosis control strategies and surveillance programs.

Biography

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