

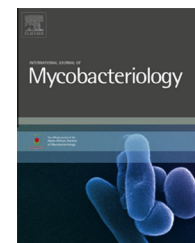
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# Determination of circulating *Mycobacterium tuberculosis* strains and transmission patterns among TB patients in Iran, using 15 loci MIRU-VNTR

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## ABSTRACT

**Aims and objectives:** Tuberculosis (TB) is considered one of the most important pathogens in the world. Iran has a moderate TB incidence, but borders two high-burden TB countries to the east and one high-burden multidrug-resistant (MDR)-TB country to the north. Limited information is available on the genetic diversity and transmission dynamics of MTB in Iran.

To determine the MTB genotypes and their transmission patterns among patients, a collection of isolates from different parts of Iran were genotyped.

**Methods:** Genotypes were generated by means of standard 15-locus variable number tandem repeat (VNTR) for 121 MTB clinical isolates collected from three provinces of Iran, including Sistan-Baluchestan (southeast province of Iran, with the highest rate of TB), Kermanshah (western part of Iran with high TB/human immunodeficiency virus [HIV] cases) and Tehran (the capital of Iran).

**Results:** Sixty-six distinct mycobacterial interspersed repetitive unit (MIRU)-VNTR patterns were detected among 121 isolates. Seventy-five strains were grouped into 20 clusters, and 46 isolates were unique. The genetic diversity of strains from Sistan-Baluchestan was higher than that in the other province. All isolates from Tehran or Kermanshah that were grouped into clusters shared more identical patterns with Sistan-Baluchestan. The Hunter-Gaston discriminatory index (HGDI) was 0.972, indicating a high power of discrimination for MIRU-VNTR typing. The MIRU 16, ETR-A, ETR-E, MTUB04 loci were designated as highly discriminative.

**Conclusions:** MIRU-VNTR typing showed a high genetic diversity and suggests the possibility of transmission from Sistan-Baluchestan to other provinces of Iran. This method could be considered a suitable tool for studying the transmission routes of TB and leading to more appropriate measures for TB control. MIRU-VNTR typing leads to a much better understanding of the bacterial population structure and phylogenetic relationships between strains of MTB in different regions of Iran.

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