

# Molecular epidemiology of *Mycobacterium tuberculosis* isolates in Iran using Spoligotyping

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## Abstract

Spoligotyping can help assess the transmission of *Mycobacterium tuberculosis* strains. We aimed to study the genotyping of *M. tuberculosis* isolated from patients with tuberculosis from the west of Iran by spoligotyping. Forty-seven *M. tuberculosis* isolates were collected from the west of Iran. All samples were cultured on Löwenstein-Jensen medium incubated at 37°C for 8 weeks. Bacterial isolates were identified as *M. tuberculosis* using standard biochemical tests. Drug resistance patterns of *M. tuberculosis* to rifampicin and isoniazid were determined, and multidrug-resistant (MDR) strains were isolated. After DNA extraction, spoligotyping was performed. We found new spoligotypes 4162 and 4163, which correlated with atypical lineage. Atypical and unknown lineages also had correlations with the MDR tuberculosis rate (4%). The most prevalent spoligointernational types were orphan (34%), 2669 (23.4%) and 127 (14.8%) types. The most prevalent clades were Ural-2 (NEW-1) (25.53%) and atypical (23.40%) lineages. The predominant clade was Ural-2 (NEW-1) and an atypical lineage restricted to Iran. The rate of MDR was low. Knowledge of the circulating isolates in the west of Iran will help implement control programmes, so knowledge of the dynamic transmission of local isolates is crucial.

**Keywords:** Epidemiology, Iran, Molecular, *Mycobacterium tuberculosis*, Spoligotyping