

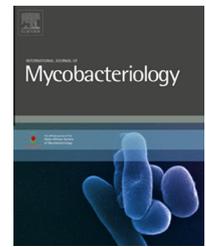
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Genomic analysis of *Mycobacterium tuberculosis* in respiratory positive-smear patients using PGRS-RFLP in northwest and west provinces of Iran

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ABSTRACT

Aims and objectives: Clustering of and determining *Mycobacterium tuberculosis* (MTB) strains is of great concern in control programs of tuberculosis (TB). Identification of transmission type and tracking the infection source is also highly necessary. The aim of the present study is to track and determine the type of MTB infection, as well as its relationship with demographic factors using PGRS-RFLP.

Methods: In this cross-sectional study, 84 smear-positive patients from 5 frontier provinces (East Azerbaijan, West Azerbaijan, Ardebil, Kurdistan, and Kermanshah) were investigated according to PGRS-RFLP. Demographic data were collected using a questionnaire. The results were analyzed by SPSS-18 and G-Box.

Result: Based on clustering, recent transmission was 66%. Most clusters were obtained from Kurdistan and Kermanshah. Vaccination record ($p = 0.49$) and treatment group (without previous treatment) ($p = 0.004$) had a significant relationship with clustering. Other demographic factors including age, gender, religion, drug abuse, smoking, history of migration, and marital status did not show a significant relationship with clustering.

Conclusion: Genetic variation of MTB is high in this region. The rate of recent transmission based on clustering was unexpected (global average is 30–40%). Recent transmission was more dynamic in west Iran than northwest Iran. The strong relationship between treatment group 1 (without previous treatment) and clustering based on PGRS-RFLP can demonstrate the high correlation between molecular and classic information. In addition, the significant relationship between vaccination record and clustering highlights the necessity to conduct more extensive studies.

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