HOSTED BY

Available at www.sciencedirect.com

ScienceDirect

journal homepage: www.elsevier.com/locate/IJMYCO

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

Bahram Golestani Eimani [a], *Maryam Seyyedi* [b,*], *Leyla Sahebi* [b], *Amir Monfaredan* [c], *Majid Khalili* [d]

[a] *Department of Biology, Islamic Azad University, Urmia Branch, Urmia, Iran*
[b] *Tuberculosis and Lung Disease Research Center, Tabriz University of Medical Science, Tabriz, Iran*
[c] *Tabriz University of Medical Sciences, Tabriz, Iran*
[d] *Medical Philosophy and History Research center, Tabriz University of Medical Sciences, Tabriz, Iran*

ARTICLE INFO

Article history:
Received 21 October 2014
Accepted 26 October 2014
Available online 22 December 2014

Keywords:
Mycobacterium tuberculosis
PGRS-RFLP
Northwest
West
Demographic

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.

© 2014 Asian-African Society for Mycobacteriology. Published by Elsevier Ltd. All rights reserved.

* Corresponding author.
E-mail addresses: golestani_bahram@yahoo.com (B. Golestani Eimani), maryamsiedy@yahoo.com (M. Seyyedi), sahebileila@yahoo.com (L. Sahebi), amir.monfaredan@yahoo.com (A. Monfaredan), khalili876@gmail.com (M. Khalili).
http://dx.doi.org/10.1016/j.ijmyco.2014.10.048
2212-5531/© 2014 Asian-African Society for Mycobacteriology. Published by Elsevier Ltd. All rights reserved.