

## Identification of Mycobacterium Tuberculosis Complex, Using Molecular Methods

**Eramabadi, M. (MSc)**

MSc of Microbiology, Islamic Azad University, Karaj Branch, Iran

**Tadayon, K. (PhD)**

Assistant Professor of Microbiology, Razi Vaccine & Serum Research Institute, Karaj, Iran

**Mosavari, N. (PhD)**

Assistant Professor of Microbiology, Razi Vaccine & Serum Research Institute, Karaj, Iran

**Keshavarz, R. (DVM)**

Doctor of veterinary medicine, Razi Vaccine & Serum Research Institute, Karaj, Iran

**Banihashemi, R. (MSc)**

MSc of Immunology, Razi Vaccine & Serum Research Institute, Karaj, Iran

**Ghaderi, Gh. (PhD)**

PhD of Microbiology, Razi Vaccine & Serum Research Institute, Karaj, Iran

**Sekhavi, M (BSc)**

BSc of Medical laboratory sciences, Razi Vaccine & Serum Research Institute, Karaj, Iran

**Ahmadi, M. (MSc)**

MSc of Microbiology, Razi Vaccine & Serum Research Institute, Karaj, Iran

**Eramabadi, P. (BSc)**

BSc of Microbiology, Islamic Azad University, Sanandaj Branch, Iran

**Khodaverdi Daryan, E. (MSc)**

MSc of Microbiology, Islamic Azad University, Karaj, Iran

**Ya Haghi, E. (MSc)**

MSc of Microbiology, Baqiyatallah University of Medical Sciences, Iran

**Mir Sharafodin, H. (MSc)**

MSc of Economy, Islamic Azad University, Firouz Kauh, Iran

**Corresponding Author:** Tadayon, K.

**Email:** k.tadayon@rvsri.ac.ir

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### Abstract

**Background and Objective:** A high level of homogeneity observed within all bacteria in the *Mycobacterium tuberculosis* complex makes a property that seriously challenges traditional biochemical-based identification methods of these pathogens in the laboratory. The work presented here was conducted to characterize *Mycobacterium tuberculosis* complex isolates in Golestan, Northern Iran.

**Material and Methods:** Between 2008 and 2010, 42 mycobacterial isolates were collected from clinical tuberculosis-suspected patients in Golestan province. The isolates were sub-cultured on fresh Mycobacterium-specific culture media including glycerinated and pyruvated Lowenstein-Jensen slopes. The isolates were subsequently subjected to a PCR-based identification scheme coined Huard-Warren method. This strategy consisted of three individual algorithms namely, 16SrRNA; RV typing (Rv0577, Rv3877.8, Rv1970, Rv3120, Rv1510 and IS1561) and RD typing (RD1, RD 4, RD9 and RD12).

**Results:** All isolates were proved to be *M. tuberculosis*. Furthermore, none of the patients were being infected with any other member of the *M. tuberculosis* complex or simultaneously co-infected with two mycobacteria. This fundamental observation was independently obtained by specific culture media, RV typing and also RD typing.

**Conclusion:** Considering the fact that cattle and sheep farming play an important role in the economy of the region, absence of *Mycobacterium bovis* in the studied isolates can be unexpected to some extent. Huard-Warren which is a simple and cost-effective identification method can be used in both reference and regional laboratory for differential diagnosis of tuberculosis.

**Keywords:** *Mycobacterium Tuberculosis* Complex, Huard-WarrenMethod, 16SrRNA, Golestan Province, RD Typing, RV Typing