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# Burden of potentially novel species of non tuberculosis mycobacteria in Iranian tuberculosis laboratories

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## ABSTRACT

**Aims and objectives:** Nontuberculous mycobacterium (NTM) infections are caused by mycobacteria that are found in water and soil. The chances of missing NTM species are higher in tuberculosis endemic countries like Iran, which are poorly equipped and overburdened with other diseases. The aim of this study is to access the diversity of rare, unusual and frequent species in Iranian tuberculosis laboratories.

**Methods:** From 2012–2014 a total of 243 different clinical isolates of NTM were recovered from Mycobacteriology Reference Laboratories across Iran (Ahvaz, Esfahan, Tehran, Gorgan, Kermanshah). The isolates identified by *rpoB* gene sequencing are useful markers in mycobacterium identification.

**Results:** Based on *rpoB* gene sequencing, 20 groups do not belong to any of the officially recognized mycobacteria. A total of 210 isolates of NTM were identified to species level, including *M. fortuitum* (66), *M. kansasii* (20), *M. simiae* (20), *M. conceptionense* (10), *M. peregrinum* (9), *M. thermoresistibile* (9), *M. gordonae* (8), *M. lentiflavum* (8), *M. phlei* (6), *M. intracellulare* (6), *M. abscessus subsp. abscessus* (5), *M. chelonae* (5), *M. abscessus subsp. bolletii* (4), *M. avium* (4), *M. flavescens* (4), *M. nonchromogenicum* (4), *M. terrae* (4), *M. branderi* (3), *M. iranicum* (3), *M. mucogenicum* (3), *M. scrofulaceum* (3), *M. smegmatis* (3) and *M. triplex* (2).

Among all isolates, *M. fortuitum* was identified as the most frequent encounter (27%) of NTM, and *M. kansasii* and *M. simiae* were the second most dominant species (8.2%) among the isolates. A total of 33 isolates (13%) were unidentifiable to species level. *M. fortuitum* was the most frequent species in Ahvaz, Esfahan, Tehran and Gorgan, but *M. simiae* was the most frequent species in Kermanshah. Thirty-three isolates (20 groups) presented unique genetic features. Further molecular tests should be carried out to reliable identification of these isolates to species level. **Conclusions:** The present study provides evidence for the importance of NTM identification in the clinical setting and the presence of diverse species in clinical samples as a causative agent of disease.

The presence of diverse species of NTM and unidentifiable strains in a clinical setting in Iran emphasizes the use of sequence analysis of genes for reliable identification.

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