

Molecular investigation of isoniazid resistant strains among mycobacterium isolates isolated from patients referred to Ardabil

Abstract

Background: Mycobacterium tuberculosis is a pathogenic species belongs to the Mycobacteriaceae family. As a causative agent of tuberculosis, was first identified in 1882 by Robert Koch. According to the epidemiological studies, almost one third of the world's people are infected with this bacterium. The emergence of MDR and XDR strains and the simultaneous infection of tuberculosis with HIV are a serious human public health threat which should be considered.

Aim: This study was conducted with the aim of identifying Mycobacterium tuberculosis and investigating their resistance to isoniazid.

Materials and methods: In this descriptive cross-sectional study, 111 sputum and BAL samples were collected from patients referred to Ardabil Health Center between 2017-2020. The samples were first examined by microscopic method, then DNA extraction was performed using boiling method. Specific primers and PCR were employed for identifying strains and resistance to isoniazid.

Results: IS6110 gene was used to identify tuberculosis complex strains, based on amplification of this gene, 17 (15.3%) samples were not part of tuberculosis complex and were classified as NTMs. 19 (17%) samples had mutations in one of the inhA and KatG genes, which is responsible for resistance to isoniazid.

Conclusion: In our study, the frequency of resistance to isoniazid was 17%, which is in line with other studies in Iran. Also, 15.3% of the isolates were NTM strain, which shows the importance of using molecular techniques in addition to direct examination and culture to identification and differentiate of this group of strains.

Key words: Mycobacterium tuberculosis, PCR, isoniazid