The relationship between embb306 and embb406 mutations and ethambutol resistant in Mycobacterium tuberculosis isolated from patients in west of Iran

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Abstract

Background: Mutations in emb gene have been reported in ethambutol (EMB) resistance Mycobacterium tuberculosis (M. tuberculosis) isolates. The aim of this study was survey on emb B 306 and 406 EMB resistant M. tuberculosis isolated from patients in West of Iran (2014-2015).

Methods: Fifty strains of M. tuberculosis from patients with pulmonary tuberculosis (TB) were considered. Drug susceptibility using proportional method was performed. Polymerase chain reaction (PCR) -DNA sequencing was applied for mutation in emb B 306 and 406 codon detection. Data were analyzed in SPSS 16 software using descriptive statistics and Fisher's exact test (p<0.05).

Results: In this study 7 (14%) M. tuberculosis isolates were resistant to EMB. 6 (85.71%) and 1 (14.28%) resistant isolates had emb B 306 and 304 codon mutations, respectively. Between embB306 mutations and resistance to EMB and MDR isolates had a significant relationship (p=0.001).

Conclusion: The data indicated that emb B 306 mutations have effect on EMB resistant. Detection of EMB resistant and these mutations prominent for antibiotic prescription.

Keywords: embB gene, Mutations, Ethambutol Resistance, Mycobacterium tuberculosis

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Introduction

Ethambutol (EMB) is one of the first-line drugs that used in the treatment of tuberculosis (TB). Mutations in the embB gene codons have effects on the resistance to EMB. Mutations in embB gene, especially those in the EMB resistance-determining region (ERDR), are considered as "hot-spots". These mutations in different embB gene codon have been frequently reported in EMB-resistant Mycobacterium tuberculosis (M. tuberculosis) isolates (1, 2). In many studies, substitution in different codon of embB gene has been considered as the main position for EMB resistance. BakuBa et al. (2013) in Poland using sequence analysis and polymerase chain reaction (PCR) reported in 17 EMB resistant M. tuberculosis isolates, mutations in codon 306 were most common and found in 9 (52.94%) EMB-resistant isolates (2). Bahrami et al. (2013) using multiplex allele-specific (MAS)-PCR from 176 M. tuberculosis isolates, 48 isolates were found to be resistant to EMB and in the 14 EMB resistant cases,

What is “already known” in this topic:
There are considerations on relationship between mutations that was occurred in embb306 and embb406 genes that lead to ethambutol and MDR resistant in Mycobacterium tuberculosis isolated from patients with TB.

What this article adds:
This study, proved occurrence of embB306 mutations in EMB-resistant M. tuberculosis isolates. A screening using molecular tools in laboratory for EMB-resistant and MDR M. tuberculosis that isolated from patients with TB is necessary before drug prescription.
embb306 and embb406 mutations and ethambutol resistant

Drug susceptibility testing

Drug susceptibility testing of M. tuberculosis (the proportional method) was done according to the standards of mycobacteriological procedures for isoniazid (INH) (0.2 µg/ml), rifampin (RIF) (40 µg/ml), streptomycin (STR) (4 µg/ml), and EMB (2 µg/ml). The H37RV reference strain of M. tuberculosis was served as quality control for EMB susceptibility testing (5).

Polymerase Chain Reaction (PCR) technique

Bacteria that were cultured on Lowenstein-Jensen media were deactivated in the temperature 80°C for one hour. Then DNAs were extracted with the cetyl-trimethyl ammonium bromide (CTAB) method. For EMB-resistant and susceptible isolates, an 863-bp fragment from the ERDR of the embB gene was PCR-amplified. The oligonucleotide primers embB F (5´-CGACGCCGTGGATAATCTTGC-3´) and embB R (5´-CCACGCGTGAATCCTTTG-3´) were used as described previously (2).

Sequencing

For all the samples (50; 100%) that had 863bp band in the electrophoresis, nucleotide sequencing was performed for embB 306 and 406 codon mutations detection automatically (by Macro Gene, a Korean company). The sequence data were analyzed with the Chromas Pro ver. 1.7.1 software program. The nucleotide sequences were translated to amino acids using the European Bioinformatics Institute (EMBL-EBI) website (http://www.ebi.ac.uk/Tools/psa/emboss_needle/index.html). The existence of mutations was determined by comparing the achieved sequences with the M. tuberculosis reference strain H37Rv (ATCC 27294) sequence of embB from the GenBank database (www.ncbi.nlm.nih.gov/genbank/) using the BLASTn algorithm (blast.ncbi.nlm.nih.gov/).

Statistically method

Data were analyzed using SPSS 16 software. Descriptive statistics to determine the frequency and percentage and also Fisher's exact test to compare qualitative findings were used (p<0.05).

Results

Drug susceptibility test result

Drug susceptibility proportional method results showed that of 50 M. tuberculosis isolates, only 17 (86%) strains were sensitive to all drugs, 8 (16%) of strains were multi-drug resistant (MDR) and 25 (50%) were non-MDR. Also 7 (14%) and 43 (86%) M. tuberculosis isolates were resistant and suspect to EMB, respectively. 5 (71.42%) EMB-resistant (100%) M. tuberculosis isolates were in MDR and 2 (28.57%) were in non-MDR group. From 43 nonresistant EMB isolates, 17 (39.53%) were found in sensitive to all drugs group and 23 (53.48%) were in non-MDR group and 3 (6.97%) samples were in MDR group.

Polymerase Chain Reaction (PCR) technique test

PCR results confirmed embB gene for all 50 samples (Fig. 1).

Sequencing results

Also PCR-DNA sequencing for embB 306 and 406 codon showed that in EMB susceptible strains, mutations at the embB 306 codon were not detected. But embB 306 codon point mutation in 6 (85.71%) and embB 406 codon point mutation in 1 (14.28%) of EMB resistant isolates were found (Table 1, Fig. 2).

Statistical results showed that embB306 mutations and resistance to EMB and MDR had a direct relationship with each other (p<0.001).

EmbB306 and embB406 mutations and ethambutol resistant

Tools/psa/emboss_needle/index.html. The existence of mutations was determined by comparing the achieved sequences with the M. tuberculosis reference strain H37Rv (ATCC 27294) sequence of embB from the GenBank database (www.ncbi.nlm.nih.gov/genbank/) using the BLASTn algorithm (blast.ncbi.nlm.nih.gov/).

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Fig. 1. Amplified Fragments of embB Gene with Electrophoresis of PCR products in M. tuberculosis isolates; Line 1, Ladder (100-1500bp); Line 2-8, embB gene in EMB resistance samples (863bp); Line 9, Positive control; Line 10, Negative control.
Discussion

EMB resistance is a serious problem in many countries, so early detection of EMB resistance is very important to avoid resistant strains spread (6). In our study, 86% of strains were sensitive to all antibiotics that were applied. But 16% of strains were MDR, also 50% were non-MDR. In a study in 2015 in Iran, Tavanaee Sani et al. using standard proportional method showed MDR-TB in 56 new cases (1.78%) and 26 (11.53%) patients with relapse during 2012-2013 that it was less than our study. Different rate of resistant can be due to obtaining sample from restricted regions with low or high rate of resistance. For example high rate of resistance can be observed in neighboring of region such as Afghanistan and Pakistan as the most prevalent area for TB (7). In our results, 14% of M. tuberculosis isolates in our results were related with EMB resistant. In other hand PCR-DNA sequencing proved that in all EMB resistant isolates point mutation were occurred. embB 306 codon mutations in 85.71% and embB 406 codon mutation in 14.28% of EMB resistant isolates were found. Nasr Esfahani et al. in Iran in 2016 using standard proportional method reported from 32 M. tuberculosis isolates, 6.25% were resistant to EMB. PCR-Single-strand conformation polymorphism (SSCP) and direct sequencing in Nasr Esfahani Esfahani study detected 2 EMB resistant isolates had mutation in codons 309 and 299 (8). Prevalence of EMB resistant isolates with mutation in our work is higher than Nasr Esfahani study. M. tuberculosis has different mechanisms to ovoid killed by drugs. One of these mechanisms is mutations in embB gene. This gene encodes an arabinosyltransferase that is involved in cell wall arabinan biosynthesis and it is the target for the EMB. Mutation in this gene causes EMB resistant (9). Mour et al. in 2014 in Spain reported that from 53 strains resistant to EMB, 77.4% of strains had mutation substitutions in the embB gene. 53.7% of them were related to codon 306 and 26.8% strains showed mutation in codon 406. Mutations in embB406 were related to EMB resistance and MDR (10). Also embB306 mutations in our study had a significant relationship with EMB resistant and MDR strains. M. tuberculosis is a human pathogen that causes TB and this disease damages the lungs, central nervous system, lymphatic system and circulatory system. So a prevention and appropriate management in treatment for this infection is necessary (11, 12).

Conclusion

In conclusion, the results presented in this study suggest that the frequency of embB306 mutations in EMB-resistant M. tuberculosis isolates, is much higher than its occurrence in EMB-susceptible isolates. These results suggest that the sequencing of this region of embB gene is sufficiently sensitive to be used as a fast screening tool for finding high-level resistance to EMB, specifically in the population served by our research laboratory.

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Conflict of Interests
The authors declare that they have no competing interests.

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