Abstract

The present study was conducted to identify the mutations in *rrs*, *rpsL* and *embB* genes responsible for streptomycin and ethambutol resistance in clinical isolates of *Mycobacterium tuberculosis*. For this purpose, 150 sputum specimens were collected from patients suspected of having pulmonary tuberculosis. Among these, 51 and 54 were smear and culture positive, respectively. Drug susceptibility testing (DST) was performed for four anti-tuberculous drugs viz. ethambutol (EMB), streptomycin (SM), isoniazid (INH) and rifampicin (RMP) by proportion method on Lowenstein-Jensen medium. DST revealed, 2 (3.7 %) *M. tuberculosis* isolates had multidrug resistance, 3 (5.5 %) were EMB resistant, 5 (9.2 %) were SM resistant, 8 (14.8 %) were INH resistant and 7 (12.9 %) were RMP resistant. The DNA of phenotypically resistant isolates was isolated and confirmed for *M. tuberculosis* by performing polymerase chain reaction (PCR) of *IS6110* insertion sequences. PCR and DNA sequencing was performed after designing of primers for *rrs*, *rpsL* and *embB* genes. Of the 5 SM-resistant isolates, 80 % (4/5) had mutations in codon 43 and 88 of *rpsL* gene i.e., AAG was substituted by AGG in resistant isolates. The 2 isolates possessing alteration of nucleotide in codon 43 also had mutations in *rrs* gene at nucleotide 513. The change in nucleotide at positions 513 and 516 in *rrs* gene was detected in 60 % (3/5) isolates which were being replaced by C or T in case of A at position 513 and by T in place of C at position 516. Of the 3 EMB-resistant isolates, nucleotide change in *embB* gene at codon 306 was not observed even in a single isolate. All isolates had wild-type sequences at that codon. Neither insertion nor deletion was observed in *rrs*, *rpsL* and *embB* genes.