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## Prevalence of mutations in drug resistance genes of MDR-TB isolates collected from South Andhra, India

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TB incidence in the developing countries has been assumed to decline as the public welfare has increased and become increasingly accessible for poor people. The onset of HIV pandemic and emergence of Multidrug resistant (MDR) which breakdown some of the national TB control programmes. In 1993, WHO declared Tuberculosis as global emergency. TB control efforts are today seriously threatened by the widespread occurrence of drug resistant strains. A particular dangerous form of drug resistant TB is multidrug resistant TB(MDR-TB) which is defined as resistance to at least isoniazid and rifampicin, the two most powerful anti TB drugs. Unlike other bacteria, in Mycobacterium tuberculosis the drug resistance is exclusively confined to mutations in the chromosomal DNA and is not transferred between bacterial cells by mobile genetic elements such as plasmids. To ensure an effective treatment, drug susceptibility of the infecting M. tuberculosis strain is to be assessed. Traditional techniques for Mycobacterial drug susceptibility testing (DST) are time consuming when a person intends in identification of mutations in resistance conferring genes a rapid detection of drug resistant isolates is very essential. Therefore, in the present paper Genotype MDR plus assay (Hainlife sciences, Germany) was used to study mutation prevalence in MDR TB isolates. The assay combines detection of MTB complex with detection of mutations in the 81-bp hotspot region of rpo B at codon 315 of the Kat G gene and in the inh A promoter region. Among the 233 rifampicin resistant MTB isolates the frequency of rpo B mutations were; 127 missing rpo B WT8 (54.5%), 123 S531L (52.7%), 52 missing WT7 (22.3%), 32 missing WT3 (13.7%), 24 H526Y (10.3%) and missing WT2(10.3%), 20 missing WT4 (8.58%), 17 H526D (8.58%), five D516V (2.14%), three missing WT5 and WT6 (1.28%) and two missing WT1(0.85%). Among the 295 INH resistant MDR-TB strains, Kat G mutations occurred in 169 strains and inh mutations occurred in 134 (45.4%) strains. The most frequently observed Kat G mutation was S315 T1 mutations (55.6%) followed by missing Kat G WT (42%), where as Kat G S315T2 (2.36%) mutation occurred less frequently. Among the 134 inh resistant isolates 65 C15T (48.5%), 66 missing WT1 (49.2%), two missing WT2 (1.5%) and one T8A (0.7%) mutations and no case with A16G and T8C inh mutations. The distribution of mutations identified in our study is significantly different from that reported from other continents. We found that S531L mutation in the rpo B gene occurred most frequently (52.7%) among Rifampicin resistant strains. For INH resistance mutation in the Kat G gene was by far most common and S315T1 mutations was found most frequently (55.6%) in our population. In our study 48.5% INH resistant MTB strains carried a mutation in the inh A promoter region C15T. Thus this study may have potentials for new therapeutic benefits in actual clinical practice.

### Biography

Ch Paramageetham completed her PhD by Winning prestigious Doctoral Fellowship from Council of Scientific and Industrial Research (CSIR), India. She qualified four National level Lecturer ship exams conducted by several National Institutes of India in different subjects. Presently she is heading Microbiology Department in Sri Venkateswara University, Andhra Pradesh, India. She has published more than 35 research papers in reputed journals. Her research interests include exploitation of biotechnological tools to develop transgenics, mining novel genes, and development of antimicrobials from photobionts, plant microbe interactions, molecular microbial diversity Infectious disease genomics and Bioremediation.

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