Abstract

“Analysis of Mutation in katG gene of Multidrug Resistant Mycobacterium tuberculosis and SLC11A1 Polymorphism in Multidrug Resistance Tuberculosis Using PCR-RFLP Technique”

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Abstract

Tuberculosis also known as the white plague has been a persistent and major cause of deaths throughout the globe. Improper use and prescription of antibiotics has caused the re-emergence of the disease in much pernicious forms like multidrug and extremely drug resistant tuberculosis. MDR-TB emerged mainly due to resistance to the two front line drugs; rifampicin (RIF) and isoniazid (INH). Majority of INH resistance occurs due to mutation in katG. Polymorphism in different locus of SLC1A11 gene like INT4 in human chromosome has also been linked with the MDR-TB. MDR screening is carried out by Acid Fast Bacilli (AFB) culture, BACTEC and Polymersase Chain Reaction (PCR) technique. The available techniques are very time consuming yet inconclusive. Even though molecular techniques such as PCR-Restriction Fragment Length Polymorphism (RFLP) is promising and robust, it is very expensive, sophisticated and it suffers from the lack of universal markers for MDR-TB.

Our study involves the screening of MDR-TB isolates from Central Development Region of Nepal for the mutation in katG gene, INT4 polymorphisms and its possible correlation with the drug resistant tuberculosis. Out of the 10 MDR-TB, AFB culture isolates, 2 of the samples were found to harbor Ser315Thr katG mutation. While none of the 10 blood samples for the MDR-TB patients showed G/C polymorphisms for INT4.

However, due to less number of samples screened, these findings do not conclusively represent the actual scenario in the whole population of Nepal. Further, we have taken H37Rv, the wide spread MTB strain, as our reference strain. But there is also a possibility of presence of other clinical strains, which
cannot be determined unless strain verification using PCR-Sequencing is done. And this situation can also create misinterpretation of data.