> Indian J Med Res. 2016 Dec;144(6):924-928. doi: 10.4103/ijmr.IJMR_684_14.

Genetic Polymorphisms of N-acetyltransferase 2 & Susceptibility to Antituberculosis Drug-Induced Hepatotoxicity

Surendra K Sharma [1], Brajesh Kumar Jha [1], Abhishek Sharma [1], V Sreenivas [2], Vishwanath Upadhyay [1], Chandrita Jaisinghani [1], Rohit Singla [1], Hemant Kumar Mishra [1], Manish Soneja [1]

Affiliations + expand

PMID: 28474630 PMCID: PMC5433286 DOI: 10.4103/ijmr.IJMR_684_14

Free PMC article

Abstract

Background & objectives: The N-acetyltransferase 2 (NAT2) gene encodes an enzyme which both activates and deactivates arylamine and other drugs and carcinogens. This study was aimed to investigate the role of NAT2 gene polymorphism in anti-tuberculosis drug-induced hepatotoxicity (DIH).

Methods: In this prospective study, polymerase chain reaction-restriction fragment length polymorphism results for NAT2 gene were compared between 185 tuberculosis patients who did not develop DIH and 105 tuberculosis patients who developed DIH while on anti-tuberculosis drugs.

Results: Frequency of slow-acetylator genotype was commonly encountered and was not significantly different between DIH (82.8%) and non-DIH (77.2%) patients. However, the genotypic distribution of variant NAT2FNx015/FNx017 amongst slow-acetylator genotypes was significantly higher in DIH (56%) group as compared to non-DIH (39%) group (odds ratio 2.02; P=0.006).

Interpretation & conclusions: The present study demonstrated no association between NAT2 genotype and DIH in the north Indian patients with tuberculosis.

Conflict of interest statement

Conflicts of Interest: None.