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Association of *NAT2* gene polymorphism with anti-tubercular drug induced hepatotoxicity in North Indian population

Background: Tuberculosis (TB) is one of the important causes of global mortality and morbidity. Hepatotoxicity is a most serious adverse drug reaction of anti-TB drugs. Various genetic factors are associated with drug-induced hepatotoxicity (DIH). Anti-tubercular drugs are mostly metabolized by N-acetyltransferase 2 (*NAT2*). Therefore, in this study we aim to assess the association between of *NAT2*genotype polymorphism and drug-induced hepatotoxicity (DIH) in North India population.

Methods: TB patients were recruited in two groups. Seventy (70) TB patients were enrolled as tolerant control group who did not develop DIH, whereas 30 TB patients in anti-tubercular DIH group who developed liver injury during treatment. The genetic polymorphisms of the *NAT2* genes were analyses by PCR-RFLP. Genotype and allele frequencies were evaluated by t-test and odds ratio (OR) with 95% confidence intervals (CIs) to evaluate the strength of associations.

Results: There is high percentage of slow acetylators among North Indian population. The 4% people were fast acetylators, 34% were intermediate acetylators and 62% were slow acetylators. Patients with the slow acetylator genotypes were most common and there was no significant difference between DIH (73.33%) and non-DIH (61.40%) patients. However, the slow-acetylator genotypes (*NAT2**6/7, *NAT2**5/7 and *NAT2**5/6) were also not significantly different in anti-tubercular DIH group and tolerant control group.

Conclusion: In present study, *NAT2* genotype polymorphism was found to have no association with development of anti- tubercular DIH

Biography

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