DNA methyltransferases 3A −448 G/A and 3B −149C/T single nucleotide polymorphisms in primary immune thrombocytopenia

Alaa S. Abd-Elkader, Tarek T.H. ElMelegy, Eman NasrEldin, Zeinab A. Abd-Elhafez

Abstract:

Background Primary immune thrombocytopenia (ITP) is a common hematological disorder of unknown etiology. DNA methylation is a major epigenetic modification of the DNA. It has a golden role in gene expression. It is mediated by DNA methyltransferases (DNMTs). The promoter of DNMT3B gene contains some single-nucleotide polymorphisms (SNPs) including that at position −149 (C/T), which was suggested to be implicated in the genetic susceptibility to ITP. The DNMT3A −448 G/A SNP in the gene promoter was found to have a protective effect against systemic lupus erythematosus. Aim The aim of the study was to investigate the association between DNMT3A −448 G/A SNP (rs1550117) and DNMT3B −149C/T SNP (rs2424913), and the risk for primary ITP and to evaluate the association between these SNPs and patients response to therapy. Participants and methods This prospective case–control study was conducted on 60 primary ITP patients and 30 healthy age-matched and sex-matched controls. Genotype analysis of DNMT3A −448 G/A and DNMT3B −149C/T was done using PCR-restriction fragment length polymorphism. Results The frequency of the DNMT3A −448 G/A SNP variant A-allele was significantly decreased in primary ITP patients compared with controls (odds ratio=0.829, 95% CI=0.097–0.964). DNMT3B −149C/T SNP variant T-allele was significantly higher in ITP patients with almost doublefold increase in the risk of ITP in comparison to controls (odds ratio=1.731, 95%CI=1.121–2.582). Conclusion The DNMT3A −448 SNP variant A-allele might has a protective effect against ITP. Also, the DNMT3B −149 SNP variant T-allele could be considered as a molecular risk factor for ITP.

Keywords:

DNMT3A, DNMT3B gene, primary immune thrombocytopenia, single-nucleotide polymorphism

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