

Investigation of GSTP1 (Ile105Val) Gene Polymorphism in Chronic Myeloid Leukaemia Patients

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ABSTRACT The factors leading to the development of Chronic Myeloid Leukemia (CML) are not fully known. Associations between polymorphisms for genes encoding Glutathione S-transferase (GST) enzymes involved in Phase II detoxification reactions and susceptibility to some cancers have been shown in several studies. The aim of the present study was to investigate the influence of the GSTP1 (Ile105Val) gene polymorphism on human susceptibility to CML. Seventy-one CML patients and 67 control subjects with no cancer history were enrolled in our study. The polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) method was used to identify the GSTP1 (Ile105Val) gene polymorphism. Genotypes were determined according to the bands that formed in agarose gels via gel electrophoresis. Leukocytes in the CML patient group were significantly different from those in the control group ($p=0.0001$). The frequency of the GSTP1 Val allele was found to be 22% in CML patients and 31% in controls. However, no statistical variation was found to exist between controls and patients in terms of the GSTP1 Val allele frequency ($p=0.199$). The relationship between the GSTP1 (Ile105Val) gene polymorphism and CML is not fully understood. Our results provide no evidence of a relationship between the GSTP1 (Ile105Val) gene polymorphism and susceptibility to CML in Turkish patients. However, these findings should be confirmed in studies with larger sample sizes.