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Letter to the Editor

Association of MMP-2 (-1306 C>T), MMP-9 (-1562 C>T) Gene Polymorphism and the Formation of the Hematological Malignancies

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Dear Editor-in-Chief

Matrix metalloproteinases (MMPs) are a large family of zinc-containing proteases several functions of the MMPs were identified in various systems such as cell migration/invasion, apoptosis/cell survival, and angiogenesis (1). Besides, MMP-2 and MMP-9 have important implications in the progression and invasiveness of several hematological malignancies, including Hodgkin lymphomas (HL), malignant non-Hodgkin lymphomas (NHL), chronic myeloid leukemia (CML) and acute myeloid leukemia (AML) (2). Functional single nucleotide polymorphisms (SNPs) have been identified for the two molecules: SNP in the promoter of the MMP-2 gene (-1306 C>T) 1 and MMP-9 gene (-1562 C>T) polymorphisms (3) that have effect the expressions of the genes. The aim of the study was to assess the relationship between the SNPs and hematological malignancies.

This cross-sectional and retrospective analysis was performed for the patients diagnosed between 2006- 2007 at Mersin University Hospital. The patient group was comprised of 52 chronic lymphocytic leukemia (CLL), 20 HL, 38 NHL, 15 acute lymphocytic leukemia (ALL), 14 multiple myeloma (MM) patients. The control group included 110 healthy individuals.

The study was approved by the local Ethic Committee and informed consent was obtained from all patients. DNA was extracted from venous blood and used for the polymerase chain reaction, restriction fragment length polymorphism (PCR-RFLP) assays. MMP-2 genotypes were CC, CT and TT and had band sizes of 193-bp, 193/167/26-bp, 167/26-bp *PCR* product and MMP-9 genotypes were CC, CT and TT and had band sizes of 436-bp, 436/242/194-bp, 242/194-bp *PCR* product, respectively for the SNPs.

All data analysis was performed using SPSS version 11.5 (Chicago, IL, USA). The average age of the control group was 56.53 yr (SD=11.37) and the patient group was 59.02 yr (SD=11.02), not calculated difference between two age groups (P=0.117, P>0.05). The patient and control subjects allele frequencies for MMP-2 (-1306 C>T) (Patient P=0.389, Control P=0.392, P>0.05) and MMP-9 (-1562 C>T) (Patient P=0.816, Control P=0.302, P>0.05) were consistent with Hardy-Weinberg equilibrium. There was no significant difference in Pearson chi square analysis between the patient and control groups in genotype distribution of MMP-2 (P>0.05). There was a significant difference in the Pearson chi square (x2) analysis between the HH group and control

groups in genotype distribution of MMP-9 SNP (HL P=0.016, P<0.005), contrarily, no statistical correlation determined by the other patient groups for the same SNP (P>0.05). The logistic regression analysis designed for this observation, then compared the CT/TT genotypes with the CC allele that taking the referent, and no significance revealed for the MMP-9 promoter high activity genotype (P=0.104, P>0.05).

So far MMPs have an important role in the progression of hematological malignancies (4). The studies with the lymphoid cell lines and animal models have shown that increased expressions of MMP2 and MMP9 have been correlated with greater invasive and metastatic potential (5). In concordance with this increased MMP-9 expression was related to adverse prognosis in patients with chronic lymphocytic leukemia, T-ALL, AML (5, 6). MMP-2 expression in adult ALL was associated with the expression levels have been found higher in extramedullary infiltration in myelodysplastic syndrome than controls (4). No significance between lymphoid malignancy formation and the genotype distributions of MMP-9 (-1562 C>T) (P>0.05) and MMP-2 (-1306 C>T) was found. The high T allele frequency of the MMP-9 (-1562 C>T) determined in our study can be associated with increased gene expression due to the high promoter activity of T allele (3) in the HL group and, this proposition has been supported by increased MMP-9 expression in HL (7) but we could not confirm this proposition with our statistical results. However, we did not follow the prognosis of the patients and didn't get any data about the SNPs and progression relation.

In conclusion, we revealed any statistical relation between the MMP2, MMP-9 SNPs and our lymphoid malignancy group. Future research will be done about the same matter with higher number of patients or about the possible relation between the hematological malignancy prognosis and the MMPs SNPs would be a contribution to the literature.

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The authors declare that there is no conflict of interests.

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