EPIGENETIC ANALYSIS OF *PTCH1* GENE IN THE PATIENTS WITH GASTRIC CANCER

SUMMARY

Gastric cancer is the fourth most common cancer diagnosed worlwide. It also has high mortality rates with poor prognosis for patients. In some molecular studies, it has been shown that the dysregulation of the PTCH1 receptor, a protein in hedgehog signaling pathway, leads to the gastric cancer. Thus, the aim of the present study was to observe the epigenetic changes of the *PTCH1* gene and related expressional differences in the gastric tumoral tissues of the patients undergone surgical gastrectomy.Both tumoral tissues and tissues far from the tumor (control) that were collected from13 male and 9 female patients (age range of 50-70 years) diagnosed with gastric cancer were included in the present study.DNA extraction procedures were performed on the included tissues with commercial extraction kit. After the determination of the concentrations of the isolated DNAs, bisulfite conversion was performed under appropriate conditions, and then quantitative real-time polymerase chain reaction (RT-qPCR),using methylated and non-methylated primers, was performed by EpiTect Methyl 2 PCR System in order to define the changes in the methylation profile of the *PTCH1* gene. Moreover, the expressions of the PTCH1 protein were measured with ELISA (Enzyme-Linked Immuno Sorbent Assay) method in homogenized tissue samples in order to observe the changes in the PTCH1 protein. According to the result of RT-PCR measurements, it was determined that 0.5 ± 0.25 degrees difference was observed in the melting temperature between tumor tissue and control tissue suggesting that methylation profiles of *PTCH1* gene in tumor tissues changed compared to that of the healthy tissues. Based on the evaluation of the protein expressions, it was found that the amount of the PTCH1 protein was significantly increased in the tumoral tissues ($p<0,05$). Depending on the data obtained from the study, PTCH1 protein expression having an effect on gastric cancer progression while no statistically significant change was observed in the methylation profile of the

PTCH1 gene, it is thought that the increase in the PTCH1 protein is not directly associated with epigenetic changes.

Keywords: Gastric cancer, *PTCH1* gene, epigenetics, RT-PCR.