

Abstract :

Breast cancer is the most common cancer among women and the second leading cause of death after lung cancer and include 32% of all kinds of cancers among women. Beside several known genetic alterations, several epigenetic alterations have been discovered that are involved in the process of tumorigenesis in breast tissue and lead to sustainable change in patherns of gene expression in cells and can cause cancer progression. *HER2* proto-oncogene encoding a protein that targets an intracellular signaling pathways and plays an important role in growth, differentiation, survival and cell adhesion. This gene is inactivated by genetic and epigenetic different mechanisms such as hypermethylation. The purpose of this study is to evaluate the methylation of promoter gene *HER2* and to determine it's possible association with prognostic factors in the studied pateints. 40 samples of blood and breast tissue of patients with invasive ductal carcinoma and 10 samples of blood and normal tissues of healthy people were collected from those who came to the cancer center academic Jahad. After DNA extraction from blood and tissue samples, concentrations were determined by spectrophotometry and then appropriate samples were placed in freezer -70°C . The methylation status of the target gene was assessed using Methylation Specific PCR method. After electrophoresis, data was analyzed using software SPSS ver 19. Ficher Exact Test and Chi square, for two-state variables and Kruskal Wallis Test and Chi square, for three-state variables with a significance level of $p>0.05$ were used. following the study, 30% of tissue samples and 30% of blood samples were hypermethylated. Evaluation results showed no significantly association between *HER2* hypermethylation and studied factors. But as expected, *HER2* hypermethylation was significantly associated ($p=0.03$) with the absence of *HER2* gene expression as a prognostic factor, that indicated the greatest role of methylation in the inactivation of this gene in Iranian patients.

Key word: Breast cancer, methylation, *HER2* gene.



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