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Investigation of Methylation Changes of VIM, CXCR4, DOK7 and SPDEF Genes by Evaluation of Peripheral Blood Leukocyte DNA in Breast Cancer

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Abstract

Introduction Breast cancer is the most common cancer in Iranian women. There are some evidences that epigenetic factors may be one of the risk factors for breast cancer. Epigenetic is defined as the study of heritable changes in gene expression, which occur in the absence of a DNA sequence change and is believed to be important in the etiology of common human diseases including cancer. Evaluating blood DNA methylation as a biomarker for cancer is of particular interest because peripheral blood DNA is a convenient tissue to assay for constitutional methylation. Molecular markers could have important applications in staging and the clinical diagnosis of breast cancer. In the present study, we investigated the methylation status of VIM, CXCR4, DOK7 and SPDEF genes in breast cancer.

Materials and Methods: 60 patients with breast cancer and 40 healthy controls were studied. Isolation of genomic DNA from peripheral blood and restriction enzyme polymerase chain reaction (REP) were applied for analysis. Real-Time PCR is used to study more closely of these genes methylation and to find the difference in methylation between normal and breast cancer in REP technique.

Results: Difference between percentage of hypermethylation of DOK7 promoter in normal and breast cancer samples was significant (P value=0.001). Also, our research indicated VIM and CXCR4 genes are significantly hypomethylated in breast cancer. Difference between percentage of hypermethylation of SPDEF promoter in normal and breast cancer samples was no significant (P value=0.2).

Conclusions: Hypermethylation of DOK7 gene in blood DNA from breast cancer patients offer as a biomarker for diagnosis of the malignancy. Also, this study indicated VIM and CXCR4 gene methylation change in breast cancer and these can be used as molecular biomarker for breast cancer prognosis.