

Expression of DNMT Enzymes-Regulated miRNAs Involving in Epigenetic Event of Tumor and Margin Tissues in Patients with Breast Cancer

Authors : Fatemeh Zeinali Sehrigh

Abstract : Background: Breast cancer is the most common and deadly cancer among women. The incidence of breast cancer depends on various genetic, epigenetic and environmental factors. DNA methylation and miRNAs are the most important epigenetic factors involved in breast cancer. miRNAs play an important role in the post-transcriptional regulation of genes, including genes involved in DNA methylation (DNMTs), and are also important regulators of oncogenic pathways. The study of microRNAs and DNMTs in Breast cancer allows the development of targeted treatments and early detection of this cancer. Methods and Materials: Experimental Statistical significance of differences in miRNAs and DNMTs relative expression results were analyzed by pair-wise fixed reallocation randomization test as a statistical model included in the REST (relative expression software tool). In silico analysis confirmed that microarray datasets miRNAs and DNMTs were downloaded from the GEO database. The analysis was defined using the Affy packages in R software to screen remarkably dysregulated miRNAs and DNMTs. the target genes in terms of molecular pathways in the web, Gestalt and GO (Gene Ontology) that specify the biological processes of molecular functions and cellular components to be investigated. In laboratory studies, sampling was done from 100 women with breast cancer and 100 healthy women with written consent. Tissue RNA was extracted using a Trizol solution. Then, using the cDNA synthesis kit, DNA was synthesized from the extracted RNAs, and the expression level of miR-509-3-5p and miR-596 was investigated using the Realtime PCR method. Results: In the present study, we found significant (p -value <0.05) changes in the expression level of miRNAs and DNMTs in patients with breast cancer. In bioinformatics studies, the GEO microarray data set, similar to qPCR results, showed a decreased expression of miRNAs and an increased expression of DNMTs in breast cancer. Conclusion: The results of the present study, which showed a decrease in the expression of miRNAs and DNMTs in breast cancer, suggest that these genes can be used as important diagnostic and therapeutic biomarkers in breast cancer.

Keywords : expression omnibus (GEO), microarray dataset, breast cancer, miRNA

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