Expression Patterns of mir181a and mir30d in Patients with Breast Cancer

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Abstract: Background: Breast cancer is common cancer among women in the world. One of the important molecular pathways in breast cancer is the PTEN-Pi3K-AKT pathway. Any change in the activity of the PTEN gene can alter the PI3K-AKT pathway. Moreover, there are subsets of genes and pathways whose expression changes by post-transcriptional regulations. For instance, gene regulation alters by non-coding RNAs such as micro-RNAs as post-transcriptional regulators that prevent the expression of the target transcript. Therefore, it is essential to assess the related alterations in micro-RNA expression patterns to find out the possible causes of conversions in related transcripts and pathways, such as the PTEN-Pi3K-AKT pathway in breast cancer. Methods: To determine the expression level of miR-181a and miR-30d in 30 breast tumor samples and 30 adjacent normal samples, the RNA extraction, and cDNA synthesis were performed by RiboEx (GeneAll, Korea). Finally, the Real-Time PCR method was used for quantitative analysis of the expression levels of these miRNAs. Results: After analyzing comparisons in the expression level of miR-181a and miR-30d in tumor and normal tissues, it was found that there was a significant increase in the expression level of miR-181a in tumor samples compared with normal samples. Also, the expression level of miR-30d in tumor samples reported a significant decrease in comparison with normal samples (P<0.05). Conclusion: In this study, we concluded that upregulation of miR-181a may affect the transcription of the PTEN gene resulting in the cell progress to cancer. The Downregulation of miR-30d may also lead to cancer cell growth due to a reduction in the affecting of the CREB gene transcript.

Keywords: breast cancer, micro RNAs, real-time PCR, post-transcriptional regulation

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