Evaluation of has-circ-00001724 gene expression in breast cancer patients and its relationship to disease prognosis

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Abstract

Introduction: Breast cancer is a leading cause of cancer-related deaths in females[1], and circular RNAs (circRNAs) have emerged as a novel class of noncoding RNAs that play regulatory roles in angiogenesis and cancer progression. The study of the expression patterns and functional roles of circRNAs in breast cancer has become an area of growing interest. The aim of this study was to investigate the relationship between hsa-circ-00001724 gene expression and breast cancer. method: Circular RNAs were extracted from tissue samples and cDNAs were synthesized, followed by RT-PCR of the glyceraldehyde-3-phosphate dehydrogenase gene as an internal control to ensure the quality of the synthesized cDNA samples. Negative controls were used in RT-PCR and qRT-PCR to exclude contamination with genomic DNA and PCR materials, and a positive control test was also performed. The most appropriate primer sequences were selected using OligoAnalyzer software and the NCBI website, and real-time PCR using SYBR Green was used to examine expression changes. The CT number was determined from the data obtained, and the resulting graphs were examined in terms of dimer formation. The Ct values of normal and tumor samples of the CIRC gene were also subjected to a parametric Kolmogorov-Smirnov test. Results: Real-time PCR reaction results revealed that the hsa-circ-00001724 gene had lower expression in cancer tumor samples than in non-tumor samples. Conclusion: Based on these results, it is hypothesized that hsa-circ-00001724 may serve as a potential biomarker for breast cancer diagnosis and prognosis, and may also be a potential target for therapeutic purposes.

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