

Investigating the Relationship between Human Breast Tumor Grading and Beta Estrogen Receptor Expression

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Abstract

Background: Breast cancer represents the most prevalent cancer among women and ranks as the third leading cause of cancer-related mortality in females. Given the critical role of early cancer detection, identifying biomarkers related to breast cancer is essential for prognosis and early identification. This study aims to explore the differential expression of the estrogen receptor- β (ESR β) gene in cancerous tissue samples compared to standard tissue samples, aiming to identify a biomarker for predicting cancer prognosis.

Method: This study collected 60 fresh tissue samples from breast cancer patients post-surgery, comprising 30 tumor samples and 30 standard samples adjacent to the tumor, which were immediately stored at -70°C . Following RNA extraction and cDNA synthesis, the expression levels of the ESR β gene and the Gapdh gene (as an internal control) were analyzed using the real-time polymerase chain reaction method.

Results: The study examined the variation in ESR β gene expression between tumor tissues and adjacent healthy tissues in breast cancer patients. An increase in gene expression was observed in tumor samples compared with the adjacent healthy tissue. Furthermore, statistical analysis using SPSS software revealed a significant correlation between the gene expression level and tumor grade across all examined groups. Additionally, the findings indicate a significant difference in gene expression between patients with and without tumor metastasis.

Conclusion: The ESR β gene holds potential as a biomarker for breast cancer prognosis.

Keywords: Breast cancer, Estrogen receptor- β , Gene, Real-time polymerase chain reaction

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