

SFRP1 Gene Expression Analysis in Tumor and Normal Breast Tissue of Breast Cancer Patients

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Abstract

Introduction: Breast cancer is the second and the most common cancers among women in the world. The diagnosis in the early stages increases patient's chance of recovery and survival. Regarding the heterogeneity of cancers, including breast cancer, participating genes in the pathways leading to this cancer and comparing their expression in different stages can be effective in prognosis, diagnosis and treatment. SFRP1 acts as moderators of the Wnt in signaling path. Considering the importance of this gene as a tumor suppressor in various cancer cell lines, in the present study SFRP1 expression in tumor and normal adjacent breast tissue were studied in breast cancer patients.

Material and Methods: In this project, the Real-Time RT-PCR technique was used to analyze expression of SFRP1 gene in tumor and normal adjacent breast tissue of 35 patients with ductal carcinoma breast cancer. SPSS software and proper statistics methods were used for statistical evaluation.

Results: Our data indicated SFRP1 gene down regulation in tumors compared with normal adjacent breast tissues.

Conclusions: The SFRP1 gene can be used as a potential biomarker related to breast cancer.