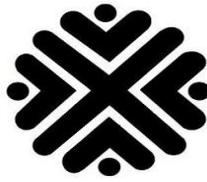


Abstract :

In many countries, including developed countries, breast cancer is the most common cancer in women. In Iran, breast cancer which has the frequency equal to 15/9 is the most common malignancy and the attacked age is 10 years less than in Western countries. New statistics reports comparing with previous reports statistics indicate a relatively rapid increase in the incidence of the disease in Iranian women. Great majority of human breast cancers arise from epithelial cell that surround lobular and ductal mammary gland. The evolution of breast cancer is accompanied by multiple genetic changes that result in qualitative and quantitative alterations in individual gene expression. Many of these quantitative genetic changes manifest themselves as alterations in the cellular complement of novel transcribed mRNAs. Identification of these mRNAs, if sufficiently characterized, could provide clinically useful information for patient management and prognosis while enhancing our understanding of breast cancer pathogenesis. One of the newest of these genes is *SCGB2A2* that alteration of its expression in breast tumor tissue has been reported in recent year's research. The function of this gene is unknown, related family members are small, epithelial secretory proteins that can either modulate inflammatory processes or bind steroid ligands. According to the importance and necessity of study of breast cancer patient, in this research we analyzed the expression of *SCGB2A2* genes in breast cancer patient of Sistan and Balouchestan, bam and Kerman. In this study, twenty-two control samples and seventeen samples of breast cancer tumour were collected. Then, to study the qualitative and quantitative *SCGB2A2* gene expression of collected tissues, RNA was extracted from all samples and expression analysed performed by real time PCR method. Data showed significant difference in *SCGB2A2* mRNA gene expressions among normal tissue and tumor ones. The results indicate that the expression of *SCGB2A2* gene in tumor breast samples is many times more than the control groups. We did not find any significant differences in *SCGB2A2* mRNA expressions in grade III tumors in contrary with Grade I and Grade II tumors.

Key words: breast cancer, gene expression, Real-Time RT PCR, tumor marker, *SCGB2A2*.



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**The Thesis Submitted for the Degree of Master of Science
(in the field of Genetic)**

**Detection of SCGB2A2 expression in
breast cancer tissue with Real-time
Reverse Transcriptase Polymerase Chain
Reaction**

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