

عنوان مقاله:

Investigation and Comparison of margin and tumor in breast cancer patient (Iominal A) by proteomic approach

محل انتشار:

هشتمین سمینار کشوری مشاوره ژنتیک و نقش آن در پیشگیری از معلولیت ها (سال: 1398)

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خلاصه مقاله:

Background and Aim : Background and Objective: According to observations of epidemiology and morphology of breast cancer, it is widely classified as In Situ Carcinoma and Invasive Carcinoma. The most common type of Invasive Ductal Carcinoma (IDC) is called Stage 1 Breast Cancer, the Early Stage. At this stage, the size of the tumor is less than 3 cm and negative lymph node involvement is reported, resulting in no metastasis called T1N0M0. At this stage, biological biomarkers also indicate that ER +, PR + and HER-2_ negative are reported. This work is done by identifying interpretive terms enriched in the list of genes with different expressions. In this study, we try to examine the expression of breast cancer tissue proteins in Stage 1 and compare it with healthy breast tissue, and analyze the expression of breast cancer induced biomarkers and analyze the pathways of Angritic biomarkers by meaningful proteins of these pathways. We compare healthy breast tissue. Finally, the biomarker panel is introduced to design a related drug. **Methods :** Materials and Methods: First, 10 patients with Stage 1 breast cancer were treated by a 150-millimeter surgeon from the breast tumor of the stomach tumor (according to the pathologic and surgical procedure) and 150 mg of tissue during surgery, is sampled. Using the standard method of trezole, we extract proteins and compare them with the help of two-dimensional and soft-electrophoresis electrophoresis and gene ontology studies and with the aid of Progenesis Same Spot software , as follows: the pattern of expression of the tumor tissue of the tumor staining and the healthy tissue of the breast. **Results :** Findings: The protein related examined revealed that there are prognostic biomarkers like BRCA1, BRCA2 and CA15-3 involved in breast cancer. As well as this we found that there are multiple protein patterns like COX2 and TACSTD1 that plays a crucial role in enhancing the development of breast cancer tumors by effecting certain cell cycle and mitosis associated biological processes. Ultimately the role of differentially expressed genes cannot be denied and some like HMGB3, CDC45 and NEB with the P values of 0.0016, 0.0036 and 0.0038 have been found to have an outstanding the breast cancer improvement in the view of proteomic approach. **Conclusion :** Conclusion: In relation with analyzing the proteomics the aimed triggers are in hand and further precaution to treat the breast cancer is possible due to the proteomic profile pattern which is ... based on the investigation of prognostic biomarkers, multiple protein patterns and diff

کلمات کلیدی:

Keywords: Biomarker, meaningful protein, 2 dimensional electrophoresis, gene oncology

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