

Alternative splicing of BRCA1 in Breast tumors

Abstract:

Background and objective : Breast cancer is the most pervasive cancer among women. About 33 percent of cancers in women is the Breast cancers.

Various evidences indicate that Breast cancer drive from various genetic and epigenetic alternations of oncogenes, tumor suppressor genes and DNA repair genes.

This study has been focused on the investigating Alternative splicing of BRCA1 genes as a tumor suppressor in the Breast tumor patient for approaching a prognostic value.

Materials and methods: 50 samples of tumor pations has been prepared through surgery prosegers with Breast concer. They were invited to Day hospital in Tehran . Then RNA were extracted from patient tumors, and first strand cDNA were synthesized Then through designed primers, cDNA had been generated through nested RT-PCR.

After electrophoresis different splicing from the splicing with complete length were separated .

Result: After verifying the alternative splicing gene of BRCA1 in the tumor sample of patient in has been recognized that there is an acceptable coordination between the stage of cancer and involved lynph node with the omitted piece of b from the exon 11. in the study other data there is no meaningful statistics between other pathologic data that include the receptor of Estrogen and progesterone, grade of tumor and the type of pathology.

Discussion: According to this study, we can use alternative splicing data of this gene beside the pathological information for specifying the malignancy situation of tumor. So we can predispose the survival of the patients with more studies.

Key word: Breast tumors, BRCA1 , Alternative splicing