عنوان مقاله:

Bioinformatic Evaluation Of miR-1278 And rs3798577 In 3'UTR of ESR1 As a Potential Prognostic Biomarker In Breast Cancer

محل انتشار:

یازدهمین کنگره بین المللی سرطان پستان (سال: 1394)

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خلاصه مقاله:

Background: Breast cancer is the most common cause of cancer death among women worldwide. Aberration in signal transduction pathway of Esr1 gene in human tumors is a common phenomenon. Esr1 overexpression has been observed in approximately 75% of breast cancer cases. miRNAs are the large subgroup of noncoding RNAs with 18-25 nucleotides inhibiting the expression of target genes by means of binding to their 3'UTR. They also can play role as an oncogene and/or tumor suppressor. In recent years, the association of some SNPs located in either miRNA seeds or 3'UTR of their target genes with the risk of breast cancer have been proved in some populations.Material and methods: miRNASNP database was used to identify the miRNAs with the ability of binding to the 3'UTR of Esr1 transcripts. In next step, miRTarBase andDAVID databases were used to investigate the function and the related signaling pathways of obtained miRNAs. Results: In silico investigation of SNPs in the 3'UTR of ESR1 gene showed that rs3798577 could alter the binding properties of miR-1278. By reviewing the literature and with regards to molecular enrichment analysis from miRWalk and DAIVID database, we realized that miR-1278 targetome could act in some molecular signaling pathways such as: PI3K-AKT, JAK/STAT and MAPK and also could target ESR1,SP1, HOXC9, SOX1, TGIF2 genes. Since rs3798577 causes change of binding between miR-1278 and its target (ESR1), this SNP could be proposed as a prognostic factor by altering the activity of miR-1278. Conclusion: According to our data, miR-1278 and its SNP may be involved in breast cancer prognosis by altering regulation of some vital signaling .pathways mRNAs

کلمات کلیدی:

Breast Cancer, Esr1, microRNA, SNP

لینک ثابت مقاله در پایگاه سیویلیکا: