

## عنوان مقاله:

In-silico analysis of hsa-mir-196a targetome pathway and its SNP function in patients with breastcancer: potential association between T allele and the risk of metastasis

## محل انتشار:

دهمین کنگره بین المللی سرطان پستان (سال: 1393)

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## خلاصه مقاله:

Prostate cancer and breast cancer are the most common neoplasia in men and women respectively. Three main treatments including surgery, chemotherapy and radiation therapy are used to treat cancer patients. However, the future of cancer treatment lies in genetic treatment options providing with a personalized medicine which will consider specific treatment individually. Nowadays treatment options based on the genetic variations occurring in specific individuals are being offered. SNPs are the most important biomarker for personalized medicine. Micro RNA regulates gene expression at the post-transcriptional level and involves in diverse biological and pathological processes including angiogenesis pathways. The miR-196a has been experimented in lung, esophageal, gastric and breast cancers. Objective: The aim of our study is to expand current knowledge about molecular function of miR-196a and its SNP in breast cancer cells by using bioinformatics tools. Methods: Validated and predicted targets of miR-196a were obtained from MiRtarbase and MiRwalk databases respectively. UniGene and DAVID databases were used for further analysis. MIRSNP database predicts single nucleotide polymorphism in miR-196a and its function. Results: It is predicted that miR-196a acts as a critical tumor suppressor micro RNA by inhibiting some important genes in sustained angiogenesis pathway such as FGFR, STAT3, ERK, ITGA and Ikb $\alpha$ . Moreover, the stability of stem loop structure of pre-mir-196a is decreased by T allele due to increasing gibbs free energy of the structure. As a result, there is a probable association between T allele carriers and poor prognostic breast cancer. In other words, T allele may contribute to intensify tumor growth and metastasis due to angiogenesis pathway alteration. Conclusion: According to our data, miR-196a and its SNP may be involved in breast cancer prognosis by altering regulation of angiogenesis and some vital signaling pathways mRNAs. To sum up, T allele in this location can have prognostic value for angiogenesis and metastasis phenotypes in patients with breast carcinoma.

## کلمات کلیدی:

Breast cancer, miR-196a, SNP, angiogenesis, metastasis

