عنوان مقاله:

in-silico analysis of hsa-mir-146a targetome pathway and its SNP function in patients with breastcancer: probable association between alleles and prognosis

محل انتشار:

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نویسندگان:

Mahboobeh Meshkat - *Division of cellular and molecular biology, Department of biology, Nourdanesh University ofMeymeh, Meymeh, Isfahan, Iran*

Hamzeh Mesrian Tanha - *Department of Biology, Faculty of Science, University of Isfahan, Isfahan, Iran*

Kamran Ghaedi - *Zistfanavari Novin biotechnology institute, Isfahan, Iran*

Mansoureh Azadeh - *Zistfanavari Novin biotechnology institute, Isfahan, Iran*

خلاصه مقاله:

Background: According to the World Health Organization, breast cancer is the most common diagnosed cancer in women. MicroRNAs (miRNAs) are causing tremendous excitement in cancer research. miRNAs have been shown to regulate oncogenes, tumor suppressors and a number of cancerrelated genes. mir-146a is a tumor suppressor miRNA proposed as a biomarker in breast cancer. Objective: the aim of our study is to expand current knowledge about molecular function of miR-146a and a potential biomarker in breast tumor cells by using bioinformatics tools.Methods: validated and predicted targets of miR-146a were obtained from miRtarbase and miRwalk databases. UniGene and DAVID databases were used for further analysis. MIRSNP database predicts single nucleotide polymorphism in miR-146a and its function. Results: Our data manifested KEGG signaling pathways pathway in cancer as the most statistical relevant pathway with miR-146a targetome. Interestingly, it revealed that miR-146a inhibit some important breast cancer-related pathways such as TGFβRI, PDGF by targeting some well-knownoncogenes such as SMAD2/3, SMAD4, PDGFR. rs2910146 is located in mir-146a seed. It is predicted that G allele could increase stability of the stem-loop structure of mir-146a. Conclusion: According to our data miR-146a may be related to breast cancer through targeting itstargetome leading to proliferation, invasion, migration and evading apoptosis in breast cancer. Therefore hsa-mir-146a is a potential tumor suppressor miRNA which could be used as worthwhile prognostic biomarker. Allele G in the SNP could have good prognostic value for breast cancer centers due to its effect on mir-146a stability.

کلمات کلیدی:

Breast cancer, miR-146a, SNP, targetome, signaling pathway

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