

عنوان مقاله:

Bioinformatics analysis of potential role of miR-662 in breast cancer patients: inhibition of cytokine-cytokine receptor pathway

محل انتشار:

دهمین کنگره بین المللی سرطان پستان (سال: 1393)

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نویسندگان:

Nastaran Riahi - *Division of cellular and molecular biology, Department of biology, Nourdanesh University of Meymeh, Meymeh, Isfahan, Iran*

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

Kamran Ghaedi - *Department of Biology, Faculty of Science, University of Isfahan, Isfahan, Iran*

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

خلاصه مقاله:

There are over 100 different known cancers that affect humans. Breast cancer is the most common malignancy in women worldwide. MicroRNAs (miRNAs) are a class of small noncoding RNAs that control gene expression by targeting mRNAs. Mir-662 is a tumor-suppressor miRNA proposed as a possible biomarker of invasiveness in breast cancer. Although several studies have validated one target of miR-662 (ING1 gene), however bioinformatics studies are needed to predict comprehensive molecular function of miR-662 in breast cancer. Objective: Using bioinformatics databases, this study aim to expand current knowledge about molecular function of miR-662 in regard to its potential as a predicted biomarker in breast cancer. Methods: Validated and predicted targets of miR-662 were regained from miRtarbase and miRwalk databases respectively. Expression of retrieved targetome in breast cancer was evaluated in UniGene database. At last breast cancer specific targetome were entered into DAVID database for molecular pathway enrichment analysis. Results: According to our data from KEGG signaling pathways Cytokine-cytokine receptor interaction, miR-662 may inhibit 11 genes such as EGFR, LTBR and KDR. Researchers have shown these genes have multiple effects on breast cancer progression. Conclusion: Our data predicts that cytokine-cytokine receptor interaction pathway is a potential target for miR-662. MiR-662 may contribute as a tumor-suppressor molecule in breast tumor cells by inhibition of some important cytokine mRNAs.

کلمات کلیدی:

Breast cancer, miR-662, signaling pathway, cytokine-cytokine receptor

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