عنوان مقاله:

Bioinformatics analysis of potential role of miR-520f in patients with breast carcinoma

محل انتشار:

دهمین کنگره بین المللی سرطان پستان (سال: 1393)

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خلاصه مقاله:

Introduction: In 2012, 6.3 million women alive who had been diagnosed with breast cancer in the previous five years. MicroRNAs (miRNAs) may act as oncogenes or tumor suppressors, so they could be used as a prognostic biomarker. miR-520f was markedly increased in breast cancer, HCC and ovarian cancer. miR-520f do not have any validated target so it is worthwhile in research Objective: This study aim to expand current knowledge about molecular function of miR-520f in regard to its potential as a predicted prognostic biomarker for patients wit h breast carcinoma.Method: With the focus on their bioinformatical aspects, miRbase and miRwalk databases have been developed for prediction and validation of miRNA targets. targetome expression in breast cancer are evaluated in uniGene database. At last use DAVID database for molecular pathwayenrichment analysis. Results: Among the 2067 predicted targets of mir-520f with 3, 4 and 5 score, 267 genes have more than 20 transcripts in breast tumor cell and mammary gland tissue. pathway in cancer as the most statistical relevant pathways. 34 genes were identified that probably indicate a role for sustained angiogenesis, evading apoptosis and proliferation in breast cancer. Discussion: The exact function of miR-520f has not been reported already. Our data suggests that miR-520f acts as an oncogenic molecule by targeting some important tumor suppressormRNAs. In additional, it is demonstrated that miR-520f involved in drug resistance phenotype in neuroblastoma.

کلمات کلیدی:

Breast cancer, miR-520f, SNP,signaling pathway

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