
عنوان مقاله:

Predicting of miR-۱۴۹ Regulatory Network and hub genes in breast cancer: an in silico study

محل انتشار:

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نویسندگان:

Farzaneh Reiisi - *Department of Genetics, Faculty of Basic Sciences, Shahrekord University, Shahrekord, Iran*

Somayeh Reiisi - *Department of Genetics, Faculty of Basic Sciences, Shahrekord University, Shahrekord, Iran*

خلاصه مقاله:

Backgrounds: Breast cancer (BC) is the most common cancer among women and one of theleading causes of death among women worldwide. Frequent studies have demonstrated the roleof miRNAs in BC. miRNAs, are small noncoding RNA, that regulate gene expression throughtarget mRNAs. Bioinformatics analysis is a valuable tool in predicting miRNA target genesinvolved in BC. Among them, miR-۱۴۹ was confirmed to be deregulated in various tumorsincluding BC. Studies showed that miR-۱۴۹ as a tumor suppressor, repressed migration, andinvasion of BC. Therefore, we aimed to identify regulatory mechanism associated of miR-۱۴۹ inBC.Materials and Methods: Targetscan, Mirmap, mirwalk and mirdb databases were used topredict miR-۱۴۹ target genes. The potential prediction of ۵۰ common miR-۱۴۹ targets and thediscovery of their potential roles in BC were performed by GEPIA. The STRING database wasthen used to identify and establish a protein-protein interaction network (PPI) and the Cytoscapetool was used to analyze the network pathway and hub genes.Results: The target genes and pathways potential by miR-۱۴۹ were analyzed using integratedenrichment prediction tools (Enrich R). KEGG pathway analysis suggested the role of miR-۱۴۹target genes in cancer pathway and Ras, MAPK, Rap۱ signaling pathways. It also GO pathwayenrichment showed regulation of apoptosis and transcription in FOS, SMAD۲, SRC, Bcl۲L۱۱ andFASLG genes.Conclusion: This study, using bioinformatics approaches, showed that the function of miR-۱۴۹and its target genes could provide new .insights into the treatment of BC

کلمات کلیدی:

Breast cancer, miR-۱۴۹, Bioinformatics analysis

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