عنوان مقاله:

Identification of effective miRNAs in breast cancer by bioinformatics analysis

محل انتشار:

اولین همایش بین المللی و دهمین همایش ملی بیوانفورماتیک ایران (سال: 1400)

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خلاصه مقاله:

Breast cancer is the greatest reason for deaths associated with cancer among women. In the latest decades, miRNAs (microRNAs) have been reported to partake in the regulation of tumorigenesis-associated various genes, tumor progress, and breast cancer metastasis. The Gene Expression Omnibus was used to download the main data set of GSE۴۵۶۶ and GSE۲۶۶۵۹. The package of LIMMA of R software was applied to identify the expressed microRNAs differentially among ۱۷۸ patients with breast tumor and ۳۲ controls. Cytoscape imagined the interaction networks of gene-miRNA and then analyzed using MCODE (Molecular Complex Detection). The candida miRNAs were chosen and investigated by the dataset of TCGA (The Cancer Genome Atlas) and the plotter of KM (Kaplan–Meier) was used to analyze the prognostic values and expression levels of the candida miRNAs. Moreover, KEGG analysis was applied to detect the common pathways that the candida miRNAs were contained. Generally, ۳۵ down-regulated and ۱۸ up-regulated DE-microRNAs were recognized. Additionally, eight candida miRNAs with four down-regulated miRNAs (hsa-miR-۱۴۳, hsamiR-۱۲۵b, hsa-miR-۴۹۷, hsa-miR-۲۶a) and four up-regulated miRNAs (hsa-miR-۱۵۵, hsa-miR-۳۷۵, hsamiR-۲۰۳a, hsa-miR-۲۱) were recognized in the network of microRNA target gene and KM found their OS(overall survival) in breast cancer significantly. Lastly, three recognized miRNAs possess the most ordinary in the majority of five pathways that detected using KEGG for instance p۵۳ signaling pathway and cell cycle. This investigation demonstrated that these five pathways might be significant in the progress of breast cancer. The three miRNAs of hsa-miR-۳۷۵, hsa-miR-۲۰۳a, and has-miR-۲۱ could be effective microRNAs in breast cancer and might be applied in breast cancer as biomarkers.

کلمات کلیدی:

Breast Cancer, signaling pathway, networks of gene-miRNA

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