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عنوان مقاله:

Study of target genes and key pathways for dysregulated microRNAs in mammosphere with breast cancer stem cells

محل انتشار:

چهارمین کنگره بین المللی و شانزدهمین کنگره ملی ژنتیک (سال: 1399)

تعداد صفحات اصل مقاله: 1

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خلاصه مقاله:

Background and Aim: MicroRNAs (miRNAs) are master regulators in cancer initiation and progression by regulating post-transcriptional gene expression. However, the exact mechanism by which miRNAs regulate breast cancer progression and recurrence using cancer stem cells is poorly studied. The aim of this study is to identify specific miRNAs and related pathways in mammospheres contain breast cancer stem cells using a multi-step approach.Methods: A multi-step method integration microarray expression profile (GSE۱۲۷۸۴۹, GSE۱۰۳۲۱۸) and bioinformatics analysis was applied to identify the mammosphere with breast cancer stem cells dysregulated miRNA-mRNA regulatory network. First, statistically significant dergulated miRNAs from breast cancer stem cells compare with adherent MCF۷ cell were identified by GEO۲R data analysis in normalized sample. Then, target genes of main miRNAs with differentially expressed were predicted by miRmap, miRDB, and Targetscan. The miRNA gene regulatory network was drawn by Cytoscape software. Enrichment analyses were performed to define the potential pathway by FunRich software.Results: Bioinformatics study demonstrated that these miRNA-mRNAs were involved in PI۳K/mTOR/Akt signaling and stemness pathway. Furthermore, ۶ up-regulated (mir-۶۶۴, mir-۱۲۹۰, mir-۱۳۲, mir-۱۳۲ and mir-۳۱۲۴, miR-۲۹b) and ۴ down-regulated (miR-۱۲۸۷, miR-۴۵۲۱, miR-۲۷a, miR-۱۷) miRNAs predicted with upper score were selected. Finally, functional analysis was performed for the target genes followed by construction of a miRNA-target gene network.Conclusion: The results in current study may be useful to further investigation to understand the underlying regulatory mechanisms of miRNA in breast cancer stem cell that may be new objectives for breast cancer therapy.

کلمات کلیدی:

Cancer stem cell, GEO analysis, microRNAs, biological pathway,

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