عنوان مقاله:

Differential Expression of EGFR, MAP2K4 and E2F3 Genes as Targets of miR-141 and Its Association with Immune System Pathway

محل انتشار:

مجله سلول و تحقیقات مولکولی, دوره 9, شماره 1 (سال: 1396)

تعداد صفحات اصل مقاله: 10

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خلاصه مقاله:

MicroRNAs by their structural complementarity capabilities have canonical roles in gene regulation. In this paper;we investigate expression of EGFR, MAP2K4 and E2F3 genes targeted by miR-141, a member of miR-200 family.EGFR, MAP2K4 and E2F3 were predicted as the potential targets of mir-141 by using online miRNA bioinformaticstools. MCF-7 cells were transfected with mir-141-precursor and inhibitor vectors. Expression of miR-141 and targetgenes was determined by using qRT-PCR. To see the most relevant pathways regulated by miR-141, we constructedtwo separate networks by NetworkAnalyst and enriched list of underlying genes by Enrichment analysis tools. Theexpression changes of all three predicted targets were higher in transfected cells with anti-mir-141 vector, comparedwith the control untransfected cells. By contrast, in transfected cells with pre-mir 141, we did not see significantexpression changes in EGFR, E2F3 and MAP2K4. List of genes in total networks as well as explored functionalmodules were enriched separately. Enrichment analysis shows that immune system pathway has the strongestrelationship with the proteins potentially targeted by miR-141. The present study demonstrated potential role of miR-141 in regulation of EGFR, MAP2K4 and E2F3 expression and suggested innate immunity pathways as the keypathway through which this regulatory network contributes to breast cancer development.

کلمات کلیدی:

Breast cancer, MiR-141, EGFR, MAP2K4, E2F3