عنوان مقاله:
Exosomal miRNAs profile in colorectalcancer: in silico analysis

محل انتشار:
اولین کنگره بین المللی ژنومیک سرطان (سال: 1402)

تعداد صفحات اصل مقاله: 1

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خلاصه مقاله:
Background: According to the available statistical data from۲۰۱۸; Colorectal cancer is the third most common type of cancerin the world and also the second most common reason ofcancer-related death. An alarming increase in the number ofearly-onset (younger than ۵۰ years of age) colorectal cancerpatients, has occured in the United States and some other highincomecountries over the past few decades. miRNAs are an important group of small non-coding RNAs which were determinedto regulate the expression of different oncogenes ortumor suppressor genes. in normal physiological situations,miRNAs play roles in feedback mechanisms by securing mainbiological processes including cell proliferation, differentiationand apoptosis. Furthermore miRNAs are very important as diagnosticand prognostic biomarkers to evaluate initiation andprogression of tumor and also response to treatment in cancerpatients.Materials and Methods: The raw data set GSE۳۹۸۳۳ wasdownloaded from the Gene Expression Omnibus, then differentiallyexpressed Exosomal miRNAs were recognized betweencontrol samples and Cancer samples from patients in differentstages of colorectal cancer by using the R packages includingGEOquery, limma, BiocGenerics, affy, and oligo. Then multi-MiR package in R was used to predict DEmiRNAs target genes.A protein-protein interaction (PPI) network was composed toshow key target genes. Next Gene ontology and KEGG pathwayanalysis were achieved to identify the potential function ofthese target genes.Results: The differential expression was calculated between thesamples of each stage and the control samples separately. Thencommon DEmiRNAs in all four stages were obtained with -۰.۵> log۲FC or log۲FC > ۰.۵ and p value <۰.۰۵; Accordingly,miRNAs that were upregulated include: hsa-miR-۱۲۸۷, hsamiR-۱۲۲۵-۵p, hsa-miR-۱۴۴, hsa-miR-۱۲۵۲, hsa-miR-۱۳۰۵,hsa-miR-۱۰۶b, hsa-miR-۶۶۲; and those were downregulated include:hsa-miR-۲۴, hsa-miR-۱۲۹, hsa-miR-۱۲۶, hsa-miR-۲۳a,hsa-miR-۲۳b, hsa-miR-۲۹۶-۵p, hsa-let-۷f-۱, hsa-miR-۱۸۲۵ andhsa-miR-۱۰b. In the next step, target genes for these DEmiRNAswere obtained by the multiMiR package in R. On the otherhand, in each specific stage, one miRNA whose expression haddifferentiated significantly compared to the other miRNAs wasselected to be introduced as a biomarker. These biomarker miRNAsare: hsa-miR-۴۵۱and hsa-miR-۱۲۴۶. GO analysis showedthat target genes were mainly enriched in RNA binding, cytoplasmicstress granule and regulation of mRNA stability. KEGGpathway analysis suggested that ... target genes were enriched inregulation of actin cytoskeleton and FC (crys

کلمات کلیدی:
colorectal cancer, Exosomal miRNAs, Gene ExpressionOmnibus, Gene ontology, KEGG pathway