عنوان مقاله:

In silico analysis of identification miRNA-mRNA regulatory network in acute myeloid leukemia (AML) patients

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خلاصه مقاله:

Backgrounds: miRNAs are a class of non-coding RNA that is involved in various biologicalprocesses and diseases including cancers. Therefore, many studies illustrating the role ofmiRNAs in acute myeloid leukemia (AML) focused on identifying AML-specific miRNAexpression patterns. AML is an invasive disease characterized by the increased proliferation andmalignancy of immature myeloid cells. Therefore this study aims to investigate putative targetgenes and interaction networks where they are involved in AML. Also, Because of the numerouspossible interactions between a single miRNA and target genes, bioinformatics analysis is veryvaluable to identifying putative pathways.Materials and Methods: The original data set GSE۱۴۲۶۹۹ was selected from the GEO dataset(NCBI), and then the differentially expressed miRNAs in cytogenetically normal acute myeloidleukemia patients were identified using the GEO۲R. Their target genes were predicted from four(Tagetscan, miRWalk, miRDB, miRmap) miRNA target prediction databases. Then, functionalanalysis was accomplished for the target genes using by the construction of a miRNAs-targetgene network.Results: In current study, described five miRs (miR-۳۸۲-۵p, hsa-miR-۱۵۱a-۳p, hsa-miR-۴۹۵-۳p,hsa-miR-۴۰۹-۳p, and miR-۱۳۵) with down-regulation and three miRs (hsa-miR-۱۹۶b-۵p, hsamiR-۳۴a-۵p, and hsa-miR-۱۸۱a-۳p) with up-regulation in patients with AML. The miRNAs wereexposed to the most used predictions software and >۲۰۰ overlap target genes predicted. Then,enrichment analysis was performed revealing the KEGG pathway, comprising the cell cycle,Transcriptional dysregulation in cancer, and cellular senescence. Network construction wasgenerated and links between the selected miRNAs and the predicted targets.Conclusion: In this study, we merged miRNA expression analysis with a bioinformatics-basedworkflow. Some genes (CDK۶, HOXA۹, RUNX۱, and ITGB۳), pathways, and interactions,putatively involved in AML development, were identified.

کلمات کلیدی:

miRNA, acute myeloid leukemia, network, bioinformatics