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عنوان مقاله:

A network-based approach to uncover the potential genes, microRNAs and pathways in colorectal cancer pathogenicity

محل انتشار:

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خلاصه مقاله:

Backgrounds: Colorectal cancer (CRC) is one of the most prevalent malignancies worldwide.Despite various conducted surveys and experiments around the CRC, the pathogenicity of thisdisease is not clear enough. The present study aimed to apply a systematic approach to makevaluable insight into the involved genes and their regulatory layers that can shed light on CRCpathogenicity.Materials and Methods: In the current survey, GSE۱۲۶۰۹۵ microRNA profiles, and genemicroarray dataset GSE۱۱۳۵۱۳ re-analyzed through P<۰.۰۵ |log fold change (FC) |≥۱ parameterto recognize differentially expressed genes (DEGs) and MicroRNAs (DEMs). The quality ofdatasets was analyzed by principal component analysis (PCA). Using the EnrichR database, theDEGs related kinases (KEA) and transcription factors (ChEA) were retrieved. Following, byusing Cytoscape application, a multi-layer network composed of DEGs, KEA, and ChEA wasconstructed and analyzed. Then functional and pathway enrichment analyses by CytoscapeClueGO plugin were applied.Results: Top ۱۰ hub genes, miRNAs, TFs and kinases extracted from multilayer network,Module ۱ of the merged network was chosen for further investigation, most of the edges andnodes were connected with RHO GTPase effectors, Cdc۲۰-mediated mitotic protein degradation,rRNA processing and the senescence-associated secretory phenotype, based on GO and pathwayenrichment analysis. Most DEGs are related to import and biological pathways such as Wnt/β-catenin, flavonoids metabolism pathway and UDP-glucuronosyltransferases pathway. Moreover,top-most central TP۵۳, AR, CTNNB, POU۳F۲, FOXA۱, NR۳C۱, PIAS۱, PPAR were identified asgenes in the network that play a significant role in CRC.Conclusion: We have here followed a systematic approach to exploring the underlyingmolecular mechanisms of CRC.

کلمات کلیدی:

Colorectal cancer, microRNAs, GSE۱۲۶۰۹۵

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