Differential gene expression study on colorectal cancer

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ABSTRACT

Colorectal cancer (CRC) is the third most diagnosed cancer worldwide and the second leading cause of cancer-related deaths in both men and women in the United States. With economic development and rising living standards, the incidence of colorectal cancer has significantly increased in recent years, while the age of onset has decreased. This trend poses a serious threat to public health. A major contributing factor is the typically late diagnosis of CRC, which often results in poor prognosis and limited treatment options. Consequently, bioinformatics approaches, particularly those involving identifying differentially expressed genes (DEGs) and pathway enrichment analysis, hold great promise for improving early detection and treatment strategies. This study retrieved microarray datasets related to colorectal cancer from the GEO database and analysed them using R software to identify DEGs. Functional enrichment analysis was performed using Gene Ontology (GO) and the Kyoto Encyclopedia of Genes and Genomes (KEGG). A total of 407 DEGs were identified, including 98 upregulated and 309 downregulated genes, based on a p-value ≤ 0.05 and an absolute log2 fold change (log2FC) ≥ 2. GO analysis revealed that the DEGs were significantly enriched in biological processes, highlighting that CRC primarily disrupts essential physiological functions. Ten DEGs—CXCL1, CXCL2, CXCL3, CXCL5, CXCL8, PPBP, MT1F, MT1G, MT1H, and MT1M—were identified as potential diagnostic biomarkers. KEGG pathway analysis showed that six upregulated DEGs were involved in 13 of 21 enriched pathways, while four downregulated DEGs were associated with one of 30 pathways. These findings provide insight into the molecular mechanisms underlying CRC and may contribute to the identification of new therapeutic targets. Further studies are necessary to construct a gene interaction network model to deepen our understanding of these genes' relationships and to support the design of targeted drug therapies.

Keywords: Colorectal cancer, differentially expressed genes (DEGs), pathway enrichment (GO and KEGG), and biomarker identification, molecular mechanisms