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BIOINFORMATIC ANALYSIS OF GENE EXPRESSION PROFILES OF CRC SAMPLES BY RNA-SEQ DATA SET

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Introduction: MicroRNAs (miRNAs) are small non-coding RNAs, approximately 22 nucleotides in length that mediate translational repression of target messenger RNA (mRNA) transcripts. MiRNAs play a key role in cellular differentiation and proliferation, regulation of cellular metabolism, and are involved in the initiation and progression of cancer. Therefore, comparing of two states can illustrate which genes cause the cancer initiation and progression. RNA-seq is the best high throughput way to study the expression level of genes and microRNAs entirely in cells with different states. Some genes are overexpressed and some of them are down-regulated in different physiological conditions or diseases especially in cancer. The main purpose of the current study is to figure out the specific miRNAs between all the microRNAs and analyze their target genes to find out the connection between the dysregulator miRNAs and CRC-related pathways.

Materials & Methods: In this study, the microRNA expression level of 1061 malignant colorectal cancer and 30 normal samples were compared using TCGA database and python programing language. Fold changes were calculated for high-grade samples related to normal ones. From total 1882 microRNAs, 10 top differentially-expressed miRNAs that had significant p values ($p<0.05$) were chosen for further analyses. Then 3000 in-common target genes, by using microRNA, miRwalk and miRmap online tools, were selected. After that Mirfocus and Diana online tools were intended to analyze miRNA-target gene pathways and the related miRNA annotations. Finally, KEGG database and Panther online tool were used to illustrate which signaling pathways are important in colorectal cancer based on microRNA function.

Results & Conclusion: Analysis of top differentially expressed microRNAs including hsa-miR-9-3, 9-1, 9-2, 200a, 1307, 191, 210, 192, 17, 1511 and hsa-miR-27a and their in-common target genes indicated that Wnt, cadherin, integrin and CCKR signaling pathways are more activated in malignant colorectal cancer than normal selected samples. Thus, these dysregulated miRNAs may have a key role in CRC initiation and progression by targeting some of the most important genes in CRC-involved signaling pathways. However, more experimental studies are needed to elucidate exact mechanism of the miRNAs function in CRC-related pathways.

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