

عنوان مقاله:

In-silico analysis of molecular association between Inflammatory Bowel Disease and colorectal cancer

محل انتشار:

چهارمین کنگره بین المللی و شانزدهمین کنگره ملی ژنتیک (سال: 1399)

تعداد صفحات اصل مقاله: 1

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خلاصه مقاله:

Background and Aim: The development of colon cancer represents a major complication in patients with inflammatory bowel disease (IBD). Colorectal cancer (CRC) is cause of large number of malignancies with high rate of mortality originated from inflammatory signaling pathway. Non-coding RNAs are one of the most important Epigenetic changes. MicroRNA's are non-coding RNAs controlling the expression of genes at the post-transcriptional level which regulate wide range of biological processes like inflammation, proliferation, differentiation and apoptosis. The aim of this study is finding common miRNAs in both of IBD and CRC developing sequences. **Methods:** in this study, by using miRs databases such as Targetscan, microRNA.org, miRWalk, miRDB were used to detect and confirm deregulated miRs which have a critical role in KEGG pathways of IBD and CRC. At the end, the hot types of target genes were used in genmania for map interconnection network drawing. **Results:** according to results we identified 5 miRs that were differentially expressed between chronically inflamed mucosae and CRC arising from IBD tissues. The has-mir-17, has-mir-20a, has-mir-20b, has-mir106a and has-mir106b, targeting the stat3, smad4, p21 in the JAK/STAT, TGF-beta, P53 signal paths, which roles in inflammatory and cancer. **Conclusion:** miRNAs have proven vital in the regulation of genetic expression. We believe that with improved understanding of miRNA biology and detection methodologies, we .will see the efficacy of miRNA use in the early diagnosis and treatment of CRC and IBD patients in the near future

کلمات کلیدی:

Computational Molecular Biology, Colorectal Cancer, Inflammatory Bowel Disease, Epigenetic, MicroRNA

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