

عنوان مقاله:

In-silico analysis of Rac1 gene and hsa-mir-۱۸۲-۵p and its related target gene of Liver Cancer

محل انتشار:

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خلاصه مقاله:

Background: Liver cancer (LC) is one of the most invasive malignancies and may derive from different types of liver cells with an estimated more than ۷۸۱۰۰۰ deaths in ۲۰۱۸. The Rho-family GTPase Rac1 plays a key role in carcinogenesis and inflammatory responses. Epidemiological studies demonstrated a relation between chronic inflammation and cancer. Most cases of hepatocellular carcinoma (approximately ۸۰ %) are associated with cirrhosis related to chronic hepatitis following viral infections. Materials and Methods: Based on bioinformatics analysis, hsa-mir-۱۸۲-۵p was selected. Using by Mirwalk database, Prediction data of genes was collected. Then in the NCBI database, at UniGene, we have checked genes expression. Functional annotation analysis has been parsed with David database. Pathways relations were collected at KEGG in David database. Results: ۴۱۵ genes were identified for LC. Information of gene expression shows that Rac1 genes were down-expression in normal livers. In the other hand, hsa-miR-۱۸۲-۵p had upexpression. Conclusion: These results suggest that Rac1 may be a new gene therapy target for LC. Blocking Rac1 expression in LC cells induces apoptosis of these tumor cells and may thus represent a new therapeutic approach.

کلمات کلیدی:

Liver Cancer, microRNA, RAC1, has-miR-۱۸۲

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