عنوان مقاله:

Identifying downregulated hub genes and key pathways in HBV-related hepatocellular carcinoma using systems biology approach

محل انتشار:

چهارمین همایش ملی تحقیقات میان رشته ای در مدیریت و علوم پزشکی (سال: 1401)

تعداد صفحات اصل مقاله: 24

نویسنده:

Sedigheh Behrouzifar - *Department of Medical Sciences, Shahrood Branch,Islamic Azad University, Shahrood, Iran*

خلاصه مقاله:

Chronic Hepatitis B (CHB) is an independent risk factor for hepatocellular carcinoma (HCC) initiation without cirrhosis occurrence. Apart from the favorable effects of some antiviral drugs following tumor resection on the survival of HCC patients, the use of these agents is essential lifelong. Thus, designing the target-oriented therapeutic strategies to increase life expectancy in HCC patients would be very important. The present study aimed to identify downregulated hub genes and enriched pathways in HB-related HCC using a systems biology-based approach. Microarray data of GSE۱۲۱۲۴۸ were downloaded from gene expression omnibus (GEO) database. The differentially expressed genes (DEGs) with the cut-off criteria of adjusted p < ۰.۰۵ and Log Fold-change (FC) < -۱.۵ were selected. Then, the genes with the highest centrality were detected. Finally, the prognostic values of the hub genes were assessed. Six under-expressed hub genes with the highest interaction degree, Betweenness and Eigenvector centrality were including IGF-۱, PTGS۲, PLG, HGF, ESR-۱ and CYP۲B۶. Among genes with high centrality, several genes including CYP۲C۹, ESR-۱, CXCL۲, CYP۲C۸, IGF-۱, CYP۳A۴, CYP۲E۱, CERPINE-۱ and PXR were prognostic in HCC. The important repressed pathways were including metabolic pathways and PI۳K-Akt and chemokine signaling pathways. The under-expression of several genes implicated in metabolism, differentiation and chemotaxis might be a hallmark of the progression of HCC that can be considered as diagnostic and therapeutic targets.

کلمات کلیدی:

Liver cancer, Hepatitis B, Network analysis