

عنوان مقاله:

A common gene expression signature in three gastrointestinal malignancies: Gastric cancer, Colorectal cancer and Hepatocellular carcinoma

محل انتشار:

اولین کنگره پزشکی شخصی (سال: 1395)

تعداد صفحات اصل مقاله: 1

نویسندگان:

Kaveh Baghaei - *Basic and Molecular Epidemiology of Gastrointestinal Disorders Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran*

Nazanin Hosseinkhan - *Research Institute for Gastroenterology and Liver Diseases*

Hamid Asadzadeh Aghdai - *Basic and Molecular Epidemiology of Gastrointestinal Disorders Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran*

Mohammad reza Zali - *Gastroenterology and Liver Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran*

خلاصه مقاله:

Recently traditional histopathologic characterizations of cancers is having been replaced by high throughput molecular based methods which study genome scale gene expressional pattern, copy number variations and epigenetic modifications. According to GLOBOCAN 2012, the incidence and the mortality rate of colorectal, gastric and liver cancers are the highest among the total gastrointestinal cancers. In this study in order to find common genes and pathways simultaneously dysregulated in the colorectal cancer, gastric cancer and hepatocellular carcinoma, we conducted differentially expression analysis between three high quality microarray gene expression datasets. The results showed 23 overlapping differentially expressed genes (DEGs) in three cancers. Inspecting the common inferred regulatory network of these genes in the understudied cancers resulted in the detection of two cases of potential feed forward loops (FFLs) indicating cross-talk between cancers associated pathways. The result of vulnerability test of the common protein protein interaction (PPI) network in the three cancers suggested three candidates which their simultaneous targeting will disintegrate the main parts of the network and consequently are potential options for efficient treatment strategies. In total the results of this study introduces new common potential biomarkers in colorectal cancer, gastric cancer and hepatocellular carcinoma that monitoring their expressional .changes in suspicious patients can be helpful in prognosis of these gastrointestinal cancers at early stages

کلمات کلیدی:

common expressional pattern, gastrointestinal cancers, regulatory network, PPI network

لینک ثابت مقاله در پایگاه سیویلیکا:

<https://civilica.com/doc/807105>



