عنوان مقاله:

Investigating the regulatory role of coagulationpathway genes in the pathogenesis of gastric cancerusing bioinformatics analysis

محل انتشار:

اولین کنگره بین المللی ژنومیک سرطان (سال: 1402)

تعداد صفحات اصل مقاله: 1

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خلاصه مقاله:

Background: Gastric cancer (GC) is one of the digestive system'smost common and deadly malignancies. Different signalingpathways are known as factors affecting this disease. Thecoagulation system promotes the growth and development ofcancer cells through the induction of angiogenesis. Accordingto recent research, coagulation factors can play a role in thepathogenesis of GC. In this study, we used bioinformatics analysisto identify important genes in GC involved in the coagulationsignaling pathway.Materials and Methods: At first, we obtained coagulationsignaling pathway genes using the MSIGDB database. In thesecond step, we used publicly available datasets such as GEOand TCGA to identify differentially expressed genes related tothe coagulation pathway in GC. Finally, we used UALCAN andGEPIA۲ databases to analyze the expression of genes commonto TCGA and GEO data to find diagnostic biomarkers in GC.Results: Using the MSigDB database, we found the genes involvedin the coagulation pathway. In the next step and afteranalyzing the GEO dataset, we filtered the genes consideringadjusted p-value <۰.۰۱ and |Log FC| >۲. After analyzing thedata, we observed key genes that passed all our filters. Thesegenes were C۳, CD۹, CTSE, FGA, FGG, FN۱, HMGCS۲,MMp۹, SERPINE۱, SPARC, THBS۱ and TIMP۱. Among the۱۲ genes obtained from the GEO dataset, nine genes that containC۳, CD۹, FGA, FGG, FN۱, MMP۹, SERPINE۱, SPARCand TIMP۱ were confirmed by the TCGA dataset.Conclusion: In this study, we introduced coagulation pathwaygenes that play an important role in angiogenesis and cancerprogression. These genes may be introduced as diagnostic andprognostic biomarkers in the future. Targeting this pathwaycould be a new therapeutic approach for GC.

کلمات کلیدی:

Gastric cancer", "coagulation", "angiogenesis", "bioinformatics

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