

عنوان مقاله:

Bioinformatics Analysis of lncRNA-mRNA Interaction Network in Different Clinical Stages of Esophageal Squamous Cell Carcinoma

محل انتشار:

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خلاصه مقاله:

Esophageal cancer is one of the most aggressive gastrointestinal malignancies, and esophageal squamous cell carcinoma (ESCC) is the most prevalent esophagus neoplastic disease with high mortality rates in some Asian countries. Nonetheless, the etiology of ESCC continues to be vaguely comprehended, and the role of long noncoding RNAs in different clinical stages of this type of malignancy remains to be clarified. Here, we aimed to investigate the crucial genes corresponding to various clinical stages of ESCC, determine the hub lncRNAs in these stages, and predict patients' overall survival time. In the current study, the cancer genome atlas (TCGA) RNA-seq public data was analyzed in order to discover novel biomarkers or therapeutic targets implicated in the progression of ESCC. Stage-related genes were analyzed, the protein-protein interaction network for any stage was constructed and the top Δ genes with the most Maximal Clique Centrality score in each network were selected as the hub mRNAs. lncRNAs interacting with each stage hub mRNA were also determined as stage-related hub lncRNAs. Gene set enrichment analysis on stage-associated modules was also carried out. Finally, Cox regression analysis was performed to assess the prognostic significance of identified hub lncRNAs in the survival of patients with ESCC. Finally, hub mRNAs and hub lncRNAs associated with ESCC progression were identified, which may have implications as biomarkers and targets for therapeutic interventions. Six lncRNAs, including AC013391.2, AC104088.1, AC026341.3, AL039023.1, AL583808.1, and LINC01707 were also identified to be significantly correlated with ESCC patients' overall survival time, which could be potential predictors for the survival rate of patients, however, more research is required in order to confirm the results experimentally.

کلمات کلیدی:

ESCC clinical stages, TCGA, WGCNA, hub mRNA, hub lncRNA, prognostic factor

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