عنوان مقاله:

Weighted Gene Co-expression Network Analysis Unveiled Key Genes Related to Progression and Prognosis of Cervical Cancer

نویسندگان:

Mina Dehghani-Samani - *Department of Genetics, Faculty of Basic Sciences, Shahrekord University, Shahrekord, Iran*

Mojtaba Emadi Baygi - *Department of Genetics, Faculty of Basic Sciences, Shahrekord University, Shahrekord, Iran*

خلاصه مقاله:

Cervical cancer is one of the most common malignancies and one of the main death causes among females all over the world. The discovery of tumor-related genes is crucial for understanding tumor biology and developing preventative and therapeutic strategies. However, genes included in the tumorigenesis of cervical cancer cells are still unclear. Due to its high prevalence and mortality, understating its pathogenesis and biomarker detection is necessary. The purpose of this study was to recognize potential biomarkers related to cervical cancer and analyze their prognostic significance. The present research used the level ٣ mRNA expression data and clinical data of cervical cancer from The Cancer Genome Atlas database to identify differentially expressed genes followed by gene ontology. Weighted co-expression Network Analysis was used to construct scale-free gene co-expression networks. In the co-expression network, the hub module and hub genes were identified. The significant modules associated with T, N, M, and FIGO staging in the network were subsequently screened. Next, overlapping genes between significant gene modules and DEGs were screened. CALML۵, TERT, PNPLA٣, CHRDL١, C٧, LEFTY٢, and PCP۴ were identified as hub genes. Survival analysis was performed to identify the association between these genes and survival using the GEPIA database. Survival analysis showed that PCP۴ was slightly less expressed in patients with primary solid tumors than normal, and related to poor prognosis in cervical cancer. These results show that these hub genes, especially PCP۴, may be a potential diagnostic biomarker for cervical cancer and provide a new perspective on the pathogenesis of cervical cancer.

کلمات کلیدی:
Cervical cancer, Differentially Expressed Genes, PCP۴, TCGA, WGCNA

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