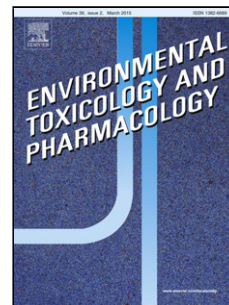


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Identification of key genes and pathways and therapeutic agents in Cadmium-treated liver cells: a bioinformatics study

Running Title: Cadmium-related genes in liver cancer

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Highlights

- The differentially expressed genes (DEGs) between Cadmium-treated liver cells and controls were screened out and their functional Enrichment Analysis was also conducted.
- The hub genes among the DEGs were screened.
- The small agents that have a potential to attenuate Cadmium-induced liver cell damage or transformation were predicted.

Abstract

Evidence indicates that Cadmium (Cd) can accumulate in liver, which results in acute or chronic cell damage with unclear complex mechanisms. Thus, we aimed to explore the possible molecules and pathways by using bioinformatics methods. Consequently, two datasets (GSE8865 and GSE31286) were retrieved and the differentially expressed genes (DEGs) were screened out. The intersection of the DEGs included seven up-regulated and forty-three down-regulated genes, which were mainly enriched in biological cell proliferation items, and were enriched in several metabolism-related pathways. Among the DEGs, several hub genes such as EGR1, FOSL1,

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