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Gene networks implicated in Acetaminophen-induced hepatotoxicity

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Abstract

Acetaminophen (APAP) is widely used as a pain reliever and a fever reducer. However, high doses of APAP will cause heptatotoxicity that can be fatal. Acetaminophen toxicity was reported by the FDA to be the most common cause of acute hepatic failure in the United States. The biochemical mechanisms for APAP-induced liver injury are complex and not fully understood, although multiple targets and pathways have been implicated. Here, we evaluated the changes of gene expression associated with APAP treatment of rat hepatocytes and provided a systematical study on gene networks implicated in APAP heptatotoxicity. We analyzed expression microarray data from primary rat hepatocytes treated for 24 and 48 hours with DMSO (as control) and two doses (0.5 mM and 5 mM) of APAP. Each treatment group had 5 biological replicates. Differentially expressed (DEX) genes between high doses of APAP treatment and the control group at different time periods were identified. Using a conservative threshold (false-discovery-rate Q value of 0.01 and 2-fold signal intensity difference), we found 157 and 130 genes were significantly differentially expressed after 24 and 48 hour APAP treatment, respectively. Gene ontology enrichment analysis of these DEX genes showed that several important metabolism-related pathways were significantly regulated by high doses of APAP. These pathways included metabolism of xenobiotics by cytochrome P450, nitrogen metabolism, fatty acid metabolism, glycine/serine/threonine metabolism, retinol metabolism, steroid hormone biosynthesis, and PPAR signaling pathways. Our analysis revealed gene pathways implicated in acetaminophen-induced hepatotoxicity and provided further insights into the toxicological mechanism of this drug.

Biography

Dr. Feng Cheng is an Assistant Professor at the USF College of Pharmacy. He received first Ph.D. in computational medicinal chemistry at the Chinese Academy of Science in 2003. After finishing his second Ph.D. in bioinformatics at the University of Virginia, Dr. Cheng received his postdoctoral training at Yale University. Dr. Cheng has published over 30 papers in prestigious journals including Nature. Presently, Dr. Cheng is an editor board member of Journal of Biomedical Science and Engineering, open bioinformatics journal and Journal of Proteomics and Bioinformatics. Dr. Cheng has been serving as a peer reviewer for more than ten journals.