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Proteomic Analysis of Liver in a Rat Model of Chronic Feeding of Ethanol diet

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The proteome is the complete set of proteins in an organism. It is considerably larger and more complex than the genome-the collection of genes that encodes these proteins. Proteomics deals with the qualitative and quantitative study of the proteome under physiological and pathological conditions (e.g., after exposure to alcohol, which causes major changes in numerous proteins especially liver tissue). The purpose of this study was to perform a comprehensive analysis of protein expression in the livers of rat treated with liquid diet containing ethanol. An ethanol- or an isocaloric control liquid diet was fed for 30 days in Male Wister rats. Serum biochemistry, liver histology and proteomic analysis of liver cytosol were performed at the end of treatment. To map large proteomes, the liver homogenates were first separated by high-resolution two-dimensional electrophoresis. Then, individual proteins are further identified by MALDI-TOF (Matrix-Assisted Laser Desorption Ionization - Time Of Flight). At the results of biochemistry and histopathology, ALT, cholesterol, HDL-Chol, and phospholipids were increased and fatty change, necrosis and expression of CYP2E1 in liver were successfully induced by ethanol ingestion. In proteomic analysis, four up-regulated proteins were significantly detected, and two proteins were down-regulated. Among these proteins, we found the novel biomarker of ethanol-induced liver damage related protein, precursor $mGluR_3$ which was up-regulated by ethanol-fed. This study supports to (1) expand the knowledge of mechanism of action of ethanol, (2) develop novel protein marker of ethanol action on the liver, and (3) illustrate the utility of proteomic analysis in alcohol-ingested gastrohepatic diseases.

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