

Proteomic Analysis of Nuclear Membrane in HCV Induced Liver Cirrhosis

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Proteomic information about the hepatitis C virus (HCV) infection leads to a better understanding of the protein function and interaction in liver cirrhosis. HCV is a causative agent of chronic liver disease leading to cirrhosis, liver failure and hepatocellular carcinoma with anticipated prevalence of 3% of the world population. In order to examine the nuclear membrane proteins of infected liver tissues, liver biopsy sample were subjected to SDS-PAGE followed by 2-DE analysis with narrow pI ranges. The expressed proteins revealed interesting results which contributes to the evaluation and understanding of HCV infection leading to cirrhosis. To support our results and to provide a conclusive data, a comparative study is carried out to elucidate the differentially expressed proteins in serum of HCV infected individuals. These results might be useful for rapid translation of findings from basic research to practical means of anticipation, control and therapeutic advancement of liver diseases.

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