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SWATH MASS SPECTROMETRY AS A TOOL FOR QUANTITATIVE PROFILING OF THE BONE MARROW PLASMA FROM ALCOHOLIC LIVER DISEASE

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Alcoholic hepatitis is characterized by acute or acute-on-chronic hepatic failure and associated with a high mortality. Specific therapies should be considered for those at high risk of mortality. Model for End-Stage Liver Disease (MELD) score is a marker of disease severity and mortality in persons with chronic alcoholic liver disease. Author's aim is to find out a diagnostic biomarker for disease severity along with the MELD score which can be used as a predictor of short term mortality in persons with alcoholic hepatitis. Understanding molecular pathogenesis is pivotal in managing the disease. They employed sequential window acquisition of all theoretical mass spectra (SWATH-MS) to seek crucial proteins involved in disease progression. Bone marrow plasma is taken from chronic liver disease patient as a part of stem cells therapy clinical trial. In this study, a quantitative proteomic of bone marrow plasma with low and high MELD scores were compared with normal bone marrow plasma from non-cirrhotic portal hypertension patient whose liver function test was normal using a SWATH-MS strategy. In total, 232 proteins were differentially expressed in all groups. 17 proteins are down regulated and 81 up regulated in patients with MELD score <15 with control. Moreover, 37 proteins are down regulated, 59 up regulated while comparison of MELD score >15 with control. Inhibition of coagulation, complement and intrinsic prothrombin pathways are revealed by functional analysis. Humoral immune response, immune cell trafficking and inflammation pathways are enriched under physiological system development. Proteins preliminarily discovered in this study may be associated with dysregulation bone marrow microenvironment during disease progression. To the author's knowledge, this study presents the most complete view of bone marrow plasma in low and high MELD score, identifying hundreds of differentially expressed proteins, which together form a rich resource for novel drug targets or diagnostic biomarker discovery.

BIOGRAPHY

Renu Goel has obtained her M.Tech and PhD degree in Biotechnology from Institute of Bioinformatics, India with Prof. Akhilesh Pandey, Johns Hopkins University, Maryland. Her research group is working on identifying pathways or proteins involved in early stages of progression of diseases such as type II diabetes, liver diseases and dengue fever by using proteomics, metabolomics and bioinformatics approaches. She has also worked on draft map of human proteome published in Nature. During this period she has published around 30 research articles in high impact factor international journals. She is an Editorial Board Member for many journals.

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