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Screening new urine biomarkers of IgA nephropathy by proteomics

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IgA nephropathy (IgAN) is one of the most common primary glomerular diseases and the main cause of chronic kidney disease (CKD) and end-stage renal disease in the world. In this study, we screened the protein profiles of IgA nephropathy by LC-MS/MS to find potential urine biomarkers for IgA. The second morning urines from Twenty-four IgA patients (20 to 50 years old) were selected and thirty healthy people second morning urines between 20 to 50 years old were selected as control. Label free LC-MS/MS were performed to screen out differentially expressed proteins and ELISA was applied for validation. Total 317 differential urinary proteins were found in IgAN patients with 152 upregulated and 165 downregulated. GO analysis and pathway enrichment results showed that these differential proteins were mainly involved in lipid metabolism blood coagulation and thrombosis iron metabolism activation of complement system cell adhesion cell motility calcium signal pathway and MAPK signal pathway. ELISA results confirmed that complement C3 Transferrin and ceruloplasmin were all increased significantly in IgAN group. More importantly, urine TF increased more than 100 times in IgAN groups, which could be served as pre-diagnosis marker and urine complement C3 was positively related to the 24-hour urinary protein quantity, which could be served as disease progression marker. In conclusion, we explored the urine protein profiles in IgAN and screened two important potential biomarkers for IgAN: Transferrin and C3, which help to improve the diagnosis and therapy of disease.

Biography

Yang Lu is a nephrology researcher in China PLA general hospital in Beijing of China. He gained his master degree in 2007 and doctor degree in 2010 from Chinese PLA Postgraduate Medical School. Dr. Lu works in Division of Nephrology of PLA general hospital for over 15 years and keeps research on the mechanism of mesangial proliferation. His main work focus on explore the molecular pathway in mesangial cell proliferation in the animal nephrology models by proteomics and genomics and published more than 30 papers in reputed journals.

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