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Urinary Proteomic Biomarkers Discovery for Prediction of Acute Rejection in Kidney Transplant Recipients

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Objectives : Early prediction and treatment of acute rejection are crucial in kidney transplant recipients (KTRs) to prevent allograft loss. Changes in the serum and urinary proteomes precede the elevation of serum creatinine concentration, the development of proteinuria, and histopathologic changes in KTRs with acute rejection. The aim of this study was to discover potential proteomic biomarkers for prediction of acute rejection in KTRs.

Methods : Twenty five KTRs with T-cell mediated rejection (TCMR), 9 KTRs with acute antibody mediated rejection (AMR), 61 normal control subjects were included in this study. We used the proteomic approach to measure the changes of urinary proteome of KTRs. The urinary exosomes were trypsin-digested using a gel-assisted protocol, and quantified by label-free LC-MS/MS, using a DDA mode.

Results : Analysis of the isolated exosomal proteins showed 100 proteins were detected in TCMR, 102 proteins in AMR. The detected proteins were quantified using the software Peaks 7. Identically detected proteins in a large amount in each group were excluded for candidate biomarkers and high-significance proteins with the fold change of at least 1.5 were selected as candidate biomarkers. Three proteins (APOA1 Apolipoprotein AI, HPX Hemopexin, PIGR Polymeric immunoglobulin receptor) and three proteins (CP cDNA FLJ58075 highly similar to Ceruloplasmin, APOA1 Apolipoprotein AI, TTR Transthyretin) were select as biomarker candidates to predict TCMR and AMR, respectively.

Conclusions : We found 6 specific proteins to predict TCMR and AMR in KTRs. Further studies are needed to validate the identified proteomic biomarkers and to apply the rejection-specific biomarkers for early prediction, diagnosis, and monitoring of clinical response of treatment of acute rejection in KTRs.

Keywords : proteomic biomarker; acute rejection; kidney transplantation