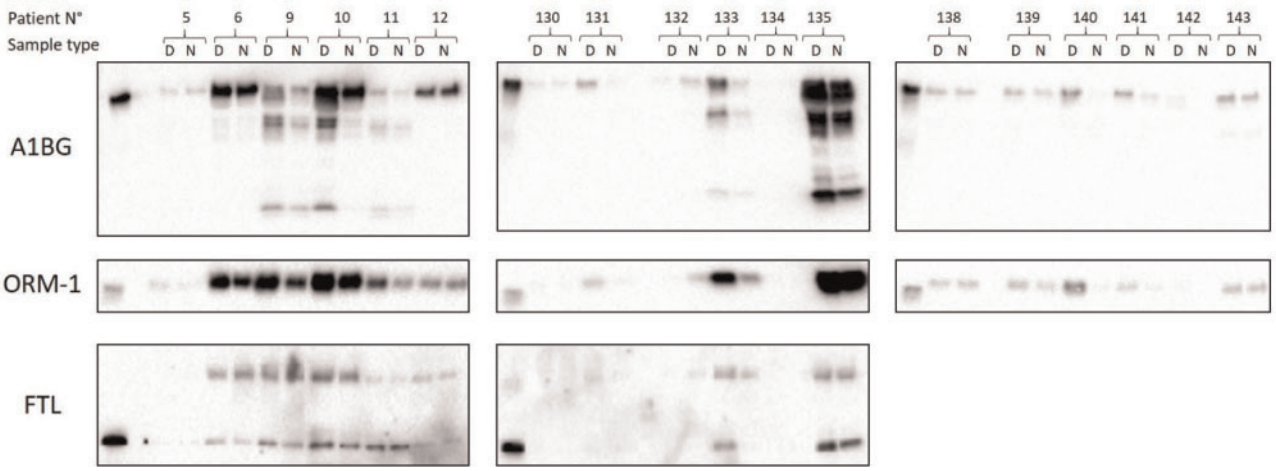


SP282 Figure

SP282 **URINARY PROTEOMIC MARKERS OF IGA NEPHROPATHY, LUPUS NEPHRITIS AND MEMBRANOUS NEPHROPATHY**

Barbara Moszczuk[1], Natalia Krata[1], Tomasz Pilżys[2], Damian Garbicz[2], Michał Marcinkowski[2], Bartosz Foroncewicz[1], Radosław Zagożdżon[2], Dominik Cysewski[2], Leszek Pączek[2], Krzysztof Mucha[2]

*[1]Medical University of Warsaw, Warsaw, Poland and [2]Polish Academy of Sciences, Warsaw, Poland*

**INTRODUCTION:** Chronic kidney disease (CKD) is a worldwide public health problem, related to increased morbidity and mortality. Glomerulopathies represent major causes of CKD and require complicated diagnostics. Standard of care includes kidney biopsy in order to confirm the type of nephropathy. However, biopsy brings specific risks. Therefore, non-invasive diagnostic and prognostic methods are sought. Urinary proteomics emerged as safe and promising tool, but still requires development and improvements. Our previous studies which are part of European Patent Application from 10th June 2016 (WO/2017/212463), identified urinary markers of IgA nephropathy. They included among others: alpha-1B-glycoprotein (A1BG), alpha-l-acid glycoprotein 1 (ORM-1), ferritin light chain (FTL) and serotransferrin (TF). The aim of this study was to evaluate them in comparison to patients with glomerulopathies of different etiologies, such as lupus nephritis (LN) and membranous nephropathy (MN).

**METHODS:** This proteomic study included patients with CKD (41 IgAN, 33 LN, 26 MN, 6 with erytrocyturia of unknown etiology) and 19 healthy controls. Urine samples were obtained from a midstream of the: first-morning (FM) and second- or third-morning (SPOT) sample. The SPOT samples were processed up to 2 h and FM samples up to 4 h after collection, by agitating and gently inverting 4-6 times, portioned into 2-ml aliquots and stored at -80°C for further measurements. Western Blotting was used for analysis of the SPOT and FM samples, ELISA and mass spectrometry for SPOT urine only. The results were related to demographic data, standard laboratory tests and GFR estimated with use of Chronic Kidney Disease Epidemiology Collaboration (CKD-EPI) equation.

**RESULTS:** The urinary concentrations of A1BG, ORM-1, FTL and TF were found to be higher in CKD patients than in healthy controls. Moreover, these proteins varied depending on the disease. According to ELISA measurements, patients with IgAN, erytrocyturia and LN had significantly more A1BG and ORM-1 ($p < 0.05$), whereas TF was more elevated in LN and MN individuals comparing to healthy controls. The western blot analysis revealed significantly elevated level of A1BG, ORM-1 and FTL in IgAN, LN and MN, comparing to healthy control. Additionally, it revealed fragmentation of A1BG in several patients and the bottom range bands tended to be most prominently elevated in IgAN patients. Mass spectrometry confirmed differences between the diseases according to the specific amino acids fragments of each tested protein. Figure 1. Western blot scans for urinary A1BG, ORM-1 and FTL in CKD patients (2-4) and healthy controls (1).

**CONCLUSIONS:** The urinary concentrations of A1BG, ORM-1, FTL and TF are elevated in CKD patients and vary depending on the type of nephropathy. This observation suggests their differential roles in the pathophysiology of the given diseases, and we believe their evaluation may help distinguishing between nephropathies. Further studies are desired to establish the role of these urinary proteins in non-invasive disease differentiation.