C8

Identification of Differentially Expressed Proteins in Human Kidney with IgA Nephropathy

Department of Clinical Pathology, Pharmacology[1], Surgery[2], Internal Medicine[3], Anatomy[4], The Catholic University of Korea*

Yeong-Jin Choi, Eun-Hui Wang, Kweon-Heang Lee[1], Yong Bok Koh[2], Dong Chan Jin[3], Chul-woo Yang[3], Yong Soo Kim[3], Byung Kee Bang[3], Chang Suk Kang , Jung Ho Cha[4]

Despite the large amount of studies, the exact etiology and pathogenesis of IgA nephropathy (IgAN) is still unclear. Proteomics has been developed and used as a powerful tool for the investigation of vast amounts of proteins simultaneously, and provide an insight for the functional aspect of the disease. We have compared proteomic difference of renal cortex from IgAN and normal control kidney to find out the potential contributing proteins related to the pathogenesis of IgAN. We used native kidneys obtained from the recipients by unilateral nephrectomy at the time of kidney transplantation. Fresh kidney tissues from ten cases of IgAN confirmed by histological and immunofluorescent examination, and from five normal kidneys as control were used. Proteins were isolated from the renal cortex and separated by two-dimensional polyacrylamide gel electrophoresis (2D-PAGE). Expression of proteins was determined by silver and Coomassie blue stains. Protein identification was done by peptide mass fingerprinting using matrix assisted laser desorption ionization-time of flight (MALDI-TOF) mass spectrometry. The expressed protein patterns of IgAN were similar in all IgAN cases. Most of the spots in IgAN were found with a similar pattern in normal control kidneys. Twenty forms of seventeen proteins were identified out of approximately 700 spots visualized on each gel. In conclusion, a large numbers of proteins and their relative expression levels from cortex of human kidneys in IgAN and normal control were found. Seventeen proteins are differentially expressed in IgAN compared with normal control. Proteomics can be used to identify the differentially expressed proteins in IgAN on a large scale, and facilitate the elucidation of pathogenesis of IgAN. Further study will be needed to identify the potentially related proteins in IgAN.