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Proteomics of kidney biopsy tissues for understanding pathophysiology

Currently proteomics has been introduced for analysis of pathophysiology of kidney tissues and biopsy specimens, and also discovery of urine biomarkers. Understanding pathophysiology of kidneys in physiologic or pathologic conditions is significant to select treatments for the diseases or to develop new therapies. By a laser microdissection system and liquid chromatography-mass spectrometry (LC-MS) we have established a method to analyze proteomes of both kidney glomerulus and other nephron compartments obtained from formalin-fixed paraffin-embedded (FFPE) sections. Thousands of proteins with high confidence were identified by LC-MS of each nephron compartment and they were semi-quantified by a non-labeled quantitation method, normalized spectral index. Bioinformatics tools for function and pathway analyses of the proteome data depicted characteristic functions of each nephron. By the proteomics analysis of 50 sections prepared from a single biopsy specimen also depicted interesting pathways in the glomerulus of each kidney disease. Proteomics and bioinformatics analysis of normal or disease kidney tissues provide new insights into molecular functions of nephron segments and pathologic pathways of glomerular diseases and may promote efficient personalized medicine and pathogenesis-based new drugs in the near future.

Biography

Tadashi Yamamoto has received his PhD in 1981 from Niigata University, School of Medicine and did Post-doctoral studies in the Scripps Research Institute, CA, USA. He is the Director of the Biofluid Biomarker Center, Niigata University. He has been chairing the Human Kidney and Urine Proteome Project of Human Proteome Organization and has published more than 25 papers in reputed proteomics journals.

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