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Perspective

Urine Proteomics: Future Diagnostic Tool for Kidney Related Diseases

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INTRODUCTION

The non-invasive nature of urine collection makes urinary proteins an ideal biomarker for diagnosing kidney disease and other diseases associated with the urinary tract, such as prostate and bladder cancer. Urine is one of the most attractive biofluids in clinical proteomics because it can be obtained noninvasively in large quantities and is stable compared to other biofluids. The urinary proteome has been studied using almost all proteomics techniques, but mass spectrometry-based profiling of urinary proteins and peptides has emerged as the most suitable for clinical application. After a period of descriptive urinary proteomics, the field is moving out of the discovery stage and into an era of validation of urinary biomarkers in larger prospective studies. Although primarily based on the location of urine production, most of these studies relate to the kidney and urinary tract, recent data suggest that analysis of the urinary proteome is also highly informative for non-genitourinary diseases. Indicating that it can be used to classify them.

DESCRIPTION

Human urine plays an important role in clinical diagnosis. For centuries, doctors have tested patients' urine samples to diagnose various diseases. Many philosophers have already said that urine color and other characteristics are indicators of certain diseases. Urine is produced by the kidneys and allows the human body to remove waste products from the blood. The kidney also maintains homeostasis throughout the body and produces hormones such as renin and erythropoietin. The human kidney is made up of millions of functional units called nephrons and can be divided into two functional parts: The glomeruli, which filter plasma to make what is called "urine," and the renal tubules, which reabsorb most of the urine. In 24 hours, about 900 liters of plasma pass through the kidneys, of which 150 liters-180 liters are filtered.

Healthy human urine contains significant amounts of peptides and proteins. The number of proteins and peptides detected in urine continues to grow. Compared to other body fluids, urine has several properties that make it suitable for biomarker discovery. First, urine can be collected in large quantities in a non-invasive manner. This allows repeated sampling of the same individual for disease surveillance. In addition, the availability of urine makes it easy to assess the reproducibility and improvement of sample preparation protocols. Second, peptides and low molecular weight proteins in urine are generally soluble. Solubilization of these low molecular weight proteins and peptides is therefore a process that has great impact on proteomic analysis of cells or tissues and is generally not a problem. Almost all known mass spectrometry techniques have been used to analyze the urine proteome, including Two-Dimensional gel Electrophoresis (2DE) 1-MS, LC-MS, SELDI-TOF, and Capillary Electrophoresis (CE)-MS. The ideal sequence for biomarker discovery is mass spectrometry based discovery followed by ELISA based validation and clinical application. Easier said than done, and till date knowledge, there are still no examples of ideal 'sequences' for urinary biomarker discovery. However, in recent years, profiling approaches have emerged that enable the use of mass spectrometry based techniques in the discovery/validation/clinical stages for the analysis of the urinary proteome. Proteomic analysis in urine has evolved into a powerful diagnostic and prognostic tool not only for kidney disease, but also for diseases of more distant organs. Although urinary proteome analysis is still far from becoming a routine tool in clinical practice, studies on larger patient cohorts demonstrate its potential in clinical diagnostics. Efforts are needed to validate panels of these biomarkers in even larger, and perhaps more important, heterogeneous cohorts, to move from disease-versus-control experimental paradigms to the bedside. However, the contribution of urinary proteomics to understanding disease pathophysiology in the analysis of the urinary proteome is still modest.

CONCLUSION

The development of mass spectrometers for high mass accuracy and resolution, new methods to study low abundance proteins and peptides, and new bioinformatics tools will enable the sequencing of more biomarkers and the understanding of underlying diseases in the near future. It should help you learn more about pathophysiology. Despite these advances in the discovery of urinary biomarkers, the contribution of urinary proteomics to understanding disease pathophysiology when

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analyzing the urinary proteome remains largely due to problems associated with sequence identification of biomarkers. Till date, research has focused on highly abundant proteins and peptides in urine, but the analysis of abundant and naturally occurring proteins and peptides in urine remains a challenge. It has emerged as one of the most attractive body fluids in clinical proteomics and may enable rapid clinical use.