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Proteomics and the Kidney: An Evolution

Proteomics is a relatively new fixture in the toolbox used to study the kidney. It is a scant 13 years since the term *proteomics* first was applied to the study of proteins on a global scale.[1] The term *proteomics* entered the renal lexicon in a prescient article authored by Mark Knepper in which he noted the potential of the approach to help understand the kidney.[2] Since that time the use of proteomic techniques in kidney research has increased dramatically. Initial studies leaned heavily on 2-dimensional gel electrophoresis methods for protein separation and quantitation, whereas protein identification was performed primarily with peptide mass fingerprinting techniques.[3] These approaches were useful, but had limited sensitivity and allowed characterization of only several hundred protein forms in a single experiment. Recent advances in protein separation and mass spectrometry have resulted in the implementation of so-called *shotgun proteomic* techniques capable of characterizing several thousand proteins in a single analysis.[4] As new and more powerful methods have become available, we have seen a shift to the study of human specimens and the beginnings of clinical proteomics in nephrology.[5,6] This issue of *Seminars in Nephrology* reflects that evolution. The first series of articles summarizes new approaches to proteomic methodology in the kidney and urine. Included in this section are 3 emerging techniques: metabolomics, imaging mass spectrometry, and differential calorimetry, which are powerful complements to standard proteomic methods. In the second section, we summarize developments in the specific areas of pediatric disease, diabetic nephropathy, and acute kidney injury. Ultimately, we hope these articles provide valuable information about current and developing proteomic tools and how they provide new insights into renal disease.

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