

Introduction

The uremic syndrome can be defined as the deterioration of multiple biochemical and physiological functions in parallel with progressive renal failure (*Vanholder et al., 2003a*).

Not all of the illness of a patient undergoing dialysis can be ascribed to uremia. Instead, patients undergoing dialysis now have a new illness which is called "residual syndrome". This illness comprises partially treated uremia, ill effects of dialysis such as fluctuation in the extracellular fluid volume and exposure to bioincompatible materials, and residual inorganic ion disturbances including acidemia and hyperphosphatemia (*Depner, 2001*).

Many uremic toxins reviewed by the European Uremic Toxin Work Group, about 92 toxins were identified and they classified them into three major groups:

- Small water soluble low molecular weight compounds,
- Protein-bound compounds
- And middle molecular weight compounds (*Vanholder et al., 2003b*).

Proteomics analysis represents a new and promising analytical tool whereby all peptides present can be registered and potentially solutes that might be of patho-physiological importance identified, offering the possibility to achieve the unbiased identification of markers or solutes. This approach is facilitated by refinements in analytical

techniques together with improvements in informatics (*Kaiser et al., 2003*).

Uremic toxicity of a compound can be proved directly by pathogenicity to a specific tissue, by relation of its concentration to mortality and morbidity and indirectly through improvement of clinical outcomes after removal of the toxin by specific dialysis modality (*Canaud, 2006*).

Nephrologists gave attention to toxicity and ways of removal of middle molecular weight and the protein-bound compounds which have evident more toxic effects than small water soluble compounds (*Depner and Himmelfarb, 2007*).

Middle molecules are very toxic to number of cells; endothelial cells, polymorphneuclear neutrophils, platelets and smooth muscle cells (*Vanholder et al., 2003c*).

P-cresol as a protein bound toxin showed to cause significant endothelial alterations and impairment of leucocyte function and activation (*Ketteler, 2006*).

Both hemodialysis and peritoneal dialysis are currently prescribed to achieve target values of urea (and the small molecular weight toxins)

clearance. Yet early studies indicated that these compounds cause only a minor part of uremic illness (*Timothy et al., 2007*).

So, many therapeutic modalities that aim to enhance removal of both middle molecules and protein-bound toxins have been developed in the last years. Protein-leaking membranes that provide more clearance of protein-bound toxins now in search of an application (*Ward, 2005*).

Adding a sorbent to the dialysate is another new different modality (*Meyer et al., 2007*).

Treatment schedule for removal of middle molecules includes : highly permeable membranes (e.g. high flux membranes), enhanced convective and/or adsorptive clearance (hemodiafiltration / hemofiltration) and extended treatment duration (*Canaud, 2006*).