

ABSTRACT

Proteomics is the large-scale study of proteins, particularly their structures and functions. Proteomics has been utilized in medicine for investigation of disease mechanisms and biomarker discovery. Instrumental methods cover sample preparation, protein and peptide separation and mass spectrometry. At present, there is no proteomic method that can be used as universal for every sample. Analytical methods need to be adapted and optimized for certain samples.

The aim of this work was to create methodic procedures and to interpret results of experimental and clinical research. The first part of the thesis includes experiments utilizing proteomics to study changes in the plasma proteome clinically relevant porcine model of sepsis-induced peritonitis. Proteomic analyzes were also starting methodological strategies in experiments aimed at kidney physiology and pathophysiology of acute kidney injury during sepsis. Renal biopsies were analyzed in order to study the time course of proteome changes caused by sepsis and surgery. The second part of the thesis contains experiments studying biocompatibility. A method for elution of proteins interacting with adsorbents used in extracorporeal liver support system and with hemodialyzer capillaries was prepared. Analysis of proteins adsorbed to polysulfone capillaries identified complement activation as an important process involved in hemodialyzer biocompatibility.