

Capillary electrophoresis coupled to mass spectrometry as a tool to define potential prostate cancer biomarkers in urine

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ABSTRACT

We describe the use of capillary electrophoresis (CE) coupled with mass spectrometry (MS) to identify single polypeptides and patterns of polypeptides specific for prostate cancer in human urine. Using improved sample preparation methods that enable enhanced comparability between different samples, we examined samples from > 100 patients that underwent prostate biopsy. Of this group, >30 patients each that had either benign pathology (BP) or prostate cancer (CaP) were used to define potential biomarkers which allow discrimination between these two states. In addition, CE-MS data from these urine samples were compared to 41 controls without known or suspected clinical CaP to further confirm the polypeptides indicative for CaP.

These analyses led to the definition of several urinary polypeptides that could serve as potential biomarkers for disease. When these were utilized in a disease-model, correct classification of the CaP patients with > 90% sensitivity and specificity was possible in the training set.

We further examined additional 474 samples from patients with renal disease enrolled in other studies and found that 14 (3%) which had polypeptides suggestive of CaP possibly indicating that they harbor clinical CaP.

In an ongoing study aimed towards the validation of these biomarkers, samples from patients scheduled for prostate biopsy are prospectively collected and examined in a blinded fashion. The comparison of these data with the biopsy data and thus the evaluation of a first blinded study will be presented.