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Validation of Prostate Cancer Biomarkers and Inflammation: A Proteomics Study

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Abstract:
Background: In this study serum protein profiles were analyzed in order to investigate possible confounding parameters in the discrimination between prostate cancer (PCa) and benign prostatic hyperplasia (BPH).
Methods: Patients with clinical suspect of PCa and candidates for trans-rectal ultrasound guided prostate biopsy (TRUS) were enrolled. Histological specimens were examined in order to identify PCa, BPH and detect inflammation. Surface En[[Unsupported Character - Codename]]hanced Laser Desorption/Ionization-Time of Flight-Mass Spectrometry (SELDI-ToF-MS) and two-dimensional gel electro[[Unsupported Character - Codename]]phoresis (2-DE) coupled with Liquid Chromatography-MS/MS (LC-MS/MS) were used to analyze immuno-depleted serum samples from patients with PCa and BPH.
Results: The comparison between PCa (in the presence or absence of inflammation) and BPH (also in the presence or ab [[Unsupported Character - Codename]]sence of inflammation) serum samples performed by SELDI-ToF-MS analysis, did not show differences in protein profiles. Differences became evident when the presence of inflammation was taken into consideration. When samples with histolo[[Unsupported Character - Codename]]gical sign of inflammation were excluded, 20 significantly different protein peaks were detected. Subsequent comparisons (PCa with inflammation vs PCa without inflammation, and BPH with inflammation vs BPH without inflammation) showed that 16 proteins appeared to be differently expressed in the presence of inflammation, while 4 protein peaks were not mo[[Unsupported Character - Codename]]dified. With 2-DE analysis, comparing PCa without inflammation vs PCa with inflammation, and BPH without inflammation vs the same condition in the presence of inflammation, were identified 29 and 25 differentially expressed protein spots, respectively. Excluding samples with inflammation the comparison between PCa vs BPH showed 9 unique PCa proteins, 4 of which overlapped with those previously identified in the presence of inflammation, while other 2 were proteins, not identified in the previous comparisons.
Conclusions: This study indicates that inflammation might be a confounding parameter during the search of candidate proteomic biomarkers of PCa. The results indicate that inflammation represents a significant confounding factor, hence, only a well-selected protein pattern should be considered as a potential biomarker of PCa.
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