Abstract

Proteomic Profiling of Prostate Cancer and Benign Prostatic Hyperplasia from Urine

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Background

Prostate cancer (CaP) is one of the most common cancers in men, and it is a leading cause of cancer deaths among men in many countries, including Canada. The diagnosis of CaP is currently based on the measurement of the serum prostate-specific antigen (PSA) level, which has several limitations. Therefore, there is a need for new biomarkers that can help in the early detection of CaP and in the differentiation between CaP and benign prostate hyperplasia (BPH).

Methods

The proteomic analysis of urine samples was performed using a combination of proteomic approaches, including liquid chromatography-tandem mass spectrometry (LC-MS/MS). The urine samples were obtained from men with BPH, CaP, and healthy individuals. The urine samples were first concentrated using a centrifugal concentrator and then protein quantification was performed using a Bradford assay. The proteins were then separated using SDS-PAGE and then analyzed using LC-MS/MS.

Results

A total of 145 proteins were identified in the urine samples, of which 14 proteins were unique to CaP, 15 proteins were unique to BPH, and 126 proteins were shared between CaP and BPH. The proteins that were overexpressed in CaP and BPH were further analyzed using statistical methods.

Conclusion

The proteomic analysis of urine samples suggests a potential role for these proteins as biomarkers for the early detection of CaP and in the differentiation between CaP and BPH. Further studies are needed to validate these findings and to develop these proteins as diagnostic biomarkers.