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Proteomics and *N*-glycosylation analysis of prostate cancer biopsies

Authors

Simon Sugár (1,2), Gábor Tóth (1,3), Fanni Bugyi (1,4), Károly Vékey (1), László Drahos (1), Lilla Turiák (1)

Affiliations

(1) MS Proteomics Research Group, Research Centre for Natural Sciences, Hungarian Academy of Sciences, Magyar tudósok körútja 2., H-1117 Budapest, Hungary

(2) Semmelweis University, PhD School of Pharmaceutical Sciences, Üllői út 26., H-1085 Budapest, Hungary

(3) Budapest University of Technology and Economics, Faculty of Chemical Technology and

Biotechnology, Műegyetem rkp. 3., H-1111 Budapest, Hungary

(4) Faculty of Science, Eötvös Loránd University, Pázmány Péter sétány 1/a, 1117 Budapest, Hungary

Introduction

Analysis of tissue specimen using mass spectrometry offers valuable information of biological processes taking place at the origin of a disease. Identifying differences in protein expression levels and site-specific *N*-glycosylation of glycoproteins among cancerous and healthy tissues can be an attractive approach in biomarker research. Our aim was to analyze prostate cancer (PCa) tissue microarray samples (n=95) and compare protein expression levels and changes in *N*-glycosylation features among various pathological grades of PCa and healthy tissues.

Methods

Following on surface proteolytic digestion [1] glycopeptides were enriched using acetone precipitation. Peptide and glycopeptide fractions were analyzed separately using reversed phase nanoHPLC-MS(MS) and nanoHPLC-MS. Label free protein quantitation was performed using MaxQuant, while glycopeptides were identified and quantified using Byonic and Glycopattern software, respectively. Statistical analysis was carried out using Perseus.

Results

Several statistically significant proteins were identified that were altered between different cancer grades and healthy tissue. STRING analysis revealed protein pathways involved in disease progression. Regarding *N*-glycosylation analysis the changes identified at specific glycosylation sites were of interest. Alterations in sialylation, fucosylation and galactosylation of individual glycosites were detected that could potentially be important targets of future studies. We found that in case of Collagen 6 subunit both protein expression levels and

fucosylation at N785 changed significantly between the different pathological grades and healthy tissue.

Conclusions

Our integrated proteomics and glycoproteomics workflow was used to identify molecular alterations occurring during PCa progression from limited size tissue samples and can also be used to analyze other types of cancerous tissue biopsies in the future.

References & Acknowledgments

1. Turiák, L., et al., *Workflow for Combined Proteomics and Glycomics Profiling from Histological Tissues.* Analytical Chemistry, 2014. **86**(19): p. 9670-9678.

LT is grateful for funding from the National Research Development and Innovation Office (NKFIH PD-121187, NKFIH FK-131603) and for the support from the János Bolyai Research Scholarship of the Hungarian Academy of Sciences.