5 Identification of cytoskeleton-associated proteins as a potential biomarkers of prostate cancer by MALDI-TOF mass spectrometry

Kmeťová Sivonova M. [1], Tatarkova Z. [1], Jurecekova J. [1], Kliment J. [2], Dusenka R. [2], Hatok J. [1], Drobkova H. [3], Grendar M. [3], Kaplan P. [1]

[1] Jessenius Faculty of Medicine in Martin Comenius University in Bratislava, Dept. of Medical Biochemistry, Martin, Slovakia, [2] Jessenius Faculty of Medicine in Martin Comenius University in Bratislava, Dept. of Urology, Martin, Slovakia, [3] Jessenius Faculty of Medicine in Martin Comenius University in Bratislava, Biomedical Center Martin, Martin, Slovakia

Introduction & Objectives: A new trend in cancer research is cancer proteomics, also termed as oncoproteomics. Alterations in prostate structure and function can predispose this tissue to the development of prostate cancer, and understanding the factors/mechanisms that regulate hormone-related changes in prostate is essential. Intracellular filaments (as a complex network of cytoskeleton) are being recognized as essential signalling proteins involved in key cancer biological functions. These include epithelial-to-mesenchymal transition, regulation of major signal transduction pathways, cell migration and invasion, the positioning and anchorage of organelles, and cell–cell and cell–substrate adhesion. The main objective of this study was to determine the possible involvement of intracellular filaments in the cytoprotective functions and explore their role as the early biomarkers of prostate cancer.

Materials & Methods: We used 2D SDS-PAGE followed by MALDI-TOF-MS to identify potentially new prognostic biomarkers in human prostate/ BPH tissues obtained from ten histologically verified prostate cancer patients (mean age 72.4 ± 2.8; Gleason score ≤ 7; mean PSA 26.2 ± 11.8 ng/ml) and ten BPH individuals (mean age 72 ± 1.4; mean PSA 1.6 ± 0.4 ng/ml) as control.

Results: Statistical analysis of the normalized quantities of matched spots revealed that, in the prostate cancer group, 17 cytoskeleton and associated protein spots were significantly > 1.5-fold changed vs BPH (p < 0.05). Among them, we identified four spots as actin, five spots as desmin, one spot as vimentin, one spot as tropomyosin, one spot as filamin A and four spots as trangelin. Importantly one identified spot was for HspB1 that interact with intracellular filaments and confer protection by preventing cytoskeleton aggregation.

Conclusions: The cytoskeleton proteins identified by this approach may be useful molecular targets for prostate cancer diagnostics and to be an attractive potential therapeutic target for future prostate cancer therapies.