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Towards cancer biomarker discovery via proteomic and metabolomic profiling of clinical specimens

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Which increasing consensus amongst cancer biologists that cancer represents a prototype of systems disease, there is an urgent need across contemporary "OMICS" technologies (e.g. genomics, proteomics, metabolomics) for integrated analysis of clinical specimens (e.g., tissue, body fluids) obtained from patients diagnosed with cancer. The integration and interpretation of these results using systems biology tools is critical for a better understanding of overwhelmingly complex cancer biology. This holistic approach should accelerate discovery of novel cancer biomarkers resulting in their subsequent translation into effective clinical assays that oncologists can use for diagnostics and targeted therapeutics of patients diagnosed with cancer. Effective integration and interpretation of data obtained from analyses of clinical specimens is critical since in many instances the data obtained from cancer cell lines and animal models are not always predictive or indicative of what is actually happening in human cancers in vivo. This presentation focuses on our recent advances in development of clinical proteomics and metabolomics technologies for biomarker discovery that involves major improvements in experimental design, upstream sample processing, and bioinformatic analysis. Advanced systems biology meta-analysis of large proteomic datasets is focused on elucidation of pathways and protein networks, showing their meaningful relation to the cancer under study. This presentation is focused on a range of proteomic and metabolomic approaches developed for biomarker research/discovery that relies on effective molecular profiling of tissues and body fluids obtained from patients diagnosed with renal cell carcinoma, Ewing's sarcoma along with method development for concomitant profiling of estrogen metabolites in thin tissues sections.

Biography

Josip Blonder received his M.D. in 1978 from the Rijeka University Medical School, Croatia. Dr. Blonder is the head of Clinical Proteomics, Laboratory of Proteomics and Analytical Technology, Advanced Technology Program, SAIC-Frederick at the Fredrick National Laboratory for Cancer Research (FNLCR). He has authored over 50 scientific publications serving as an associate editor of the BMC Cancer. He is a member of the American Society for Mass Spectrometry and the American Association for Cancer Research. Dr. Blonder brings unique combination of expertise in medicine, clinical proteomics, and bioinformatics to FNLCR where he promotes the application of shotgun proteomics and systems biology to important problems in cancer biology and translational medicine.

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