

International Conference on

Euro Oncology, Breast Cancer & Biomarkers

October 18-19, 2018 | Amsterdam, Netherlands

Proteomic fingerprint of rearrangement of the lung function in a breast cancer lung metastases – in a search for the molecules for detection of metastases and potential therapeutic targets

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Breast cancer is characterized by a strong ability to metastasize, specifically to lungs. The study aimed at the proteomic characterization of the changes in the function of lungs in relation to metastases development in the experimental model of tumor metastasis in murine 4T1 mammary adenocarcinoma. The 4T1 tumor cells were orthotopically inoculated into the mammary fat pad of the BALB/c female mice. Analysis was performed in lungs, four weeks after cancer cell transplantation. 2D-DIGE as well as label-free comparative proteomics with the aid of nano LC-MS/MS technique was applied. Histological analysis confirmed the presence of the metastases in the 4th week after the tumor cell inoculation. The label-free proteomic analysis revealed 168 differentially expressed proteins involved in multiple biological processes related to inter alia: gene expression, cell differentiation, organelle and cellular component organization, localization, response to stress, multiple metabolic processes. Most of the differentially expressed proteins were involved in binding of different molecules. The results for complementary techniques used in the study greatly overlapped, with additional information provided by label-free comparative analysis. The prominent changes were reported for proteins involved in inter alia: immunological response e.g., protein S100-A9, protein S100-A8, cathelicidin antimicrobial peptide, integrin alpha M, neutrophilic granule protein, myeloperoxidase, neutrophil cytosol factor 2, retinoic acid-induced protein 3 and cysteine-rich protein 2. The proteomic profiling enabled to reveal the pattern of changes in metastatically affected lungs. Differentially expressed proteins may be considered in further analysis as potential therapeutic targets as well as the fingerprints for discerning between healthy and metastatic tissue.

Biography

Anna Kurpinska has completed her PhD at West Pomeranian University in Szczecin, Poland. She has published more than 13 papers in reputed journals. She has involved in non-targeted proteomics (nano LC-MS/MS) - screening of alterations of protein repertoire and targeted proteomic analysis (LC/MS-MRM) of the endothelium-related proteins in animal models of breast cancer, endotoxemia and obesity. She is a Principal Investigator of the National Science Centre MINIATURA grant entitled: "Analysis of the molecular mechanisms of metastasis in murine model of breast cancer with the aid of the comprehensive analysis of the changes in protein expression in lungs".

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