

POSTER PRESENTATION

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Profiling metabolic changes in breast cancer with targeted proteomics

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Background

Breast cancer is one of the most common causes of death from cancer among women. Significant but yet insufficient progress has been achieved due to the introduction of targeted therapeutics [1]. Nevertheless, advancing personalized medicine requires a detailed and comprehensive molecular characterization, particularly at the protein level. This project aims to advance the understanding of crosstalk between cancer-relevant signaling and metabolism.

Materials and methods

Based on a constructed flux distribution model, targets were chosen to be analyzed in breast cancer cell lines and tumor samples. The RPPA (reverse phase protein microarray) technology a micro-scaled dot-blot approach is used. RPPA allows to quantify protein expression and activation states in a large panel of samples. In addition, RPPA has a remarkable high sensitivity and is able to analyze many proteins in a single experiment. Therefore this method presents a powerful approach for targeted hypothesis-based proteome research [2].

Results

As a first step, based on publically available transcript data a model describing the deregulation especially of glutamine and nitrogen metabolism in breast cancer was developed [3]. Key features of our model are currently evaluated by RPPA in cell lines representing the different breast cancer subtypes. Metabolic enzymes confirmed on the cell line level as de-regulated will be evaluated in tumor samples and tested as putative drug targets in *in vitro* models.

Conclusion

Based on the bioinformatic model and proteomic validation our aim is to introduce options for new co-treatment concepts that target key metabolic enzymes to harm tumor cells and disable their malignant anabolic processes, as well as energy consumption. The resulting data will provide a basis to calculate new models explaining the metabolic shift in breast cancer cells and to identify signaling molecules that contribute to malignant transformation.

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