Summary

Better cure of the breast cancer requires switch to the individualized treatment of patients. Presented here study describes development of tools for individualized treatment of patients, and provides insights in the complexity of cancer-related signaling in breast epithelial cells. Described by us results showed feasibility of application of proteomics to individualization of treatment of breast cancer patients. We expect that the combination of tissue-proteomics and the case-study approach have a great potential for identification of novel markers for better diagnostics of breast cancer.

The case-by-case approach to proteome profiling of IDC and ILC will help to identify individual changes in protein expression and\or modifications. This will lead to discoveries of novel proteins involved in cancer, and development potential markers.

Transforming growth factor-β (TGFβ) is a potent regulator of tumorigenesis. In our study of the clinical cases, we demonstrated that TGFβ signaling might be influenced in breast tumorigenesis. We found that 14-3-3σ was of a crucial importance for the cross-talk between TGFβ and p53 signaling. We identified also more than 100 proteins that were regulated by TGFβ in human epithelial cells, and involved in carcinogenesis.

We believe that our results will help better understand of the mechanisms involved in cancer development, better diagnostic and treatment for patients.