Nuclear matrix protein alterations in triple-negative breast cancer

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Abstract

Breast cancer is a heterogeneous disease that can be characterized by different patterns of histology, receptor status as well as gene and molecular classifications. All these factors influence the therapy, the prognosis and the outcome for each individual patient. Triple-negative breast cancer (TNBC) is a certain subgroup of breast cancer that is negative for hormone receptors (ER and PR) and lacks overexpression of the Her2/neu protein. This subgroup accounts for 15-20% of all breast cancer cases. Due to its aggressive behavior, the increased risk for metastases and the lack of targeted therapies TNBC has gained major interest in recent years.

Methods

This proteomic analysis focused on the nuclear structure of human breast cancer tissue, which has been shown to be a promising tool for biomarker development in cancer. The nuclear matrix composition of human triple-negative breast cancer (n=4) and matched human non-TNBC controls (n=10) with different patterns of hormone receptors and Her2/neu status was analyzed by high-resolution two-dimensional gel electrophoresis and silver-staining.

Results

Performing a computer-based comparison of all 2-dimensional gels by PDQuest 2D analyzing software, three protein spots (TNBC-A, -B, -C) were identified to be specifically upregulated in triple-negative breast cancer tissues (4/4). TNBC-A was found exclusively in TNBC and was absent in all of the non-TNBC controls (0/10; p=0.001). TNBC-B and TNBC-C were upregulated in all triple-negative breast cancer tissues, but also present in two samples of the non-TNBC controls (2/10; p=0.015).

Conclusion

We were able to identify three nuclear matrix proteins that appear to be specific for triple-negative breast cancer. Further studies are required to investigate the potential role of these proteins as biomarkers for triple-negative breast cancer and have to clarify their function in the management of this disease.