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Elucidation of a Conserved Proteomic Pattern of Breast Cancer Tissue and Metastatic Axillary Lymph Node

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Abstract
Objective: Breast cancer is one of the most devastating cancer types affecting women. For critical decision making regarding the fate of cancerous breast tissue, the assessment of axillary lymph node (ALN) involvement is required. However, such ALN involvement is difficult to predict without surgical intervention. Therefore, an easy predictive test using protein markers may be a desirable approach. In this study, we performed a whole proteome analysis to reveal the presence of a putative biomarker panel using primary breast tumor tissue.
Materials and Methods: Proteins were extracted from tumor tissues and were subjected to two dimensional (2D) gel electrophoresis. The resulting gel images were used for inter-gel spot comparisons using PDQuest Advance software. The paterns thus obtained were used for differentiating invasive tumor types from non-invasive ones.
Results: The analysis of 2D gel images revealed the presence of 24 conserved protein spots whose intensities were moderately regulated high on the gels. Those protein spots were used to create a conserved 2D pattern spanning a pH range of 4 to 8.
Conclusion: Protein spots generating a preserved model among pattern between primary breast cancer and its axillary lymph node indicated that a robust and highly reliable proteomic approach, e.g., 2DE may be used to differentiate metastatic forms of breast cancer from non-metastatic ones.
Key words: breast cancer, axillary, lymph node, 2D, proteomics