



Proteomic analysis of non-tumoral breast tissue

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ABSTRACT. Breast cancer is a complex and heterogeneous disease. In spite of the advances made in recent decades, a better understanding of the intrinsic mechanisms of this disease is crucial. The development of new biomarkers is absolutely necessary to improve diagnosis and prognosis. Research using the proteomic approach has generated interesting results; however, the complexity of the mammary gland and of breast tumors remains a major limitation to the development of new markers. An initial step is to characterize non-tumoral human breast tissue. We present data from classical proteomic analysis based on 2-D electrophoresis and peptide mass fingerprinting identification, which were performed on six non-tumoral samples from patients with invasive ductal breast carcinomas. Forty-four different proteins from 70 spots were identified and classified according to their biological function. Cytoskeleton and associated proteins represent the largest class (30%) followed by the proteins with binding function (27%). Several of the proteins have been described in breast tumors, such as vimentin, endoplasmic reticulum chaperones, small heat shock beta-6, disulfide isomerase

and some cell growth, and proliferation regulators, suggesting the importance of including data on the characterization of non-tumoral breast and to studies on differential expression in cancer tissue.

Key words: Non-tumoral breast tissue; Proteomics; Biomarkers