

Gene expression profiling of breast cancer in Lebanese women

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Background and Aims: Breast cancer is the most common cancer in women worldwide. Elucidation of its underlying biology and molecular pathways is necessary for improving therapeutic options, hence, improving clinical outcomes. As molecular alterations in breast cancer are complex and involve cross-talk between multiple cellular signaling pathways, the application of gene expression profiling using microarray technologies provides a window to compare expression patterns across multiple samples from different populations. The aim of this study is to extract a unique mRNA fingerprint of breast cancer in Lebanese women. **Methods:** Gene expression profile of 94 fresh breast tissue samples (84 cancerous and 10 non-tumor samples) were analyzed using GeneChip Human Genome U133 Plus 2.0 arrays. Quantitative real-time PCR was subsequently carried out to validate candidate genes. **Results:** Differentially expressed genes between breast cancer and non-tumor control tissues were screened. Significant differences in gene expression between breast cancer and normal non-tumor tissues were established for COL11A1, COL10A1, MMP1, COL6A6, DLK1, S100P, CXCL11, SOX11, LEP, ADIPOQ, OXTR, FOSL1, ACSBG1, and C21orf37. Relevant pathways and diseases representing the genes were retrieved and linked using PANTHER® and Pathway Studio®. The analysis revealed that many of the deregulated genes are associated with extracellular matrix, inflammation, angiogenesis, metastasis, differentiation, cell proliferation, and tumorigenesis. **Conclusion:** These findings add a better understanding of molecular mechanisms in breast cancer, particularly in Lebanese women. More importantly, key genes were uncovered which could

serve as potential biomarkers or novel drug targets for breast cancer.