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ORIGINAL REPORT

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Supervised Risk Predictor of Breast Cancer Based on Intrinsic Subtypes

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A B S T R A C T

Purpose
To improve on current standards for breast cancer prognosis and prediction of chemotherapy benefit by developing a risk model that incorporates the gene expression–based "intrinsic" subtypes luminal A, luminal B, HER2-enriched, and basal-like.

Methods
A 50-gene subtype predictor was developed using microarray and quantitative reverse transcriptase polymerase chain reaction data from 189 prototype samples. Test sets from 761 patients (no systemic therapy) were evaluated for prognosis, and 133 patients were evaluated for prediction of pathologic complete response (pCR) to a taxane and anthracycline regimen.

A Comparison of PAM50 Intrinsic Subtyping with Immunohistochemistry and Clinical Prognostic Factors in Tamoxifen-Treated Estrogen Receptor–Positive Breast Cancer

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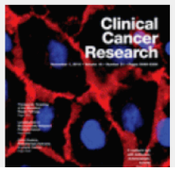
Abstract

Purpose: To compare clinical, immunohistochemical (IHC), and gene expression models of prognosis applicable to formalin-fixed, paraffin-embedded blocks in a large series of estrogen receptor (ER)–positive breast cancers from patients uniformly treated with adjuvant tamoxifen.



Gene expression patterns of breast carcinomas distinguish tumor subclasses with clinical implications

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Contributed by David Botstein, July 17, 2001

The purpose of this study was to classify breast carcinomas based on variations in gene expression patterns derived from cDNA microarrays and to correlate tumor characteristics to clinical outcome. A total of 85 cDNA microarray experiments representing 78 cancers, three fibroadenomas, and four normal breast tissues were analyzed by hierarchical clustering. As reported previously, the cancers could be classified into a basal epithelial-like group, an *ERBB2*-overexpressing group and a normal breast-like group based on variations in gene expression. A novel finding was that the correlations between gene expression patterns and clinically relevant parameters. We found that classification of tumors based on gene expression patterns can be used as a prognostic marker with respect to overall and relapse-free survival in a subset of patients that had received uniform therapy. One finding was the separation of estrogen receptor (ER)-positive tumors into at least two distinctive groups with characteristic gene expression profiles and different prognosis.

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ORIGINAL REPORT

Molecular Classification of Tamoxifen-Resistant Breast Carcinomas by Gene Expression Profiling

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Presented in part at the San Antonio Breast Cancer Conference (oral

A B S T R A C T

Purpose
To discover a set of markers predictive for the type of response to endocrine therapy with the antiestrogen tamoxifen using gene expression profiling.

Patients and Methods
The study was performed on 112 estrogen receptor–positive primary breast carcinomas from patients with advanced disease and clearly defined types of response (ie, 52 patients with objective response *v* 60 patients with progressive disease) from start of first-line treatment with tamoxifen. Main clinical end points are the effects of therapy on tumor size and time until tumor progression (progression-free survival [PFS]). RNA isolated from tumor samples was amplified and hybridized to 18,000 human cDNA microarrays.