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Gene expression profiling

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Valerie Speirs,[Aff1]

Aff1 University of Leeds, UK

Keywords

DNA arrays, recurrence

Context

The most important prognostic indicators to predict patient outcome in breast cancer are hormone receptor status, axillary lymph node status and histological grade; although these give a broad overview of outcome, they cannot predict for all patients. The recent development of cDNA array analysis provides the opportunity for a more refined approach based on molecular classification of individual tumours (see Additional information [1]). A previous study by the same authors identified molecular profiles in a cohort of nine benign and 72 malignant breast tumours (see Additional information [2]). The aim of this work was to use this technology to identify patients at increased risk of tumour recurrence.

Significant findings

Hierarchical cluster analysis of data revealed two clusters, class A - which consisted of a high proportion of node-negative patients with metastases at time of diagnosis - and non-class A (all other patients). Median follow up data (23.5 months) from 55 of these patients were analysed. Of 22 patients in class A, 11 progressed to metastatic disease and 9 out of 20 had recurrences, compared to 3 out of 27 of non-class A. Additionally, three out of five patients originally classified as N0 in class A developed metastatic disease.

Comments

Although based on a small number of patients, these results illustrate the potential use of cluster analysis in identifying patients at greater risk of recurrence. Larger scale studies are warranted to examine the impact of gene expresion profiling in predicting patient outcome and response to therapy on a more individualised basis. The data presented here and in another related study (see Additional information [3]) are promising and suggest that this technology could be used routinely in a clinical setting in the not too distant future.

Methods

DNA arrays

Additional information

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