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Breast cancer prognosis

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No-one really understands why some women with **breast cancer** respond well to chemotherapy while others do not, or how to predict an individual patient's chances of survival. In the January 31 *Nature*, Laura van't Veer and colleagues describe a gene-expression profiling study of breast tumours (*Nature* 2002, **415**:530-536). They chose around 100 primary breast cancers (with and without metastases or *BRCA1* mutations) and looked at the relative expression levels of 25,000 genes. They used a three-step **supervised classification** method to distinguish groups of tumours with good or poor prognosis. An **expression signature panel** of 70 genes could accurately predict 'poor prognosis' patients. This set includes genes encoding proteins involved in cell invasion, metastasis and angiogenesis. Women under 55 who are diagnosed with lymph-node-negative breast cancer have a 28-fold higher chance of developing distant metastases within 5 years if they have a 'poor prognosis signature' rather than a 'good prognosis signature'. This predictor is better than current clinical and histopathological prognostic factors, and may help to improve the criteria for selecting patients for adjuvant therapy.

References

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