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LUNG ALERT

Gene profiling to predict recurrence in lung cancer

▲ Potti A, Mukherjee S, Petersen R, *et al*. A genomic strategy to refine prognosis in early-stage non-small-cell lung cancer. *N Engl J Med* 2006;**355**:570–80

Patients with stage I non-small cell lung cancer are traditionally treated with surgical resection alone. However, 30–35% will relapse and these patients may therefore have benefited from adjuvant chemotherapy. The current clinicopathological classification system is an imprecise prognostic indicator, and the authors have evaluated the use of gene expression profiling to predict recurrence.

One hundred and ninety eight tumour samples from three separate groups were used. One group was used to identify gene expression profiles (the lung metagene model), and samples from the other two groups were used to assess the predictive value of the model in comparison with clinical variables known to be of prognostic significance.

The results showed that the lung metagene model was superior to clinical data in predicting recurrence. The model was 93% accurate in the identification group compared with 64% for clinical data alone. The samples in the other two groups were used to validate the predictive model. Using univariate and multivariate analysis, the results once again illustrated the significantly greater accuracy of the model for predicting recurrence ($p < 0.001$): 72% (69% positive predictive value, 78% negative predictive value) and 79% (79% positive predictive value, 80% negative predictive value) in the two cohorts, respectively.

The data suggest that patients with stage I disease and likely recurrence may be identified using the lung metagene model. The role of adjuvant chemotherapy in these patients would require a phase 3 clinical trial.

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