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## Lung alert

### Gene expression: the key to treatment decisions in early-stage adenocarcinoma?

Recent evidence shows that adjuvant chemotherapy significantly improves the survival of patients with early-stage lung cancers. There are, however, groups of patients who do not fit neatly into prognostic categories according to stage, and tumour biology is likely to play an important role. This retrospective blinded validation study aimed to identify predictors of survival (classifiers) using gene expression profiling.

Data were collected about 442 patients with stage I, II or III lung adenocarcinoma, including gene expression data, clinical variables and outcome data (survival). To allow comparison between data sets from separate laboratories, standardised protocols were used for all aspects of data generation and collection. The data were split into two groups according to the laboratory which performed the initial analysis. One data set was used for “training” of classifiers and the other to validate these approaches. Each investigating team developed classifiers to predict the outcome for each patient, aiming to discover if these could be predicted based on gene expression alone or when combined with simple clinical information (sex, stage and age). Of the numerous classifiers generated, one showed the most consistent performance over the range of hypotheses. This method involved 100 gene clusters and ridge regression analysis to predict outcome. Prediction was poorer for stage I disease and better when clinical data were included in the analysis for all stages.

The study was not adequately powered to compare the classifiers with high significance, and used survival as the outcome measure rather than recurrence which may reflect tumour biology more accurately. However, the study has proved the principle of cooperation between institutions and, using standardised protocols, has generated a large data set which can be further analysed for better classifiers.

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