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## Lung alert

### Survival prediction in early squamous cell lung cancer

Current staging methods of squamous cell carcinoma (SCC) do not provide information regarding long-term prognosis. Gene expression profiling may be useful in this area.

In this study, lung SCC tumours resected from 66 patients between 2000 and 2004 in a Polish centre were identified for gene transcriptional analysis. A second cohort (validation group) of 26 patients was also studied. Tumour samples resected at surgery were used to study gene expression. A risk score model was designed to classify patients into good and poor survival groups. The degree of expression of 10 genes (CSF1, EGFR, CA IX, PH4, KIAA0974, ANLN, VEGFC, NTRK1, FN1 and INR1) was found to correlate with survival. In a subsequent multivariate analysis, three-gene signature (CSF1, EGFR, CA IX) and tumour size were found to have further independent useful predictive value for survival.

This study does have limitations; the range of the confidence interval is large due to the small sample size. Although the authors conclude the three genes are strongly associated with prognosis, this non-interventional study does not confirm the survival benefit of adjuvant chemotherapy. Also, the follow-up period is only 3 years and the sample size in the validation group is too small to give any convincing long-term conclusions.

- Skrzypski M, Jassem E, Taron M, *et al*. Three-gene expression signature predicts survival in early-stage squamous cell carcinoma of the lung. *Clin Cancer Res* 2008;**14**:4794–9.

#### K Wu

**Correspondence to:** Dr K Wu, Specialist Registrar, St James' University Hospital, Leeds, UK; kenwu@doctors.org.uk