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## Lung alert

### Genetic determinants of lung cancer micrometastasis

Complete resection of non-small cell lung cancer without lymph node or distant metastasis has a relapse rate within 2 years of surgery of approximately 40%. This study is the first to show a pattern of genomic profiles that appear to be specific to early micrometastasis.

Primary tumour cells were collected from 62 patients with non-small cell lung cancer undergoing surgical resection. These were subsequently divided into two groups based on the absence or presence of disseminated tumour cells (DTC) in bone marrow using immunocytochemical staining. Genomic aberrations were detected by microarray and fluorescence in situ hybridisation (FISH) analyses.

The most significant finding was loss of a region of chromosome 4q in bone marrow-positive patients and a gain in bone marrow-negative cases. Additional FISH analysis was also performed on a tissue microarray of 36 brain metastases of the lung, with 39% of samples showing a one allele loss of 4q. 4q loss was more commonly found in squamous cell carcinoma than adenocarcinomas. Brain metastases showed more losses of 4q21 than primary lung tumours overall.

The authors conclude that lung cancer development is a multistep genomic process and a 4q loss has a highly significant association with bone marrow-positive status. Further studies are required in this highly complex area before genomic aberrations can be used as a prognostic marker in the treatment of lung cancer.

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