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Metastatic signature

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Metastasis is responsible for determining the fate of many patients with cancer. But little is know about the molecular events by which tumor cells acquire metastatic capacity. In an Advanced Online Publication in Nature Genetics Ramaswamy *et al.* report microarray profiling analysis of metastatic tumours to define a 'metastatic signature' (*Nature Genetics,*9 December 2002, DOI:10.1038/ng1060). Comparison of expression profiles from 12 metastatic adenocarcinoma nodules with those from 64 primary adenocarcinomas identified 128 genes that were differentially expressed. Analysis of additional primary tumor samples revealed that the metastasis-associated genes were also detectable in a subset of primary lung tumors, specifically in patients with a poorer clinical outcome. The metastasis-linked gene set could be reduced to a 17-gene signature with good diagnostic potential. Thus, metastatic potential appears to be contained within the primary tumor gene program, rather than residing in a few rare cells within the tumor mass.

References

1. The pathogenesis of cancer metastasis

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