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Adenocarcinoma survival

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Clinical and histopathological examination of biopsy samples can generate a large amount of medically important information, but cannot predict disease progression and outcome in many cancers. In the 15 July [Nature Medicine](#), David Beer and colleagues at the [University of Michigan](#), Ann Arbor, show that gene expression profiles can be used to predict patient survival in early-stage lung adenocarcinomas (*Nat Med* 2002, DOI:10.1038/nm733).

Beer *et al.* examined gene-expression profiles based on microarray analysis and the clinical outcome for a cohort of patients with lung adenocarcinoma. They observed that expression of specific genes could predict patient survival in early-stage lung adenocarcinomas. In addition, Beer *et al.* developed a risk index based on the top 50 genes identified in low-risk and high-risk adenocarcinomas, and this risk index predicted survival in an independent cohort of patients with lung adenocarcinomas.

"Clearly, the identification of a high-risk group among patients with stage I disease would lead to consideration of additional therapeutic intervention for this group, possibly leading to improved survival of these patients," conclude the authors.

References

1. Beer DG, Kardia SLR and Huang C-C: Gene-expression profiles predict survival of patients with lung adenocarcinoma. *Nat Med* 2002, DOI:10.1038/nm733., [<http://medicine.nature.com>]
2. University of Michigan, [<http://www.umich.edu/>]

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