## **RESEARCH HIGHLIGHTS**

## 4 GENES FOR BLADDER CANCER PROGNOSIS

Quantifying the expression of just four genes can accurately predict the likelihood of bladder cancer progression. "The concise nature of the panel makes it far superior to existing prognostic panels for bladder cancer, which often consist of hundreds of genes. It also renders the panel an extremely cost-effective tool, which could be implemented clinically almost immediately," reports senior author Richard Cote.

Cote describes his team's unique approach as a "paradigm shift". Instead of employing the commonly used 'shotgun' technique, via which the entire genome is profiled, Anirban Mitra, Cote and colleagues adopted a hypothesis-driven strategy. Pathways and molecules that have been implicated generally in tumorigenesis, and that are known to be involved in the development and progression of bladder cancer, were targeted. "We have identified gene alterations that have the strongest prognostic impact across all disease stages; this focused approach helped us identify a four-gene panel that can predict an individual patient's prognosis, independent of standard clinicopathologic criteria," explains Cote.

Overexpression of the four genes— JUN, MAP2K6, STAT3 and ICAM1—was associated with poor outcomes. The difference between patients (n=52) at the two ends of the expression spectrum was striking. Those who expressed three of the four oncogenes at low or normal levels had a 5-year overall survival probability of 61%. This dropped to 5% in patients who had favorable expression levels for only two of the four genes.

"Further retrospective and prospective trials to confirm the prognostic potential of the identified gene panel are now in progress," adds Cote. These trials should validate the utility of the panel for identification of patients who are likely to benefit from additional therapy.

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