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PROSTATE CANCER

Genomic information improves risk prediction

> “67% of patients would be assigned to different risk groups using the new system”

The US National Comprehensive Cancer Network (NCCN) classification system, commonly used to determine the prognosis of patients with localized prostate cancer, incorporates data on PSA levels, grade group and T stage. This system was developed to predict the chance of biochemical recurrence, an end point subsequently shown to be a poor surrogate of overall survival outcomes. To overcome this limitation, Dan Spratt and colleagues have developed a method that incorporates genomic information, now described in the *Journal of Clinical Oncology*.

Nearly 7,000 patients were involved in this multicentre study, which included two prospective cohorts ($n = 5{,}937$) and two retrospective cohorts ($n = 991$) with long-term outcomes data (median follow-up duration of 8 years). Data from the two retrospective cohorts were used for training and validation of the new risk-grouping system. “Earlier this year, we demonstrated the robustness of the Decipher genomic classifier for risk prediction across nearly all patient subgroups. We have now used modelling methods to generate a combination of clinical and genomic information. We found that a simple summation of the NCCN and Decipher scores results in an optimal model that is very easy to use,” Spratt describes.

In this new system, six groups are defined according to the risk of prostate cancer recurrence (from very low to very high). These categories were converted into the three defined by the NCCN (low, intermediate and high) for comparison purposes. The risk of distant metastasis in patients in the validation cohort was calculated, and the new method showed superior performance over the NCCN system (area under the curve 0.84 versus 0.62). Further analysis of the prospective cohorts indicated that 67% of patients would be assigned to different risk groups using the new system.

“Most clinicians operate in the confines of NCCN risk groups, and not by risk of recurrence. We already knew that gene expression classifiers can provide additional data. Now we provide a new system that is simple and easy to use to personalize treatment,” Spratt explains, adding, “we plan to readily incorporate this risk-grouping system into practice, because the Decipher classifier test is already commercially available.”

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