

Methylation of PITX2 DNA feasible in prostate biopsies

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(HealthDay)—For patients with prostate cancer (PCa), methylation of

the paired-like homeodomain transcription factor 2 (*PITX2*) gene is feasible for individualized risk assessment in prostate core biopsies before surgery, according to a study published online Dec. 8 in the *Journal of Molecular Diagnostics*.

Barbara Uhl, from the University Hospital Bonn in Germany, and colleagues examined whether *PITX2* methylation is feasible for individualized [risk assessment](#) in prostate core biopsies before surgery. *PITX2* was measured using a quantitative, methylation-specific real-time [polymerase chain reaction](#) (PCR) in three cohorts: matched samples of neoplastic and non-neoplastic tissue from 24 PCa patients; a cohort of 300 patients with PCa after radical prostatectomy; and core biopsy specimens from 32 PCa patients and 31 patients with benign prostatic disease.

The researchers found that in patients with PCa, *PITX2* methylation discriminated between neoplastic and non-neoplastic tissue (P *PITX2* methylation correlated with clinicopathologic parameters in the second cohort, and *PITX2* hypermethylation predicted an elevated risk of biochemical recurrence. Overall, 720 of 753 [prostate biopsies](#) were applicable for analysis; *PITX2* methylation was increased in tumor-positive biopsies and correlated with the International Society of Urological Pathology grade groups.

"This study indicates that the *PITX2* methylation assay is feasible in prostate biopsies and might add valuable prognostic information for risk assessment in a presurgical diagnostic setting," the authors write.

More information: [Full Text \(subscription or payment may be required\)](#)

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