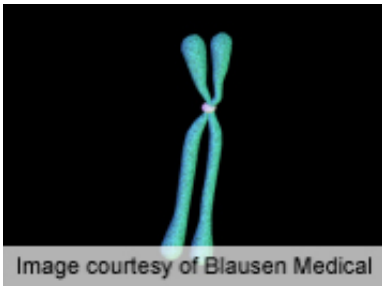


Three DNA methylation markers ID recurrence in bladder cancer

April 2 2014



(HealthDay)—For patients with noninvasive urothelial carcinoma, three DNA methylation markers are able to accurately predict tumor recurrence, according to a study published in the April 1 issue of *Clinical Cancer Research*.

Sheng-Fang Su, from USC Norris Comprehensive Cancer Center at the University of Southern California in Los Angeles, and colleagues analyzed DNA methylation levels of six markers in 368 urine sediment samples from 90 patients with noninvasive [urothelial carcinoma](#) to assess their use in longitudinal [tumor recurrence](#) surveillance. Five-fold cross-validation was used to identify the optimum marker combination, which was then validated in separate samples.

The researchers identified a panel of three markers which were able to

discriminate between patients with and without recurrence. The area under the curve was 0.90 in the testing set and 0.95 in the validation set, while sensitivity was 86 and 89 percent and specificity 80 and 97 percent, respectively. Tumor recurrence was reliably predicted by the three-marker test in 80 percent of patients, which was superior to cytology and cystoscopy (35 and 15 percent, respectively). The test accurately predicted no recurrence for 74 percent of patients who scored negative on the test.

"Given their superior sensitivity and specificity in urine sediments, a combination of hyper- and hypomethylated markers may help avoid unnecessary invasive exams and reveal the importance of DNA methylation in bladder tumorigenesis," the authors write.

One author disclosed financial ties to the pharmaceutical industry.

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

Copyright © 2014 [HealthDay](#). All rights reserved.

Citation: Three DNA methylation markers ID recurrence in bladder cancer (2014, April 2) retrieved 24 May 2024 from <https://medicalxpress.com/news/2014-04-dna-methylation-markers-id-recurrence.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.
