# Detection of Promoter Methylation of CCND2, CCNA1, and CALCA Genes in Urine Samples for Early Detection and Monitoring of Low Grade Papillary Urothelial Cell Carcinoma Patients

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## Technology description

Unmet Need:

Urothelial cell carcinoma (UCC) constitutes over 90% of bladder cancers in the Western world, non-muscle invasive UCC being the most common and treated by trans-urethral resection of bladder tumor (TURBT) with or without Bacillus Calmette-Guerin (BCG), the main intravesical immunotherapy for treating early-stage bladder cancer. 20% of patients will be cured while 70% will recur at least once every 5 years, and the remaining will progress to muscle-invasive disease with poor prognosis. Since, conventional approaches (computed tomography, urine cytology, histopathology, or tumor-node-metastasis classification) are not ideal to predict risk of recurrence, there is a crucial need to develop well validated molecular markers that can predict recurrence at the time of diagnosis.

Technical Overview:

By analyzing the promoter methylation status of candidate genes in over 100 urine samples of noninvasive low grade urothelial cell carcinoma patients through methylation specific PCR (QMSP), JHU researchers have identified three genes (CCND2, CCNA1, and CALCA) were highly methylated in the promoter regions in recurrent cohort compared to non-recurrent control. The research supports methods for detecting, diagnosing, providing prognosis for and treating urothelial cancers by detecting methylation changes in the regulatory region of three genes.

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