

Genetic signature and epigenetic markers in bladder cancer

Wun-Jae Kim M.D., Ph.D.

Department of Urology, College of Medicine, Chungbuk National University, Cheongju,
South Korea

Transitional cell carcinomas of the urinary bladder have diverse biological and functional characteristics. Many bladder cancer markers have been evaluated for detecting and monitoring tumors using serum, bladder washes, and urinary specimens. However, none of the biomarkers reported to date have shown sufficient sensitivity and specificity for detecting the whole spectrum of bladder cancer diseases in routine clinical practice. The limited value of the established prognostic markers requires the analysis of new molecular parameters of interest for predicting the prognosis of bladder cancer patients, particularly with respect to patients who are at high-risk of recurrence and progression. Over the past decade, there has been major progress elucidating of the molecular genetic and epigenetic changes leading to the development of bladder cancer. Because multiple genetic and epigenetic alterations are required for the transformation of a normal cell into a cell with a malignant and ultimately metastatic phenotype, assessment of multiple markers as a whole might better describe the biological phenotype of a particular cancer. For these reasons, the role of multiple biomarkers in

regulating tumorigenesis and prognosis is of particular interest. Recently, new high-throughput microarray technology makes it possible to gain comprehensive insight into the molecular basis of human diseases. With this technology, hundreds or even thousands genetic and epigenetic alterations in a tumor can be surveyed simultaneously. This presentation focuses on the recent advances of genetic and epigenetic aspects in bladder cancer, and emphasizes how molecular biology would be likely to affect the future research and clinical aspects.