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Biomarkers in bladder cancer: Translational and clinical implications

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Abstract

Bladder cancer is associated with high recurrence and mortality rates. These tumors show vast heterogeneity reflected by diverse morphologic manifestations and various molecular alterations associated with these disease phenotypes. Biomarkers that prospectively evaluate disease aggressiveness, progression risk, probability of recurrence and overall prognosis would improve patient care. Integration of molecular markers with conventional pathologic staging of bladder cancers may refine clinical decision making for the selection of adjuvant and salvage therapy. In the past decade, numerous bladder cancer biomarkers have been identified, including various tumor suppressor genes, oncogenes, growth factors, growth factor receptors, hormone receptors, proliferation and apoptosis markers, cell adhesion molecules, stromal factors, and oncoproteins. Recognition of two distinct pathways for urothelial carcinogenesis represents a major advance in the understanding and management of this disease. Nomograms for combining results from multiple biomarkers have been proposed to increase the accuracy of clinical predictions. The scope of this review is to summarize the major biomarker findings that may have translational and clinical implications.

Keywords: Urinary bladder; Urothelial carcinoma; Biomarkers; Prognosis; Tumorigenesis

1. Introduction

Urothelial carcinoma is the 5th most common cancer in industrialized countries, accounting for approximately 5% of all cancers [1–3]. The associated risk factors for bladder cancer include tobacco smoking, aromatic amine exposure, arsenic exposure, chronic infection with *Schistosoma* species, radiation therapy, and exposure to alkylating agents [4,5].

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