

Comprehensive Evaluation of the Bax Gene in Urothelial Bladder Carcinoma: The Role of Single Nucleotide Polymorphisms in Bax Gene Underexpression

Introduction and Objective: Bax under-expression is known as an adverse prognostic factor in urothelial bladder cancer. In this study, the level of bax gene expression was determined in urothelial bladder cancer tissues and compared with control tissues, normal tissues adjacent to the tumor, and blood lymphocytes. Furthermore, complete sequencing of the bax gene was performed to assess the role of potential mutations and polymorphisms that may interfere with gene expression.

Materials and Methods: Tissue samples were obtained from 31 patients with bladder cancer and 26 cancer-free controls, who were candidates for surgical treatment of benign prostatic hyperplasia. Quantitative real-time polymerase chain reaction was applied to determine and compare bax gene expression in different tissues. Sequencing of the bax gene was also performed to correlate potential genetic variations with the level of bax expression.

Results: Nineteen (61.3%) patients showed a tumor expression level of more than 2 times higher than adjacent normal tissue. The expression level of bax in normal adjacent tissues and blood lymphocytes was similar to that of control tissues. Complete sequencing of the bax gene revealed 3 single-nucleotide polymorphisms (SNPs) at three loci of the bax gene. The genetic variation of the promoter region was associated with bax under-expression and occurred in both tumor tissues and lymphocytes, concomitantly.

Conclusions: The observed SNP in promoter region of bax gene is associated with bax under-expression and may be also seen in lymphocytes. These findings may be considered as a starting point for further investigation of serum biomarkers indicative of bladder cancer.