



MEETING ABSTRACT

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The A148T variant of *CDKN2A* gene in bladder cancer

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Background

Cancer of the urinary bladder is a common malignant disease in Poland. Molecular genetic alterations play a key role in bladder cancer carcinogenesis. Understanding genetic events that lead to initiation and progression of bladder cancer remains an important challenge in urological research.

Materials and methods

44 lesions were determined to be non-invasive tumors (pTa), whereas 36 tumors were invasive (pT1-T4). Tumor grade was noted low (G1) in 46 cases and high (G2-3) in 34 cases. DNA samples were evaluated for *CDKN2A* mutations with the use of MSSCP and sequencing method.

Results

We found common polymorphic variants reported in the literature at codon 148 in exon 2 (Arg148Thr) and at nucleotides 500 and 540 in the 3'untranslated region which were not considered to be functional variants. We compared the obtained frequencies for the particular *CDKN2A* variants with the control group for the Polish population examined by Debniak and colleagues (Cancer Research 2005) and we found a significant difference in A148T polymorphism occurrence in the group of the bladder cancer patients (G test, table 2 × 2: $N_{\text{BLADDER CANCER}}=80$, $N_{\text{CONTROL}}=1210$, $G=10.214$, $p<0.01$). The Nt 500c>g, Nt540c>t polymorphisms recorded in the group of the bladder cancer patients in our study is not different from those recorded in the control group.

Conclusion

The A148T variant of *CDKN2A* gene seems to be associated with an increased risk of bladder cancer development.

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