

Significant association of catechol-O-methyltransferase Val158Met polymorphism with bladder cancer instead of prostate and kidney cancer.

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Abstract

BACKGROUND: Urological cancers occur worldwide. Many factors, among which the catechol-O-methyltransferase (COMT) Val158Met polymorphism, are said to be associated with the cancer risk. We conducted a meta-analysis to investigate the association between urological cancer susceptibility and COMT Val158Met in different genetic models.

METHODS: This study was based on material obtained from the PubMed, HuGENet and Embase databases. Four models including dominant (AA + AG vs. GG), recessive (AA vs. AG + GG), codominant (AA vs. AG, AA vs. GG) and per-allele analysis (A vs. G) were applied. Odds ratios (OR) and the corresponding 95% confidence intervals (CI) were used to evaluate the power of the associations.

RESULTS: Fourteen eligible studies comprising 3,285 cases and 3,594 controls were included. Although we could not detect a positive function of the COMT Val158Met polymorphism in urological cancers, the polymorphism might be significantly associated with bladder cancer risk (dominant model [AA + AG vs. GG]: OR = 0.736, 95% CI = 0.586-0.925, I² = 0.00%; recessive model [AA vs. AG + GG]: OR = 0.822, 95%CI = 0.653-1.035, I² = 6.30%; codominant model [AA vs. AG]: OR = 0.908, 95% CI = 0.710-1.161, I² = 0.00%; codominant model [AA vs. GG]: OR = 0.693, 95% CI = 0.524-0.917, I² = 30.20%; allele analysis [A vs. G]: OR = 0.826, 95%CI = 0.717-0.951, I² = 30.20%). The same significant associations were not found for kidney cancer and prostate cancer risk in different ethnicities. There also seemed to be no distinct effect of the polymorphism on benign prostatic hyperplasia.

CONCLUSIONS: We suggest that bladder cancer but not prostate cancer and kidney cancer could be significantly associated with the Val158Met polymorphism. Interaction of COMT genetic and related environmental factors for urological cancers should not be ignored in future.