Meta-analysis demonstrates association of XRCC1 genetic polymorphism Arg399Gln with esophageal cancer risk in the Chinese population

Z.Y. Zhang, Y. Xuan, X.Y. Jin, X. Tian and R. Wu

Department of Medical Oncology, Shengjing Hospital, China Medical University, Shenyang, China

Corresponding author: Z.Y. Zhang
E-mail: cmuliangyuan@163.com

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ABSTRACT. We made a meta-analysis of the association between X-ray cross-complementing gene 1 (XRCC1) genetic polymorphism Arg399Gln and esophageal cancer (EC) risk. Statistical analysis was performed with the Review Manager version 4.2.8 software program and STATA version 11.0. We selected 16 case-control studies for this meta-analysis, including 3591 EC cases and 5752 controls. Overall, the Gln399 allele was not associated with EC risk, compared with the Arg399 allele in the populations included in the analysis. However, stratified analysis revealed that the Gln399 allele was associated with increased EC risk among the Chinese population in a recessive model [odds ratio (OR) = 1.42; 95% confidence interval (95%CI) = 1.07-1.90; P = 0.02 for heterogeneity] and by homozygote contrast (OR = 1.43; 95%CI = 1.05-1.96; P = 0.02 for heterogeneity), particularly for the tumor histology of squamous cell carcinoma (OR = 1.46; 95%CI = 1.10-1.95 for the recessive model and OR = 1.42; 95%CI = 1.03-1.95 for the homozygote contrast). We conclude that the XRCC1 Arg399Gln
polymorphism has potential as a biomarker for EC susceptibility in the Chinese population, particularly for squamous cell carcinoma.

Key words: Esophageal cancer; Gene polymorphism; Meta-analysis; X-ray cross-complementing gene 1