GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Lack of association between the *hOGG1* gene Ser326Cys polymorphism and gastric cancer risk: evidence from a case-control study and a meta-analysis

W.G. Hu[1]*, R.J. Pan[1]*, W. Cai[1], Z.T. Wang[2] and Z.G. Zhu[1]

[1]Department of General Surgery, Ruijin Hospital,
Shanghai Jiaotong University School of Medicine, Shanghai, China
[2]Department of Gastroenterology, Ruijin Hospital,
Shanghai Jiaotong University School of Medicine, Shanghai, China

*These authors contributed equally to this study.
Corresponding author: Z.T. Wang
E-mail: dake_wang@126.com

Genet. Mol. Res. 14 (4): 14670-14679 (2015)
Received December 1, 2014
Accepted May 26, 2015
Published November 18, 2015
DOI http://dx.doi.org/10.4238/2015.November.18.31

ABSTRACT. The association between the human 8-oxoguanine glycosylase 1 (*hOGG1*) gene Ser326Cys polymorphism (rs1052133) and gastric cancer has been widely evaluated, yet a definitive answer to whether this association exists is lacking. We first conducted a case-control study to assess this association in a large Han Chinese population, and then performed a meta-analysis to further address this issue. This case-control study involved 448 patients clinically diagnosed with gastric cancer and 372 cancer-free control individuals from China. Genotyping was conducted using the polymerase chain reaction-ligase detection reaction method. Meta-analysis was performed by the STATA software. Data and study quality were assessed in duplicate. Our case-control association study indicated that there were no significant differences in the genotype and allele distributions of the Ser326Cys

 ©FUNPEC-RP www.funpecrp.com.br

polymorphism between gastric cancer patients and controls (P = 0.8026 for genotype, and P = 0.5857 for allele), consistent with the results of the subsequent meta-analysis involving 2745 patients and 4588 controls under both allelic [odds ratio (OR) = 1.02; 95% confidence interval (CI) = 0.91-1.14; P = 0.739] and dominant (OR = 0.97; 95%CI = 0.78-1.21; P = 0.803) models. Further subgroup analyses by ethnicity, source of controls, and sample size also did not detect any positive associations in this meta-analysis. Overall, our study in the Han Chinese population, along with the meta-analysis, failed to confirm the association of the *hOGG1* gene Ser326Cys polymorphism with gastric cancer risk, even across different ethnic populations.

Key words: Gastric cancer; *hOGG1* gene; Polymorphism; Risk association study; Meta-analysis