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

Lack of association between *Cyclin D1* gene G870A polymorphism and esophageal cancer: evidence from a meta-analysis

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Genet. Mol. Res. 12 (4): 6636-6645 (2013)
Received July 23, 2012
Accepted January 20, 2013
Published April 26, 2013
DOI http://dx.doi.org/10.4238/2013.April.26.1

ABSTRACT. The association between the *Cyclin D1* gene (*CCND1*) G870A polymorphism and esophageal cancer has been widely evaluated, with conflicting results. As meta-analysis is a reliable approach to resolving discrepancies, we aimed to evaluate this association. Data were available from 9 study populations incorporating 1898 cases and 3046 controls. Overall, the allelic/genotypic association between the G870A polymorphism and esophageal cancer was nonsignificant [for allele: odds ratio (OR) = 1.14, 95% confidence interval (95%CI) = 0.94-1.38, P = 0.184; for genotype homozygous comparison: OR = 1.36, 95%CI = 0.90-2.06, P = 0.140; for dominant model: OR = 1.24, 95%CI = 0.88-1.75, P = 0.222; for recessive model: OR = 1.13, 95%CI = 0.90-1.43, P = 0.292]. Moreover, subgroup analyses according to study designs, geographic areas, types of esophageal cancer, genotyping methods, and ethnicities failed to demonstrate a significant association between this polymorphism and esophageal cancer. In addition, there was significant publication bias as reflected by funnel plots and the

Egger test (P = 0.042). Taken together, our results suggest that the *CCND1* G870A polymorphism might not be a potential candidate for predicting esophageal cancer risk.

Key words: Esophageal cancer; *CCND1* gene; Polymorphism; Meta-analysis; Genetic association

