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

Meta-analysis of epidemiological studies of association of two polymorphisms in the interleukin-10 gene promoter and colorectal cancer risk

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Genet. Mol. Res. 11 (3): 3389-3397 (2012)
Received October 13, 2011
Accepted March 16, 2012
Published September 25, 2012
DOI http://dx.doi.org/10.4238/2012.September.25.7

ABSTRACT. In order to make a comprehensive assessment of the potential association between two genetic variants in the IL-10 gene promoter, -1082 A>G (rs1800896) and -592 C>A (rs1800872), and colorectal cancer (CRC) risk, we conduced a meta-analysis of seven epidemiological studies, which included 1469 colorectal cancer cases and 2566 controls. Neither of the two polymorphisms had any association with increased CRC risk in overall population [for rs1800896: odds ratio (OR) = 0.90, 95% confidence interval (95%CI) = 0.76-1.06 in the dominant model and for rs1800872: OR = 1.06, 95%CI = 0.91-1.23 in the dominant model]. In subgroup analysis of the rs1800896 polymorphism, the results did not change when the analyses were restricted to individual studies, or those fulfilling Hardy-Weinberg equilibrium, or according to the source of controls. For rs1800872,

however, when stratifying by the source of controls, the A allele had a significant increased risk of CRC among studies with population-based controls in the codominant model (AC *vs* CC: OR = 1.30, 95%CI = 1.04-1.63) and dominant model (AA/AC *vs* CC: OR = 1.25, 95% CI = 1.01-1.55). Based on this meta-analysis, we conclude that the IL-10 rs1800872 polymorphism could be a risk factor for CRC development among European populations. However, we found no association between the IL-10 rs1800896 polymorphism and CRC risk. Further studies, either with larger sample size or involving other SNPs and haplotypes of the IL-10 gene, are necessary to clarify the contribution of IL-10 genetic variations in colorectal carcinogenesis.

Key words: Interleukin-10; Colorectal cancer; Polymorphism; Meta-analysis