Correlation between IRGM genetic polymorphisms and Crohn’s disease risk: a meta-analysis of case-control studies

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Received November 8, 2013
Accepted April 28, 2014
Published December 18, 2014
DOI http://dx.doi.org/10.4238/2014.December.18.15

ABSTRACT. This meta-analysis was performed to evaluate the relationships between single-nucleotide polymorphisms (SNPs) in the immunity-related GTPase M (IRGM) gene and the risk of Crohn’s disease (CD). Eleven case-control studies were included, for a total of 5183 CD patients and 5571 healthy controls. Three common SNPs (rs13361189 C>T, rs10065172 C>T, and rs4958847 A>G) in the IRGM gene were assessed. We found that the IRGM rs13361189 polymorphism was significantly associated with an increased risk of CD [C allele vs T allele: odds ratio (OR) = 1.30, 95% confidence interval (CI) = 1.05-1.61, P = 0.017; CC + CT vs TT: OR = 1.32, 95%CI = 1.06-1.64, P = 0.013]. However, we observed no correlation between the rs10065172 and rs4958847 polymorphisms in the IRGM gene with susceptibility to CD (all P > 0.05). Subgroup analysis by ethnicity revealed significant associations between IRGM genetic polymorphisms and an increased risk of CD.
among Caucasian populations (C allele vs T allele: OR = 1.22, 95%CI = 1.07-1.40, P = 0.004; CC + CT vs TT: OR = 1.22, 95%CI = 1.05-1.41, P = 0.009), but not among Asian populations (all P > 0.05). Meta-regression analysis also confirmed that ethnic differences may be an important source of heterogeneity (P = 0.003). Our meta-analysis results indicate that the IRGM rs13361189 polymorphism contributes to the susceptibility to CD. Thus, the IRGM rs13361189 polymorphism is promising as a biomarker for early diagnosis of CD. However, the IRGM rs10065172 and rs4958847 polymorphisms may not be the major determinants of CD risk.

**Key words:** Crohn’s disease; IRGM; Single nucleotide polymorphism; Meta-analysis