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

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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

