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Association analysis of colorectal cancer susceptibility variants with gastric cancer in a Chinese Han population

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ABSTRACT. Evidence suggests that some genetic variants are risk factors for both colorectal cancer (CRC) and gastric cancer (GC). Thus, we selected 12 reported single nucleotide polymorphisms (SNPs) from genome-wide association studies of CRC and conducted this case-control study to assess the associations between these SNPs and the risk for GC in a southern Chinese population. All SNPs were genotyped in 249 individuals with GC and 292 healthy population-matched subjects using the Sequenom MassArray iPLEX System. Association analyses based on the χ^2 test and binary logistic regression were performed to determine the odds ratio (OR) and 95% confidence interval (95%CI) for each SNP. A stratified analysis by gender was also performed. Borderline significant associations were observed for rs4444235 (P = 0.070) and rs10411210 (P = 0.084), both fitting the overdominant model. The rs4444235 CT genotype showed a protective

effect (OR = 0.72, 95%CI = 0.50-1.03), while the rs10411210 CT genotype was a risk factor (OR = 1.40, 95%CI = 0.96-2.05) as compared with the CC+TT genotype. In the female subgroup, the rs6983267 GT genotype (compared with TT, OR = 2.31, 95%CI = 1.07-4.99) and the rs10505477 CT genotype (compared with TT, OR = 2.36, 95%CI = 1.09-5.11) significantly increased the risk for GC. No significant association was detected for the other SNPs. These results provide evidence that known genetic variants associated with CRC risk may also confer risk for GC.

Keywords: Single nucleotide polymorphism; Susceptibility; Gastric Cancer; Colorectal cancer;

