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Association between five common polymorphisms in microRNA genes and the risk of gastric cancer: a meta-analysis

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ABSTRACT. Gastric cancer (GC) is a prevalent disease with a high mortality rate, especially in developing countries. Accumulating evidence suggests that single nucleotide polymorphisms in microRNA (miRNA) genes might influence the susceptibility to GC; such sequence variation might contribute to the development of disease by altering crucial cellular pathways. In this study, we assessed the correlation between the miR-146a G>C, miR-196a-2 C>T, miR-499 T>C, miRNA-27a A>G, and miRNA-149 T>C polymorphisms and the susceptibility to GC. A comprehensive literature search for relevant studies published prior to August 2014 was conducted using PubMed/Medline, Embase, Web of Science, the Cochrane Library, and CNKI databases along with Google Scholar. Meta-analysis was performed using odds ratios (ORs) and 95% confidence intervals (CIs) as effect measures, incorporating 19 studies encompassing 8285 patients and 10,716 controls. Allelic, dominant, recessive, homozygous, and heterozygous genetic models were examined. Pooled results showed that none of the

five polymorphisms studied were statistically related to GC. Stratified analyses by ethnicity and source of controls were conducted for miR-146a G>C and miR-196a-2 C>T. Subgroup analysis suggested that the miR-146a G allele might increase the risk of GC in hospital-based case-control (HCC) but not in population-based case-control studies (HCC: recessive model: OR = 1.23, 95%CI = 1.10-1.37, P < 0.001; heterozygous model: OR = 1.19, 95%CI = 1.06-1.34, P = 0.004). Overall, this meta-analysis failed to detect an association between five common miR-146a gene polymorphisms and GC susceptibility. However, this does not necessarily completely rule out a correlation between miRNA polymorphisms and GC susceptibility.

Key words: Gastric cancer; MicroRNA; Polymorphism; Meta-analysis

