



Common polymorphisms in the *HIF-1 α* gene confer susceptibility to digestive cancer: a meta-analysis

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ABSTRACT. Recent evidence suggests that common functional polymorphisms in the hypoxia inducible factor-1 α (*HIF-1 α*) gene may play an important role in the development and progression of digestive cancer, but individually published results are inconclusive. Our meta-analysis is aimed to derive a more precise estimation of the relationships between *HIF-1 α* gene polymorphisms and digestive cancer risk. An extensive literature search for relevant studies was conducted on Pubmed, Embase, Web of Science, Cochrane Library, and CBM databases from their inception through May 1, 2013. This meta-analysis was performed using the STATA 12.0 software. The crude odds ratios (OR) with 95% confidence interval (CI) were calculated. Eight case-control studies were included with a total of 1276 digestive cancer patients and 3392 healthy controls. Our meta-analysis revealed that the A variant of *HIF-1 α* G1790A polymorphism might be associated with increased risk of colorectal, esophageal, gastric, and liver cancers, especially among Asian populations. However, no statistically significant associations were found between *HIF-1 α* C1772T polymorphism and susceptibility

to digestive cancer. No publication bias was detected in this meta-analysis. The current meta-analysis suggests that the *HIF-1 α* G1790A polymorphism may increase the risk of colorectal, esophageal, gastric, and liver cancers, especially among Asian populations.

Key words: Digestive cancer; Hypoxia inducible factor-1 α ; Polymorphism; Susceptibility; Meta-analysis