



Association between the CYP1A1 polymorphisms and hepatocellular carcinoma: a meta-analysis

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ABSTRACT. Numerous studies have evaluated the association between CYP1A1 gene polymorphisms and hepatocellular carcinoma (HCC) risk. However, the specific association is still controversial. The aim of our study was to clarify the effects of CYP1A1 gene polymorphisms (3801 T>C and A2455G) on HCC risk by conducting a meta-analysis. We conducted searches of the literature published in PubMed and EMBASE databases up to April 2014. We estimated the pooled odds ratio with its 95% confidence interval to assess the association using a fixed or random-effects model. Publication bias was investigated by the Begg funnel plot. Meta-analysis was performed using the STATA package version 12.0. Meta-analysis results showed no significant association between the CYP1A1 3801 T>C polymorphism and HCC risk. In a subgroup analysis by nationality, we found a significant association between 3801 T>C polymorphism and HCC risk in Asians

(TT vs TC: OR = 0.77, 95%CI = 0.60-0.99). As for A2455G, the meta-analysis indicated no significant association between the CYP1A1 A2455G polymorphism and HCC risk. In conclusion, the 3801 T>C polymorphism in the CYP1A1 gene may be related to increased risk of HCC in Asians. Conclusive evidence on the effects of the variants in HCC should be addressed in further studies.

Key words: CYP1A1; Gene polymorphism; Meta-analysis; Hepatocellular carcinoma