



Relationship between *RUNX3* methylation and hepatocellular carcinoma in Asian populations: a systematic review

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ABSTRACT. Runt-related transcription factor 3 (*RUNX3*) is a potential tumor suppressor that is frequently hypermethylated in hepatocellular carcinoma (HCC). The present meta-analysis of case-control studies was carried out to determine whether *RUNX3* hypermethylation is associated with HCC. The PubMed, Embase, and Chinese National Knowledge Infrastructure databases were searched for all relevant studies published between May 2000 and May 2012. A total of 11 studies were identified, and 8 studies involving 491 patients with HCC and 409 patients without tumors were found to satisfy the inclusion criteria for the meta-analysis. All tissue samples were from Asian populations. There was significant heterogeneity between the studies. Over the entire sample, the odds ratio (OR) of *RUNX3* promoter methylation was 18.5 [95% confidence interval

(CI), 11.6-29.6] for HCC tissues relative to control tissues. The ORs of *RUNX3* methylation were 16.6 (95%CI = 6.5-42.4) for tumor tissues relative to tumor-adjacent tissues in patients with HCC, 67.3 (95%CI = 13.0-348.5) for tumor tissues from patients with HCC relative to liver tissues from patients with non-neoplastic liver diseases, and 3.26 (95%CI = 1.54-6.90) for tissues from patients with hepatitis C virus (HCV)-related HCC relative to liver tissues from patients with HCC unrelated to HCV. There was no association between *RUNX3* methylation and age, gender, pathological stage, or hepatitis B virus infection in HCC tissues. Methylation of the *RUNX3* promoter strongly correlated with HCC in Asian populations, especially in individuals with HCV-related HCC, and may be a useful marker for HCC diagnosis in these populations.

Key words: *RUNX3*; Methylation; Meta-analysis; Asian; Hepatocellular carcinoma