



Functional polymorphisms in microRNA gene and hepatitis B risk among Asian population: a meta-analysis

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ABSTRACT. Genetic mutations in microRNA gene can alter expression, which may interact to increase the risk of developing various diseases, including hepatitis B. However, published results are inconclusive or ambiguous. The aim of this review and meta-analysis is to more precisely estimate the association between polymorphisms in microRNA genes and hepatitis B risk. A digital search was performed of the MEDLINE EMBASE, CNKI, and CBM databases to identify relevant articles published up to February 18, 2014. Ten case-control studies were included, with a total of 6042 patients with hepatitis B and 6834 healthy controls. Nine single-nucleotide polymorphisms in the miRNA gene were examined, including miR-34b/c [rs4938723 (T>C)], miR-196a-2 [rs11614913 (C>T)], miR-146a [rs2910164 (G>C)], miR-499 [rs3746444 (T>C)], miR-122 [rs3783553 (ins/del)], miR-149 [rs2292832 (C>T)], miR-106b-25 [rs999885 (A>G)], miR-let-7c [rs6147150 (ins/del)], and miR-218 [rs11134527 (A>G)]. The meta-analysis results indicated that the miR-196a-2*T, miR-122*del, miR-106b-25*A, and miR-let-7c*del alleles/carriers increase the risk of

hepatitis B among the Asian population. However, the miR-146a, miR-499, miR-149, miR-218, and miR-34b/c polymorphisms may not be linked with the risk of hepatitis B. Further investigations are warranted to determine the exact associations between microRNA mutations and hepatitis B susceptibility.

Key words: Hepatitis B; Meta-analysis; MicroRNA; Polymorphism