Functional polymorphisms in microRNAs and susceptibility to liver cancer: a meta-analysis and meta-regression

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ABSTRACT. MicroRNAs (miRNAs) are small non-coding RNA molecules that play a fundamental role in controlling a variety of biological functions. Emerging evidence has shown that common genetic polymorphisms in miRNAs may be associated with the development of liver cancer; however, several individually published studies showed inconclusive results. This meta-analysis aimed to derive a more precise estimation of the association between functional polymorphisms in miRNAs and susceptibility to liver cancer. A literature search of PubMed, Embase, Web of Science, and China BioMedicine (CBM) databases was conducted on articles published before May 1, 2012. Crude odds ratios with 95% confidence intervals were calculated. Fourteen case-control studies were included with a total of 6824 liver cancer patients and 7674 healthy controls. Nine single nucleotide polymorphisms in miRNAs were assessed, including miR-146a G>C (rs2910164), miR-499 T>C (rs3746444), miR-218 A>G (rs11134527), miR-let-7c Ins/Del (rs6147150), miR-106b-25 A>G (rs999885), miR-34b/c T>C (rs4938723), miR-196a-2 C>T (rs11614913), miR-920 Ins/Del (rs16405), and miR-122 Ins/Del (rs3783553). The meta-analysis
results showed that miR-let-7c*Del, miR-34b/c*C, and miR-122*Del variants may be associated with increased liver cancer risk. Conversely, miR-920*Del variant may decrease the risk of liver cancer. However, miR-146a G>C, miR-196a-2 C>T, miR-499 T>C, and miR-218 A>G polymorphisms showed no significant association with liver cancer risk. In conclusion, the current meta-analysis suggests that miR-let-7c*Del, miR-34b/c*C and miR-122*Del variants may be associated with increased liver cancer risk, while miR-920*Del variant may be a protective factor against liver cancer.

**Key words:** Liver cancer; Single nucleotide polymorphism; MicroRNA; Meta-analysis