



# Association between polymorphisms in the promoter region of pri-miR-34b/c and risk of hepatocellular carcinoma

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**ABSTRACT.** Hepatocellular carcinoma (HCC) is a major cause of cancer-related deaths worldwide. MicroRNA-34 (*miR-34*) gene plays a key role in altering the apoptotic cycle and pathways of downstream

cells, and therefore influences carcinogenesis. In this case-control study, we assessed the role of the pri-miR-34b/c rs4938723 polymorphism in HCC risk. The pri-miR-34b/c polymorphic genotype was determined in 286 patients with HCC and 572 controls using polymerase chain reaction-restriction fragment length polymorphism. The male gender ( $\chi^2 = 12.95$ ,  $P < 0.001$ ), regular alcohol consumption ( $\chi^2 = 16.81$ ,  $P < 0.001$ ), and a family history of cancer ( $\chi^2 = 11.88$ ,  $P = 0.001$ ) were associated with HCC risk. However, the age ( $t = 1.19$ ,  $P = 0.12$ ) and tobacco smoking habit ( $\chi^2 = 0.64$ ,  $P = 0.42$ ) of HCC patients were comparable to those of the controls. The TC (adjusted OR = 1.46, 95%CI = 1.06-2.01) and CC (adjusted OR = 3.07, 95%CI = 1.77-5.34) genotypes of pri-miR-34b/c rs4938723 were correlated with a higher risk of HCC compared to the TT genotype. Moreover, the TC+CC genotype was correlated with an increased risk of HCC compared to the TT genotype (adjusted OR = 1.64, 95%CI = 1.21-2.22). In the recessive model, the CC genotype of pri-miR-34b/c rs4938723 was significantly correlated with an elevated risk of HCC compared to the TT+TC genotype (adjusted OR = 2.50, 95%CI = 1.49-4.22). Further large-scale and multi-center studies are required to confirm these results.

**Key words:** pri-miR-34b/c; Polymorphism; Hepatocellular carcinoma