

A variant in microRNA-196a2 is associated with susceptibility to hepatocellular carcinoma in Chinese patients with cirrhosis

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polymorphism was genotyped by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP). In addition, tumour tissues of liver (n = 59) were obtained from the studied HCC patients for measurement of miR-196a expression levels.

Results: The frequency of the CC genotype among HCC patients was higher than that in the control group, implying that the cirrhotic patients with the CC genotype or C allele containing genotypes (CT and CC) may have a higher risk of HCC. However, in a subsequent analysis of the association between this polymorphism and clinicopathological characteristics, there was an association between rs11614913 genotype and tumour size ($p = 0.046$), but not with tumour number, grade, stage, invasiveness or Child-Pugh grade. In a genotype-phenotype correlation analysis using 59 tumour tissues of liver, rs11614913 CC or carrying at least one C allele was associated with significantly increased mature miR-196a expression ($p = 0.006$ or $= 0.002$).

Conclusions: Our results suggest, for the first time, that miR-196a2 polymorphism may contribute to cirrhosis-related HCC susceptibility in Chinese patients through influencing mature miR-196a expression.

Key words:

- Cirrhosis
- hepatocellular carcinoma
- MiR-196a2
- single nucleotide polymorphism




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