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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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