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Molecular Pathology

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

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Abstract

Aims: Cirrhosis is an important risk factor for hepatocellular carcinoma (HCC) in China, while little is known of the genetic susceptibility to hepatocarcinogenesis. Traditional approaches to identification of novel genetic predisposition genes have focused on

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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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