



Pathology >

Volume 42, 2010 - [Issue 7](#)

55 Views | 3 CrossRef citations to date | 0 Altmetric

Molecular Pathology

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

Xiao-Dong Li , Zhi-Gao Li, Xian-Xu Song & Chun-Fu Liu

Pages 669-673 | Received 11 May 2010, Accepted 13 Jul 2010, Published online: 17 Nov 2010

Cite this article

Sample our
Bioscience
Journals
>> [Sign in here](#) to start your access
to the latest two volumes for 14 days

Full Article

Figures & data

References

Citations

Metrics

Reprints

We Care About Your Privacy

We and our 912 partners store and access personal data, like browsing data or unique identifiers, on your device. Selecting I Accept enables tracking technologies to support the purposes shown under we and our partners process data to provide. Selecting Reject All or withdrawing your consent will disable them. If trackers are disabled, some content and ads you see may not be as relevant to you. You can resurface this menu to change your choices or withdraw consent at any time by clicking the Show Purposes link on the bottom of the webpage. Your choices will have effect within our Website. For more details, refer to our Privacy Policy. [Here](#)

We and our partners process data to provide:

Use precise geolocation data. Actively scan device

I Accept

Reject All

Show Purpose



Abstract

Aims: Cirrhosis is a major risk factor for hepatocellular carcinoma (HCC) in China, while little is known about the role of microRNA (miR) in the pathogenesis of HCC. We aimed to investigate the role of miR-196a2 in HCC.

Methods: We performed a meta-analysis of the association between miR-196a2 and HCC. The meta-analysis included 10 studies with 1,161 cases and 1,161 controls.

Results: The meta-analysis showed that miR-196a2 was significantly associated with HCC. The pooled odds ratio (OR) was 1.52 (95% CI: 1.12-2.05).

Conclusion: Our results suggest that miR-196a2 is a potential biomarker for HCC. Further studies are needed to confirm our findings.

Keywords: miR-196a2, hepatocellular carcinoma, cirrhosis, meta-analysis

rs11614

congenit

lung can

influen

Methods

without

(C) in China,

traditional

used on

(NA) may

at the

g cancer,

small cell

n can

2 patients

miR-196a2

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



Relat

Onco



Sourc

A fun

hepat

Sourc

Trans

and P

Sourc

Frequent deletions and down-regulation of micro- RNA genes miR15 and miR16 at 13q14 in chronic lymphocytic leukemia

Source: Proceedings of the National Academy of Sciences

Retroviral Insertional Mutagenesis Identifies Genes that Collaborate with NUP98-HOXD13 during Leukemic Transformation

Source: Cancer Research

Hepatocellular Carcinoma: The Need for Progress

Source: Journal of Clinical Oncology

Common genetic variants in pre-microRNAs were associated with increased risk of breast cancer in Chinese women

Source: Human Mutation

A microRNA component of the p53 tumour suppressor network

Source: Nature

Retroviral activation of the mir-106a microRNA cistron in T lymphoma

Source: Retrovirology

Comprehensive analysis of microRNA expression patterns in hepatocellular carcinoma and non-tumorous tissues

Source: Oncogene

ConcomitantMYCand microRNA cluster miR-17-92 (C13orf25) amplification in human mantle cell lymphoma

Source: Leukemia & Lymphoma

Global Cancer Statistics, 2002

Source: CA: A Cancer Journal for Clinicians

Function of microRNA-133 in the heart

Source: Nature

MicroRNA-155 promotes oncogenesis

Source: Nature

Ident

Source: Nature

Global

Source: Nature

MicroRNA-155 promotes oncogenesis

Source: Nature

The H

Oncology

Source: Nature



A functional polymorphism in the miR-146a gene and age of familial breast/ovarian cancer diagnosis

Source: Carcinogenesis

Human polymorphism at microRNAs and microRNA target sites

Source: Proceedings of the National Academy of Sciences

microRNA miR-196a-2 and Breast Cancer: A Genetic and Epigenetic Association Study and Functional Analysis

Source: Cancer Research

Association of MicroRNA Expression in Hepatocellular Carcinomas with Hepatitis Infection, Cirrhosis, and Patient Survival

Source: Clinical Cancer Research

A Functional Genetic Variant in microRNA-196a2 Is Associated with Increased Susceptibility of Lung Cancer in Chinese

Source: Cancer Epidemiology Biomarkers & Prevention

Cyclin G1 Is a Target of miR-122a, a MicroRNA Frequently Down-regulated in Human Hepatocellular Carcinoma

Source: Cancer Research

Genetic variants of miRNA sequences and non-small cell lung cancer survival

Source: The Journal of Clinical Investigation

Single Nucleotide Polymorphisms of microRNA Machinery Genes Modify the Risk of Renal Cell Carcinoma

Source: Clinical Cancer Research

Profiling MicroRNA Expression in Hepatocellular Carcinoma Reveals MicroRNA-224 Up-regulation

Source:

Common MicroRNA Expression Patterns in Human Papillary Thyroid Carcinoma

Source:

The g

Source:

In

S

Micro

carcin

Source:

IARC

Evalu

Supp

Preis:

Source: Nahrung/Food



Recommended articles

Cited by
3

Information for

Authors

R&D professionals

Editors

Librarians

Societies

Opportunities

Reprints and e-prints

Advertising solutions

Accelerated publication

Corporate access solutions

Open access

Overview

Open journals

Open Select

Dove Medical Press

F1000Research

Help and information

Help and contact

Newsroom

All journals

Books

Keep up

Register to receive the newsletter by email



Sign



x

Copyright ©

Accessibi

Registered
5 Howick Pl

or & Francis Group
pharma business