BMJ Open Genetic polymorphism of NFKB1 and NFKBIA genes and liver cancer risk: a nested case–control study in Shanghai, China

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ABSTRACT

Objectives: Genetic variations of nuclear factor-κB (NF-κB) signalling pathway were found to be associated with inflammatory diseases and several malignancies. However, little is known about NF-κB pathway gene polymorphisms and susceptibility of liver cancer. The aim of this study was to investigate whether genetic variants of NFKB1 and NFKBIA were associated with risk of liver cancer in a Chinese population.

Design: The study was designed as a nested case–control study within two prospective cohorts (the Shanghai Women’s Health Study, SWHS, 1996–2000 and the Shanghai Men’s Health Study, SMHS, 2002–2006).

Settings: This population-based study was conducted in urban Shanghai, China.

Participants: A total of 217 incident liver cancer cases diagnosed through 31 December 2009 and 427 healthy controls matched by sex, age at baseline (±2 years) and date (±30 days) of sample collection were included in the study.

Primary and secondary outcome measures: Genetic polymorphisms of NFKB1 and NFKBIA were determined blindly by TaqMan single-nucleotide polymorphism (SNP) genotyping assay. OR and its 95% CIs were estimated by an unconditional logistic regression model to measure the association between selected SNPs and the risk of liver cancer.

Results: After adjusted for potential confounding factors, rs230362491 ins/del or del/del genotypes were associated with higher risk of liver cancer with an adjusted OR 1.54 (95% CI 1.04 to 2.28), rs230496 AG and GG genotypes were also noted with higher risk of liver cancer with an adjusted OR 1.54 (95% CI 1.04 to 2.28). Haplotype analysis indicated that carriers of the NFKB1 GA and AA (rs230525-rs230530) haplotypes had higher risk of liver cancer under an additive model. No association was observed between NFKBIA variants and risk of liver cancer.

Conclusions: Our results suggest that genetic variants of NFKB1 influence liver cancer susceptibility in Chinese population, although replication in other studies is needed.

INTRODUCTION

Liver cancer is a common disorder worldwide which ranks the fifth and seventh most common cancer among men and women. It was estimated that more than 80% of liver cancers occur in developing countries and about 54% occur in China.1 Among the main risk factors for liver cancer, chronic infections of hepatitis B virus (HBV) and hepatitis C virus (HCV) are the most important in humans, accounting for more than 70% of liver cancer cases worldwide.2–4 Liver cirrhosis, heavy alcohol consumption, exposure to aflatoxin and diabetes also account for part of liver cancer occurrence.2–4 Chronic inflammation has been widely accepted to play an important role in hepatocarcinogenesis. Most of the known risk factors of liver cancer such as HBV, HCV infection and alcohol drinking can cause persistent inflammatory reaction of the liver and promote cancer development.5 6 However, the molecular and cellular mechanisms linking inflammation and liver cancer remain unclear. Recent findings have
suggested that nuclear factor-xB (NF-xB) may play a

role in bridging the actions of growth factors and

cellular inflammation to hepatic oncogenesis.7–10

NF-xB, a collection of dimeric transcription factors,

was originally identified as a nuclear factor bound to the

enhancer of the immunoglobulin x-light chain gene11

specific to B cells and presents in all cell types.12 It is a

major transcription regulator of the immune response,

cell adhesion, differentiation, proliferation and apop-
tosis.13 NF-xB dimers are formed by seven distinct pro-

teins: NF-xB1 (p105 and p50), NF-xB2 (p100 and p52),

RelA (p65), RelB and c-Rel, of which NF-xB p50/RelA is

the most common dimer form.9 In the resting cell, most

NF-xB dimers are inactivated in the cytoplasm by

binding to specific inhibitors: IxB family, of which IxBz

is the most common one. In the classical activation

pathway, IxB is phosphorylated and degraded by IxB

kinase complex, and then NF-xB dimers are released

to the nucleus where they coordinate the transcriptional

activation of target genes.14 Several genetic variations of NF-xB signalling pathway have been reported to be associated with cancer risks such as breast,15 prostate,16 stomach,17 colorectum18 and mouth.19 However, little is known about the role of genetic polymorphisms of NF-xB genes and susceptibil-

ity of liver cancer.

In a population-based case–control study nested in

two prospective cohorts of the Shanghai Women’s (SWHS) and Men’s Health Studies (SMHS), we investi-
gated the relationships between genetic variants of

NFKBI and NFKBIA, two key genes involved in classical

signalling pathway of NF-xB, and the risk of liver cancer

among Chinese men and women.

MATERIALS AND METHODS

Study population

Participants of this study came from the SWHS and

SMHS. The design and methods used in these two

studies have been described in detail elsewhere.20–23

Briefly, the SWHS enrolled 74,941 women aged 40–74 years between 1 March 1997 and 31 May 2000, with

a response rate of 92.7%. SMHS enrolled 61,491 men aged 40–74 years without history of cancer at recruit-

ment from 1 April 2002 to 30 June 2006, with a response

rate of 74.1%. Both studies were approved by the rele-

vant Institutional Review Boards for human research in

China and the USA, and a written informed consent was

obtained from all participants.

In-person interview was conducted by trained inter-

viewers using a structured questionnaire at baseline to

obtain information on demographics, lifestyle, dietary

habits, medical history and other characteristics.

Anthropometric measurements, including current

weight, height and circumferences of the waist and hips,

were also measured. Of the eligible participants, 56,831

(75.8%) of the SWHS and 46,392 (75.3%) of the SMHS

provided a 10 mL blood sample at baseline. The samples

were drawn into an EDTA Vacutainer tube and then kept

in a portable styrofoam box with ice packs (at approxi-
mately 0–4°C) and processed within 6 h for long-term

storage at –70°C. A biospecimen collection form was

completed for each participant at the time of sample

collection, time of last meal, and date of last menstruation,

intake of selected foods, smoking, as well as use of any

medications over the previous 24 h and during the previ-

ous week.

Cohort follow-up and outcome ascertainment

Both cohorts were followed for occurrence of cancer and other chronic diseases by active in-person surveys con-
ducted every 2–3 years as well as annual record linkage to

the databases of the population-based Shanghai Cancer

Registry, Shanghai Vital Statistics Registry and Shanghai

Resident Registry. For the SWHS, four rounds of in-person follow-ups were completed, and the response


third (2004–2007) and fourth (2008–2011) follow-up surveys were 99.8%, 98.7%, 96.7% and 92%, respec-
tively. For the SMHS, two rounds of follow-up surveys were com-

pleted. The response rates for the first (2004–2008) and

second (2008–2011) follow-up surveys were 97.6% and

93.6%, respectively. For cohort members who developed

liver cancer during the follow-up, medical charts were

reviewed by a panel of oncologists to verify the diagnosis.

Liver cancer data through 31 December 2009 was used

for the present study.

Included in this nested case–control study are 217 inci-
dent liver cancer cases and 427 matched controls who

had donated blood sample. Liver cancer cases were

defined as having an International Classification of

Disease, Ninth Revision (ICD-9), codes of 155.0

(primary malignant neoplasms), 155.1 (malignant neo-

plasms of the intrahepatic bile ducts) or 155.2 (unspeci-

fied malignant neoplasms of the liver).24 Two control

subjects were randomly selected from the cohorts who

donated a blood sample at baseline and matched to
each case for sex, age at baseline (±2 years) and date
(±30 days) of sample collection. All controls were free of

any cancer at the time of cancer diagnosis for the corre-
sponding case.

Genotyping

Single-nucleotide polymorphisms (SNPs) were selected

based on tag SNP and their putative functional signifi-
cance. Tagging SNPs were selected by searching the Han

Chinese data from the HapMap project.25 The following
criteria were used to identify tagging SNPs: (1) SNPs

located in the genes or within the 5 kb flanking region,

(2) a minor allele frequency ≥0.05 and (3) other unse-
lected SNPs could be captured by one of the tagging

SNPs with a linkage disequilibrium of r² ≥ 0.90. A total

of eight SNPs were selected for genotyping which were

rs28362491, rs230530, rs230525, rs230496 for NFKBI

and rs3138053, rs3138055, rs2273650, rs696 for NFKBIA.
(table 1). Genomic DNA was extracted from buffy coat using Promega DNA Extraction Kit according to the manufacturer’s instructions (Promega Corporation, Madison, Wisconsin, USA). Genotyping were performed by the TaqMan assay, using the ABI PRISM 7900HT Sequence Detection System (Applied Biosystems, Foster City, California, USA), in 384-well format, with dual fluorescent reporter probes VIC and FAM. rs28362491 was genotyped using custom-designed probes and primers. The primer sequences were: 5'-GGCCTCGCTGG TGCCT-3' (forward primer), 3'-AGGGAAGCCCGCAG AA-5' (reverse primer). The probe sequences were: 5'-TTCCCCGACCATGG-3' (del), 5'-CCGACCATTGAT TGG-3' (ins). Other SNPs were genotyped using predesigned assays (Applied Biosystems). The quality and potential misclassification of the genotyping results were assessed by evaluating 5% of duplicate DNA samples that were randomly selected from the whole samples. Their replicates were 100% concordant. All serum samples were tested blindly and were identified only by a unique identification number blinded with case-control status.

Statistical analysis

Subjects with both survey data and genotyping results were included in the final analysis. Means and percentages of selected characteristics for cases and controls were calculated. The distributions of selected characteristics were compared between cases and controls by either Student t test (continuous variables) or \(\chi^2\) test (categorical variables). OR and its 95% CI were estimated by unconditional logistic regression model to measure the association between selected SNPs and the risk of primary liver cancer. In the multivariable analysis, potential confounding factors were adjusted for, which included age (continuous variable); education level (four categories: elementary school or less, middle school, high school and college or above); history of hepatitis (yes or no); family history of liver cancer (yes or no); and history of other chronic liver diseases or cirrhosis (yes or no). Statistical analyses were carried out using the SAS software package (V.9.2; SAS Institute, Cary, North Carolina). Tests for trend were performed by entering categorical variables as continuous variables in the regression model. All p values were calculated by two-sided tests and were considered statistically significant if p value was less than 0.05.

Hardy-Weinberg equilibrium and linkage disequilibrium were accessed with HaploView V.4.0. Associations between haplotypes and the risk of liver cancer were evaluated with HAPSTAT V.3.0 using the most common haplotype as the referent category, assuming an additive model.

RESULTS

Selected baseline characteristics of study participants were presented in table 2. The average ages of cases and controls were 59.61 and 59.47, respectively. Compared with controls, liver cancer cases were more likely to have a lower education level, a history of hepatitis, a family history of liver cancer in first degree relatives and history of chronic liver diseases or cirrhosis. Besides, men with liver cancer were more probable to have lower body mass index and be non-regular exercisers compared with controls, although the difference was at borderline significance. Whereas in women, cases were more likely to have a history of type 2 diabetes than controls. No differences were observed in family income, smoking, drinking habits, waist-to-hip ratio and family history of other cancers between the two groups.

The associations of NFKB1 SNPs with liver cancer risk were summarised in table 3. The genotypes of rs28362491, rs230530 and rs230525 showed no deviation from Hardy-Weinberg equilibrium in controls except for rs230496. After adjusted for potential confounding factors, rs28362491 ins/del or del/del genotypes were associated with higher risk of liver cancer with an OR 1.54 (95% CI 1.04 to 2.28). rs230496 AG and GG genotypes were also noted with higher risk of liver cancer with an adjusted OR 1.53 (95% CI 1.03 to 2.26). Carriers of rs230525 AG or GG genotypes had about 30% increased risk of liver cancer, but the risk was insignificant. No association was found between rs230530 and liver cancer risk.

Table 4 presents the distribution of NFKBIA SNPs in cases and controls. The genotypes of rs3138055, rs696
<table>
<thead>
<tr>
<th>Characteristics</th>
<th>All participants</th>
<th>Male</th>
<th>Female</th>
<th>p Value</th>
<th>Male</th>
<th>Female</th>
<th>p Value</th>
<th>Male</th>
<th>Female</th>
<th>p Value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Cases</strong> (n=217)</td>
<td></td>
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<tr>
<td>Age at interview, mean±SD</td>
<td>59.61±9.56</td>
<td>60.05±9.93</td>
<td>59.86±9.95</td>
<td>0.853</td>
<td>58.95±8.98</td>
<td>58.85±8.87</td>
<td>0.928</td>
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<td>Education level (%)</td>
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<tr>
<td>Elementary school or less</td>
<td>63 (29.30)</td>
<td>18 (13.95)</td>
<td>35 (13.41)</td>
<td>–</td>
<td>45 (52.33)</td>
<td>80 (48.48)</td>
<td>–</td>
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<tr>
<td>Middle school</td>
<td>69 (32.09)</td>
<td>54 (41.86)</td>
<td>104 (39.85)</td>
<td>–</td>
<td>15 (17.44)</td>
<td>44 (26.67)</td>
<td>–</td>
<td></td>
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<tr>
<td>High school</td>
<td>62 (28.84)</td>
<td>41 (31.78)</td>
<td>61 (23.37)</td>
<td>–</td>
<td>21 (24.42)</td>
<td>30 (18.18)</td>
<td>–</td>
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<tr>
<td>College or above</td>
<td>21 (9.77)</td>
<td>16 (12.40)</td>
<td>61 (23.37)</td>
<td>0.053</td>
<td>5 (5.81)</td>
<td>11 (6.67)</td>
<td>0.341</td>
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<tr>
<td>Family income (%)†</td>
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<tr>
<td>Low</td>
<td>50 (23.04)</td>
<td>17 (12.98)</td>
<td>37 (14.12)</td>
<td>–</td>
<td>33 (38.37)</td>
<td>53 (32.32)</td>
<td>–</td>
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<tr>
<td>Medium</td>
<td>112 (51.61)</td>
<td>76 (58.02)</td>
<td>130 (49.62)</td>
<td>–</td>
<td>36 (41.86)</td>
<td>78 (47.56)</td>
<td>–</td>
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</tr>
<tr>
<td>High</td>
<td>55 (25.35)</td>
<td>38 (29.01)</td>
<td>95 (36.26)</td>
<td>0.271</td>
<td>17 (19.77)</td>
<td>33 (20.12)</td>
<td>0.606</td>
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<tr>
<td>Ever smoked (%)</td>
<td>93 (42.86)</td>
<td>90 (68.70)</td>
<td>163 (62.21)</td>
<td>0.206</td>
<td>3 (3.49)</td>
<td>10 (6.06)</td>
<td>0.384</td>
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<tr>
<td>Ever drank alcohol (%)</td>
<td>45 (20.74)</td>
<td>42 (32.06)</td>
<td>97 (37.02)</td>
<td>0.333</td>
<td>3 (3.49)</td>
<td>1 (0.61)</td>
<td>0.084</td>
<td></td>
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<tr>
<td>Body mass index, kg/m², mean±SD</td>
<td>23.79±3.65</td>
<td>23.16±3.25</td>
<td>23.77±2.89</td>
<td>0.06</td>
<td>24.75±4.02</td>
<td>24.78±3.80</td>
<td>0.961</td>
<td></td>
<td></td>
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</tr>
<tr>
<td>WHR, mean±SD</td>
<td>0.87±0.07</td>
<td>0.90±0.06</td>
<td>0.82±0.05</td>
<td>0.383</td>
<td>0.83±0.06</td>
<td>0.83±0.06</td>
<td>0.261</td>
<td></td>
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<td></td>
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<tr>
<td>Regular physical activity (%)</td>
<td>94 (43.32)</td>
<td>49 (37.40)</td>
<td>124 (47.33)</td>
<td>0.062</td>
<td>45 (52.33)</td>
<td>83 (50.30)</td>
<td>0.761</td>
<td></td>
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</tr>
<tr>
<td>Physical activity, MET-h/week</td>
<td>81.58±47.12</td>
<td>66.86±40.33</td>
<td>68.00±34.61</td>
<td>0.78</td>
<td>104.00±48.09</td>
<td>108.60±44.83</td>
<td>0.450</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>History of hepatitis (%)</td>
<td>74 (34.10)</td>
<td>57 (43.51)</td>
<td>16 (6.11)</td>
<td>&lt;0.001</td>
<td>17 (19.77)</td>
<td>9 (4.95)</td>
<td>&lt;0.001</td>
<td></td>
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<td></td>
</tr>
<tr>
<td>History of cancer (%)</td>
<td>69 (31.80)</td>
<td>41 (31.30)</td>
<td>70 (26.72)</td>
<td>0.342</td>
<td>28 (32.56)</td>
<td>46 (27.88)</td>
<td>0.441</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Family history of liver cancer (%)</td>
<td>28 (12.90)</td>
<td>20 (15.27)</td>
<td>10 (3.82)</td>
<td>&lt;0.001</td>
<td>8 (9.30)</td>
<td>8 (4.85)</td>
<td>0.171</td>
<td></td>
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<td></td>
</tr>
<tr>
<td>History of type 2 diabetes (%)</td>
<td>25 (11.52)</td>
<td>25 (9.54)</td>
<td>11 (4.22)</td>
<td>0.171</td>
<td>14 (10.69)</td>
<td>6 (3.72)</td>
<td>0.068</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>History of chronic liver disease or cirrhosis (%)</td>
<td>35 (16.13)</td>
<td>26 (19.85)</td>
<td>10 (3.82)</td>
<td>&lt;0.001</td>
<td>9 (10.47)</td>
<td>1 (0.61)</td>
<td>&lt;0.001</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Missing data were excluded from the analysis.
†Family income level (low income for <¥5000/year in the SWHS and <¥12 000/year in the SMHS; medium income for ¥5000 to <¥10 000/year in the SWHS and ¥12 000 to <¥24 000/year in the SMHS; and high income for >¥10 000/year in the SWHS and >¥24 000/year in the SMHS).

SMHS, Shanghai Men’s Health Study; SWHS, Shanghai Women’s Health Study.
haplotypes had higher risk of liver cancer. In addition, haplotype analysis indicated that carriers of the NFKB1 GA and AA (rs230525-rs230530) haplotypes had higher risk of liver cancer under the additive model, although this association was only observed in men. These findings suggested that variants of NF-κB signalling pathway may play a role in liver cancer susceptibility.

NFKB1 gene was mapped on chromosome 4q23-q24 and composed of 24 exons. This gene encodes p105 which is a non-DNA binding protein. As an inactive precursor, it is activated to p50, a DNA binding protein by proteasome-mediated degradation. Several genetic polymorphisms were defined in NFKB1, and researches have been focused on a common polymorphism of -94 del/ins (rs28362491) in the promoter region. Recent studies show that genetic polymorphism of rs28362491 was associated with a number of cancer risks including sporadic breast, prostate, gastric, colorectal and oral cancers, but little is known about its relationship with liver cancer. He et al conducted a case–control study of 202 hepatocellular carcinoma (HCC) cases of HBV carrier and 404 healthy controls without HBV infection. Results showed that after adjusting for age and gender, -94 ins/del and ins/ins genotypes might increase the risk of HCC, with ORs 1.60 (95% CI 1.01 to 2.53) and 3.01 (95% CI 1.87 to 4.85), respectively. A report from Taiwan also found ins allele more prevalent in patients with HCC (OR=2.23, 95% CI 1.32 to 3.77). In our study, we found that ins/del and del/del genotypes were significantly associated with liver cancer.

**DISCUSSION**

In this nested case–control study, we found that the variants of rs28362491 and rs230496 of NFKB1 gene might be associated with risk of primary liver cancer. After adjusting for possible confounders, rs28362491 deletion allele and rs230496 AG or GG genotype were found to increase the risk of liver cancer. In addition, haplotype analysis indicated that carriers of the NFKB1 GA and AA (rs230525-rs230530) haplotypes had higher risk of liver cancer.
Table 4  NFKBIA genetic polymorphisms with the risk of primary liver cancer

<table>
<thead>
<tr>
<th>SNPs</th>
<th>Cases</th>
<th>Controls</th>
<th>p Value</th>
<th>OR*</th>
<th>95% CI</th>
<th>OR†</th>
<th>95% CI</th>
<th>OR‡</th>
<th>95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs3138053</td>
<td>AA</td>
<td>173</td>
<td>336</td>
<td>1.00</td>
<td>1.00</td>
<td>1.00</td>
<td>1.00</td>
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<td>1.00</td>
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<tr>
<td></td>
<td>AG</td>
<td>21</td>
<td>48</td>
<td>0.85</td>
<td>0.49 to 1.47</td>
<td>0.84</td>
<td>0.48 to 1.45</td>
<td>0.97</td>
<td>0.54 to 1.74</td>
</tr>
<tr>
<td></td>
<td>GG</td>
<td>19</td>
<td>40</td>
<td>0.823</td>
<td>0.52 to 1.64</td>
<td>0.94</td>
<td>0.52 to 1.68</td>
<td>0.98</td>
<td>0.51 to 1.88</td>
</tr>
<tr>
<td>p value for trend</td>
<td>–</td>
<td>–</td>
<td>0.638</td>
<td>–</td>
<td>0.653</td>
<td>–</td>
<td>0.920</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>AG or GG</td>
<td>40</td>
<td>88</td>
<td>0.556</td>
<td>0.58 to 1.34</td>
<td>0.88</td>
<td>0.58 to 1.34</td>
<td>0.97</td>
<td>0.61 to 1.54</td>
<td></td>
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<tr>
<td>rs3138055</td>
<td>CC</td>
<td>62</td>
<td>128</td>
<td>1.00</td>
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<tr>
<td></td>
<td>CT</td>
<td>109</td>
<td>215</td>
<td>1.05</td>
<td>0.72 to 1.54</td>
<td>1.05</td>
<td>0.72 to 1.54</td>
<td>1.22</td>
<td>0.79 to 1.87</td>
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<td></td>
<td>TT</td>
<td>42</td>
<td>81</td>
<td>0.956</td>
<td>0.66 to 1.73</td>
<td>1.07</td>
<td>0.66 to 1.73</td>
<td>1.33</td>
<td>0.78 to 2.27</td>
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<tr>
<td>p value for trend</td>
<td>–</td>
<td>–</td>
<td>0.772</td>
<td>–</td>
<td>0.771</td>
<td>–</td>
<td>0.276</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>CT or TT</td>
<td>151</td>
<td>296</td>
<td>0.778</td>
<td>0.74 to 1.51</td>
<td>1.06</td>
<td>0.74 to 1.52</td>
<td>1.25</td>
<td>0.83 to 1.88</td>
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<tr>
<td>rs696</td>
<td>CC</td>
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<td>149</td>
<td>1.00</td>
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<td>CT</td>
<td>115</td>
<td>196</td>
<td>1.35</td>
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<td>1.35</td>
<td>0.93 to 1.96</td>
<td>1.47</td>
<td>0.97 to 2.23</td>
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<tr>
<td></td>
<td>TT</td>
<td>33</td>
<td>76</td>
<td>0.210</td>
<td>0.60 to 1.64</td>
<td>0.99</td>
<td>0.60 to 1.64</td>
<td>1.17</td>
<td>0.67 to 2.03</td>
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<td>–</td>
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<td>–</td>
<td>0.695</td>
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<td>0.360</td>
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<td>CT or TT</td>
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<td>272</td>
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<td>0.88 to 1.78</td>
<td>1.25</td>
<td>0.88 to 1.78</td>
<td>1.38</td>
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<tr>
<td>rs2273650</td>
<td>CC</td>
<td>108</td>
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<td>1.00</td>
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<tr>
<td></td>
<td>CT</td>
<td>84</td>
<td>173</td>
<td>0.97</td>
<td>0.68 to 1.37</td>
<td>0.97</td>
<td>0.68 to 1.37</td>
<td>0.86</td>
<td>0.58 to 1.26</td>
</tr>
<tr>
<td></td>
<td>TT</td>
<td>20</td>
<td>37</td>
<td>0.938</td>
<td>0.60 to 1.95</td>
<td>1.07</td>
<td>0.59 to 1.94</td>
<td>0.89</td>
<td>0.45 to 1.73</td>
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<td>–</td>
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<td>–</td>
<td>0.945</td>
<td>–</td>
<td>0.493</td>
<td>–</td>
<td>–</td>
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<tr>
<td>CT or TT</td>
<td>104</td>
<td>210</td>
<td>0.933</td>
<td>0.71 to 1.38</td>
<td>0.99</td>
<td>0.71 to 1.37</td>
<td>0.86</td>
<td>0.60 to 1.24</td>
<td></td>
</tr>
</tbody>
</table>

*Adjusted for age.  †Adjusted for age and sex.  ‡Adjusted for age, sex, education level, family history of liver cancer, history of hepatitis and chronic liver diseases or cirrhosis.

SNP, single-nucleotide polymorphism.

genotypes were more prevalent in liver cancer cases than controls. It was observed that the association of rs28362491 polymorphism with cancer susceptibility varied with cancer site and study populations. Ins allele was reported to increase the risk of oral cancer, melanoma, prostate cancer, gastric cancer, nasopharyngeal carcinoma and cervical cancer. Two studies in European population found that del allele might increase the risk of colorectal cancer, while in Chinese population, none or even reverse association was observed. Two studies in Chinese mainland population found rs230530 polymorphism associated with liver cancer susceptibility. A study in European American descent found rs230530 polymorphism associated with alcohol dependence, and the evidence came primarily from those individuals who met the criteria for alcoholism earlier. As alcohol is one of the major risk factors of liver cancer, rs230530 might play a role in alcohol associated liver cancer. Unfortunately, subject to the limitation of relatively small sample size, we were not able to explore this issue. In addition, although the functions of intronic SNPs are still obscure, studies have indicated that they can affect the secondary structure of either local DNA or RNA, thereby regulating gene expression.39–41

NFKBIA gene, which encodes IkBα, the inhibitor of NFKB, was mapped to 1q413 with six exons spanning approximately 3.5 kb. As a major component of the IκB family, the dysfunction or down regulation of IκBα will lead to over activation of NFKB. Epidemiological studies on NFKBIA were relatively rare. A 2758G/A polymorphism (rs696) in 5′-untranslated region might regulate the expression of IκBα and thus affect the activation of NF-xB. Sun and colleagues found that frequency of AG genotype was increased in Chinese patients ≥50 years of age (OR=3.06, 95% CI 1.55 to 6.02) with colorectal cancer.24 Another study on breast cancer fails to obtain a significant association. There was no previous report on rs696 and risk of liver cancer.

Of the four SNPs of NFKBIA gene evaluated, we did not observe a significant association. In previous studies, the rs3138053 variant was found to be associated with HCC in a Chinese mainland population but not Taiwanese.29 Two studies on European American descent found rs230530 polymorphism associated with alcohol dependence, and the evidence came primarily from those individuals who met the criteria for alcoholism earlier. The best of our knowledge, it was the first population-based study to evaluate the polymorphic variants of NF-xB and risk of liver cancer. All study participants were ethnic Chinese and residents of Shanghai with similar genetic backgrounds, which minimised the
potential confounding due to ethnics. Only incident cases were included which ruled out the possibility of recall and selection bias. Liver cancer cases were carefully verified with multiple approaches which minimised the disease misclassification. Also, we controlled potential confounding variables in the analysis. The limitations of our study should also be noted. First, we focused on only two genes involved in the canonical pathway of NF-κB, other regulatory genes in the NF-κB signalling pathway may also contribute to the pathogenesis of liver cancer. Second, we did not test for HBV infection, HCV infection or aflatoxin exposure, so we cannot rule out possible confounding due to that although the presence of HCV infection and aflatoxin is very low in the study population, but we did take into consideration the participants’ history of hepatitis and liver cirrhosis. Finally, owing to the relatively small sample size, the frequencies of some homozygous variants were low in subgroups and therefore reduced the statistical power and limited us from evaluating the joint effects in stratified analysis. Replication in other studies is needed.

In summary, in this nested case–control study, we provided additional evidence for the role of NF-κB SNPs and haplotypes in the aetiology of liver cancer. Studies in larger, varied populations are warranted to confirm these findings. Furthermore, functional studies are required in order to explore the underlying mechanisms.

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Contributors Y-BX obtained the funding, developed the research design, drafted the manuscript, interpreted the results, and also had primary responsibility for the final content; WZheng and X-OS designed, directed and obtained funding for the parent cohorts, and contributed to the revisions and interpretation of the results; JG obtained part of the funding, drafted the manuscript, analysed the data and interpreted the results; JG and H-LX conducted experiments; all authors critically reviewed and approved the manuscript.

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Competing interests None.

Ethics approval Vanderbilt University IRB and Shanghai Cancer Institute IRB.
REFERENCES


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