

Original research article

Genetic polymorphisms in the *SLC27A5* gene are associated with biochemical characteristics of HBV patients in Yunnan

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Abstract

Background: Lipid droplets could influence hepatitis B virus (HBV) replication and release, as well as disease progression in patients with chronic HBV. The solute carrier family 27 member 5 (*SLC27A5*) gene is highly expressed in the liver and possessed bile acid-CoA ligase activity. However, no previous study has investigated the role of the *SLC27A5* gene in HBV infection or disease progression.

Methods: A total of 400 chronic HBV patients and 300 controls were collected in Yunnan Province to genotype three single nucleotide polymorphisms (SNPs) of the *SLC27A5* gene and investigate potential association between SNPs and HBV infection or biochemical characteristics of HBV patients. *In silico* prediction and dual-luciferase reporter assay were performed to explore the role of alleles of each SNP.

Results: No association was found between HBV infection and genotypes and alleles of three SNPs (rs4801275, rs2278497, and rs56225452) in the *SLC27A5* gene. However, alanine transaminase (ALT) and lymphocytes (LYM) levels differed significantly among HBV patients carrying different genotypes of rs4801275. When HBV patients were stratified into HBsAg-positive and HBsAg-negative subgroups, most hepatic functional features showed significant differences between the two subgroups. Furthermore, RNA structures containing the alleles of two SNPs were predicted, and the results indicated that different alleles could partially alter RNA structures. Dual-luciferase reporter assay also demonstrated that different alleles of the three SNPs significantly influenced firefly luciferase expression level.

Conclusion: This study is the first to identify that genetic polymorphisms of the *SLC27A5* gene are associated with biochemical characteristics of HBV patients in Yunnan. Furthermore, the RNA structure prediction and dual-luciferase reporter assays suggest that different alleles of the three SNPs might alter the *SLC27A5* gene expression levels.

Keywords: Biochemical characteristics; Genetic polymorphisms; HBV patients; The *SLC27A5* gene

Highlights:

- No association between genetic variants of the *SLC27A5* gene and HBV infection in Yunnan population.
- Biochemical levels were affected by genotypes of SNPs in the *SLC27A5* gene.
- The alleles of two SNPs could change the particle structures of RNA.

Introduction

Hepatitis B virus (HBV) infection led to hepatitis B, which could further progress to cirrhosis and hepatocellular carcinoma (HCC). Moreover, HBV and hepatitis C virus (HCV) infection were the major risk factors for HCC occurrence (Yip et al., 2022). In 2023, about 254 million people were living with HBV infection, many of whom were neither diagnosed with HBV, nor with hepatitis (WHO, 2024). Approximately 1.3 million persons died of viral hepatitis, 87% of whom caused by HBV infection (WHO, 2024). Thus, HBV infection is one of the serious public problems worldwide. Although HBV vaccines have been widely used in many countries, there were still many per-

sons exposed to HBV infection. The lack of effective medicines to cure HBV patients meant that studying mechanisms of HBV infection was needed.

Lipid metabolism of the host is closely related to the life cycle of HBV. Moreover, HBV infection also changes lipid metabolism of the host (Zhang et al., 2021). HBV X protein (HBx) can increase hepatic lipid accumulation and induce hepatic steatosis by activating SREBP1 and PPAR α pathway (Kim et al., 2007). Na⁺/taurocholate co-transporting polypeptide (NTCP), a protein specifically expressed in hepatocytes and a bile acid transporter, is the receptor for HBV infection (Yan et al., 2012). Genetic polymorphisms of the *NTCP* gene were associated with HBV infection (Xu et al., 2023). A clinical study showed that lipid characteristics of chronic HBV patients were

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significantly higher than those of controls (Arain et al., 2017). All these reports suggest lipid metabolism is altered by HBV infection, and that HBV proliferation *in vivo* also depends on host lipid droplets.

The solute carrier family 27 member 5 (SLC27A5 or FATP5) encodes an isozyme of very long-chain acyl-CoA synthetase. On one hand, it acts as an acyl-CoA synthetase, which catalyzes the ATP-dependent activation of bile acids into CoA thioester. On the other hand, it mediates the import of long-chain fatty acids (LCFA) by facilitating their transport across cell member. Additionally, it is capable of activating very long-chain fatty acids containing 24 and 26 carbons (Doege et al., 2006). Recently, many studies investigated the function of SLC27A5 in relation to liver fibrosis and HCC, including the disease progression and treatment efficacy (Gao et al., 2020; Wu et al., 2024; Xu et al., 2023). However, no research has been performed to study the role of the SLC27A5 gene in HBV infection. In this study, the association between genetic polymorphisms of the SLC27A5 gene and HBV infection in Yunnan population was investigated.

Materials and methods

Individuals

The blood samples of persons with chronic HBV infection ($N = 400$) and general controls ($N = 300$) were collected by doctors at First People's Hospital of Yunnan Province. For each subject, 3 ml of whole blood was collected by using EDTA anticoagulant tube and serum separator tube before breakfast in the morning, along with their basic information (including gender and age), blood routine parameters (including white blood cells [WBC], neutrophilic granulocyte [NEUT], lymphocytes [LYM], monocytes [MONO], glucose [GLU], eosinophil [EO], and basophil granulocyte [BASO]), and hepatic and renal function features (including alanine transaminase [ALT], aspartate transaminase [AST], total bilirubin [TBIL], direct bilirubin [DBIL], indirect bilirubin [IBIL], total protein [TP], albumin [ALB], and globin [GLOB], blood urea nitrogen [BUN], serum creatinine [CREA], and serum uric acid [UA]) for further analysis. Hepatitis B surface antigen (HBsAg) was detected in each HBV infected person. Written informed consents conforming to the tenets of the Declaration of Helsinki were obtained from each participant prior to the study. The institutional review board of Kunming University of Science and Technology approved this study (No. KMUST-MEC-2025-029).

Selecting and genotyping single nucleotide polymorphisms (SNPs)

Genomic DNA was extracted from whole blood of each individual using TIANamp Genomic DNA Kit (TIANGEN, Chi-

na). Tag SNPs were selected from the CHB and CHD populations using the SNPinfo Web Server, covering a region from 5000 bp upstream to 5000 bp downstream of the SLC27A5 gene flanking regions. Subsequently, two tag SNPs (rs4801275 and rs2278497 are intron variants in the SLC27A5 gene) and one SNP (rs56225452) located in the promotor region of the SLC27A5 gene were collected for further study. Sanger sequencing method was used to analyze the genotypes of three SNPs.

In silico prediction

Two SNPs in the SLC27A5 gene were predicted to evaluate whether different alleles could change RNA structure. The potential function of the two SNPs was predicted using RegulomeDB database and HaploReg v4.1 website.

Cell culture and Plasmids construction

HepG2 cells were cultured in Dulbecco's modified eagle medium (DMEM, Hyclone, USA) supplemented with 10% fetal bovine serum (FBS), 1 mM pyruvate, 2 mM L-glutamine, 100 µg/ml streptomycin and 100 U/ml penicillin at 37 °C in a 5% CO₂ incubator.

DNA regions containing both alleles of each SNP were amplified to verify the function of predicted SNPs. For each SNP, two fragments were amplified using the primers listed in Table 1. The PCR products were cloned into the pGL3-basic plasmid using the restriction endonuclease method, with *Kpn* I and *Xho* I added at the 5' end of forward and reverse primers, respectively.

Transfection and dual-luciferase reporter assay

Cells were cultured and transfected with a mixture of 4.2 µg plasmid (including 4.0 µg firefly luciferase pGL3-basic plasmids and 0.2 µg renilla luciferase pRL-SV40 plasmids) and 3 µl Lipofectamine 3000 (Life, USA) in a 12-well plate. The cells were then harvested at 24, 48, and 72 hours for further studies. Dual-luciferase reporter assays (Beyotime, China) were performed to evaluate the function of both alleles of each SNP. The intensities of firefly luciferase and Renilla luciferase (used as a control) were detected at 560 and 465 nm, respectively, using Victor X Multimode Plate Reader (PerkinElmer, USA). Finally, the firefly/Renilla ratio was calculated to analyze the expression levels of firefly luciferase.

Statistical analysis

The Hardy-Weinberg equilibrium (HWE) was assessed for each variant to identify the deviation. The differences in the genotypes and alleles of each SNP between patients and normal controls were evaluated using Pearson Chi-square test or Fisher's exact test. The odds ratio (OR) and 95% confidence intervals (95% CI) were calculated using the observed values

Table 1. Primers to amplify the regions containing three SNPs for plasmid construct

Primers	Sequence (5'-3')	Annealing temperature
rs56225452-F	GGGGTACCCTGACTGGAAGATCTATGGG	55 °C
rs56225452-R	CCGCTCGAGGGTGGGCTGCATATATAACC	
rs4801275-F	GGGGTACCTGAGCACCACCTTCCTTG	55 °C
rs4801275-R	CCGCTCGAGCATAGGTTACCCAGCACCTG	
rs2278497-F	GGGGTACCCTTCGCGTGAGAAGTCCTGA	55 °C
rs2278497-R	CCGCTCGAGCGGAAGGCTTCCTCTACT	

Note: The underlined sequences were the restriction endonuclease sites

and expected values of the genotype and allele frequency in the HBV patients and the controls. The upper and lower limits of 95% provided a range within which the population parameter was probable to fall at a 95% confident level. Student's *t* test (unpaired, two-tailed) was used to analyze the biochemical characteristics (Mean $\pm$ SD) among different groups. Statistical analysis of the data was performed using the GraphPad Prism 9. A *p*-value less than 0.05 was considered statistically significant.

Results

The basic information and biochemical characteristics of the two groups are listed in Table 2. The HBV patients contained 211 males (53%) and 189 females (47%), while the control group included 185 males (62%) and 115 females (38%). The mean ages of HBV patients and controls were 43 and 42 years, respectively. The levels of AST, ALT, TBIL, DBIL, and IBIL were significantly higher in HBV infected persons than those in the controls. However, the levels of TP and ALB in HBV patients were lower than those in the controls. These results indicated that liver function was impaired in HBV patients.

Genotyping results of three SNPs are showed in Table 3 and Suppl. Fig. S1 (representative genotypes of each SNP are showed). No deviation from HWE was found for the three SNPs

in both HBV patients and control population (Table 3). Moreover, there was no association between genotypes or alleles and HBV infection in Yunnan population (Table 3). Among 400 HBV infected individuals, 135 were detected as HBsAg-negative and 265 as HBsAg-positive. There were no associations between genotypes or alleles of each SNP and HBsAg-positive status (Table 4).

After analyzing the biochemical characteristics of HBV patients with different genotypes of each SNP, significant differences in ALB and LYM levels were found among HBV patients carrying different genotypes of rs4801275 (Fig. 1). The ALB level was statistically higher in HBV patients with genotype GG (41.79 ± 5.85) than in those with genotype AA and AG (40.05 ± 5.99 , $P = 0.031$). Similarly, the LYM was higher in HBV patients with genotype GG (1.83 ± 0.64) than in those with genotype AA and AG (1.62 ± 0.71 , $P = 0.019$).

Liver function showed significant difference between HBsAg-positive HBV patients and HBsAg-negative patients carrying the same genotype of the three SNPs (Fig. 2). ALT, AST, TBIL, DBIL, and IBIL levels were significantly higher in HBsAg-positive HBV patients than HBsAg-negative patients carrying genotype CC of rs56225452 or genotype GG of rs4801275. Excluding ALT level, AST, TBIL, DBIL, and IBIL also showed higher levels in HBsAg-positive HBV patients carrying genotype GG of rs2278497.

Table 2. Comparison of basic and biochemical information between HBV patients and general controls

Basic and biochemical information	HBV patients (<i>n</i> = 400)	General controls (<i>n</i> = 300)	<i>P</i> -value
Gender			
Male (%)	211 (52.75%)	185 (61.67%)	0.023
Female (%)	189 (47.25%)	115 (38.33%)	
Age	43.27 $\pm$ 0.69	41.75 $\pm$ 0.74	0.142
AST (U/l)	43.53 $\pm$ 4.45	24.06 $\pm$ 0.56	<0.0001
ALT (U/l)	46.33 $\pm$ 4.25	27.89 $\pm$ 1.18	0.0001
TBIL (μ mol/l)	18.65 $\pm$ 1.63	11.39 $\pm$ 0.31	<0.0001
DBIL (μ mol/l)	8.16 $\pm$ 1.23	3.96 $\pm$ 0.11	0.0021
IBIL (μ mol/l)	10.50 $\pm$ 0.46	7.45 $\pm$ 0.22	<0.0001
TP (g/l)	73.19 $\pm$ 0.37	78.34 $\pm$ 0.23	<0.0001
ALB (g/l)	41.48 $\pm$ 0.31	46.97 $\pm$ 0.13	<0.0001
GLOB (g/l)	31.60 $\pm$ 0.28	31.57 $\pm$ 0.21	0.9493
GLU (mmol/l)	5.10 $\pm$ 0.11	5.34 $\pm$ 0.07	0.0543
BUN (mmol/l)	4.93 $\pm$ 0.13	5.00 $\pm$ 0.07	0.6575
CREA (μ mol/l)	72.73 $\pm$ 3.96	72.13 $\pm$ 1.00	0.8861
UA (μ mol/l)	366.9 $\pm$ 23.25	352.9 $\pm$ 5.43	0.5686
WBC (10^9 /l)	6.79 $\pm$ 0.15	6.78 $\pm$ 0.17	0.9685
NEUT (10^9 /l)	4.35 $\pm$ 0.14	3.80 $\pm$ 0.07	0.0010
LYM (10^9 /l)	1.79 $\pm$ 0.03	2.27 $\pm$ 0.04	<0.0001
MONO (10^9 /l)	0.43 $\pm$ 0.01	0.54 $\pm$ 0.13	0.3429
EO (10^9 /l)	0.13 $\pm$ 0.01	0.14 $\pm$ 0.006	0.5441
BASO (10^9 /l)	0.03 $\pm$ 0.001	0.03 $\pm$ 0.001	0.0183

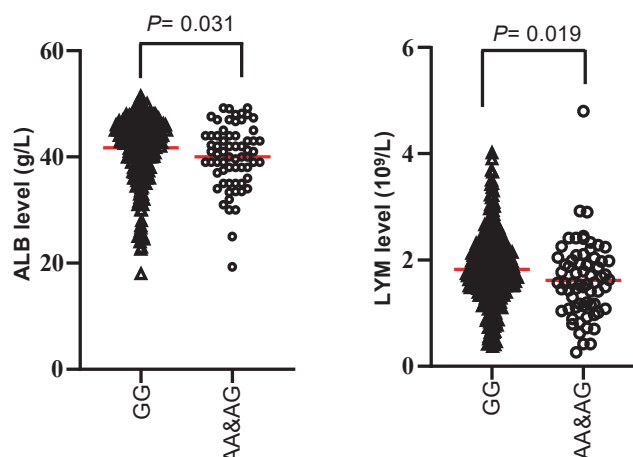
Note: aspartate transaminase (AST), alanine transaminase (ALT), total bilirubin (TBIL), direct bilirubin (DBIL), indirect bilirubin (IBIL), total protein (TP), albumin (ALB), globin (GLOB), glucose (GLU), blood urea nitrogen (BUN), serum creatinine (CREA), and serum uric acid (UA), white blood cells (WBC), neutrophilic granulocyte (NEUT), lymphocytes (LYM), monocytes (MONO), eosinophil (EO), basophil granulocyte (BASO)

Table 3. Frequency of genotypes and alleles between HBV infected persons and general controls

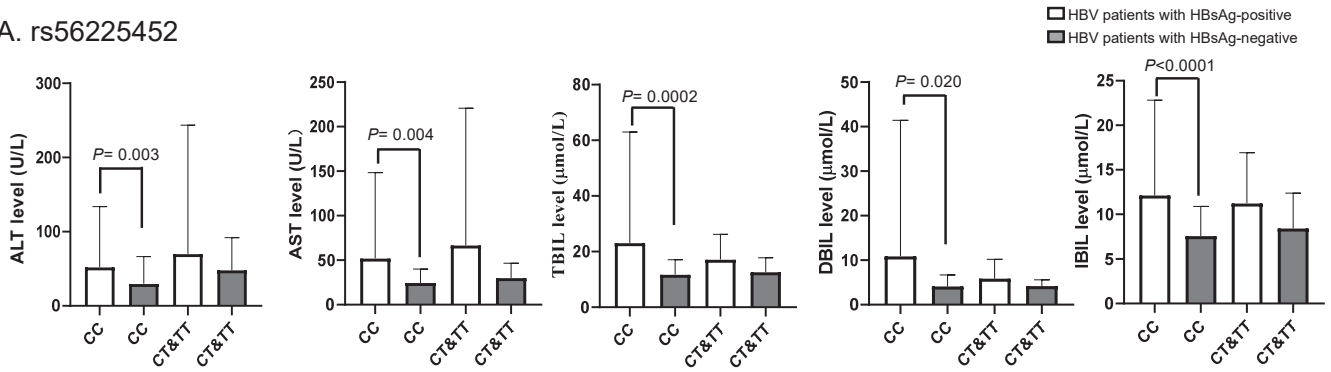
SNP (genotypes/alleles)	HBV infected persons (n = 400)	General controls (n = 300)	P-value	OR (95% CI)
rs56225452	HWE <i>P</i> = 0.995	HWE <i>P</i> = 0.559		
CC	353 (88.25%)	268 (89.33%)	0.743	0.897 (0.563–1.423)
CT	45 (11.25%)	32 (10.67%)	0.903	1.062 (0.663–1.702)
TT	2 (0.50%)	0 (0%)	0.609	–
C	751 (93.88%)	568 (94.67%)	0.609	0.864 (0.273–1.357)
T	49 (6.12%)	32 (5.33%)		1.158 (0.739–1.847)
rs4801275	HWE <i>P</i> = 0.891	HWE <i>P</i> = 0.997		
AA	2 (0.50%)	2 (0.67%)	0.828	0.749 (0.117–4.806)
AG	68 (17.00%)	49 (16.33%)	0.895	1.049 (0.708–1.560)
GG	330 (82.50%)	249 (83.00%)	0.943	0.966 (0.647–1.446)
A	72 (9.00%)	53 (8.83%)	0.989	1.021 (0.704–1.481)
G	728 (91.00%)	547 (91.17%)		0.980 (0.676–1.421)
rs2278497	HWE <i>P</i> = 0.980	HWE <i>P</i> = 0.514		
GG	187 (46.75%)	144 (48.00%)	0.802	0.951 (0.702–1.290)
GT	171 (42.75%)	118 (39.33%)	0.406	1.152 (0.853–1.562)
TT	42 (10.50%)	38 (12.67%)	0.440	0.8089 (0.513–1.287)
G	545 (68.13%)	406 (67.67%)	0.901	1.021 (0.812–1.281)
T	255 (31.87%)	194 (32.33%)		0.979 (0.781–1.231)

Table 4. Frequency of genotypes and alleles between HBV patients with HBsAg negative or positive

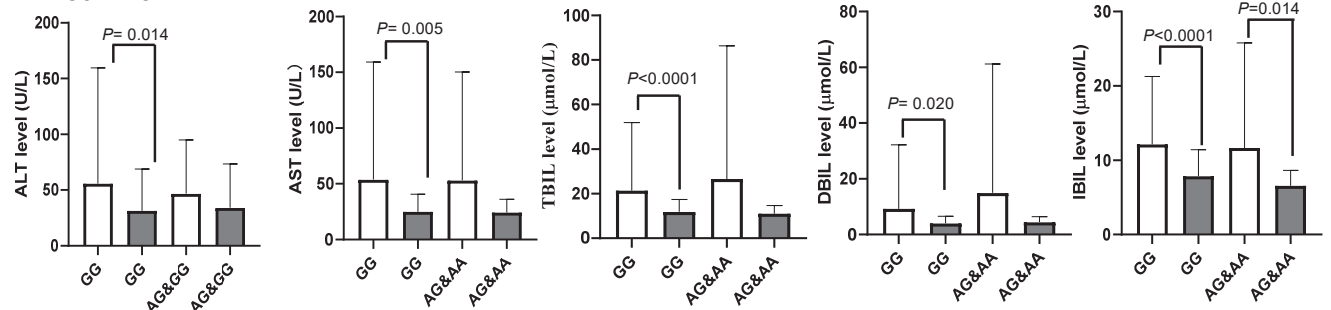
SNP (genotypes/alleles)	HBV patients with HBsAg negative (n = 135)	HBV patients with HBsAg positive (n = 265)	P-value	OR (95% CI)
rs56225452				
CC	117 (86.67%)	236 (89.06%)	0.591	0.799 (0.419–1.473)
CT	16 (11.85%)	29 (10.94%)	0.917	1.094 (0.558–2.044)
TT	2 (1.48%)	0 (0%)	0.216	–
C	250 (92.59%)	501 (94.53%)	0.356	0.724 (0.408–1.300)
T	20 (7.41%)	29 (5.47%)		1.382 (0.770–2.454)
rs4801275				
AA	2 (1.48%)	0 (0%)	0.216	–
AG	19 (14.07%)	49 (18.49%)	0.332	0.722 (0.405–1.264)
GG	114 (84.44%)	216 (81.51%)	0.554	1.231 (0.696–2.125)
A	23 (8.52%)	49 (9.25%)	0.834	1.231 (0.696–2.125)
G	247 (91.48%)	481 (90.75%)		1.094 (0.648–1.803)
rs2278497				
GG	67 (49.63%)	120 (45.28%)	0.473	1.191 (0.794–1.785)
GT	51 (37.78%)	120 (45.28%)	0.184	0.734 (0.476–1.109)
TT	17 (12.59%)	25 (9.44%)	0.423	1.383 (0.711–2.655)
G	185 (68.52%)	360 (67.92%)	0.928	1.028 (0.749–1.412)
T	85 (31.48%)	170 (32.08%)		0.973 (0.708–1.336)

**Fig. 1.** Comparison of biochemical characteristics of HBV patients with different genotypes of rs4801275. ALB: albumin; LYM: lymphocytes; GG: HBV patients with genotype GG of rs4801275; AA&AG: HBV patients with genotype AA or AG of rs4801275

A. rs56225452



B. rs4801275



C. rs2278497

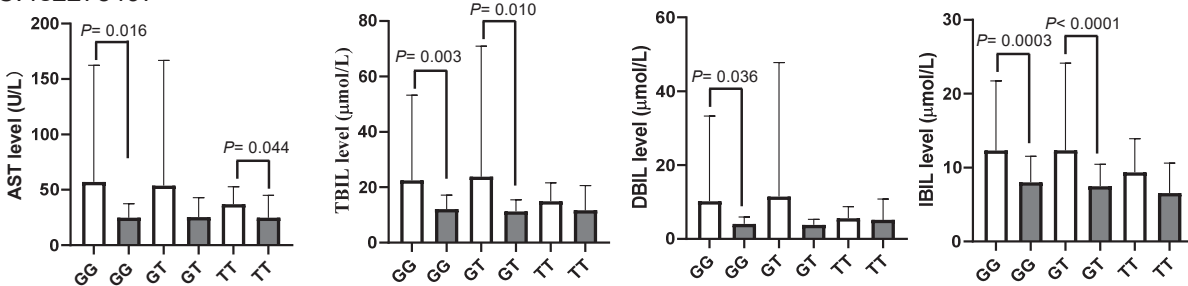


Fig. 2. Comparison of biochemical characteristics between HBsAg-positive and HBsAg-negative HBV patients with various genotypes of three SNPs. (A) The ALT, AST, TBIL, DBIL, and IBIL level in patients with genotype CC and CT&TT of rs56225452; (B) The ALT, AST, TBIL, DBIL, and IBIL level in patients with genotype GG and AG&AA of rs4801275; (C) The AST, TBIL, DBIL, and IBIL level in patients with genotype GG, GT and TT of rs2278497. AST: aspartate transaminase; ALT: alanine transaminase; TBIL: total bilirubin; DBIL: direct bilirubin; IBIL: indirect bilirubin.

In order to evaluate the potential susceptibility of these SNPs to hepatic function and disease progression of HBV patients, the RNA structure and function of these SNPs were predicted. The results showed that RNA structures could be altered by different alleles of rs4801275 and rs2278497 (Fig. 3). rs56225452 has been reported to be located in the promoter region of the *SLC27A5* gene, and we suggested the alleles of rs56225452 might change the promoter activity. rs4801275 and rs2278497 were predicted to be modified by H3K4me1, H3K4me3k, H3K27ac and H3K9ac, which act as an activator of promoters or enhancers. These results suggested that different alleles of the three SNPs might influence the transcription activity of the *SLC27A5* gene.

The dual-luciferase reporter assays (Fig. 4) showed that allele T of rs56225452 led to a higher firefly luciferase expression level than allele C of this SNP. At 48 hours after transfection, the expression level of firefly luciferase was significantly higher in cells transfected with allele A of rs4801275 (1.16 ± 0.05) compared to the allele G (0.89 ± 0.03). Allele G of rs2278497 resulted in a lower firefly luciferase expression level than allele T of this SNP. These results suggested that different alleles of three SNPs might influence the expression level of the *SLC27A5* gene.

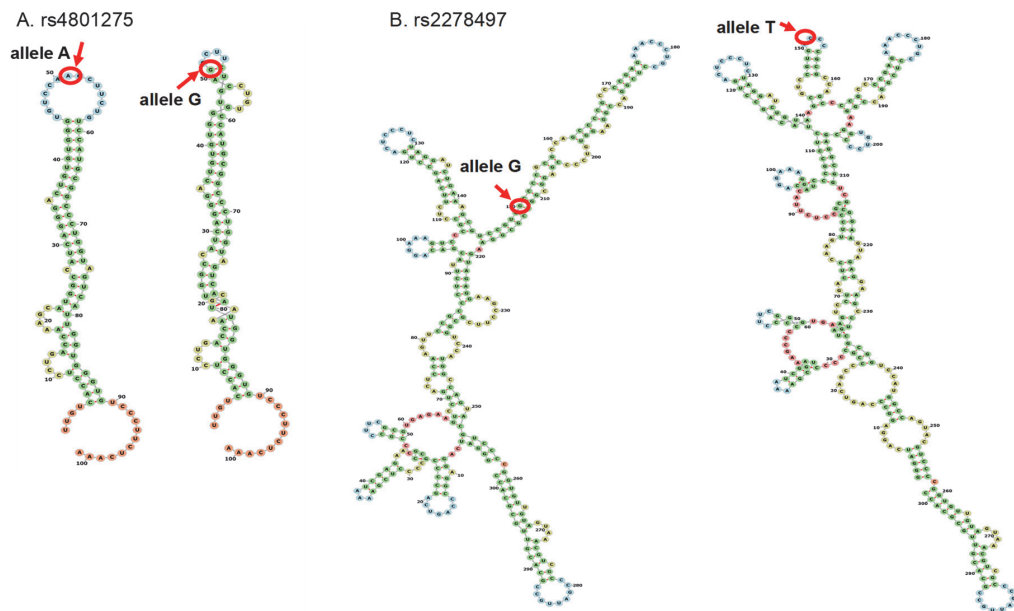


Fig. 3. RNA structure prediction of various alleles of SNPs. The nucleotides marked by red circle were genotyping SNPs in this study.

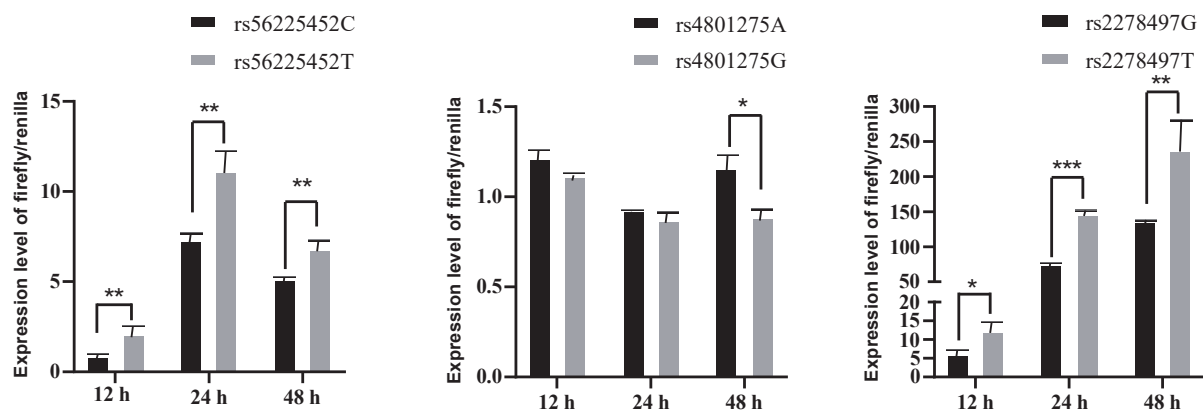


Fig. 4. Dual-luciferase reporter assay. * means $P < 0.05$, ** means $P < 0.01$, *** means $P < 0.001$.

Discussion

Genetic factors have been identified to be associated with HBV infection or treatment effects in HBV patients, but most of these studies focused on immune genes. The genome-wide association study (GWAS) showed that SNPs in the *HLA-DP* gene contributed to the risk of chronic HBV infection in Chinese and Japanese populations (Guo et al., 2011; Mbarek et al., 2011). rs455804 in the *GRIK1* gene was identified as a susceptibility factor for HBV-related HCC (Li et al., 2012). Many genetic variations in other immune genes have been reported in cohort studies. rs10838543 in the *TRIM22* gene was correlated with PegIFN α treatment of HBeAg-positive patients (Wang et al., 2023). Fang et al. (2025) investigated that SNPs in the *IL37* gene were associated with HBV infection and clinical outcomes of HBV patients in Chinese Han cohort.

In our previous study, the SNPs in the *IFNL4*, *MxA*, and *MxB* gene were associated with biochemical characteristics of

HBV patients (Zheng et al., 2022). These findings indicated that genetic polymorphisms of host genes played important roles in HBV infection and disease progression. However, few studies have been performed to investigate the role of lipid genes.

Serum lipidomics of patients with non-alcoholic fatty liver disease (NAFLD) could be altered by chronic HBV infection in Li's study (Li et al., 2021). Additionally, lipid metabolism was reported to participate in HBV infection, replication, release, and disease progression. Inhibition of human low-density lipoprotein receptor (LDLR) decreased HBV replication by reducing the expression of apolipoprotein E (Li and Luo, 2021). Lipid phosphatase SAC1 played key role in production of phosphatidylinositol lipids, which promoted HBV replication. SAC1-mediated phospholipid metabolism could regulate HBV life-cycle (Zheng et al., 2023). Chen and colleagues constructed a model to investigate lipid metabolisms as a key factor for HBV-related HCC (Zhou et al., 2023). Emerging evidence has established that SNPs in lipid metabolism-related genes play

a pivotal role in the pathogenesis and prognosis of HBV or HBV-related HCC. All these studies suggested HBV infection and replication were closely related to lipid metabolism, and many genes involved in lipid metabolism might influence HBV infection, replication, or disease progression.

rs738409 in the *PNPLA3* gene, a well-known risk allele for hepatic steatosis, has been significantly associated with an increased incidence of HCC development in HBV-infected patients (Wang et al., 2020). rs1570247 in the *GBA2* gene, a key gene in sphingolipid metabolism pathway, was significantly associated with survival of HBV-HCC patients, potentially by modulating *GBA2* mRNA expression and influencing immune cell infiltration within the tumor microenvironment (Jiang et al., 2023). The *SLC10A1* (also known as *NTCP*) gene serves as the import receptor for HBV entry into cells, and its function is sodium-dependent bile acids uptake. The SNP (p.Ser267Phe) played protective role against liver cirrhosis, hepatocellular carcinoma, and liver failure in Chinese CHB patients (Yang et al., 2019). Similarly, rs2296651 in the *SLC10A1* gene was associated with HBV infection in Ghanaian population (Xu et al., 2023). The *SLC27A5* gene showed lower expressing levels in HCC patients and served as a suppressor in sorafenib-resistant HCC patients (Xu et al., 2023). Loss of *SLC27A5* function promoted hepatic stellate cell activation and liver fibrosis through accumulation of unconjugated cholic acid, which might drive the transition from NAFLD to cirrhosis and HCC. Moreover, *SLC27A5* expression was significantly reduced in cirrhotic liver tissues and HBV-associated HCC, and ectopic expression of *SLC27A5* suppressed hepatoma cell proliferation and metastasis (Wu et al., 2024). These studies suggested a tumor-suppressive role of *SLC27A5* in HBV-related liver disease progression.

Although the *SLC27A5* gene appeared to be important in lipid metabolism and HCC disease progression, no study has been performed to investigate the role of this gene in HBV infection or disease progression. In this study, we identified an association between SNPs in the *SLC27A5* gene and biochemical characteristics of HBV patients in Yunnan province. When HBV patients with same genotypes were divided into HBsAg-positive and HBsAg-negative groups, liver functional features showed statistically significant differences (Fig. 2). Additionally, we observed that the proportion of males was lower in the HBV patients compared to the controls. Since the normal parameters of biochemical indicators were same for adult males and females, the differences of biochemical indicators between HBV patients and controls were not attributable to gender bias. Similarly, the genotype and allele frequencies of genetic polymorphisms were not influenced by gender. These results suggested that genetic variants of the *SLC27A5* gene might alter the expression level of *SLC27A5*. Furthermore, RNA structure prediction and dual-luciferase reporter assays indicated that different alleles of three SNPs might play roles in HBV patients through altering the expression level of the *SLC27A5* gene. However, further validation is needed in HBV patients to determine whether the genotype changes of the three SNP sites in the *SLC27A5* gene do indeed affect the expression level of this gene.

Conclusion

In summary, we have identified for the first time an association between genetic polymorphisms of the *SLC27A5* gene and hepatic function in HBV patients in Yunnan Province. This finding might provide basic evidence for development of novel anti-HBV medicines.

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Ethical aspects and conflict of interest

The authors have no conflict of interest to declare.

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