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***Case Control Study***

**Associations of *PNPLA3* and *LEP* genetic polymorphisms with metabolic-associated fatty liver disease in Thai people living with human immunodeficiency virus**

Choochuay K *et al*. *PNPLA3* and *LEP* genetic polymorphisms in MAFLD

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**Abstract**

BACKGROUND

The prevalence of metabolic-associated fatty liver disease (MAFLD) is a growing public health issue in people living with human immunodeficiency virus (PLWH). However, the pathophysiology of MAFLD is still unknown, and the role of genetic variables is only now becoming evident.

AIM

To evaluate the associations of gene-polymorphism-related MAFLD in PLWH.

METHODS

The study employed transient elastography with a controlled attenuation parameter ≥ 248 dB/m to identify MAFLD in patients from a Super Tertiary Hospital in central Thailand. Candidate single-nucleotide polymorphisms (SNPs) were genotyped using TaqMan® MGB probe 5' nuclease assays for seven MAFLD-related genes. Statistical analyses included SNP frequency analysis, Fisher's Exact and Chi-square tests, odds ratio calculations, and multivariable logistic regression.

RESULTS

The G-allele carriers of *PNPLA3* (rs738409) exhibited a two-fold rise in MAFLD, increasing by 2.5 times in MAFLD with human immunodeficiency virus infection. The clinical features and genetic patterns imply that *LEP* rs7799039 A-allele carriers had a nine times (*P* = 0.001) more significant chance of developing aberrant triglyceride among PLWH.

CONCLUSION

The current study shows an association between *PNPLA3* rs738409 and *LEP* rs7799039 with MAFLD in PLWH.

**Key Words:** *PNPLA3*; *LEP*; Metabolic-associated fatty liver disease; People living with HIV; Thai

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**Core Tip:** The prevalence of metabolic-associated fatty liver disease (MAFLD) in people living with human immunodeficiency virus (PLWH) is increasing, becoming a public health concern. The current evidence suggests that aspartate transaminase, fasting plasma glucose, triglyceride, total cholesterol, low-density lipoprotein, and the genetic factors *PNPLA3* rs738409 and *LEP* rs7799039 indicate genetic susceptibility for PLWH, leading to improvements in MAFLD.

**INTRODUCTION**

Metabolic-associated fatty liver disease (MAFLD) related to systemic insulin resistance is defined as an accumulation of fat in the hepatocytes of more than 5%, consisting of steatosis, non-alcoholic steatohepatitis, fibrosis, and cirrhosis[1,2]. Nowadays, the pathogenesis of MAFLD remains unclear. Furthermore, the prevalence of MAFLD in people living with human immunodeficiency virus (PLWH) was reported to be 40%-55%, based on different MAFLD phenotype-proven techniques in multiple ethnicities[3,4]. Additionally, liver disease is the second leading cause of death in PLWH[5]. Since 2005, several studies have suggested that MAFLD is common in human immunodeficiency virus (HIV) patients, and its prevalence appears to be increasing. Therefore, HIV infection remains a contributing factor of MAFLD that directly activates insulin resistance in adipose tissue and generates mitochondrial toxicity and reactive oxygen species in hepatocytes, which worsens the MAFLD prognosis[6].

Genetic differences in the risk of MAFLD or NASH progression in the general population are well described[7]. One of the strongest and most consistent associations with the presence and progression of MAFLD in certain populations is associated with the single-nucleotide polymorphism (SNP) on the *PNPLA3* rs738409[8-12]. However, only limited studies exist regarding the role of rs738409 SNP on the *PNPLA3* gene among people living with HIV. A previous report analyzed the association between *PNPLA3* rs738409 polymorphism and the severity of liver disease, insulin resistance, and obesity in patients co-infected with HIV/hepatitis C virus, which was not associated with the duration of the HIV infection or antiretroviral therapy (ART), specific antiretroviral drugs, a history of opportunistic infection, the patient’s immune status, or the duration of the aminotransferase elevation[13,14]. Additionally, other studies indicate that genes involved in the lipid metabolism pathway, such as *APOC3, APOB, APOA5,* and *LIPC*, areassociated with MAFLD[15-22]. Moreover, *GHRL* and *LEP* also exhibit an association with MAFLD pathogenesis[23-25]. In a previous study, it was shown that the *APOC3* rs2854116 is associated with elevated serum levels of triglycerides, while this genotype did not affect the incidence of lipoatrophy after adjusting for gender and stavudine (d4T)-containing regimens in Thai people living with HIV[26]. Importantly, *GHRL* gene polymorphism was significantly correlated with insulin resistance, which is a hallmark of MAFLD and increased type 2 diabetes mellitus risk, particularly among Chinese people and in other populations[27-29]. However, the genome-wide associations replicated in people living with HIV and MAFLD remain inconclusive. A previous study showed both positive and negative associations between candidate SNP and MAFLD, making it difficult to determine the significance of these findings[7,30]. Hence, our study aimed to evaluate the association between several genes related to MAFLD in Thai people living with HIV.

**MATERIALS AND METHODS**

***Study subjects***

We enrolled patients from a Super Tertiary Hospital in central Thailand and classified them into 4 groups: 83 PLWH and MAFLD (Group 1); 94 people living with HIV and without MAFLD (Group 2); 145 with NAFLD without HIV infection (Group 3), and 93 Chinese Dai genotyping data from the 1000 Genome Project phase ([http://www.1000genomes.org](http://www.1000genomes.org/)) used to represent the Thai ethnicity (Group 4). The presence of MAFLD was confirmed *via* transient elastography with a controlled attenuated parameter ≥ 248 dB/m, as prescribed by our colleague in a previous study[31]. The Infectious Disease Clinic enrolled PLWH who were on ART with full viral suppression and had no history of alcohol consumption in the trial. The key inclusion criteria were as follows: PLWH receiving ART with an undetectable HIV viral load for at least 6 months. Patients co-infected with hepatitis B or C virus, other known liver disorders such as cirrhosis or hepatocellular carcinoma, and critical liver disease were all excluded. The study protocol is shown in Figure 1.

***Genotyping analysis***

The genotyping of seven genes related to MAFLD was performed using an allele-specific TaqMan® MGB probe 5’ nuclease assay with a real-time polymerase chain reaction (PCR) ViiA7™ system (Applied Biosystems, Life Technologies). The allele-specific TaqMan® MGB probe 5’ nuclease chain reaction assay was performed with primers of *PNPLA3* (rs738409); *APOC3* (rs2854116); *APOA5* (rs662799); *APOB* (rs10495712); *LIPC* (rs1800588); *LEP* (rs7799039); and *GHRL* (rs27647). Each 6 μL of the PCR mixture contained 2 μL of genomic DNA in a concentration of 5 ng/μL, 2.5 μL of the TaqMan® Genotyping Master mix, 0.25 μL of allele-specific TaqMan® MGB probe and a sequence-specific primer kit, and 1.25 μL of DNase-free water. The thermal cycler program started with 10 min at 95°C, followed by 50 cycles of 15 s at 92°C and 90 s at 60°C. The allelic discrimination plot was analyzed using ViiA7™ software (Applied Biosystems, Life Technologies). Allele 1 was labeled with VIC® dye fluorescence, and allele 2 was labeled with FAM® dye fluorescence.

***Statistical analysis***

The frequencies of all SNPs were checked for Hardy-Weinberg equilibrium using the R statistic, version 3.6.1, from the R Foundation for Statistical Computing. Fisher’s Exact and Chi-square tests were used to determine the statistical difference between the minor alleles between MAFLD patients and control patients using SPSS version 22.0 for Windows, SPSS Inc., Chicago, IL, United States. The association of the candidate genes’ polymorphisms with MAFLD was assessed by calculating the odds ratios and the corresponding 95% confidence intervals. Backward stepwise multivariable logistic regression analysis was used to assess whether one or more genetic factors predicted MAFLD. A *P* value of less than 0.05 was considered significant.

**RESULTS**

***Characteristics of people living with HIV and with MAFLD (Group 1) and of non-MAFLD patients (Group 2) and MAFLD patients (Group 3)***

When comparing the people living with HIV and with andwithout MAFLD, we enrolled a higher proportion of males with a higher BMI. The levels of fasting glucose, HbA1C, triglyceride, aspartate transaminase (AST), alanine transaminase (ALT), and gamma-glutamyl transferase were significantly higher in the MAFLD group compared to the non-MAFLD group in the metabolic profiles and liver function tests. When comparing the HIV treatment regimens, the proportion of non-nucleoside reverse transcriptase inhibitor, nucleoside reverse transcriptase inhibitor (NRTI), protease inhibitor (PI)-based, or alternative regimens did not differ between the two groups (*P* = 0.573), but comorbidities of dyslipidemia, hypertension, and diabetes mellitus were higher in people living with HIV and MAFLD (*P =* 0.002; *P* = 0.001 and *P* = 0.005, respectively) (Table 1).

***Distribution of SNPs in people living with HIV and MAFLD (Group 1) or without MAFLD (Group 2), with MAFLD (Group 3), and Chinese Dai (Group 4)***

All the SNP genotyping experiments were successful. Throughout the entire study, the genotype frequencies of each SNP did not deviate from Hardy-Weinberg equilibrium (*P* > 0.05). Table 2 shows the genotype distribution and minor allele frequency of the investigated SNPs in people living with HIV with or without MAFLD, MAFLD patients, and Chinese Dai. All potential SNP genotype distributions (*PNPLA3* rs738409*, APOC3* rs2854116*, APOA5* rs662799*, APOB* rs10495712*, LIPC* rs1800588*, LEP* rs7799039, and *GHRL* rs27647) in people living with HIV with MAFLD were similar to those seen in patients living with HIV without MAFLD. In comparison to Chinese Dai, patients with MAFLD had a higher frequency of the *PNPLA3* G-allele (*P* = 0.035). The frequencies of the other SNPs were not significant in persons living with HIV and those with or without MAFLD.

***Association between PNPLA3 and other candidate SNPs with MAFLD***

the data given in Tables 3 and 4 show the well-established *PNPLA3* rs738409 gene, which is found on chromosome 22 and has a function related to lipid droplet formation in the hepatocytes; the G-carrier patients had an approximately two-fold higher risk of developing MAFLD when compared to MAFLD with Chinese Dai (*P* = 0.012).Importantly, people living with HIV and MAFLD exhibited a 2.5-fold increased risk (*P* = 0.002) when compared to Chinese Dai (Group 4). In addition, *GHRL* (Ghrelin) rs27647 is a promising susceptibility gene for insulin regulation; the C-allele carrier has exhibited a protective effect in MAFLD in people living with HIV. The odds of having MAFLD is 53% lower if the people living with HIV are C-carriers of *GHRL* rs27647 than if they are not C-carriers (*P* = 0.047). However, there was no statistically significant association with *GHRL* in the other groups. Furthermore, *APOC3*rs2854116 C-allele carriers were also statistically significant in the MAFLD group, exhibiting a six-fold higher risk in the dominant model with Chinese Dai as the comparison (*P* < 0.001).

***Association between candidate SNPs and the lipid profile, liver function, and glucose metabolisms***

We performed a subgroup analysis of people living with HIV in terms of their metabolic profiles and compared the genotypes of candidate genes. As shown in Table 5, the mean or median values of the lipid profile [triglyceride, total cholesterol, LDL]; liver function (AST, ALT); and glucose metabolisms (HbA1C and fasting plasma glucose) were higher in the people living with HIV and MAFLD than in the control group (people living with HIV and non-MAFLD). The association between the genotypes of the *APOA5* rs662799 SNP and serum lipid parameters in the control group is presented in Table 5 and Supplementary Table 1. Serum total cholesterol levels in control patients differed between the AA and AG/GG genotypes (*P* < 0.05). The *APOA5* rs662799 G allele carriers had a lower proportion of total cholesterol levels in the normal range (< 200 mg/dL) than the A allele non-carriers and indicated the protective effect of *APOA5* rs662799 in an abnormal range of total cholesterol (> 200 mg/dL); these results showed statistical significance (*P* = 0.045). Furthermore, *LEP* rs7799039 AG and AA carriers exhibited a significant nine-fold higher risk in an abnormal range of triglyceride (> 150 mg/dL) when compared with non-carriers (*P* = 0.001). Unfortunately, none of the individual SNPs were associated with LDL. Moreover, in men, *APOC3* rs2854116 TT alleles also showed a protective effect on the high-density lipoprotein (HDL) profile (Table 5 and Supplementary Table 1). Furthermore, AST is known to be a reliable surrogate marker for outcome measures in MAFLD. Table 6 shows that *PNPLA3* rs738409 G-carrier patients have an approximately 2.5 times higher chance of AST abnormality (> 34 U/L) when compared with non-carriers (statisticallysignificant at *P* = 0.010).

***Association between the genetic profile, clinical factors, and MAFLD***

A stepwise multiple logistic regression was performed to investigate the relationship between the genetics profiles, clinical factors, and MAFLD. Sixteen variables, including gender, AST, ALT, total cholesterol, triglycerides, HDL, LDL, fasting plasma glucose, HbA1C, and the genetic profiles of *PNPLA3* rs738409*, APOC3* rs2854116*, APOA5* rs662799*, APOB* rs10495712*, LIPC* rs1800588*, LEP* rs7799039*,* and *GHRL* rs27647 were entered into the original equation. The results showed that seven variables, namely, AST, total cholesterol triglycerides, LDL, fasting plasma glucose, *APOB* rs10495712, and *APOA5* rs662799, were significantly associated with MAFLD (Table [7](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3432067/table/pone-0044136-t003/)).

**DISCUSSION**

Risk factors for MAFLD in people living with HIV (PLWH) include the normal factors seen in the general population, such as components of metabolic syndrome (obesity, diabetes, hypertension, dyslipidemia, a sedentary lifestyle, and excessive dietary intake)[1]. Hepatic steatosis and mitochondrial oxidative stress are pivotal to MAFLD pathogenesis. In PLWH with MAFLD, HIV-specific factors such as lipodystrophy, ART, and HIV infection itself are strongly linked to the development of MAFLD[31,32]. However, our study did not find NRTI-based and PI-based regimens to be predictive factors for MAFLD.

The strongest and most consistent associations with the presence and progression of MAFLD in the studied populations are related to the SNP on the *PNPLA3* rs738409, which was discovered by the first GWAS in 2003[8]. Our study demonstrated the significance of *PNPLA3* rs738409 in MAFLD when compared to the general population, indicating the impact of genetic factors. Moreover, we evaluated the effect of both HIV infection and genetic factors by conducting a comparison between people living with HIV and Chinese Dai, finding that it increased the chance of the development of MAFLD between 2 and 2.5 times when compared to the genetic factor alone. Moreover, our results agree with previous studies that demonstrated the significant association with *PNPLA3* rs738409 and biopsy-proven fibrosis or steatosis among HIV/hepatitis C virus or HBV co-infected patients, HIV-mono infection, and the group with no viral infection[33-35].

Insulin resistance has been characterized as the crucial pathophysiological factor in MAFLD.The advanced reports found that insulin resistance is associated with the reduction of circulating ghrelin level[21,36,37]. Interestingly, our study has shown that the G/A genotype and G/G genotype of *GHRL* rs27647 were associated with a 53% decreased risk of MAFLD in people living with HIV when compared with non-MAFLD patients. Moreover, a previous study observed higher levels of ghrelin in patients with hypertriglyceridemia, as well as a positive correlation between ghrelin and triglyceride levels in patients with hypertriglyceridemia[38,39]. Unfortunately, our study failed to detect the association between SNP and triglyceride levels in people living with HIV.

The *APOC3* gene plays a crucial role in the circulation and clearance of very-low-density lipoprotein, HDL, and chylomicron remnants[40,41]. The polymorphism in the promotor region of the *APOC3* rs2854116 (-455T>C) gene has been extensively studied and has been found to be related with insulin resistance at the transcriptional level. Consequently, the overexpression of *APOC3*, which functions to inhibit lipoprotein lipase and the cellular uptake of triglyceride-rich lipoprotein particles, may result in hypertriglyceridemia, as has been confirmed by *in vivo* and clinical studies[23,24,42-44]. In this study, we showed that *APOC3* rs2854116 C-allele carrier patients have a six-fold higher risk of developing MAFLD in a dominant model. Our findings are also consistent with previous reports that the *APOC3rs2854116* genetic variant leads to increased plasma concentrations of apolipoprotein C3, resulting in hepatic insulin resistance and MAFLD in multiethnic populations[23,45,46].

Our results show a similar trend to those of a previous report, which demonstrated a positive correlation between AST levels and the accumulation of intrahepatic triglyceride[47]. Interestingly, our results indicate a robust association in *LEP* rs7799039 with the lipid profile, especially with triglyceride levels. According to a subgroup analysis of patients infected with HIV, a patient who is a carrier of the A-allele (AG and AA) has a nine-times-higher risk of exhibiting abnormal triglyceride levels (> 150 mg/dL). Further information suggests that *LEP* rs7799039, located on chromosome 7, encodes 167 amino acid peptide variants with a molecular weight of 16 ku, which may subsequently affect the biological functions of *LEP*[48]. In recent years, *LEP* has been found to regulate the energy balance in coordination with the regulation of the glucose and lipid metabolisms. Thus, it plays a vital role in the development of MAFLD. This finding aligns with that of previous reports that evaluated the association between *LEP* rs7799039 and diabetes mellitus, metabolic syndrome, MAFLD, and cardiovascular disease[49,50].Our findings should be interpreted while bearing in mind several potential limitations. First, the small sample size of each group may have limited the study’s ability to detect a significant relationship. Second, the patients included in this study were exclusively Thai, so our findings may not apply to patients of other ethnic origins. Further, long-term studies are still needed to confirm these findings in other ethnicities. Although the results of the available research are satisfactory, they have not been proven in randomized control trials. Further studies of genetic predispositions for MAFLD with the absence or presence with MAFLD will certainly provide a better understanding of the molecular mechanisms of MAFLD.

**CONCLUSION**

The prevalence of MAFLD in people living with HIV is increasing, representing a public health concern. The existing evidence suggests that AST, fasting plasma glucose, triglyceride, total cholesterol, LDL, and the genetic factors *PNPLA3* rs738409 and *LEP* rs7799039 indicate genetic susceptibility for PLWH, leading to improvements in the treatment of MAFLD.

**ARTICLE HIGHLIGHTS**

***Research background***

Metabolic-associated fatty liver disease (MAFLD), which is characterized by hepatocyte fat accumulation, poses substantial health risks; it affects a significant number of people globally, especially those living with obesity, diabetes, dyslipidemia, hypertension, and metabolic syndrome. Despite its prevalence, the precise mechanisms underlying MAFLD, which involve factors including viral hepatitis, human immunodeficiency virus (HIV), antiretroviral treatment, and genetics, remain unclear.

***Research motivation***

MAFLD is prevalent among individuals with HIV, with rates ranging from 40% to 55%; it is influenced by both antiretroviral medications and specific genetic variants. Notably, the *PNPLA3* rs738409 variant, a genetic factor, plays a significant role in the development of MAFLD.

***Research objectives***

The present investigation sought to assess the correlation between gene polymorphisms and MAFLD in individuals living with HIV.

***Research methods***

We employed transient elastography and set a threshold for the controlled attenuated parameter at ≥ 248 dB/m for the identification of MAFLD. All participants underwent genotyping for candidate single-nucleotide polymorphisms.

***Research results***

Individuals carrying the G-allele of *PNPLA3* (rs738409) demonstrated a two-fold increased risk of developing MAFLD; this risk rose to 2.5 times in cases of MAFLD with HIV infection. The clinical characteristics and genetic profiles suggested that carriers of the A-allele of *LEP* rs7799039 had a nine-fold higher likelihood of developing abnormal triglyceride levels among individuals living with HIV.

***Research conclusions***

The present research reveals a connection between *PNPLA3* rs738409 and *LEP* rs7799039 and MAFLD in individuals with HIV.

***Research perspectives***

Genetic factors play a crucial role in the pathophysiology of MAFLD. In upcoming research, targeting the *PNPLA3* gene in clinical trials may emerge as a promising direction for precision medicine in the treatment of MAFLD.

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**REFERENCES**

1 **Fouad Y**, Waked I, Bollipo S, Gomaa A, Ajlouni Y, Attia D. What's in a name? Renaming 'NAFLD' to 'MAFLD'. *Liver Int* 2020; **40**: 1254-1261 [PMID: 32301554 DOI: 10.1111/liv.14478]

2 **Verna EC**. Non-alcoholic fatty liver disease and non-alcoholic steatohepatitis in patients with HIV. *Lancet Gastroenterol Hepatol* 2017; **2**: 211-223 [PMID: 28404136 DOI: 10.1016/S2468-1253(16)30120-0]

3 **Non-alcoholic Fatty Liver Disease Study Group**, Lonardo A, Bellentani S, Argo CK, Ballestri S, Byrne CD, Caldwell SH, Cortez-Pinto H, Grieco A, Machado MV, Miele L, Targher G. Epidemiological modifiers of non-alcoholic fatty liver disease: Focus on high-risk groups. *Dig Liver Dis* 2015; **47**: 997-1006 [PMID: 26454786 DOI: 10.1016/j.dld.2015.08.004]

4 **Rinella ME**. Nonalcoholic fatty liver disease: a systematic review. *JAMA* 2015; **313**: 2263-2273 [PMID: 26057287 DOI: 10.1001/jama.2015.5370]

5 **Smith CJ**, Ryom L, Weber R, Morlat P, Pradier C, Reiss P, Kowalska JD, de Wit S, Law M, el Sadr W, Kirk O, Friis-Moller N, Monforte Ad, Phillips AN, Sabin CA, Lundgren JD; D:A:D Study Group. Trends in underlying causes of death in people with HIV from 1999 to 2011 (D:A:D): a multicohort collaboration. *Lancet* 2014; **384**: 241-248 [PMID: 25042234 DOI: 10.1016/S0140-6736(14)60604-8]

6 **Coronel-Castillo CE**, Qi X, Contreras-Carmona J, Ramírez-Pérez OL, Méndez-Sánchez N. Nonalcoholic fatty liver disease and nonalcoholic steatohepatitis in HIV infection: a metabolic approach of an infectious disease. *Expert Rev Gastroenterol Hepatol* 2019; **13**: 531-540 [PMID: 30905208 DOI: 10.1080/17474124.2019.1599284]

7 **Soti S**, Corey KE, Lake JE, Erlandson KM. NAFLD and HIV: Do Sex, Race, and Ethnicity Explain HIV-Related Risk? *Curr HIV/AIDS Rep* 2018; **15**: 212-222 [PMID: 29671204 DOI: 10.1007/s11904-018-0392-1]

8 **Romeo S**, Kozlitina J, Xing C, Pertsemlidis A, Cox D, Pennacchio LA, Boerwinkle E, Cohen JC, Hobbs HH. Genetic variation in PNPLA3 confers susceptibility to nonalcoholic fatty liver disease. *Nat Genet* 2008; **40**: 1461-1465 [PMID: 18820647 DOI: 10.1038/ng.257]

9 **Kitamoto T**, Kitamoto A, Yoneda M, Hyogo H, Ochi H, Nakamura T, Teranishi H, Mizusawa S, Ueno T, Chayama K, Nakajima A, Nakao K, Sekine A, Hotta K. Genome-wide scan revealed that polymorphisms in the PNPLA3, SAMM50, and PARVB genes are associated with development and progression of nonalcoholic fatty liver disease in Japan. *Hum Genet* 2013; **132**: 783-792 [PMID: 23535911 DOI: 10.1007/s00439-013-1294-3]

10 **Speliotes EK**, Yerges-Armstrong LM, Wu J, Hernaez R, Kim LJ, Palmer CD, Gudnason V, Eiriksdottir G, Garcia ME, Launer LJ, Nalls MA, Clark JM, Mitchell BD, Shuldiner AR, Butler JL, Tomas M, Hoffmann U, Hwang SJ, Massaro JM, O'Donnell CJ, Sahani DV, Salomaa V, Schadt EE, Schwartz SM, Siscovick DS; NASH CRN; GIANT Consortium; MAGIC Investigators, Voight BF, Carr JJ, Feitosa MF, Harris TB, Fox CS, Smith AV, Kao WH, Hirschhorn JN, Borecki IB; GOLD Consortium. Genome-wide association analysis identifies variants associated with nonalcoholic fatty liver disease that have distinct effects on metabolic traits. *PLoS Genet* 2011; **7**: e1001324 [PMID: 21423719 DOI: 10.1371/journal.pgen.1001324]

11 **Kozlitina J**, Smagris E, Stender S, Nordestgaard BG, Zhou HH, Tybjærg-Hansen A, Vogt TF, Hobbs HH, Cohen JC. Exome-wide association study identifies a TM6SF2 variant that confers susceptibility to nonalcoholic fatty liver disease. *Nat Genet* 2014; **46**: 352-356 [PMID: 24531328 DOI: 10.1038/ng.2901]

12 **Namjou B**, Lingren T, Huang Y, Parameswaran S, Cobb BL, Stanaway IB, Connolly JJ, Mentch FD, Benoit B, Niu X, Wei WQ, Carroll RJ, Pacheco JA, Harley ITW, Divanovic S, Carrell DS, Larson EB, Carey DJ, Verma S, Ritchie MD, Gharavi AG, Murphy S, Williams MS, Crosslin DR, Jarvik GP, Kullo IJ, Hakonarson H, Li R; eMERGE Network, Xanthakos SA, Harley JB. GWAS and enrichment analyses of non-alcoholic fatty liver disease identify new trait-associated genes and pathways across eMERGE Network. *BMC Med* 2019; **17**: 135 [PMID: 31311600 DOI: 10.1186/s12916-019-1364-z]

13 **Jiménez-Sousa MA**, Berenguer J, García-Álvarez M, Gutierrez-Rivas M, Aldámiz-Echevarria T, Tejerina F, Diez C, Vázquez-Morón S, Resino S. Impact of patatin-like phospholipase domain-containing 3 gene polymorphism (rs738409) on severity of liver disease in HIV/hepatitis C virus-coinfected patients. *AIDS* 2016; **30**: 465-470 [PMID: 26760234 DOI: 10.1097/QAD.0000000000000908]

14 **Deprince A**, Haas JT, Staels B. Dysregulated lipid metabolism links NAFLD to cardiovascular disease. *Mol Metab* 2020; **42**: 101092 [PMID: 33010471 DOI: 10.1016/j.molmet.2020.101092]

15 **Puppala J**, Siddapuram SP, Akka J, Munshi A. Genetics of nonalcoholic Fatty liver disease: an overview. *J Genet Genomics* 2013; **40**: 15-22 [PMID: 23357341 DOI: 10.1016/j.jgg.2012.12.001]

16 **Taliento AE**, Dallio M, Federico A, Prati D, Valenti L. Novel Insights into the Genetic Landscape of Nonalcoholic Fatty Liver Disease. *Int J Environ Res Public Health* 2019; **16** [PMID: 31375010 DOI: 10.3390/ijerph16152755]

17 **Geng Y**, Faber KN, de Meijer VE, Blokzijl H, Moshage H. How does hepatic lipid accumulation lead to lipotoxicity in non-alcoholic fatty liver disease? *Hepatol Int* 2021; **15**: 21-35 [PMID: 33548031 DOI: 10.1007/s12072-020-10121-2]

18 **Abu-Farha M**, Ghosh A, Al-Khairi I, Madiraju SRM, Abubaker J, Prentki M. The multi-faces of Angptl8 in health and disease: Novel functions beyond lipoprotein lipase modulation. *Prog Lipid Res* 2020; **80**: 101067 [PMID: 33011191 DOI: 10.1016/j.plipres.2020.101067]

19 **Posadas-Sánchez R**, Ocampo-Arcos WA, López-Uribe ÁR, Posadas-Romero C, Villarreal-Molina T, León EÁ, Pérez-Hernández N, Rodríguez-Pérez JM, Cardoso-Saldaña G, Medina-Urrutia A, Vargas-Alarcón G. Hepatic lipase (LIPC) C-514T gene polymorphism is associated with cardiometabolic parameters and cardiovascular risk factors but not with fatty liver in Mexican population. *Exp Mol Pathol* 2015; **98**: 93-98 [PMID: 25550127 DOI: 10.1016/j.yexmp.2014.12.010]

20 **Li XL**, Sui JQ, Lu LL, Zhang NN, Xu X, Dong QY, Xin YN, Xuan SY. Gene polymorphisms associated with non-alcoholic fatty liver disease and coronary artery disease: a concise review. *Lipids Health Dis* 2016; **15**: 53 [PMID: 26965314 DOI: 10.1186/s12944-016-0221-8]

21 **Petersen KF**, Dufour S, Hariri A, Nelson-Williams C, Foo JN, Zhang XM, Dziura J, Lifton RP, Shulman GI. Apolipoprotein C3 gene variants in nonalcoholic fatty liver disease. *N Engl J Med* 2010; **362**: 1082-1089 [PMID: 20335584 DOI: 10.1056/NEJMoa0907295]

22 **Lin B**, Huang Y, Zhang M, Wang J, Wu Y. Association between apolipoprotein C3 Sst I, T-455C, C-482T and C1100T polymorphisms and risk of coronary heart disease. *BMJ Open* 2014; **4**: e004156 [PMID: 24430880 DOI: 10.1136/bmjopen-2013-004156]

23 **Stagi S,** Bianconi M, Sammarco MA, Artuso R, Giglio S, de Martino M. New thoughts on pediatric genetic obesity: pathogenesis, clinical characteristics and treatment approach. InAdiposity: omics and molecular understanding 2017; **22:** 1320-1678. InTechOpen, London [DOI: 10.5772/66128]

24 **Cappiello V**, Ronchi C, Morpurgo PS, Epaminonda P, Arosio M, Beck-Peccoz P, Spada A. Circulating ghrelin levels in basal conditions and during glucose tolerance test in acromegalic patients. *Eur J Endocrinol* 2002; **147**: 189-194 [PMID: 12153739 DOI: 10.1530/eje.0.1470189]

25 **Barazzoni R**, Zanetti M, Ferreira C, Vinci P, Pirulli A, Mucci M, Dore F, Fonda M, Ciocchi B, Cattin L, Guarnieri G. Relationships between desacylated and acylated ghrelin and insulin sensitivity in the metabolic syndrome. *J Clin Endocrinol Metab* 2007; **92**: 3935-3940 [PMID: 17652221 DOI: 10.1210/jc.2006-2527]

26 **Likanonsakul S**, Rattanatham T, Feangvad S, Uttayamakul S, Prasithsirikul W, Srisopha S, Nitiyanontakij R, Tengtrakulcharoen P, Tarkowski M, Riva A, Nakayama EE, Shioda T. Polymorphisms in Fas gene is associated with HIV-related lipoatrophy in Thai patients. *AIDS Res Hum Retroviruses* 2013; **29**: 142-150 [PMID: 22775001 DOI: 10.1089/AID.2012.0114]

27 **Zhuang L**, Li M, Yu C, Li C, Zhao M, Lu M, Zheng T, Zhang R, Zhao W, Bao Y, Xiang K, Jia W, Wang N, Liu L. The Leu72Met polymorphism of the GHRL gene prevents the development of diabetic nephropathy in Chinese patients with type 2 diabetes mellitus. *Mol Cell Biochem* 2014; **387**: 19-25 [PMID: 24132517 DOI: 10.1007/s11010-013-1865-6]

28 **Li YY**, Lu XZ, Yang XX, Wang H, Geng HY, Gong G, Zhan YY, Kim HJ, Yang ZJ. GHRL Gene Leu72Met Polymorphism and Type 2 Diabetes Mellitus: A Meta-Analysis Involving 8,194 Participants. *Front Endocrinol (Lausanne)* 2019; **10**: 559 [PMID: 31440212 DOI: 10.3389/fendo.2019.00559]

29 **Huang R**, Tian S, Cai R, Sun J, Shen Y, Wang S. Ethnicity-Specific Association Between Ghrelin Leu72Met Polymorphism and Type 2 Diabetes Mellitus Susceptibility: An Updated Meta-Analysis. *Front Genet* 2018; **9**: 541 [PMID: 30487812 DOI: 10.3389/fgene.2018.00541]

30 **Maurice JB**, Patel A, Scott AJ, Patel K, Thursz M, Lemoine M. Prevalence and risk factors of nonalcoholic fatty liver disease in HIV-monoinfection. *AIDS* 2017; **31**: 1621-1632 [PMID: 28398960 DOI: 10.1097/QAD.0000000000001504]

31 **Jongraksak T**, Sobhonslidsuk A, Jatchavala J, Warodomwichit D, Kaewduang P, Sungkanuparph S. Prevalence and predicting factors of metabolic-associated fatty liver disease diagnosed by transient elastography with controlled attenuation parameters in HIV-positive people. *Int J STD AIDS* 2021; **32**: 266-275 [PMID: 33334267 DOI: 10.1177/0956462420960997]

32 **Williams CD**, Stengel J, Asike MI, Torres DM, Shaw J, Contreras M, Landt CL, Harrison SA. Prevalence of nonalcoholic fatty liver disease and nonalcoholic steatohepatitis among a largely middle-aged population utilizing ultrasound and liver biopsy: a prospective study. *Gastroenterology* 2011; **140**: 124-131 [PMID: 20858492 DOI: 10.1053/j.gastro.2010.09.038]

33 **Romeo S**, Sentinelli F, Cambuli VM, Incani M, Congiu T, Matta V, Pilia S, Huang-Doran I, Cossu E, Loche S, Baroni MG. The 148M allele of the PNPLA3 gene is associated with indices of liver damage early in life. *J Hepatol* 2010; **53**: 335-338 [PMID: 20546964 DOI: 10.1016/j.jhep.2010.02.034]

34 **Zou Y**, Zhong L, Hu C, Sheng G. Association between the alanine aminotransferase/aspartate aminotransferase ratio and new-onset non-alcoholic fatty liver disease in a nonobese Chinese population: a population-based longitudinal study. *Lipids Health Dis* 2020; **19**: 245 [PMID: 33239040 DOI: 10.1186/s12944-020-01419-z]

35 **López-Amador N,** Nolasco-Hipolito C, Rojas-Jimeno MD, Carvajal-Zarrabal O. Liver enzymes in patients diagnosed with non-alcoholic fatty liver disease (NAFLD) in Veracruz: a comparative analysis with the literature. *Clinical Investigation* 2017; **7**: 25-32 [DOI: 10.4172/Clinical-Investigation.1000107]

36 **Zhang X**, Zhai L, Rong C, Qin X, Li S. Association of Ghrelin Gene Polymorphisms and Serum Ghrelin Levels with the Risk of Hepatitis B Virus-Related Liver Diseases in a Chinese Population. *PLoS One* 2015; **10**: e0143069 [PMID: 26599409 DOI: 10.1371/journal.pone.0143069]

37 **Estep M**, Abawi M, Jarrar M, Wang L, Stepanova M, Elariny H, Moazez A, Goodman Z, Chandhoke V, Baranova A, Younossi ZM. Association of obestatin, ghrelin, and inflammatory cytokines in obese patients with non-alcoholic fatty liver disease. *Obes Surg* 2011; **21**: 1750-1757 [PMID: 21744131 DOI: 10.1007/s11695-011-0475-1]

38 **Falasca K**, Manigrasso MR, Racciatti D, Zingariello P, Dalessandro M, Ucciferri C, Mancino P, Marinopiccoli M, Petrarca C, Conti P, Pizzigallo E, Guagnano MT, Vecchiet J. Associations between hypertriglyceridemia and serum ghrelin, adiponectin, and IL-18 Levels in HIV-infected patients. *Ann Clin Lab Sci* 2006; **36**: 59-66 [PMID: 16501238]

39 **Meier U**, Gressner AM. Endocrine regulation of energy metabolism: review of pathobiochemical and clinical chemical aspects of leptin, ghrelin, adiponectin, and resistin. *Clin Chem* 2004; **50**: 1511-1525 [PMID: 15265818 DOI: 10.1373/clinchem.2004.032482]

40 **Groenendijk M**, Cantor RM, de Bruin TW, Dallinga-Thie GM. The apoAI-CIII-AIV gene cluster. *Atherosclerosis* 2001; **157**: 1-11 [PMID: 11427198 DOI: 10.1016/s0021-9150(01)00539-1]

41 **Jong MC**, Hofker MH, Havekes LM. Role of ApoCs in lipoprotein metabolism: functional differences between ApoC1, ApoC2, and ApoC3. *Arterioscler Thromb Vasc Biol* 1999; **19**: 472-484 [PMID: 10073946 DOI: 10.1161/01.atv.19.3.472]

42 **Young K,** Bjerregaard P. Health Transitions in Arctic Populations. *University of Toronto Press* 2008 [DOI: 10.3138/9781442688193]

43 **Li MR**, Zhang SH, Chao K, Liao XH, Yao JY, Chen MH, Zhong BH. Apolipoprotein C3 (-455T>C) polymorphism confers susceptibility to nonalcoholic fatty liver disease in the Southern Han Chinese population. *World J Gastroenterol* 2014; **20**: 14010-14017 [PMID: 25320541 DOI: 10.3748/wjg.v20.i38.14010]

44 **Lu H**, Sun J, Sun L, Shu X, Xu Y, Xie D. Polymorphism of human leptin receptor gene is associated with type 2 diabetic patients complicated with non-alcoholic fatty liver disease in China. *J Gastroenterol Hepatol* 2009; **24**: 228-232 [PMID: 18713300 DOI: 10.1111/j.1440-1746.2008.05544.x]

45 **Marzuillo P**, Miraglia del Giudice E, Santoro N. Pediatric fatty liver disease: role of ethnicity and genetics. *World J Gastroenterol* 2014; **20**: 7347-7355 [PMID: 24966605 DOI: 10.3748/wjg.v20.i23.7347]

46 **Wang J**, Ye C, Fei S. Association between APOC3 polymorphisms and non-alcoholic fatty liver disease risk: a meta-analysis. *Afr Health Sci* 2020; **20**: 1800-1808 [PMID: 34394242 DOI: 10.4314/ahs.v20i4.34]

47 **Chen Z**, Han CK, Pan LL, Zhang HJ, Ma ZM, Huang ZF, Chen S, Zhuang XJ, Li ZB, Li XY, Li XJ, Yang SY. Serum alanine aminotransferase independently correlates with intrahepatic triglyceride contents in obese subjects. *Dig Dis Sci* 2014; **59**: 2470-2476 [PMID: 24861033 DOI: 10.1007/s10620-014-3214-3]

48 **Wang H**, Wang C, Han W, Geng C, Chen D, Wu B, Zhang J, Wang C, Jiang P. Association of leptin and leptin receptor polymorphisms with coronary artery disease in a North Chinese Han population. *Rev Soc Bras Med Trop* 2020; **53**: e20190388 [PMID: 32049202 DOI: 10.1590/0037-8682-0388-2019]

49 **Swellam M**, Hamdy N. Association of nonalcoholic fatty liver disease with a single nucleotide polymorphism on the gene encoding leptin receptor. *IUBMB Life* 2012; **64**: 180-186 [PMID: 22215535 DOI: 10.1002/iub.597]

50 **Zain SM**, Mohamed Z, Mahadeva S, Cheah PL, Rampal S, Chin KF, Mahfudz AS, Basu RC, Tan HL, Mohamed R. Impact of leptin receptor gene variants on risk of non-alcoholic fatty liver disease and its interaction with adiponutrin gene. *J Gastroenterol Hepatol* 2013; **28**: 873-879 [PMID: 23278404 DOI: 10.1111/jgh.12104]

**Footnotes**

**Institutional review board statement:** The study was approved by the ethics committee of the Faculty of Medicine, Ramathibodi Hospital, Mahidol University (Bangkok, Thailand) (COA. MURA2019/645). All study procedures were conducted in accordance with the 1964 Helsinki Declaration.

**Informed consent statement:** In this investigation, genomic material was isolated from residual specimens of the study subjects, demonstrating minimal risk to patients and participant consent was not necessary.

**Conflict-of-interest statement:** No benefits in any form have been received or will be received from a commercial party related directly or indirectly to the subject of this article.

**Data sharing statement:** No additional data are available.

**STROBE statement:** The authors have read the STROBE Statement – checklist of items, and the manuscript was prepared and revised according to the STROBE Statement – checklist of items.

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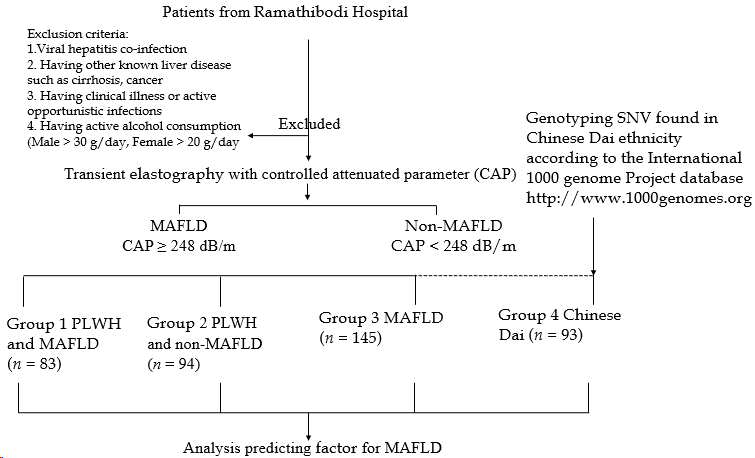
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**Figure Legends**



**Figure 1 Protocol flowchart.** MAFLD: Metabolic-associated fatty liver disease; PLWH: People living with HIV; SNV: Single nucleotide variant.

**Table 1 Baseline characteristics of metabolic-associated fatty liver disease patients and controls**

| **Characteristics** | **PLWH and MAFLD (*n* = 83)** | **PLWH and non-MAFLD (*n* = 94)** | ***P* value** | **MAFLD (*n* = 145)** | ***P* value** | **Chinese Dai (*n* = 93)** | ***P* value** |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Age (yr) | 51.99 ± 7.65 | 49.55 ± 8.27 | 0.044a | 65.00 | < 0.001b | N/A | N/A |
| Gender |  |  |  |  |  |  |  |
| Male | 54 (65.10) | 48 (51.10%) | 0.060 | 68 (46.90%) | 0.008b | 44 (47.30%) | 0.950 |
| Female | 48 (34.90%) | 46 (48.90%) |  | 77 (53.10%) |  | 49 (52.70%) |  |
| BMI (kg/m2) | 25.42 | 21.79 | < 0.001a | 27.67 | < 0.001b | N/A | - |
| CD4 (cells/mm3) | 619.00 | 570.50 | 0.033a | N/A | - | N/A | - |
| %CD 4 | 26.10 ± 0.83 | 25.76 ± 0.81 | 0.853 | N/A | - | N/A | - |
| Hb (g/dL) | 14.36 ± 1.62 | 13.84 ± 1.90 | 0.015a | N/A |  | N/A |  |
| Platelets (-/mm3) | 259063 ± 77332 | 261694 ± 66966 | 0.744 | N/A |  | N/A |  |
| AP (U/L) | 85.00 | 86.00 | 0.821 | 72.00 | 0.001b | N/A | - |
| AST (U/L) | 33.00 | 28.00 | < 0.001a | 38.00 | 0.015b | N/A | - |
| ALT (U/L) | 38.00 | 25.00 | < 0.001a | 50.00 | 0.004b | N/A | - |
| GGT (U/L) | 47.00 | 35.50 | < 0.001a | 51.50 | 0.853 | N/A | - |
| Total protein (g/L) | 79.60 ± 0.56 | 78.28 ± 0.47 | 0.071 | 75.96 ± 0.42 | < 0.001b | N/A | - |
| Albumin (g/L) | 40.80 | 38.35 | < 0.001a | 40.65 | 0.255 | N/A | - |
| Total bilirubin (mg/dL) | 0.60 | 0.50 | 0.759 | 0.70 | 0.10 | N/A | - |
| Direct bilirubin (mg/dL) | 0.20 | 0.20 | 0.862 | 0.30 | 0.007b | N/A | - |
| HbA1C (mmol/L) | 5.68 | 5.38 | < 0.001a | 6.36 | < 0.001b | N/A | - |
| Fasting plasma Glucose (mg/dL) | 98 | 93 | 0.026 | 108 | < 0.001b | N/A | - |
| Triglyceride (mg/dL) | 169 | 109 | < 0.001a | 123 | < 0.0001b | N/A | - |
| Total Cholesterol (mg/dL) | 206.78 ± 5.57 | 199.10 ± 3.57 | 0.212 | 183 | 0.428 | N/A | - |
| HDL (mg/dL) | 44 | 49 | 0.004a | 49 | 0.10 | N/A | - |
| LDL (mg/dL) | 130.67 ± 4.27 | 122.46 ± 2.98 | 0.086 | 114.94 ± 2.83 | 0.001b | N/A | - |
| Drug-regimen, *n* (%) |  |  |  |  |  |  |  |
| NRTI+NNRTI | 62 (74.7) | 71 (75.5) | 0.573 | N/A | - | N/A | - |
| NRTI+PI | 19 (22.9) | 18 (19.1) |  | N/A | - | N/A | - |
| Alternative | 2 (2.4) | 5 (5.3) |  | N/A | - | N/A | - |
| Co-morbidities |  |  |  |  |  |  |  |
| Dyslipidemia | 30 (36.1) | 15 (16.0) | 0.002a | 82 (56.9) | 0.002b | N/A | - |
| Hypertension | 21 (25.3) | 6 (6.4) | 0.001a | 64 (44.1) | 0.003b | N/A | - |
| Diabetes mellitus | 16 (19.3) | 5 (5.3) | 0.005a | 63 (43.4) | < 0.001b | N/A | - |

a*P* value < 0.05 compared between people living with human immunodeficiency virus (PLWH) and metabolic-associated fatty liver disease (MAFLD) *vs* PLWH and non-MAFLD.

b*P* value < 0.05 compared between PLWH and MAFLD *vs* MAFLD.

Data represent as mode, mean ± standard deviation or *n* (%), differences between groups were tested by Chi-square test or one-way ANOVA as appropriate. AP: Alkaline phosphatase; AST: Aspartate aminotransaminase; ALT: Alanine aminotransaminase; ALP: Alkaline phosphatase; Hb: Henoglobin; TB: Total bilirubin; MAFLD: Metabolic-associated fatty liver disease; N/A: Not available; PLWH: People living with human immunodeficiency virus; GGT: Gamma-glutamyl transferase; HbA1C: Hemoglobin A1C; HDL: High-density lipoprotein; LDL: Low-density lipoprotein; NRTI: Nucleoside reverse transcriptase inhibitor; NNRTI: Non-nucleoside reverse transcriptase inhibitor; PI: Protease inhibitor.

**Table 2 Genotype distributions and Minor allele frequency of candidates single-nucleotide polymorphisms**

| **Polymorphism** | **PLWH and MAFLD (*n* = 83)** | **PLWH and non-MAFLD (*n* = 94)** | ***P* value** | **MAFLD (*n* = 145)** | **Chinese Dai (*n* = 94)** | ***P* value** |
| --- | --- | --- | --- | --- | --- | --- |
| *PNPLA3* rs738409 |  | | | | | |
| MAF = G | 57 (34.33) | 56 (29.78) | 0.413 | 92 (31.73) | 43 (23.12) | 0.035a |
| *APOC3* rs2854116 |  |  |  |  |  |  |
| MAF=T | 81 (47.09) | 87(46.28) | 0.691 | 128 (44.14) | 88 (47.31) | < 0.001b |
| *LEP* rs7799039 |  | | | | | |
| MAF=G | 57 (33.14) | 57 (30.32) | 0.738 | 85 (29.31) | 48 (25.81) | 0.674 |
| *GHRL* rs27647 | | | | | | |
| MAF = C | 13 (7.56) | 25 (13.30) | 0.055 | 28 (9.66) | 18 (9.68) | 0.702 |
| *LIPC* rs1800588 | | | | | | |
| MAF = T | 70 (42.17) | 70 (37.33) | 0.421 | 101 (34.83) | 67 (36.02) | 0.872 |
| *APOB* rs10495712 |  | | | | | |
| MAF = A | 15 (8.06) | 14 (7.45) | 0.853 | 22 (7.59) | 8 (4.30) | 0.339 |
| *APOA5* rs662799 |  | | | | | |
| MAF = G | 41 (22.04) | 51 (27.13) | 0.766 | 75 (25.86) | 52 (27.96) | 0.834 |

a*P* value < 0.05 compared between people living with human immunodeficiency virus (PLWH) and metabolic-associated fatty liver disease (MAFLD) *vs* PLWH and non-MAFLD.

b*P* value < 0.05 compared between PLWH and MAFLD *vs* MAFLD MAF minor allele frequency, Chinese Dai was represented as general population. Data represented as *n* (%), PLWH and MAFLD *vs* other groups, differences between groups were tested by Chi-square test. MAFLD: Metabolic-associated fatty liver disease; PLWH: People living with human immunodeficiency virus; MAF: Metabolic-associated fatty.

**Table 3 Genotype and allele frequencies of the single-nucleotide polymorphisms in the people living with human immunodeficiency virus and metabolic-associated fatty liver disease compared with people living with human immunodeficiency virus and non-metabolic-associated fatty liver disease group**

| **Gene** | **SNP** | **B allele** | **Dominant model** | | | | **Recessive model** | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **PLWH and MAFLD *vs* PLWH and non-MAFLD** | | **PLWH and MAFLD *vs* Chinese Dai** | | **PLWH and MAFLD *vs* PLWH and non-MAFLD** | | **PLWH and MAFLD *vs* Chinese Dai** | |
| **OR (95%CI)** | ***P* value** | **OR (95%CI)** | ***P* value** | **OR (95%CI)** | ***P* value** | **OR (95%CI)** | ***P* value** |
| *PNPLA3* | rs738409 | G | 1.476 (0.809-2.694) | 0.204 | 2.539 (1.382-4.665) | 0.002b | 0.94 (0.276-3.202) | 0.921 | 0.929 (0.273-3.166) | 0.907 |
| *APOC3* | rs2854116 | C | 1.117 (0.543-2.297) | 0.764 | 1.203 (0.588-2.462) | 0.613 | 0.798 (0.411-1.550) | 0.506 | 0.828 (0.425-1.614) | 0.579 |
| *LEP* | rs7799039 | G | 0.704 (0.287-1.727) | 0.422 | 0.408 (0.146-1.142) | 0.080 | 0.886 (0.491-1.601) | 0.689 | 0.730 (0.403-1.322) | 0.298 |
| *GHRL* | rs27647 | G | 0.466 (0.217-1.001) | 0.047a | 0.704 (0.317-1.566) | 0.388 | 2.146 (1.832-2.514) | 0.469 | 2.134 (1.823-2.499) | 0.472 |
| *LIPC* | rs1800588 | T | 1.506 (0.806-2.815) | 0.198 | 1.676 (0.898-3.128) | 0.104 | 1.053 0.452-2.456) | 0.905 | 1.040 (0.446-2.427) | 0.928 |
| *APOB* | rs10495712 | A | 1.264 (0.557-2.871) | 0.575 | 2.156 (0.855-5.436) | 0.098 | 1.134 (0.070-18.422) | 1.000 | 2.134 (1.823-2.499) | 0.472 |
| *APOA5* | rs662799 | G | 0.914 (0.505-1.654) | 0.766 | 0.960 (0.330-2.790) | 0.940 | 0.629 (0.177-2.231) | 0.470 | 0.734 (0.200-2.697) | 0.751 |

Data expressed as OR odds ratio, CI confidence interval.

a*P* value < 0.05 compared between people living with human immunodeficiency virus (PLWH) and metabolic-associated fatty liver disease (MAFLD) *vs* PLWH and non-MAFLD.

b*P* value < 0.05 compared between PLWH and MAFLD *vs* Chinese Dai was represented as general population, B-allele expressed risk allele. MAFLD: Metabolic-associated fatty liver disease; PLWH: People living with human immunodeficiency virus; SNP: Single-nucleotide polymorphism.

**Table 4 Genotype and allele frequencies of the single-nucleotide polymorphisms in the metabolic-associated fatty liver disease compared with Chinese Dai**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **SNP** | **B allele** | **Dominate model** | | **Recessive model** | |
| **OR (95%CI)** | ***P* value** | **OR (95%CI)** | ***P* value** |
| *PNPLA3* | rs738409 | G | 1.970 (1.160-3.345) | 0.012a | 1.074 (0.377-3.061) | 0.894 |
| *APOC3* | rs2854116 | C | 6.109 (2.490-14.986) | < 0.001a | 0.485 (0.259-0.907) | 0.022b |
| *LEP* | rs7799039 | G | 0.840 (0.300-2.355) | 0.740 | 0.790 (0.469-1.332) | 0.376 |
| *GHRL* | rs27647 | G | 0.953 (0.491-1.850) | 0.888 | 1.646 (1.486-1.823) | 1.000 |
| *LIPC* | rs1800588 | T | 0.889 (0.525-1.504) | 0.661 | 1.042 (0.494-2.199) | 0.914 |
| *APOB* | rs10495712 | A | 1.799 (0.762-4.251) | 0.176 | 1.642 (1.486-1.823) | 1.000 |
| *APOA5* | rs662799 | G | 0.854 (0.507-1.438) | 0.552 | 0.960 (0.330-2.790) | 0.940 |

a*P* value < 0.05 compared between metabolic-associated fatty liver disease (MAFLD) *vs* Chinese Dai in dominant model.

b*P* value < 0.05 compared between MAFLD *vs* Chinese Dai in recessive model, B-allele expressed risk allele. Data expressed as *n* (%). MAFLD: Metabolic-associated fatty liver disease; PLWH: People living with human immunodeficiency virus; SNP: Single-nucleotide polymorphism; OR: Odds ratio.

**Table 5 Association between genetic polymorphism and Lipid profile**

| **Genetic polymorphisms** | **Lipid parameters** | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Triglyceride (mg/dL), ( *n* = 177)** | | **Total cholesterol (mg/dL), (*n* = 177)** | | **LDL-cholesterol (mg/dL), (*n* = 177)** | | **HDL-cholesterol (mg/dL), (*n* = 66)** | **HDL-cholesterol (mg/dL), (*n* = 111)** |
|  | **< 150** | **≥ 150** | **< 200** | **≥ 200** | **< 130** | **≥ 130** | **Men ≥ 40 mg/dL, women ≥ 50 mg/dL** | **Men < 40 mg/dL, women < 50 mg/dL** |
| *PNPLA3* rs738409 CC *vs* CG+GG | | | | | | |  |  |
| OR (95%CI) | 0.699 (0.383-1.277) | | 1.053 (0.580-1.912) | | 1.088 (0.597-1.981) | | 0.9967 (0.538 -1.846) | |
| *P* value | 0.243 | | 0.865 | | 0.784 | | 0.992 | |
| *APOC3* rs2854116 TT *vs* CT+CC | | | | | | |  | |
| OR (95%CI) | 0.796 (0.387-1.635) | | 1.611 (0.780-3.328) | | 1.173 (0.568-2.423) | | 0.4696 (0.253-0.873) | |
| *P* value | 0.534 | | 0.195 | | 0.666 | | 0.017a | |
| *APOA5* rs662799 AA *vs* AG+GG | | | | | | |  |  |
| OR (95%CI) | 1.021 (0.562-1.855) | | 0.543 (0.299-0.989) | | 0.595 (0.326-1.084) | | 0.739 (0.374-1.461) | |
| *P* value | 0.946 | | 0.045a | | 0.089 | | 0.385 | |
| *APOB* rs10495712 (GG *vs* AG+AA) | | | | | | |  |  |
| OR (95%CI) | 0.749 (0.322-1.743) | | 0.719 (0.315-1.639) | | 0.807 (0.351-1.855) | | 0.816 (0.343-1.938) | |
| *P* value | 0.501 | | 0.431 | | 0.613 | | 0.645 | |
| *LIPC* rs1800588 CC *vs* CT+TT | | | | | | |  |  |
| OR (95%CI) | 0.870 (0.467-1.621) | | 0.732 (0.393-1.363) | | 0.607 (0.326-1.132) | | 0.911 (0.482-1.722) | |
| *P* value | 0.661 | | 0.325 | | 0.115 | | 0.774 | |
| *LEP* rs7799039 GG *vs* AG+AA | | | | | | |  |  |
| OR (95%CI) | 9.316 (2.064-40.428) | | 1.623 (0.655-4.017) | | 1.518 (0.602-3.825) | | 1.317 (0.507-3.419) | |
| *P* value | 0.001a | | 0.292 | | 0.374 | | 0.572 | |
| *GHRL* rs27647 (AA *vs* AG+GG) | | | | | | |  |  |
| OR (95%CI) | 0.570 (0.265-1.224) | | 0.997 (0.483-2.058) | | 0.905 (0.436-1.878) | | 0.889 (0.417-1.895) | |
| *P* value | 0.147 | | 0.993 | | 0.788 | | 0.761 | |

a*P* < 0.05 compare between normal level *vs* abnormal level. OR: Odds ratio; HDL: High-density lipoprotein; LDL: Low-density lipoprotein.

**Table 6 Association between genetic polymorphism and metabolic traits**

| **Genetic polymorphisms** | **Metabolic traits** | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **FPG (mg/dL), *n* = 175** | | **HbA1C (mmol/L), *n* = 159** | | **AST (U/L), *n* = 175** | | **ALT (U/L), *n* = 177** | |
|  | **< 100** | **≥ 100** | **< 6.5** | **≥ 6.5** | **<34** | **≥ 34** | **< 40** | **≥ 40** |
| *PNPLA3* rs738409 (CC *vs* CG+GG) | | | | | | | | |
| OR (95%CI) | 0.354 (0.063-1.984) | | 1.055 (0.437-2.543) | | 2.568 (1.243-5.305) | | 1.679 (0.713-3.953) | |
| *P* value | 0.219 | | 0.906 | | 0.010a | | 0.232 | |
| *APOC3* rs2854116 (TT *vs* CT+CC) | | | | | | | | |
| OR (95%CI) | 0.956 (0.923-0.991) | | 1.553 (0.495-4.897) | | 0.735 (0.335-1.614) | | 0.630 (0.253-1.570) | |
| *P* value | 0.342 | | 0.448 | | 0.442 | | 0.318 | |
| *APOA5* rs662799 (AA + AG+GG) | | | | | | | | |
| OR (95%CI) | 1.167 (0.229-5.946) | | 1.213 (0.509-2.893) | | 0.823 (0.421-1.611) | | 0.730 (0.320-1.664) | |
| *P* value | 1.000 | | 0.663 | | 0.570 | | 0.453 | |
| *APOB* rs10495712 (GG *vs* AG+AA) | | | | | | | | |
| OR (95%CI) | 1.100 (0.123-9.802) | | 1.150 (0.356-3.720) | | 2.063 (0.879-4.840) | | 1.255 (0.431-3.651) | |
| *P* value | 0.923 | | 0.815 | | 0.092 | | 0.774 | |
| *LIPC* rs1800588 (CC *vs* CT+TT) | | | | | | | | |
| OR (95%CI) | 0.947 (0.907-0.989) | | 1.709 (0.636-4.592) | | 1.476 (0.719-3.027) | | 2.208 (0.844-5.776) | |
| *P* value | 0.093 | | 0.284 | | 0.287 | | 0.100 | |
| *LEP* rs7799039 (GG *vs* AG+AA) | | | | | | | | |
| OR (95%CI) | 0.268 (0.046-1.561) | | 1.008 (0.272-3.746) | | 1.329 (0.462-3.827) | | 2.016 (0.444-9.155) | |
| *P* value | 0.166 | | 1.000 | | 0.579 | | 0.535 | |
| *GHRL* rs27647 (AA *vs* AG+GG) | | | | | | | | |
| OR (95%CI) | 1.045 (1.009-1.083) | | 0.700 (0.222-2.206) | | 0.676 (0.285-1.605) | | 0.795 (0.280-2.256) | |
| *P* value | 0.345 | | 0.541 | | 0.373 | | 0.666 | |

a*P* value < 0.05. AST: Aspartate aminotransaminase; ALT Alanine aminotransaminase; OR: Odds ratio; FPG: Fasting plasma glucose; HbA1C: Hemoglobin A1C.

**Table 7 Logistic regression analysis of factors associated with metabolic-associated fatty liver disease (people living with human immunodeficiency virus and metabolic-associated fatty liver disease *vs* people living with human immunodeficiency virus and non-metabolic-associated fatty liver disease)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Factor** | **Exp**(**B**) | **95**%**CI** | ***P*** **value** |
| AST | 4.615 | 1.081-19.709 | 0.039a |
| Fasting Plasma glucose | 21.5 | 5.327-86.767 | < 0.001a |
| Triglyceride | 6.747 | 1.747-26.047 | 0.006a |
| Total cholesterol | 0.125 | 0.019-0.819 | 0.030a |
| LDL | 12.97 | 1.983-84.827 | 0.007a |
| *APOB rs*10495712 | 4.195 | 1.304-18.532 | 0.019a |
| *APOA5* rs662799 | 0.012 | 0.002-0.770 | < 0.001a |
| *LEP* rs7799039 | 0.321 | 0.070-1.469 | 0.143a |

a*P* value < 0.2. AST: Aspartate aminotransaminase; FPG: Fasting plasma glucose; LDL: Low-density lipoprotein.