The Metabolic Status In Non-Alcoholic Fatty Liver Disease And Its Subtypes: A Pilot Study

Yanqi Lan^a, Ying Lu^a, Shiqi Hu^a, Shuohua Chenb, Yanhong Wang^a, **ShoulingWub * and Li Wanga ***

a Department of Epidemiology and Biostatistics, Institute of Basic Medical Sciences Chinese Academy of Medical Sciences; School of Basic Medicine Peking Union Medical College, Beijing, China

b Cardiology Department, Kailuan General Hospital, Tangshan, China

Author Contributions:

These authors contributed equally to this work.

Corresponding author.

Shouling Wu,

Cardiology Department, Kailuan General Hospital, Tangshan 063000, China. **E-mail address:** drwusl@163.com

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1. Abstract

1.1 Aim: To unravel novel circulating metabolites relevant to nonalcoholic fatty liver disease (NAFLD) and its subtypes, lean NAFLD (LN) and overweight/obese NAFLD (ON).

1.2 Methods: A case-control study was undertaken involving 72 newly onset NAFLD and 72 sex-, age-matched non-NAFLD inKailuan cohort. Untargeted liquid chromatography-tandem mass spectrometry was performed to detect serum metabolomics. Significantly altered metabolites were selected. Logistic regressions were used to validate the associations between candidate metabolites and diseases.

1.3 Results: Compared to non-NAFLD, the glycerophospholipid metabolism pathway was evidently changed in NAFLD, LN, and ON. Panels containing seven, sixteen, and four specific glycerophospholipids were found to discriminate NAFLD, LN, and ON. The glycerophospholipid metabolism pathway was also reprogrammed in LN vs. ON. There was a positive correlation between choline and LN [odds ratio(OR)=4.35, 95% confidence interval(95% CI): 1.36-13.90]. A panel containing choline, PC, and LPC had an AUC of 0.73 to distinguish LN from ON. Moreover, a positive relationship was discovered between LPC(20:3(8Z,11Z,14Z))

and very-low-density lipoprotein (OR=3.13, 95% CI: 1.20-8.19).

1.4 Conclusions: The reprogramming of the glycerophospholipid metabolism pathway may be principal in NAFLD and its subtypes.The disruption of PC synthesis and subsequent dysfunctional very-low-density lipoprotein secretion may be responsible for the development of LN.

2. Keywords:

Non-alcoholic fatty liver disease; Lean non-alcoholic fatty liver disease; Untargeted metabolomics; Choline; Glycerophospholipid; Very-lowdensity lipoprotein Shouling Wu,

3. Introduction

Non-alcoholic fatty liver disease (NAFLD) is rapidly becoming one of the most common liver diseases and often increases intra- and extra-hepatic disease risks[1-3]. Despite its importance in clinical practice, there is a lack of easily accessible biomarkers for early diagnosis[4]. Metabolomics may be helpful for research of NAFLD,a disease with a dynamic and complex phenotype, resulting from the multiple-level interactions between genetic and environmental factors[5-7]. Potential circulating metabolites and several metabolic pathways in NAFLD have been found by means of metabolomics, such as variations in amino acid metabolism and key aspects of lipid metabolism, including fatty acids, triglycerides, bile acids, and phospholipids[8, 9]. However, the findings are inconclusive and inconsistent. Further investigations are needed to gain insights into other new early biomarkers and principal metabolic pathways influenced by NAFLD. Notably, a subset of patients with NAFLDis lean[10]. Growing evidence implicates that lean NAFLD (LN) may be a distinct entity with respect to pathophysiological mechanism. Several cohort studies have reported a higher all-cause[11, 12], liver-related mortality, and higher occurrence ofsevere liver disease[13, 14] in LN patients than their counterparts with overweight/obese NAFLD (ON). Additional evidence from recent metabolomics studies also showed a distinctive metabolite profile in LN from ON, indicating different metabolic reprogramming and adaptation between LN and ON. Results from targeted metabolomics studies in Caucasians revealed changes in circulating phospholipids, including phosphatidylcholines (PCs), lysophosphatidylcholines (LPCs), amino acids[15], and bile acids[16] in LN compared to ON. A study in the Chinese population reported distorted metabolism characterized by disordered fatty acid and amino acid profiles in LN and ON patients in comparison to non-NAFLD[17], but they failed to compare LN and ON directly. More studies based on metabolomics are needed to unravel the unique mechanisms of LN and develop subtype-specific markers for clinical applications, particularly in Chinese population. Therefore, employing a case-control design nested within the Kailuan cohort, this

pilot study aimed to identify metabolic markers of NAFLD, and to reveal the metabolic discrepancies between LN and ON. Our results will hopefully provide insightful evidence for establishing diagnosis biomarkers and developing clinically relevant targets for pharmacological interventions of NAFLD and its subtypes.

4. Methods

4.1 Study design and participants

This study adopted a cohort-based case-control design. The Kailuan cohort (Chinese Clinical Trial Registry number: ChiCTR-TNRC-11001489) is a prospective community cohort built in Kailuan of Tangshan City, Hebei Province, China, to evaluate non-communicable diseases in Chinese population. The cohort recruited 101,510 research objects who finished a baseline investigation in 2006-2007 and underwent a regular biennial follow-up in 11 local hospitals. We included 72 cases with incident NAFLD from September 1, 2017, to December 31, 2017. We defined incident NAFLD as those newly diagnosed with fatty liverusing abdominal ultrasound imaging (HD-15; Philips, Netherlands) afterexcludingsecondary causes of hepatic lipid accumulation, including viral hepatitis and excessive drinking [18]. We also selected 72 controls without NAFLD who were 1:1 matched to cases by age $(\pm 3 \text{ years})$ and sex during the same follow-up period. All the controls were excluded from NAFLD using the same diagnostic criteria as cases. The study was carried out in obeyance of the tenets of the Declaration of Helsinki. Ethical approval was obtained from both the Ethics Committee of the Kailuan General Hospital and the Institute of Basic Medical Sciences Chinese Academy of Medical Sciences(2016-IFMS-006). Additionally, written informed consent was retrievedfrom all participants.

4.2 Covariates

Sociodemographic characteristics were collected by questionnaire investigation. E Height, weight, waist circumference, systolicand diastolic pressure were also measured. BMI was calculated as body weight divided by the square of height (kg/m2). Total serum cholesterol (TC), triglycerides (TG), low-density lipoprotein cholesterol (LDL-C), high-density lipoprotein cholesterol (HDL-C), fasting blood glucose (FBG), alanine transaminase, c-reactive protein were quantified using an auto-analyzer (Hitachi 747; Hitachi, Tokyo, Japan) at the central lab in Kailuan General Hospital.VLDL was estimated as TC minus LDL-C and HDL-C[19]. Two insulin resistance-related indexes, including triglyceride glucose index (TyG index) and TG/HDL-C ratio[19], were also computed,among which, the TyG index was denoted as ln[TG(mmol/L)*FBG (mmol/L)/2]. Serum hepatitis B surface antigen was tested by enzyme-linked immunosorbent assay (Shanghai Kehua Bio-Engineering, KHB).

4.3 Metabolomics profiling

The serum metabolomic profiling was examined using high-throughput untargeted liquid chromatography (LC)-tandem mass spectrometry (MS) system, the reproducibility and reliability of which were assessed by quality control (QC) samples.

4.4. Serum sample preparation

100μL of serum was poured into 10μL of L-2-chlorophenylalanine, and the mixture was vortexed for 10 sec. Subsequently, a 300μL mix of methanol and acetonitrile (2/1, v/v) was added. After vortex mixing for 1 min, the extract was centrifuged at a speed of 13,000 rpm, 4℃ for 10 min. 300μL of supernatant was dried in a glass vial. Then, a 400μL mixture of methanol and water (1/4, v/v) was added and vortexed for 30 sec. The tube was then centrifuged again at 13,000 rpm, 4℃, for 10 min, after which 150μL of supernatant was filtered through 0.22μm micro-filters and relocated to an LC vial. The vial was reserved at -80℃ tillfurther LC-MSoperation. A total of 14 QC samples were formulated as a pooled sample by mixing aliquots of all samples and used to balance the LC-MS system.

4.5. LC-MS/MS analysis

ADionex Ultimate 3000 ultra-high pressure LC system equipped with Q Exactive Plus Hybrid Quadrupole-Orbitrap MSinstalled with a heated electrospray ionization source was used to characterize the metabolite landscape in both electrospray ionization positive and negative ion modes, in which an ACQUITY UPLC HSS T3 (1.8μm, 100nm×2.1mm) was employed. The binary solvent gradient elution composed of solvent A (0.1%, v/v, formic acid dissolved in water) and solvent B (0.1%, v/v, formic acid dissolved in acetonitrile). Separation was completed by the following gradient: 0 min, 5% B; 2 min, 5% B; 4 min, 25% B; 8 min, 50% B; 10 min, 80% B; 14 min, 100% B; 15 min, 100% B; 15.1 min, 5% B; 16 min, 5% B. The injection volume was at 2μL each time. We injected QC samples every ten samples throughout the analytical run. The detailed MS conditions was showed in Supplementary Table 4.6. Raw data preprocessing and metabolite identification. The acquired raw data were preprocessed and analyzed by Progenesis QI software v2.3 (Nonlinear Dynamics, Newcastle, UK) through baseline filtering, peak identification, peak integration, retention time correction, peak alignment, and normalization. In addition, metabolites were annotated on the basis ofprecise mass, secondary fragments, and isotope distribution by mapping on the Human Metabolome Database (HMDB), the Lipid Metabolites and

Pathways Strategy (LIPID MAPS) v2.3, Metabolite Link (METLIN), and a self-built library. The extracted data included mass-to-charge ratio (m/z), peak RT andintensities, and the RT-m/z pair was linked as the label for each ion. Ion peaks with a relative standard deviation >40% were deleted. The ion peaks with >50% missing values were also deleted, and missing values ≤50% were displacedby half of the minimal level. The quality of compound annotation was ensured by scoring. If the score was less than 36 (a total score of 60), the identification results were considered incorrect and would be deleted. In the end, data from both positive and negative ion modes were combined to form a matrix containing all the signals extracted from the raw data.

4.7 Statistical analyses

Baseline characteristics weredemonstrated as median (interquartile range) or mean \pm standard deviation for continuous variables and frequency (percentage) for categorical variables, which werecompared between groups by Student's t-test or Mann-Whitney U test for continuous variables and Pearson chi-square test or Fisher exact probability method for categorical variables.SAS software, version 9.4 (SAS Institute, Cary, NC), was utilized, with two-sided P< 0.05 considered as statistically significant. We further categorized the NAFLD patients into two groups: LN (BMI <23 kg/m2) and ON (BMI≥23 kg/m2) considering BMI ≥ 23.0 kg/m2 is the cut-off recommended for the diagnosis of overweight in Asian adults[20]. Three subjects without data on BMI in 2016-2017 were excluded, and 20 LN and 49 ON were finally included. Orthogonal partial least squares discriminant analysis (OPLS-DA) after Pareto scaling was carried out to visualize the metabolite landscapeof different groups, including NAFLD vs. non-NAFLD, LN vs. non-NAFLD, ON vs. non-NAFLD, and LN vs. ON. The response permutation testing (permutation number=200) was operated to validate the robustness of the OPLS-DA model. Variable importance in projection (VIP) ranked the relative contribution of each metabolite to the OPLS-DA model. Candidate metabolites were selected referred to VIP values of the OPLS-DA model (VIP>1) together with the P value of analysis of covariance adjusted for age and sex on the logtransformed normalized peak areas (P<0.05). Differential metabolites were enriched by Homo sapiens (Kyoto Encyclopedia of Genes and Genomes) library in MetaboAnalyst 5.0 to identify significantly altered metabolic pathways. We visualized the selected metabolites in heat maps to show differences between groups using MetaboAnalyst 5.0. Logistic regressions were also used to estimate odds ratios (ORs) and 95% confidence intervals (95% CIs) to further validate the relationships between candidate metabolites (divided into two groups using the median of relative abundance as a cut-off point) and diseases in NAFLD vs. non-NAFLD,LN vs. non-NAFLD, ON vs. non-NAFLD, and LN vs. ON. A panel of significant candidate metabolites selected by logistic regression in each pairwise comparison was used to discriminate two states,and the area under the curve (AUC) was calculated.

5. Results

5.1 Baseline characteristics of NAFLD cases and non-NAFLD controls

The baseline characteristics of the NAFLD patientsand healthy controls were depicted in Table 1. The NAFLD cases tended to have higher blood concentrations of TG, LDL-C, TG/HDL-C ratio, TyG index, and lower blood concentrations of HDL-C (P<0.05) than healthy controls. Noapparent differences were observed between two groups in age, sex, BMI, waist circumference, SBP, DBP, TC, FBG, c-reactive protein, and alanine transaminase (P>0.05).

Supplementary Table 1. Mass spectrometry conditions

5.2 Metabolite comparison NAFLD vs.non-NAFLD

The metabolite landscapes of the NAFLD cases and non-NAFLD controls were further deciphered from the 6132 annotated metabolites(3614 and 2518 detected from positive and negative ion mode, respectively). The QC samples were tightly clusteredin the score plot of unsupervised principal component analysis (Supplementary Figure 1), implicating the LC-MS system's good repeatability, reliability, and stability. The 400-times response permutation testing demonstrated R2Y and Q2Y values of 0.165 and -0.187, respectively (Supplementary Figure 2). The grey regression line of Q2 value with Y-axis intersect below zero validated the OPLS-DA model.

Supplementary Figure 1. Principal component analysis of quality control samples to assess the reliability of the system. Abbreviations: QC, quality control.

Supplementary Figure 2. Response permutation testing (400 times) of the prediction model by orthogonal partial least-squares-discriminant in NAFLD vs. non-NAFLD.

The Q2 value represents the predictability of the model. The R2Y value represents the goodness of fit of the model. The grey regression line of Q2 value with Y-axis intersect below zero suggests the validity of the orthogonal partial least-squares-discriminant analysis model. Abbreviations: NAFLD, non-alcoholic fatty liver disease.

Overall, 77 differential metabolites were screened out according to the rule (VIP>1 and P<0.05), and among them, 48 are lipids and lipid-like molecules. Glycerophospholipids covering PC (n=11), LPC (n=3), phosphatidylethanolamine (PE) (n=5), phosphatidylserine (PS) (n=2), phosphatidylinositol (PI) (n=2), phosphatidic acid (PA) (n=1), and lysophosphatidic acid (LPA)(n=1) accounted for 52.1% (25/48) of the total lipids and lipid-like molecules found (Supplementary Table 2-1, Figure 2).Pathway analysis showed a significantly enriched pathway involvingglycerophospholipid metabolism (FDR P=0.018; pathway impact 0.252; Figure 1A).We further validated the associations between differential metabolites in the glycerophospholipid pathway and NAFLD. Specific PCs $(n=6)$ and PE $(n=1)$ were found to be associated with NAFLD (Supplementary Table 3). A panel consisting of the above seven metabolites reached an AUC of 0.73 in discriminating NAFLD from non-NAFLD (Table 2).

5.3 Metabolite comparison LN vs. non-NAFLD and ON vs. non-NAFLD

To further identify candidate metabolites with potential to make a distinction between subtypes of NAFLD (LN and ON), two subcomparisons were performed (LN vs. non-NAFLD and ON vs. non-NAFLD). Supplementary Table 1 showed the characteristics of subgroups. The TG, LDL-C, HDL-C, TG/HDL-C ratio, and TyG index of the LN group were between those of the ON and non-NAFLD group. In comparison between LN and non-NAFLD, 70 differential metabolites were identified, with 58 of them belonging to the categoryof lipids and lipid-like molecules (Supplementary Table 2-2).

Among the 58 lipids and lipid-like molecules, 40 were glycerophospholipids. Furthermore, pathway analysis showed a significantly enriched pathway involving glycerophospholipid metabolism (FDR P=0.032; pathway impact 0.138) (Figure 1B).Choline, PC (n=21), LPC (n=8), PE (n=6), lysophosphatidylethanolamine (LPE) (n=1), PS (n=1),and phosphatidylinositol (PI) (n=2)were identified in the glycerophospholipid metabolism pathway (Figure 2).Logistic regression revealed choline andspecific PCs (n=9), LPCs (n=2), PE (n=1), PIs (n=2), and PS (n=1) to be associated with LN. A panel of the above 16 metabolites achieved an AUC of 0.87 in discriminating LN from non-NAFLD (Table 2).

Supplementary Table 2-1. Differential metabolites in NAFLD vs. non-NAFLD.

ID	Retention time (min)	m/z	Error (ppm)	Scan mode	Postulatedidentity	Super class	Class	Sub class	Molecu- le comp osition
0.73 ¹¹⁵ . 0635n	0.733067	116. 0707	1.217482	Pos	L-Proline	Organic acids and derivatives	Carboxylic acids and derivatives	Aminoacids, peptides, and analogues	C5H 9NO ₂
12.35_549. 3788n	12.35067	550. 3861	-1.15616	Pos	LysoPC(20:1 (11Z)	Lipids and lipid -like molecules	Glycerophos- pholipids	Glyceropho sphocholines	C28H5 6NO7P
13.30_551. 3953n	13.2991	552. 4026	0.35191	Pos	LysoPC(20:0/0:0)	Lipids and lipid -like molecules	Glycerophos- pholipids	Glycerophos phocholines	C28H5 8NO7P
12.00 297. 2419m/z	12.00175	297. 2419	-1.68835	Pos	12R-hydroxy-9Z,15Z -octadecadienoic acid	Unclassified	Unclassified	Unclassified	C18H3 203
14.29_780. 5505m/z	14.28892	780. 5505	-1.16765	Pos	PC(16:0/18:2) (11Z, 13Z))	Lipids and lipid -like molecules	Glycerophos -pholipids	Glycerophos phocholines	C42H8 0NO8P

In ON vs. non-NAFLD, 73 differential metabolites were obtained, and 40 of them were categorized into the classification of lipids and lipidlike molecules (Supplementary Table 2-3). Of the 40 lipids and lipidlike molecules, 16 were glycerophospholipids. Glycerophospholipid metabolism (FDR P=0.004; pathway impact 0.339) was significantly altered (Figure 1C). PC (n=5), PE (n=6), LPE (n=1), PS (n=1), PA (n=1),and LPA (n=1) were identified in the glycerophospholipid metabolism pathway (Figure 2).Specific PCs (n=2), PE (n=1), and PS (n=1) showed associations with ON. A panel of the above four metabolites had an AUC of 0.70 in discriminating ON from non-NAFLD (Table 2).

5.4 Metabolite comparison LN vs. ON

The same analyses were performed for LN and ON subjects, where

27 differential metabolites were identified, and 12belonged to lipids and lipid-like molecules (Supplementary Table 2-4). Six of the 12 lipids and lipid-like molecules were glycerophospholipids. Pathway analysis showed that a significantly enriched pathway involved glycerophospholipid metabolism (FDR P=0.004; pathway impact 0.183, Figure 1D).In the glycerophospholipid metabolism pathway, choline and choline-related lipids includingPC(20:3(5Z,8Z,11Z)/0:0), PC(22:4(7Z,10Z,13Z,16Z)/0:0), LPC(20:3(8Z,11Z,14Z)), LPE(22:5 (7Z,10Z,13Z,16Z,19Z)/0:0), LPA(18:2(9Z,12Z)/0:0) were identified (Figure 2). Choline was significantly higher, while other choline-related lipids weresignificantly lower in LN compared to ON (Figure 3).The associations of choline and specific PC, LPC, LPE, and LPA above with LN were further evaluated in LN vs. ON. Patients with higher levels

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of PC and LPC had lower odds of LN. At the same time, choline was positively correlated with LN (Table 2).A panel containing choline, PC, and LPC had an AUC of 0.73 in distinguishing LN from ON. To elucidate the clinical relevance of the selected metabolites, including choline, PC, and LPC, we analyzed the relationships between these metabolites and VLDL (data not shown). A positive relationship was found between LPC(20:3(8Z,11Z,14Z)) and VLDL (OR=3.13, 95% CI:1.20-8.19).

Figure 2 (B) Lean NAFLD vs.non-NAFLD

6. Discussion

In the current cohort-based case-control pilot study conducted in China, we discovered that the glycerophospholipid metabolism pathway was altered in NAFLD vs. non-NAFLD, LN vs. non-NAFLD, and ON vs. non-NAFLD. Specific glycerophospholipids may have the potential to distinguish NAFLD and its subtypes from non-NAFLD. The glycerophospholipid metabolism pathway was also reprogrammed in LN vs. ON, and the differential metabolites included choline and specific PC, LPC, LPE, and LPA. The relative concentration of choline was obviously higher in LN, while that of the other differential metabolites was considerably lower. Choline was positively associated with LN, while specific PC and LPC were negatively associated with LN. The disruption of PC synthesis may be responsible for the development of LN. A series of metabolites and key metabolic pathways have been discovered to be influenced by NAFLD[8, 9], including phospholipid found in this study. Glycerophospholipids and PC, for example, are the most ubiquitous and abundant phospholipids in the composition of biological membranes[21-23]. The disorder of PC may lead to oxidative stress, membrane impairment, and subsequent hepatocyte injury associated with NAFLD[21-23]. As the hub of the lipid network, the metabolic reprogramming of PC can also result in the imbalance of hepatic lipid export related to NAFLD[21-23]. Although the biological function of PC is closely related to NAFLD, very few population-based studieshave reported specific PC to be associated with NAFLD[8, 9]. The study by Oresic et al. showed that a triplet of TG(16:0/18:0/18:1), PC(18:1/22:6), and PC(O-24:1/20:4) could predict NAFLD with an AUC of 0.79[24]. Our study found that a panel of six specific PCs and one PE was associated with NAFLD, with an AUC of 0.73. Similarly, diagnostic

Supplementary Table 2-2. Differential metabolites in lean NAFLD vs. non-NAFLD.

panels containing specific glycerophospholipids at the center of PC were revealed for both LN and ON, further implicating the importance of PC and its related metabolites along the pathway in the pathogenesis of NAFLD and the diagnostic potential of specific glycerophospholipids.

Apart fromthe overall NAFLD, the metabolism of glycerophospholipid was also reprogrammed when comparing two NAFLD subtypes, LN vs. ON. The differential metabolites included choline and specific PC, LPC, LPE, and LPA. LN had significantly increased choline and decreased specific PC, LPC, LPE, and LPA than ON, indicating that the production of PC from various routes starting from choline, PE, and PA was reduced (SupplementaryFigure 3). Accordingly, we observed that choline was positively associated with LN while PC and its derivative LPC were negatively associated with LN, suggesting that choline, PC, and LPC might be a hallmark of LN. Choline is an essential nutrient and may synthesize PC through multiple routes[21-23].The significantly higher relative abundance of choline but lower PC in LN than ON may be due to decreased bioavailability of serum choline in LN[25]. Decreased PC may further result in NAFLD through membrane instability, oxidative stress, endoplasmic reticulum stress, ordecreased VLDL assembly and export[21-23]. An experimental study[26] showed that betaine homocysteine methyltransferase gene knockout mice and PE N-methyltransferase gene knockout mice had decreased liver choline, increased energy consumption, and less weight gain compared with wildtype mice. In other words,decreased bioavailability of serum choline in LN may subsequently increase energy consumption and contribute to obesity resistance in patients with LN. Population-based genetic findings also implicated the indispensable role of PC-synthesizing enzyme in the occurrence of LN [27]. The aforementioned hypothesis is also supported

by our results, i.e., decreased LPC is related to decreased VLDL secretion and increase the odds of developing LN, and a decreased trend of VLDL in LN compared to ON was found though not statistically significant. Based on the existing evidence, we considered that choline and cholinerelated metabolites along the pathway of PC production might mediate the pathogenesis of LN.

Figure 3 (C) Overweight/obese NAFLD vs.non-NAFLD

metabolites with only relative abundance obtained.

Supplementary Figure 3. Description of the glycerophospholipid metabolism pathway-related metabolites changes in lean NAFLD vs. overweight/obese NAFLD.

Lean NAFLD had significantly increased choline and decreased specific PC, LPC, LPE, and LPA than overweight/obese NAFLD. The significantly higher concentration of choline but lower PC in lean NAFLD than in overweight/obese NAFLD may be due to the decreased bioavailability of serum choline in lean NAFLD. Decreased PC may further result in decreased VLDL and the development of liver damage.

Abbreviations: NAFLD, non-alcoholic fatty liver disease; PC, phosphatidylcholine; LysoPC, lysophosphatidylcholine; PE, phosphatidylethanolamine; LysoPE, lysophosphatidylethanolamine; PA, phosphatidic acid; LPA, lysophosphatidic acid; VLDL, very-low-density lipoprotein.

Further targeted metabolomics detection is needed to accurately quantify the candidate metabolites for diagnostic applications and for the study reproducibilityin general [8]. Third, the inaccuracy of ultrasound in fatty liver diagnosis may result in non-differential misclassification and underestimation of the actual effect size.Despite possible sample overlap and model overfitting, significantly differential metabolites do exist between groups.Last but not least, the underlying mechanisms of the candidate metabolites driving NAFLD, LN, and ON awaits further investigation. We assume that under the obesogenic stress, compared with ON patients, LN patients may have different metabolic adaptations probably arising from intra-individual variations in gene or microbiome[33], which leads to the reprogramming of choline and glycerophospholipid metabolism, and this metabolic adaptation may possibly influence some unknown factors for example, membrane stability or protein[34] and finally results in the characteristics and long-term outcomes of LN(Supplementary Figure 4).

We observed that LN subjects featured higher serum choline, lower specific PC, lower blood lipids such as TG, VLDL, and lower insulin resistance indicators than ON. Alonso et al.[28] discovered two NAFLD subtypes in humans: The m-subtype of NAFLD showed decreased PC synthesis and impaired VLDL secretion, which was similar to the LN phenotype in our study, while the non-M-subtype had a phenotype of increased liver lipid de novo synthesis, normal VLDL secretion, and increased serum TG and TC levels, in line with ON phenotype. Also, the feature of LN in our study seemed to be consistent with the genetic subtype of NAFLD [29], which is characterized by impaired hepatic mitochondrial function, no insulin resistance and decreased VLDL secretion. This could be supported by the fact that LN subjects may have a higher frequency of PNPLA3 rs738409 GG genotype [30, 31] and TM6SF2 rs58542926 T allele [16, 32] than ON. In contrast, the metabolic component of NAFLD [29], corresponding to ON, is characterized by insulin resistance, hepatic oversupply of substrates, and increased VLDL secretion. Therefore, these findings may indicate that LN is generated by decreased PC synthesis and hepatic VLDL secretion or impaired hepatic mitochondrial function, whereas liver lipid de novo synthesis or insulin resistance may play a vital part in the onset of ON. We need further study to determine whether VLDL secretion is reduced in LN and, in contrast, hepatic lipid de novo synthesis is upregulated in ON [Supplementary Figure 3]. Our study still has several limitations. First, the current sample size is relatively small because of the pilot study's exploratory nature, which may lead tothe wide CIsof selected metabolite, but still goodmodeldiscriminationis achieved. Second, untargeted metabolomics was used to explore the candidate

ID Retention time (min) m/z Error (ppm) Scan mode Postulated identity Super class Class Sub class Molecule composition 12.35_549 .3788n 12.35067 550.3861 -1.15616 pos LysoPC(20:1(11Z)) Lipids and lipid-like molecules Glycerophos pholipids Glycerophospho cholines C28H56NO7P 11.96_523 .3631n 11.95655 546.3523 -1.37431 pos PC(0:0/18:0) Lipids and lipid-like molecules Glycerophos pholipids Glycerophospho cholines C26H54NO7P 8.29_465 .3084n 8.285067 466.3157 -1.2948 pos Glycocholic acid Lipids and lipid-like molecules Steroids and steroid deriva tives Bile acids, alco hols and deriva tives C26H43NO6 11.51_478 .2942m/z 11.50975 478.2942 0.643562 neg PE(18:1(9Z)/0:0) Lipids and lipid-like molecules Glycerophos pholipids Glycero phosphoethanol amines C23H46NO7P 13.30_551 .3953n 13.2991 552.4026 0.35191 pos LysoPC(20:0/0:0) Lipids and lipid-like molecules Glycerophos pholipids Glycerophospho cholines C28H58NO7P 11.47_521 .3475n 11.46953 $\left| \begin{array}{c} 522.3548 \\ -1.15072 \end{array} \right|$ pos $\left| \begin{array}{c} P\text{C}(18:1(11\text{Z})/0:0) \end{array} \right|$ Lipids and lipid-like molecules Glycerophos pholipids Glycerophospho cholines C26H52NO7P 11.26_546 .3544m/z 11.26103 | 546.3544 | -1.81846 | pos PC(20:3(5Z,8Z,11Z) $(0:0)$ Lipids and lipid-like molecules Glycerophos pholipids Glycerophospho cholines C28H52NO7P 8.94_318 .2997m/z 8.9353 $\begin{array}{|l|c|c|c|c|}\n\end{array}$ 318.2997 -2.06001 pos 17-hydroxy stearic acid $\begin{array}{|l|c|c|c|}\n\end{array}$ Lipids and lipid-like The results Fatty Acyls Cotadecanoids C18H36O3 10.96_519 .3315n 10.9624 520.3392 -1.88609 pos PC(18:2(9Z,12Z)/0:0) Lipids and lipid-like molecules Glycerophospholipids Glycerophosphocholines C26H50NO7P 10.85_481 .3163n 10.84537 482.3235 -1.17968 pos PC(15:0/0:0) Lipids and lipid-like molecules Glycerophospholipids Glycerophosphocholines C23H48NO7P 11.08_507 .3318n 11.07903 $\left| \begin{array}{c} 508.3391 \end{array} \right|$ -1.40844 $\left| \begin{array}{c} 908 \end{array} \right|$ PC(17:1(10Z)/0:0) $\left| \begin{array}{c} \text{Lipids and lipid-like} \end{array} \right|$ molecules Glycerophospholipids Glycerophosphocholines C25H50NO7P 11.16_569 .3474n 11.15525 | 570.3547 | -1.24228 | pos LysoPC(22:5(4Z,7Z, 10Z,13Z,16Z)) Lipids and lipid-like molecules Glycerophospholipids Glycerophosphocholines C30H52NO7P 11.01_612 .3311m/z 11.00758 612.3311 0.642615 neg LysoPC(22:6(4Z,7Z, 10Z13Z,16Z,19Z)) Lipids and lipid-like molecules Glycerophospholipids Glycerophosphocholines C30H50NO7P 10.96_567 .3317n 10.9624 568.339 -1.37532 pos PC(22:6(4Z,7Z,10Z, 13Z,16Z,19Z)/0:0) Lipids and lipid-like molecules Glycerophospholipids Glycerophosphocholines C30H50NO7P 10.99_543 .3318n 10.99095 544.339 -1.3519 pos LysoPC(20:4(5Z,8Z, 11Z,14Z)) Lipids and lipid-like molecules Glycerophospholipids Glycerophosphocholines C28H50NO7P 11.69_547 .3630n 11.69448 | 548.3703 | -1.35738 | pos LysoPC(20:2(11Z ,14Z)) Lipids and lipid-like molecules Glycerophos pholipids Glycerophosphocholines C28H54NO7P 11.02_564 .3309m/z 11.02308 564.3309 0.41043 neg 2-linoleoyl-sn-glycero-3-phosphocholine Lipids and lipid-like molecules Glycerophos pholipids Glycerophosphocholines C26H50NO7P 11.32_590 .3466m/z 11.32428 590.3466 0.553556 neg LysoPC(20:3(8Z,11Z ,14Z)) Lipids and lipid-like molecules Glycerophos pholipids Glycerophosphocholines C28H52NO7P 1.36_132 .1018m/z 1.3554 132.1018 -0.59934 pos L-Isoleucine Organic acids and derivatives Carboxylic ac ids and deriva Amino acids, peptides, and an-C6H13NO2

Supplementary Table 2-3. Differential metabolites in overweight/obese NAFLD vs. non-NAFLD.

10.77_400 .3414m/z

11.04_588 .3309m/z

11.03847 588.3309 0.438121 neg

Lipids and lipid-like

10.7676 400.3414 -1.78694 pos Palmitoylcarnitine Benzenoids Phenols Benzenediols C23H45NO4

molecules

LysoPC(20:4(8Z,11Z,

14Z,17Z))

tives

Glycerophos pholipids

alogues

Glycerophospho cholines

C28H50NO7P

Figure 4 (D) Lean NAFLD vs.Overweight/obese NAFLD

The bubble plot indicated alterations in the primary metabolic pathways,with impact and P-value attributed to the accumulation of differential metabolites along each enriched pathway. The bubble

In conclusion,alterations in the glycerophospholipid metabolism pathway may be principal in NAFLD and its subtypes.Specific glycerophospholipids may have the potential to distinguish NAFLD and its subtypes from non-NAFLD. The disruption of PC synthesis may be responsible for the development of LN.Our results have translational implications in dietary recommendations and interventions for lean NAFLD patients, who would probably benefit from more PC intake and supplementation with diet. Further targeted metabolomics studies with larger sample size and in-vitro functional validation are needed to investigate the effect and mechanisms of choline and choline-related metabolites on NAFLD and its subtypes, especially on LN, and develop potential clinically relevant targets for early intervention and treatment.

Figure 1.Pathway analyses of thedifferential metabolitesin various comparisons.

Supplementary Table 2-4. Differential metabolites in lean NAFLD vs. overweight/obese NAFLD.

7. Ethics approval and consent to participate

We obtained approval from the Ethics Committee of the Kailuan General Hospital and the Institute of Basic Medical Sciences Chinese Academy of Medical Sciences. In addition, we got written informed consent from all participants. Availability of data and materials The datasets used during the current study are available from the corresponding author on reasonable request. Competing interests The authors declare that they have no competing interests.

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Authors' contributions

LW and SLW designed the study. SHC collected the data. SQH processed the data. YQL and YL performed the statistical analysis. SQH and YHW interpreted the data. YQL and YL drafted the manuscript. LW and SLW revised the manuscript critically. All authors read and approved the final manuscript.

9. Abbreviations:

NAFLD, non-alcoholic fatty liver disease; BMI,body mass index; LN, lean NAFLD; ON, overweight or obese NAFLD; TG, triglyceride; TC, total cholesterol; LDL-C, low-density lipoprotein cholesterol; HDL-C, high-density lipoprotein cholesterol; FBG, fasting blood glucose; VLDL, very-low-density lipoprotein;TyG Index, triglyceride glucose index; TG/ HDL-C ratio, triglyceride to high-density lipoprotein cholesterol ratio; LC-MS, liquid chromatography-tandem mass spectrometry; QC, quality control; OPLS-DA, orthogonal partial least squares discriminant analysis; VIP, variable importance in projection; OR, odds ratio; 95%CI, 95% confidence interval; AUC, area under the curve; PC, phosphatidylcholine; LPC, lysophosphatidylcholine; PE, phosphatidylethanolamine; LPE, lysophosphatidylethanolamine; PA, phosphatidic acid; LPA, lysophosphatidic acid; PS, phosphatidylserine; PI, phosphatidylinositol.

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