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Plasma and Liver Metabolomic Profiling in Hispanic and Caucasian Subjects with  
Nonalcoholic Fatty Liver Disease

By

TAGREED ABDULHALEM MAZI  
DISSERTATION

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in the

OFFICE OF GRADUATE STUDIES

of the

UNIVERSITY OF CALIFORNIA

DAVIS

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## Abstract

**Background/Objective:** Nonalcoholic fatty liver disease affects 30% of the world adult population. It comprises a spectrum of liver histopathological presentation that varies from hepatocellular lipid accumulation, or nonalcoholic fatty liver (NAFL), to nonalcoholic steatohepatitis (NASH). Mechanism(s) of NAFLD onset and progression are modulated by a multilayered interaction between genetics, environmental factors, and comorbidities. In the US., the Hispanic population presents with higher rate of NAFLD, and more advanced histological scores compared to other ethnicities. However, the underlying metabolic drivers of these observations are not clear. Previous metabolomic studies revealed that NAFLD is associated with several metabolic dysregulations in lipid, carbohydrate, and amino acid metabolism. Also, alterations in polyunsaturated fatty acids (PUFA) and downstream oxidized lipids as oxylipins (OXLs) and endocannabinoids (eCBs) are reported to distinguish different stages of NAFLD. However, is not clear if ethnicity-related metabolomic differences exist in NAFLD. The identification of ethnicity-related metabolomic differences will expand current knowledge with on mechanism(s) of NAFLD onset and progression. It can also identify unshared mechanism(s) that may explain the observed ethnicity-related disparity in NAFLD rate and severity. The objective of this “proof of principle” analyses is to explore metabolomic profiles of a group of Hispanic (HIS) and Caucasian (CAU) subjects with NAFLD undergoing bariatric surgery **Methods:** We compared metabolomic profiles in a group of obesity NAFL-HIS and NAFL-CAU subjects to ethnicity-matched lean and healthy control subjects. We also compared the profiles of subjects with NASH to NASH-free (0-NASH) subjects. For this we profiled plasma and liver samples using untargeted, semi-quantitative metabolomic approaches for metabolites related to primary metabolism using gas chromatography/time-of-flight mass spectrometry (GC-TOF MS); complex lipids using charged surface hybrid liquid chromatography/quadrupole time of flight mass spectrometry (CSH-QTOF MS/MS); choline and related metabolites using hydrophilic interaction liquid chromatography/quadrupole time of flight mass spectrometer (HILIC-QTOF MS/MS). We also performed a targeted and quantitative lipidomic analysis to profile for plasma fatty acids and related downstream lipid mediators using ultra-high-performance liquid chromatography-electrospray ionization-

tandem mass spectrometry (UPLC-ESI-MS/MS). **Results:** Findings from current analyses reveal ethnicity-related metabolic perturbation, independent of obesity. Specifically, lean, and healthy HIS subjects showed higher plasma profiles of triglycerides, acylcarnitines, free fatty acids and downstream lipid mediators. Our finding also shows that in NAFL there are ethnicity-related differences in plasma profiles of fatty acids and acylcarnitines. In specific, NAFL-CAU was characterized by higher arachidonic acid, while NAFL-HIS showed lower n-3 PUFA. With the progression to NASH, comparison within ethnicity groups indicated that the hepatic lipidomic profile in NASH-HIS was characterized higher levels of free fatty acids and lipotoxic lipids, suggesting lipotoxicity is involved in the progression of NASH. We also observed a higher hepatic triglyceride with signs of impaired mitochondrial  $\beta$ -oxidation. Remarkably, the plasma OXLs and eCBs profiles discriminated ethnicities with NASH, independent of histological severity. In specific, NASH-HIS was characterized with lower arachidonic acid derived OXLs, and findings suggest a downregulated lipoxygenase(s) and upregulated soluble epoxide hydrolase(s) activities. **Conclusion:** The analyses presented in this dissertation highlights the existence of ethnicity-related metabolomic variations in NAFLD that could potentially modulate disease risk and severity in HIS. It also indicates that ethnicity-specific lipidomic signature can distinguish NASH, which needs to be verified in larger studies.

## **Chapter 1**

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### ***Literature Review***



## **1. Definitions**

Described first in 1980, [1], nonalcoholic fatty liver disease (NAFLD) is a range of abnormal histopathological presentations that include hepatocellular triglycerides (TGs) accumulation, also known as steatosis or nonalcoholic fatty liver (NAFL), necrosis and inflammation, or nonalcoholic steatohepatitis (NASH), which can advance to cirrhosis and hepatocellular cancer [2,3]. NAFL is defined by imaging or histology as the presence of hepatocellular lipid droplets, accounting for >5% the total liver weight; absence of hepatocellular injury, defined by hepatocyte ballooning, mild inflammation with or without fibrosis; after excluding secondary causes of hepatic fat accumulation. Other causes of hepatocellular fat accumulation include excessive alcohol consumption, (defined as the intake of >14 drinks/week in women or >21 drinks/week in men, or a daily intake of >10 g/day of alcohol); the use of steatogenic medication (e.g., corticosteroids, mipomersen, lomitapide, methotrexate, amiodarone); starvation; total parenteral nutrition; other coexisting liver disease etiologies, such as viral or autoimmune hepatitis, hemochromatosis, and Wilson disease [3]. On the other side, NASH is defined as the presence of NAFL in combination with histological evidence of inflammation and hepatocytes injury with or without fibrosis [3].

## **2. Epidemiology**

According to a recent global meta-analysis that included 8.5 million subjects from 22 countries, the worldwide prevalence of NAFLD was estimated to be 25% of the general population, and this prevalence is expected to rise parallel to the metabolic syndrome (MetS) pandemic [4]. NAFLD is highly prevalent in the Middle East 32% and South America 31%, followed by the U.S. 24%, and with the rate lowest in Africa 14% [4]. When investigating NAFLD prevalence among subjects with multiple comorbidities, as obesity and type 2 diabetes mellitus (T2DM), the prevalence of NAFLD was 50% in this high-risk group compared to 16% in the general population, independent of ethnicity [5]. The prevalence of NASH in the general population is estimated to be between 2 to 6%. In morbidly obese subjects, this rate increases to 59%, whereas it is lower, being 7 to 30%, in low-risk subjects who undergoing liver biopsy without clinical suspicion [4].

### **3. Risk factors**

#### **3.1. *The metabolic syndrome***

The MetS is a cluster of metabolic derangements that include hypertension (HTN); low level of high-density lipoprotein-cholesterol (HDL-C) or dyslipidemia; high level of TGs or hypertriglyceridemia; elevated glucose level or T2DM; and visceral adiposity [6]. Clinically, MetS is defined as the existence of three or more of the for mentioned abnormal metabolic manifestations [6]. NAFLD is strongly associated with all components of MetS, including T2DM, dyslipidemia, TGs, and obesity [7,8]. MetS affects about 43% of subjects with NAFLD and 71% of subjects with NASH [4], with about 90% of NAFLD subjects presenting with at least one component of MetS [9-11]. Owing to this strong correlation, it is argued that NAFLD is the hepatic presentation of the MetS. However, evidence indicate that this link is bidirectional, as components of MetS can predict NAFLD onset and progression [12-14], and NAFLD may precede the development of MetS [15-17].

There are data suggesting that the effect of MetS on the risk of NAFLD may be influenced by ethnicity. In a study based on data from the U.S. Third National Health and Nutrition Examination Survey (1988–1994) and employing confirmatory factor analysis to challenge the notion that NAFLD is the hepatic continuum of MetS, a basic model constructed with components of MetS exhibited strong goodness-of-fit, whereas the addition NAFL decreased the model fit statistics [18]. When analysis was repeated by ethnicity, the addition of NAFL resulted in higher model fit for Hispanics and non-Hispanic Blacks compared to Whites, indicating that the association between MetS and NAFLD may be influenced by ethnicity [18]. In support of this evidence, findings from the NASH-Clinical Research Network (NASH-CRN) indicated that the effect of IR on the risk of NASH was modified by ethnicity, where IR was a strong predictor of NASH in non-Hispanics whites, but not in Hispanics [19].

#### **3.2. *Type 2 diabetes mellitus and insulin resistance***

In patients with T2DM, the estimated worldwide prevalence of NAFLD and NASH was 55.5% and 37.3%, respectively [20]. It is estimated that about 23% of NAFLD and 44% of NASH subjects present with T2DM [4]. Compared to non-diabetic, subjects with T2DM are at higher risk for the

progression to NASH [21], fibrosis, and hepatocellular carcinoma [22]. This strong link between NAFLD and T2DM was found to be reciprocal, as results from a recent meta-analysis including studies of nondiabetic subjects show that NAFLD diagnosis increases the risk for T2DM [23].

Insulin resistance (IR), a condition characterized by impaired glucose disposal in the periphery, including muscle and adipose tissues [24,25], is thought to be a key player in the pathology of NAFLD [26,27]. In subjects with NAFL and NASH compared to healthy control and under euglycemic-clamp test, the rate of glucose disposal in response to glucose infusion was decreased and the ability to suppress adipose tissue lipolysis in response to insulin was impaired, indicating a state of peripheral IR that was evident at the level of skeletal muscle and adipose tissues [28]. Hepatic IR, or the inability of insulin to suppress hepatic glucose production in fasted state, with subsequent hyperglycemia and hyperinsulinemia [29], was also reported in NAFLD with T2DM [30] and in non-diabetic subjects [31]. The metabolic effect of IR state in the context of NAFLD is discussed in section 6.

### **3.3. Obesity**

It was estimated that about 51% of NAFLD subjects and 82% of NASH subjects are obese [4]. Moreover, obesity was found to increase the risk of NAFLD by 3-fold compared to none-obese subjects [32-34]. In the U.S., NAFLD was estimated to affect 5 to 10% of non-obese subjects [35], and this rate increases to 95% in morbidly obese subjects [36]. The distribution of adiposity was found more determinant to NAFLD risk than amount of adiposity. This was demonstrated with a strong linear association between visceral adiposity and NAFLD [37-40], which could be explained by IR, which is associated with visceral adiposity [24,25]. The implications of obesity in the development and progression of NAFLD are discussed in section 6.

### **3.4. Dyslipidemia**

Dyslipidemia affects about 43% of subjects with NAFLD and 71% of subjects with NASH [4]. In NAFLD, dyslipidemia mainly manifests as elevated TGs, elevated low-density-lipoprotein cholesterol (LDL-C) count or particle size, and decreased HDL-C [41,42]. The implications of dyslipidemia in the development and progression of NAFLD are discussed in section 6.

### **3.5. Hypertension**

NAFLD is strongly associated with HTN [43,44], and arterial stiffness was found to correlate with NAFLD diagnosis, severity [45], and progression to fibrosis [46]. According to a global analysis, HTN was prevalent among 39% of subjects with NAFLD and 68% of subjects with NASH [4]. This link between NAFLD and HTN was shown to be bidirectional, as HTN increased the risk of NAFLD onset and progression, NAFLD was also found to be a strong predictor for HTN [47].

### **3.6. Age and sex**

NAFLD diagnosis occurs more frequently after the fourth decade of life [20]. Advanced age was found to be a predictor for NAFLD development and progression to NASH [48]. This may be attributed to the fact that most NAFLD-related risk factors increase with age, as MetS, T2DM, and HTN [49,50]. The prevalence of NAFLD was reported to be higher in males compared to females [51-53]. In female, NAFLD prevalence increases significantly after the age of 50, and was found higher in postmenopausal women, compared to premenopausal, suggesting a protective role of female hormones [54-56]. The risk of NAFLD progression to fibrosis was higher in males compared to females [57,58]. Up to date, the mechanisms explaining this sex-related differences in NAFLD prevalence are not clear.

### **3.7. Genetics**

Genome-wide association studies and exome-wide association studies revealed an association of multiple genes variants with risk of NAFLD development and progression. The identified genes were involved in the regulation of lipid and carbohydrate metabolism, mitochondrial function, insulin signaling, oxidative stress, inflammation, immune response, and fibrogenesis [59-61].

The rs738409 [C] > [G] variant of the patatin-like phospholipase domain-containing gene (*PNPLA3*), with the substitution of isoleucine to methionine at position 148 was associated with the full spectrum of NAFLD [62-68]. This association was also established in studies that included multiple ethnicities cohorts [68-73] and found to be independent of age, sex, T2DM [67], total or visceral adiposity [62,74], IR and dyslipidemia [75]. The potential mechanism by which the *PNPLA3* variant is involved in the pathogenesis of NAFLD is discussed in section 6.

The rs58542926 [C] > [T] variant of the transmembrane 6 superfamily member 2 (*TM6SF2*), with glutamate to lysine substitution at residue 167 was associated with an increased hepatic TGs content [76-78] and a higher risk of NASH [79]. This gene variant was also associated with a marked reduction in apoB-100, very-low density lipoprotein (VLDL) particle count and size, as well as in the VLDL and LDL TGs and cholesterol content [77,78,80]. The *TM6SF2* gene encodes a trans-membrane protein that regulates the lipidation and secretion of VLDL and cholesterol synthesis [76,78,80,81]. The rs58542926 variant of *TM6SF2* results in a loss-of-function of the enzymatic activity with consequent NAFL due to reduced lipidation and/or secretion of VLDL [59].

The single nucleotide polymorphism in glucokinase regulator (*GCKR*) at rs780094 was associated with NAFLD in multiple ethnicities [73,82-85]. The *GCKR* gene encodes a protein that functions as a negative regulator of glucokinase, a hepatic enzyme responsible for glucose uptake [86,87]. The missense mutation impairs the protein's function, results in increased hepatic glucose uptake and malonyl Co-A production, which serves as substrate for hepatic *de novo* lipogenesis (DNL), a process that inhibits mitochondrial  $\beta$ -oxidation of fatty acids [88].

In a group of high-risk subjects of European descent, the rs641738 [C] > [T] gene variant of the membrane bound o-acyltransferase domain-containing 7 (*MBOAT7*) was found to be associated with a higher risk of NAFL and NASH [89], and with an increased risk of progression to hepatocellular carcinoma in NAFLD patients without cirrhosis [90]. The *MBOAT7* gene encodes for the enzyme lysophosphatidylinositol acyltransferase 1, responsible for incorporating arachidonic acid (AA, 20:4n-6) and other polyunsaturated fatty acids (PUFAs) into phospholipids (PLs) in remodeling pathways [91]. The rs641738 [C] > [T] variant is associated with a down-regulation of *MBOAT* gene transcripts and protein levels, with impaired incorporation of AA (20:4n-6) in PLs [89,92].

### **3.8. Diet**

#### **3.8.1. Hyper-caloric diet**

A hyper-caloric diet may induce NAFLD by promoting obesity, which is a major risk factor for NAFLD [32-34]. However, NAFLD can occur in a smaller rate in non-obese subjects [35], suggesting the involvement of mechanisms that are not exclusively related to obesity. However, the link between

caloric-content and NAFLD may be influenced by weight status and dietary composition. In morbidly obese subjects, there was a lack of association between caloric content and the NAFLD spectrum, while the risk of inflammation was associated with a higher intake of carbohydrates and lower intake of fat [93]. Also, in animal models, NAFLD can be induced by caloric-restricted diet containing high sucrose or high fructose in the absence of weight gain [94,95].

### *3.8.2. Fructose and fructose-containing sugars*

In experimental animals, dietary fructose, sucrose, or high-fructose corn syrup are commonly used to induce NAFL and NASH [95-98]. In humans, multiple observational studies pointed toward a strong association between fructose and fructose-containing sugar intake and the risk of NAFLD development and progression [93,99-104]. The intake of fructose and fructose-containing sugar was also associated with the development of unfavorable metabolic outcomes strongly linked to NAFLD, including dyslipidemia and HTN [105,106]. However, the effect of fructose-containing sugar on the development of NAFLD is controversial. There is a lack of large, long-term studies to assess this relationship. Nevertheless, in short-term setting, this relation may be confounded by excessive dose, caloric content, and weight status [107]. Results from one meta-analysis that inspected the short-term effect ( $\leq 10$  weeks) of fructose or sucrose intake on hepatic fat content, DNL, liver enzymes in normal and overweight subjects concluded that there is lack of evidence supporting the role of isocaloric or hypocaloric fructose or sucrose as cause of NAFLD [108]. Another meta-analysis that included normal and overweight subjects concluded that short-term hypercaloric and high-fructose diets increased hepatic fat content by 54%, while the intake of fructose with isocaloric diet did not induce NAFLD [109].

### *3.8.3. Fatty acids and cholesterol*

In animals, a diet high in saturated fatty acids (SFAs) [110,111] and PUFAs deficiency was associated with development of NAFL [112-115]. In obese subjects with NAFLD, the diagnosis of NASH was associated with a high dietary intake of cholesterol [116], high SFAs and PUFAs dietary intake [99,116]. An excess dietary n-6 with reduced n-3 PUFAs was associated with NAFLD [117,118], and an increased SFA:PUFA ratio was associated with NASH [99,116]. Moreover, results

from two meta-analysis showed that n-3 PUFAs supplementation alleviated hepatic lipid content [119,120], with no effect on NASH histological outcomes [119]. Another meta-analysis concluded that n-3 PUFAs supplementation significantly reduced plasma/serum alanine aminotransferases (ALT), aspartate aminotransferases (ASL) and TGs level, however, with marginal reduction in hepatic fat content. In the same study, a dose-response analysis showed that an intake of 1.0 g/day of eicosapentanoic acid (EPA, 20:5n-3) and docosahexaenoic acid (DHA, 22:6n- 3) predicted a 2.74% decrease of hepatic fat content and 9.97 mg/dL reduction in TGs levels [121]. Monounsaturated fatty acids (MUFA) intake, mainly as component of the Mediterranean diet [122], has been shown to be effective in reducing hepatic fat content, liver enzymes, and circulating lipid profile in subjects with NAFLD [123,124].

### **3.9. Ethnicity**

In the U.S., disparity in NAFLD prevalence is reported, with Hispanics being impacted at higher prevalence [4,52,125-128] and severity [5,19,129]. Furthermore, this disparity trend was consistent when comparing Hispanic to non-Hispanic children and adolescents [130], suggesting that the ethnical disparity of NAFLD prevalence is independent of age [131]. However, the ethnical disparity in NAFLD prevalence was more profound in the general population, than in high-risk groups with other existing co-morbidities. In a study that examined NAFLD prevalence in high-risk cohort with obesity and T2DM, NAFLD prevalence rate was 50% and not associated with ethnicity [5]. However, in the same study, the risk of NASH among subjects with NAFLD was highest in Hispanics and lowest in African Americans, with no significant difference between ethnicities in fibrosis scores [5].

Gender disparity in the distribution of NAFLD according to ethnic group was also reported, as NAFLD in Caucasians was more prevalent in men than in women. However, this difference was not observed in Hispanic and African American [132]. Up to date, the mechanisms underpinning these ethnic disparities are not clear. Potential factors contributing to the higher rate of NAFLD in Hispanics are discussed in section 7.

#### **4. Natural history**

Both NAFL and NASH are recognized as progressive liver conditions that increase the risk for developing advanced liver disease and mortality [46,57,133-139]. It is estimated that about 30% of individuals with NAFL will eventually develop NASH [140-142]. Compared to subjects with NAFL, NASH patients are at increased risk for developing liver and non-liver-related complications [46]. About 40-50% of patients with NASH will develop fibrosis [133], with an estimated average progression of 0.09 fibrosis stages per year [4].

Mortality in NAFLD patients is mainly due cardiovascular disease, followed by non-liver malignancy, and then liver-related deaths, which is primary due to hepatocellular carcinoma [4,57,134,135]. Despite the low rate of liver-related mortality, it corresponds to 20,000,000 estimated deaths among subjects with NAFLD [4,143]. When NASH is present, this risk of liver-related mortality increases by 5 to 10-fold [144]. In another analysis, the presence of NASH with fibrosis was associated with lower survival, and this was not true for NAFL alone [145]. In the U.S., about 10% of NASH subjects receive liver transplantation [146]. NASH is considered a major indication for liver transplant [3] and was projected to be main indication in the U.S. by 2020 [146].

#### **5. NAFLD diagnosis and treatment**

Early diagnosis of NASH is determinant for its prognosis. Specifically, the identification of NASH in the pre-fibrotic stage can significantly improve the response to therapy [147]. Liver biopsy and histological confirmation are the gold standard to establish NAFLD diagnosis. On histological examination, the principal features of NAFLD are microvascular steatosis with or without the presence of lobular inflammation, peri-sinusoidal fibrosis, and hepatocellular ballooning [148]. The NAFLD activity score (NAS) is commonly used to establish a histopathological diagnosis and characterization of NASH, and it accounts for steatosis, hepatocellular ballooning, and lobular inflammation [3]. The NASH-CRN scoring system is commonly used to determine the stage of fibrosis [148]. In general, liver biopsy is an invasive procedure, subjected to risk of complications [149,150] and inter-observer variability of pathology interpretation [151].



NAFLD can also be identified and diagnosed by various abdominal imaging modalities. These include ultrasound, computed tomography, magnetic resonance elastography, and transient elastography. These imaging techniques vary according to sensitivity, specificity, and ability to quantify steatosis, necroinflammatory activity, and fibrosis [147]. The disadvantages of these imaging modalities include the high costs, radiation exposure, and limited applicability for morbidly obese patients, inability to detect low-moderate grades of fibrosis or to characterize necroinflammatory activity [152].

Despite the epidemic and significance of NAFLD, there are no FDA-approved treatments [153,154]. Clinical approaches to manage NAFLD are mainly directed to manage the concurrent components of MetS. Effective approaches include lifestyle changes, dietary modifications and increased physical activity aimed to body weight reduction [155-157]. However, lifestyle interventions are hard to comply to [158]. Bariatric surgery is indicated for a subset of subjects [159], with the benefits of reversal of NAFLD shown in long term follow up studies [160].

## **6. Pathophysiology**

Steatosis develops when fatty acids availability exceeds the liver's disposal capacity [161]. Specifically, when the hepatic uptake of non-esterified fatty acids (NEFAs) from the circulation and lipid synthesis from DNL, outweighs the disposal rate, mainly by  $\beta$ -oxidation of FA and export of TGs with VLDL particles, the net result is hepatocellular lipid accumulation [162].

The mechanism of NAFLD progression was previously explained by the "two hits" hypothesis [163]. Hepatic lipid accumulation composes the "first hit". As hepatic lipid accumulation overwhelms the disposal and storage capacity, excess lipids will induce oxidative stress, inflammation, the "second hit", with ultimate progression to NASH [163]. Later, the "multiple hit" model was proposed to explain the heterogeneous presentation and disease course of NAFLD, and to include a multi-layered interaction between host genetics, environmental factors, and microbiome [164]. In the "multiple hit" model, following the accumulation of hepatocellular lipids, a cascade of metabolic insults orchestrates multiple cellular and systemic responses, including oxidative stress and lipid peroxidation, lipotoxicity, glucotoxicity, inflammation, endoplasmic reticular stress, mitochondrial dysfunction,

apoptosis, and intestinal dysbiosis, that will collectively alter lipid metabolism, induce hepatocytes injury, and provoke NAFLD development and progression [161,165-167].

Within the context of obesity and MetS, IR is considered a component of the ‘multiple hits’ in the pathogenesis of NAFLD [26,27]. IR is characterized by impaired glucose disposal in peripheral tissues [24,25] and results in impaired suppression of adipose tissue lipolysis, a state known as adipose tissue dysfunction, with consequent increased efflux of NEFA [168]. Adipose tissue and skeletal muscle IR were reported in NAFLD subjects compared to healthy controls [169,170]. In NAFLD patients, the insulin-mediated inhibition of adipose tissue lipolysis was found impaired and plasma NEFAs was found persistently elevated [28,171-173]. Moreover, in patients with NAFLD, adipose tissue lipolysis was identified as the major source of fatty acids in hepatocellular TGs store [174,175]. The uncontrolled lipolysis of visceral adipose tissue may further exacerbate the state of IR with the release of pro-inflammatory cytokines, which in turn triggers peripheral tissues inflammation and impair insulin signaling [176,177].

The increased flux of NEFA into the circulation is efficiently cleared by hepatic uptake [178]. Data on hepatic  $\beta$ -oxidation of fatty acids are inconsistent with reported increase [28,179] and decrease in NAFLD subjects compared to controls under basal conditions [180]. An impaired metabolic flexibility, or the inability to alternate between fat and carbohydrate oxidation as a source of energy during insulin infusion was also reported in NAFLD [181] and is thought to be an adaptive mechanism against excess hepatic free fatty acids (FFAs) buildup [182].

Hepatic IR, or the inability of insulin to suppress hepatic glucose production in fasted state [29], was reported in NAFLD subjects with [30] and without diabetes [31,169,170]. The extent of adipose, hepatic and skeletal muscle IR was comparable to that in T2DM patients, independently from the degree of steatosis [181]. Hepatic IR is accompanied by uncontrolled hepatic glucose production and a compensatory hyperinsulinemia, both stimulating hepatic DNL [183,184]. Accordingly, DNL was reported to be 3-fold higher in subjects with NAFLD, compared with healthy controls [175,185]. The ability of insulin to suppress hepatic DNL in fasted state was impaired in NAFLD subjects and hepatic DNL was comparable in fed and fasted states, this indicate metabolic inflexibility, which is

believed to contribute to the development of NAFL [174]. The ability of insulin to suppress VLDL production was impaired in NAFLD [186] and NAFL was found associated with increased production of TG-rich VLDL [187,188], which contributes to the development of hypertriglyceridemia and dyslipidemia.

Hepatic TGs accumulation is thought to be a protective mechanism from the metabolic burden of increased hepatic fatty acids availability [182,189,190]. However, this concept is questioned [191], as evidence from longitudinal studies show that substantial number of subjects with NAFL, in the absence of necroinflammation and ballooning, may progress to advanced fibrosis over a relatively short period of time [136,137]. Moreover, a role for hepatocellular lipids in mediating inflammation is proposed, as indicated by an up-regulation of genes involved in inflammatory response in subjects with NAFL [192].

Evidence indicates a potential role of specific lipid species in histological changes observed during NAFLD progression, and the involvement of mechanisms related to TGs, diglycerides (DGs), and PLs remodeling in NAFLD progression. In a recent study using Mass Spectrometry (MS) imaging techniques to study spatial distribution of lipids in liver tissue, it was found that in both animal models and humans, there was a loss of hepatic lipid zonation and marked remodeling of PLs with NAFLD progression, with enrichment of AA (20:4n-6) acid in PLs located in the pericentral hepatocytes zone, potentially to serve as a source for eicosanoid synthesis. In the same study, the transcript levels of lysophosphatidylcholine Acyltransferase 2 (*LPCAT2*) and cytosolic phospholipases A2 (*cPLA2*) involved in membrane remodeling; arachidonate 15-lipoxygenase (*ALOX15*) involved in eicosanoid production were increased [193]. In support of this evidence, genome-wide association studies identified a robust association of *PNPLA3* G allele with the full spectrum of NAFLD [62-68]. In hepatocytes, the *PNPLA3* protein is thought to be involved in lipid remodeling, as it was shown to have a transacylase activity that facilitates the direct fatty acid transfer between lipids [194], and an acyltransferase activity catalyzing the conversion of lysophosphatidic acid to phosphatidic acid [195]. Also, in vitro studies showed the *PNPLA3* protein modulates the activity of adipose TG lipase (ATGL) or Patatin Like Phospholipase Domain Containing 2 (*PNPLA2*) via sequestering the cofactor,

comparative gene identification-58, which is essential for ATGL function [196-198]. The net effect of PNPLA3 and ATGL activity is to induce the hydrolysis of fatty acid ester bonds of glycerolipids, with a high preference for oleic acid (OA,18:1n-9) among other fatty acyl moieties to be incorporated into complex lipids as TGs, DGs, and phosphatidylcholine [199-201]. The *PNPLA3* I148M variant results in a loss-of-function of the enzymatic activity, impairs the ATGL activity with consequent TGs accumulation, altered saturation of hepatocellular lipids [196-199,202-204], and impairment of hydrolysis and incorporation of OA (18:1n-9) moiety from TGs pool [205]. In hepatic stellate cells, the PNPLA3 protein is involved in retinol metabolism with potential role in fibrogenesis. The PNPLA3 has a retinyl-palmitate lipase activity that promotes the release of retinol from hepatic stellate cells [206,207]. The *PNPLA3* I148M variant results in reduced retinol release and bioavailability, which promotes inflammation and fibrogenesis [206,208].

Collectively, the combination of increased hepatocellular lipid retention and dysregulation in lipid remodeling, increases the demand on the liver to handle metabolic burden from excess energy substrates and may direct lipids to pathways that generate hepatotoxic lipid species, also known as lipotoxicity [209-211]. Lipotoxicity correlates with the severity of NAFLD [212] and induces production of reactive oxygen species and lipid peroxidation [213], as well as stress cellular-response and apoptosis [212,214]. Up to date, the lipotoxic lipid specie(s) promoting hepatocellular injury and the NASH phenotype are not identified. However, *in vitro* and *in vivo* evidence indicate the SFA, palmitate (PA,16:0) [110,215,216], DGs and ceramides (CERs) [217-219], lysophosphatidylcholines [220], and free cholesterol [221,222] as lipotoxic species with potential role in NAFLD.

## **7. Factors contributing to the high prevalence and severity of NAFLD in Hispanics**

Multiple factors can come into interplay to explain the reported ethnic disparities in NAFLD rate and severity, these factors include the presence of comorbidities as MetS; genetic predisposition; environmental factors such as diet, socioeconomic status, and inaccessibility to health care [126,127,223]. The prevalence of MetS and its components is higher in Hispanics compared to non-Hispanic whites and African American [224]. Hispanics are also reported to have higher body mass index (BMI), visceral adiposity, and IR for BMI compared to other ethnicities [225-227].The

prevalence of T2DM is higher in Hispanics compared to non-Hispanic whites, however, comparable to that of African Americans [127,228]. Plasma TGs levels are significantly lower in African Americans compared to Hispanics and Caucasians, who have comparable TGs profile [229]. However, the extent by which these variations may explain the observed disparity in NAFLD prevalence and severity is unclear.

The homozygous carriers of the rs738409 [G] allele in *PNPLA3* gene, discussed in detail in section 3.7 and 6, has the highest frequency in Hispanics compared to other ethnicities. In one study, the frequency of the I148M variant was reported to be 49%, 23%, and 17% in Hispanics, Whites, and African Americans, respectively [62]. A following study reported the allelic frequency in a group of subjects with biopsy-confirmed NAFLD to be 91% and 70% in Hispanics and non-Hispanics, respectively [67]. Similar findings have been replicated in following studies [72,73,230].

Other environmental and life-style factors include diet, physical activity and socioeconomic status, based on data from the NASH-CRN, and compared to non-Hispanic Whites, Hispanics with NASH were younger, consumed higher amount of carbohydrates and less fat, performed less physical activity, and came from lower socio-economical background [19]. The acculturation of the Hispanics to the U.S. dietary habits and lifestyle was reported with a change in diet with successive generations of Hispanics in which fruit and vegetable intake decreased and sugar-sweetened beverages intake increased in third-generation Hispanics compared to first-generation [231]. Acculturation to American society was also found to be associated with a more sedentary lifestyle, as multiple studies have reported lower physical activity among Hispanics as compared with other ethnicities [232] [233].

## **8. Metabolomics for the study of NAFLD**

Metabolomics is the comprehensive characterization of small molecules, or metabolites, in a biological matrix by applying analytical chemistry methods [234]. The high-throughput range of detected metabolites reflects substrates, intermediates, and products of metabolic processes that are direct product of gene-environment (exposome) interactions. Therefore, metabolomics has the advantage of better reflecting the phenotype, compared to genomics and proteomics [235,236]. Metabolomic approaches are with diverse scientific applications. The ability to predict a given

phenotype with a metabolomic signature is a common application of biomarker discovery.

Characterizing changes in metabolomic profile between two disease states, or exposures, may provide insights into altered metabolic pathways to pin out mechanisms and potential therapeutic targets [234,236].

Mass spectrometry is a commonly used method with high sensitivity and the ability to detect metabolites in very low abundance. It includes gas chromatography-mass spectrometry (GC-MS) which characterizes thermally stable, volatile metabolites and liquid chromatography-mass spectrometry (LC-MS) which can profile more polar metabolites with lower thermal stability and higher relative molecular mass [237,238].

Previous metabolomic profiling studies on liver biopsies revealed that NAFLD is associated with defects in the tricarboxylic acid cycle (TCA) resulting in metabolic perturbations including alterations in amino acids, lipids, and bile acids profiles [239,240], impaired antioxidant capacity, and PLs composition [240]. In situ analysis of tissue lipidomic composition and distribution revealed that there are differential distribution of lipids within the liver lobule, and the progression of NAFL to NASH impacts lipid zonation and, possibly, remodeling [193,241-243]. Last, the employment of metabolomic for biomarker discovery enabled the identification of a plasma lipidomic signature that can distinguish NASH from NAFL [244-248].

## **9. Justifications and aims**

NAFLD is a major health concern and a heavy economic burden on health systems. It is a frequent indication for liver transplant [3]. It is also associated with high risk of morbidity and mortality [249,250]. In the U.S., the annual cost of NAFLD is estimated to be 103 billion dollars [249]. The Hispanic population is a fast-growing population and expected to account for 30% of the U.S. population by 2060 [251]. Alongside, the economic impact of NAFLD is expected to inflate. The pathophysiology of NAFLD is not clearly understood, especially with regard to the progression from NAFL to NASH. Ethnicity-related disparity in NAFLD prevalence and severity are reported with Hispanics being affected disproportionately at higher rate compared to other ethnicities [5,125-127]. To date, the biological mechanism(s) underlying these observations is not clear. The characterization of

metabolomic profile associated with a given phenotype is a valid way to understand its biochemical underpinning. Within this context, metabolomics offers a valuable tool to expand our understanding of NAFLD etiology and pathophysiology. To our knowledge, ethnicity was not addressed before in a metabolomic profiling study conducted in NAFLD.

The standard method for establishing NAFLD diagnosis, liver biopsy, is invasive and subjected to limitations [149,150]; and a clinically feasible, non-invasive biomarker to characterize NASH is an unmet necessity. Moreover, with histopathological changes occurring with progression from NAFL to NASH, little is known about the correlation of liver histological features with liver tissue or plasma metabolome in NAFLD subjects. Most of the available literature focuses on plasma or serum, with few available data on liver metabolites.

A guiding principle for our methodology is that there are biochemical differences between Hispanic and Caucasian subjects with NAFLD that could explain, at least in part, the ethnicity-related disparity observed in NAFLD prevalence and progression. In this dissertation, as a “proof of principle”, the objective is to explore metabolomics profiles of a group of Hispanic and Caucasian bariatric surgery subjects with NAFLD. In specific, we conducted this study to: (i) characterize liver and plasma metabolomic profiles by ethnicity groups; (ii) determine the role of specific biochemical pathway(s) involved in NAFLD in the study groups; (iii) identify if ethnicity-specific panel of metabolites characterizes NASH.

Results of this work will expand our understanding of mechanism(s) underlying NAFLD onset and progression and shed light on potential unshared mechanism(s) for NAFLD between ethnicities. Our results will provide bases for hypothesis generation for future research aiming to find therapeutic targets and to identify ethnicity- specific metabolomic signatures that differentiate stages of NAFLD, which with future validation, can aid in clinical practices.

## **10. Chapters overview**

Lipid species as DGs, CERs, and FFAs are thought to be key factors in the progression to NASH [240]. Previous literature identified alterations in plasma FFAs and lipid composition in patients with NAFL vs. NASH [244,248]. The comparison of lipidomic profiles in relation to ethnicity in NAFLD

may provide insights into potential lipotoxic lipid specie(s) and pathway(s) that are unshared between ethnicities. In chapter two, published in [252], we conducted an untargeted lipidomic profiling of plasma and liver tissues for metabolites related to primary metabolism, including fatty acids and complex lipids; choline and related metabolites in a group of Hispanic and Caucasian bariatric surgery subjects with NAFLD. Our findings revealed ethnicity-related differences in plasma profiles, independent of obesity, with Hispanics showing higher plasma TGs, acylcarnitines, and FFAs. Also, in NASH, there were ethnicity-related differences in hepatic profile with Hispanics having higher FFAs, TGs and lysophospholipids. Our findings suggest that impaired mitochondrial  $\beta$ -oxidation and lipotoxicity are involved in the progression of NASH in Hispanics.

In chapter three, published in [253], we examined a targeted and quantitative lipidomic profiling of plasma oxylipins in a group of Hispanic and Caucasian bariatric surgery subjects with NAFLD. Oxylipins, including eicosanoids, prostaglandins, and leukotrienes, are biologically active lipids with implication in various pathological conditions, including diabetes, cardiovascular disease and cancer [254,255]. The study of oxylipins in NAFLD is a relatively new area [256]. Investigating oxylipins in NAFLD with regards to ethnicity can identify potential role of dietary PUFAs and down-stream inflammatory-mediators in NAFLD progression. Findings indicate that in NAFLD, there are ethnicity-related differences in plasma profiles with Hispanic having lower long chain PUFAs, independent of histological severity. Also, when comparing between ethnicity groups, differences in plasma lipid mediators distinguished ethnicities with NASH. Importantly, our findings point out to a lower lipoxygenase(s) activities and higher soluble epoxide hydrolase(s) activities in Hispanics with NASH.

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## **Chapter 2**

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### ***Untargeted metabolomic profiling***

## 1. Introduction

Nonalcoholic fatty liver disease (NAFLD) is a continuum of liver pathology that includes steatosis (NAFL), hepatocellular inflammation and ballooning, or nonalcoholic steatohepatitis (NASH) and cirrhosis [1]. It affects 25% of the general population and up to 95% of individuals with medically complicated obesity [2,3]. Based on the strong correlations of NAFLD with metabolic syndrome and its components, NAFLD is argued to be its hepatic manifestation [4,5]. In the U.S., disparity in NAFLD prevalence is reported, with Hispanics (HIS) being impacted at higher rate and severity compared to other ethnicities [6-11]. To date, the biological background underlying this disparity remains unclear.

NAFL develops when fatty acid availability, from the hepatic uptake of free fatty acids (FFA) and *de novo* lipogenesis (DNL), outweighs the utilization and disposal capacity, mainly by synthesis of triglycerides (TG) and other lipids, mitochondrial  $\beta$ -oxidation and export as very low-density lipoprotein [12]. Mechanisms of NAFLD progression are explained by the “multiple hit” model, in which lipid overload, the first hepatic hit, overwhelms the disposal, utilization and storage capacity. This results in a cascade of metabolic insults including oxidative stress, lipotoxicity, endoplasmic reticular stress, mitochondrial dysfunction and apoptosis, collectively, provoking hepatocyte injury, inflammation and disease progression [12,13].

Mitochondrial function is altered in NAFLD and hepatic  $\beta$ -oxidation of fatty acids is reported to be both increased and decreased [14-16]. This inconsistency is thought to reflect a process of mitochondrial adaptation to compensate for the increased availability of FFAs, with an initial increase in  $\beta$ -oxidation, tricarboxylic acid cycle and oxidative phosphorylation [14,15,17]. Eventually, the metabolic capacity and antioxidant defenses are overwhelmed, resulting in hepatic oxidative stress and diverting FFAs to the production of hepatotoxic lipids [18,19]. It is thought that accumulation and generation of hepatotoxic lipids is critical to NAFLD progression [20]. As mentioned above, lipotoxicity is considered a component of the “multiple hit” and may result from the accumulation of hepatotoxic lipids or intermediates, such as saturated fatty acids (SFA), ceramides (Cer) and

lysophosphatidylcholine (LPC) [21-24]. Lipotoxicity can also result from a deficiency or imbalance in lipids essential for cellular integrity and function, including polyunsaturated fatty acids (PUFA) [24].

Previous metabolomic analysis of liver tissue and plasma have shown that NAFLD is associated with derangements of lipid, carbohydrate, and amino acid metabolism [25-29]. Dysregulation in one-carbon metabolism, including alterations in choline, betaine, methionine and in the universal methyl donor, S-Adenosyl-L-methionine (S-AdoMet), is also implicated in NAFLD development and NASH severity, as shown from animal studies [30]. In humans, a recent metabolomic analysis identified a subtype of NAFLD subjects characterized by impaired one-carbon metabolism with NASH progression [31]. However, to our knowledge, no previous metabolomic profiling study has addressed ethnicity-related variations with regards to NAFLD.

The objective of this study was to investigate metabolomic profiles in a group of Hispanic (HIS) and White Caucasian (CAU) with obesity and biopsy-confirmed NAFLD. The identification of metabolomic differences between HIS and CAU subjects with NAFLD may provide a new research direction pointing towards ethnicity-specific changes as potential drivers for the disparity observed in NAFLD rate and progression. To this end, we employed untargeted metabolomic profiling of primary metabolism, complex lipids, choline and related metabolites in a group of Hispanic (NAFL-HIS) and Caucasian (NAFL-CAU) subjects with obesity and NAFLD of comparable histological presentations, as compared to a group of ethnicity-matched lean healthy control subjects. We also compared liver and plasma metabolomic profiles in a group of NASH (NASH-HIS) and (NASH-CAU) subjects with similar NAFLD Activity Score (NAS), to a group of BMI-matched NASH-free (0-NASH) subjects in both ethnicities.

## **2. Subjects and methods**

### **1.1. Subjects**

Liver biopsies ( $n = 17$ ) and plasma samples ( $n = 15$ ) were retrieved from the biobank repository at the Division of Gastroenterology and Hepatology, UC Davis Medical Center. Samples were collected from bariatric surgery patients who self-identified ethnicity as either HIS or CAU. Included subjects were both males and females; age range 18–75 years; with class II and III obesity (body mass index

(BMI) > 35.0 kg/m<sup>2</sup>); no previous diagnosis of acute or chronic diseases except for obesity or type 2 diabetes based on medical history. Exclusion criteria were diagnosis of secondary causes of chronic liver disease based on medical history, including viral and autoimmune hepatitis, HIV, hemochromatosis, alpha 1 anti-trypsin deficiency, Wilson disease and drug-induced liver disease; excessive alcohol intake (defined as >20 g/day for women and >30 g/day for men); and subjects with advanced fibrosis (stage >2). Healthy control subjects (HC; *n* =22) were recruited via public postings. Both male and female subjects were included; age between 18–75 years; BMI between 18 and 25 kg/m<sup>2</sup>; no current or previous diagnosis of chronic diseases; absence of signs of acute diseases.

For subjects with NAFLD, demographic, anthropometric and clinical data were collected retrospectively using data recorded within 7 days of bariatric surgery procedure. For HC subjects, demographic data were self-reported and anthropometric measurements were collected during one in-clinic visit. All subjects were consented with a signed form and the study protocol was approved by the Institutional Review Board at the University of California, Davis (protocol # 856052).

### **1.2. *Biological samples***

Liver tissue samples were collected by intraoperative core biopsy during bariatric surgery (time of collection is not available). For each subject, one sample was submitted in 10% formalin to the Department of Pathology for routine diagnostic interpretation. A second sample was flash-frozen in liquid nitrogen immediately after harvest and subsequently transferred and stored at –80 °C until analysis. Blood samples were collected by veno-puncture in EDTA-containing pre-cooled tubes after a 10-hour overnight fasting on the day of operation for NAFL group or in clinic for HC (time of collection is not available). Samples were centrifuged and stored at –80 °C until analysis.

### **1.3. *Histopathology***

Specimens received by the Department of Pathology were processed as per routine protocol. After diagnostic interpretation was completed, biopsy slides were retrieved and scored using the NASH Clinical Research Network (NASH-CRN) histology scoring system, which includes steatosis, hepatocellular ballooning, lobular inflammation, and fibrosis, by a gastrointestinal pathologist blinded to the subject's clinical data. The NAFLD Activity Score (NAS) and fibrosis score were tabulated

[32]. NASH diagnosis was determined by incorporating the histology scores into a diagnostic algorithm [33].

#### **1.4. *Untargeted metabolomics***

Untargeted, semi-quantitative metabolomic profiling for plasma and liver samples was performed at the UC Davis West Coast Metabolomics Center. Samples were extracted using methanol: methyl tert-butyl ether (MTBE):water as previously described [34]. To profile metabolites related to primary metabolism including carbohydrates, sugar phosphates and amino acids, the aqueous phase was dried and subjected to trimethylsilylation and methoximation and analyzed by gas chromatography/time-of-flight mass spectrometry (GC-TOF MS) [35]. Spectral data were processed and annotated using BinBase [36]. To profile FFAs and complex lipids, including mono-, di- and TGs, cholesteryl ester (CE), phospholipids (PL), sphingolipids (SL), the organic phase was dried, resuspended and analyzed by charged surface hybrid liquid chromatography/quadrupole time of flight mass spectrometry (CSH-QTOF MS/MS) [37]. Data collected in both positive and negative ion mode and processed using MassHunter (Agilent Technologies, Inc., Santa Clara, CA, <http://www.agilent.com>). Lipids were identified based on MS/MS fragmentation patterns using Lipidblast software [38]. To profile acylcarnitine, choline, betaine, S-Adenosyl-L-methionine (SAME) and related metabolites, aqueous phase was analyzed by the biogenic amines platform using hydrophilic interaction liquid chromatography/quadrupole time of flight mass spectrometer (HILIC-QTOF MS/MS) [37]. Data were collected in both positive and negative mode. MS-DIAL was used for data processing [39]. For annotations, the three-levels of compound annotation by the Metabolomics Standards Initiative (MSI) was employed [40]. Metabolites with MSI level 1 annotation (i.e., an MS/MS spectral library with retention time and precursor mass) were excluded from statistical analyses. All mass spectra are available at Massbank of North America (<http://mona.fiehnlab.ucdavis.edu>). The study details are available on The Metabolomics Workbench (<http://www.metabolomicsworkbench.org>), ID number (ST000977).

In this study, fatty acids and complex lipids are described by name and lipid class, respectively, followed by number of (carbons, double bounds) of the fatty acyl moiety (i.e., linoleic acid (18:2n6)

and TG(50-52:0-6)). The index of fatty acid desaturase-1(FADS1,  $\Delta$ -5 desaturase) was estimated as the product to precursor ratio or arachidonic acid (20:4n6)/dihomo- $\gamma$ -linolenic acid (20:3n6). Stearoyl-CoA desaturase (SCD1, or  $\Delta$ -9 desaturase) was estimated as palmitoleic acid (16:1n7)/palmitic acid (16:0). The hepatic relative ratio of free n6 to n3 PUFAs was calculated as arachidonic acid (20:4n6)/eicosapentaenoic acid (20:5n3) and arachidonic acid (20:4n6)/docosahexaenoic acid (22:6n3).

### **1.5. Statistical analysis:**

Statistical analysis was performed using JMP Pro 14.1 (SAS Institute Inc., Cary, NC; <http://www.jmp.com>). Unknowns and metabolites and with MSI level 1 identification from HILIC-QTOF MS/MS platform were excluded. Outliers were detected and excluded using the robust Huber M test and missing data were imputed using multivariate normal imputation if greater than 70% complete. Metabolites with more than 30% missing data were excluded. The Johnson's transformation was used to attain normal data distributions for statistical assessment.

Metabolite means were calculated using Log normalized data, fold changes were calculated as the mean of NAFL/HC for comparison between NAFL and HC or NASH/0-NASH for comparison between NASH and 0-NASH. Students' *t*-test was used to compare means. Differences were considered likely at  $p < 0.05$ , and possible if the  $p$ -value was  $\geq 0.05$  and  $< 0.1$ .

To examine if ethnicity-specific differences exist in NAFLD and to evaluate the interaction of ethnicity x health status (i.e., NASH or NAFL), full factorial analysis of covariates (ANCOVA) was employed. This model included ethnicity, health status, ethnicity x health status interaction as fixed effects, and age and sex as covariates. Benjamini-Hochberg false discovery rate (FDR) correction for multiple comparisons using a  $q = 0.2$  was performed, given the pilot nature and small sample number of this study [41]. To reduce data dimensionality and facilitate visualization, metabolites were clustered using the JMP implementation of the SAS VARCLUS procedure, a principal component analysis (PCA)-based clustering algorithm, with cluster components calculated as the linear sum of all variables in a cluster.



For NAFL vs. HC comparisons and to focus on ethnicity-specific differences, we only clustered metabolites with  $p < 0.1$  for ethnicity x NAFL interaction. Next, cluster components were subjected to partial least square-discriminant analysis (PLS-DA) separately in each ethnicity with leave-one-out cross validation (LOOCV) [42]. A variable importance in projection (VIP) score of  $>1$  was set as a threshold for variable selection [43]. Because the PLS-DA model was constructed using reduced set of data to highlight only ethnicity-specific differences between NAFL and HC, the VIP scores should not be directly compared between the two analyses.

For NASH vs. 0-NASH comparisons and to focus on ethnicity-specific differences, we clustered metabolites with  $p < 0.05$  for the NASH effect within ethnicity groups or with  $p < 0.05$  for the ethnicity x NASH interaction. To further examine the effect of ethnicity between NASH and 0-NASH, cluster components were reevaluated using  $t$ -test for group comparison within ethnicity and ANCOVA to check on interaction (ethnicity x NASH).

To examine the association between metabolomic profiles and liver histological scoring, Spearman's rank correlations was performed. To correct for multiple testing, Benjamini-Hochberg FDR adjustment was performed with  $q = 0.2$  [41].

### **1.6. Over representation analysis**

To provide an overview on the general changes in metabolomic profile, we employed ChemRICH [44], a statistical enrichment analysis based on chemical similarity. This approach clusters metabolites into non-overlapping chemical groups using Tanimoto substructure chemical similarity coefficients and calculates cluster  $p$ -values using the Kolmogorov–Smirnov test.

### **1.7. Pathway enrichment analysis**

Pathway analysis was performed using MetaboAnalyst (McGill University, Quebec, CA; <http://metaboanalyst.ca>) [45]. Metabolites with differential alterations between ethnicity in NASH ( $p < 0.05$ ) were compared against pathway-associated metabolite sets from Kyoto Encyclopedia of Genes and Genomes (KEGG) [46]. Fisher's Exact test was used to assess over-representation and the relative betweenness centrality was used for topology analysis.

### 3. Results

#### 1.8. Subject characteristics

The clinical and histological features for NAFL and NASH subjects are presented in Table 1 and Table 2. When comparing between ethnicities, both NAFL and NASH groups showed no difference in age, BMI and other clinical parameters including histology NAS scores.

In NAFL groups, the mean age was  $45 \pm 16$  and  $50 \pm 16$  years in HIS and CAU, respectively ( $p > 0.05$ ); 29% of HIS and 30% of CAU had moderate to severe steatosis; 43% of HIS and 50% of CAU were diagnosed with NASH and exhibited various degrees of lobular inflammation. One NAFL-CAU subject had portal/periportal fibrosis, or stage 1A. The mean NAS score for NAFL subjects was  $2.4 \pm 2.4$  and  $2.9 \pm 1.5$  for HIS and CAU, respectively ( $p > 0.05$ ). When compared to HC, BMI was 80% higher in NAFL-HIS and 70% higher in NAFL-CAU. In NASH subjects, the mean NAS score was  $4.7 \pm 0.58$  and  $4 \pm 1$  for HIS and CAU, respectively ( $p > 0.05$ ). Compared to 0-NASH, both ethnicities showed no difference in age, BMI or other clinical parameters.

#### 1.9. Ethnicity-specific differences in plasma metabolome in NAFL

Given the low sample size and broad analysis in this study, we first evaluated NAFL-dependent changes by chemical classes separately in each ethnicity, effectively reducing the number of comparisons (Fig. 1). In both ethnicities, when compared to corresponding HC, NAFL was associated with lower plasma phosphatidylcholines (PC), unsaturated LPCs, galactosyl Cers, CEs and amino acids. Specific to CAU, NAFL showed higher levels of ACs and unsaturated FFAs, driven by elevated PUFAs including linoleic acid (18:2n6),  $\alpha$ -linolenic acid (18:3n3), eicosadienoic acid (20:2n6) and MUFAs, heptadecenoic acid (17:1n7) and physeteric acid (14:1n7). Also, NAFL-CAU showed a reduction in many PLs including ether-linked PLs (Table S1). These differences in ACs and in unsaturated fatty acids were not evident in the NAFL-HIS group, which was characterized by alterations in sphingomyelins (SM) and xanthines, with higher level hydroxybutyrates, trimethyl ammonium compounds and sugar alcohols (Table S2).

To further examine this ethnicity-associated divergence in metabolomic profile, ANCOVA was performed with interaction (ethnicity x NASH). Of the 940 metabolites detected, 46 plasma

metabolites (4.9%) were found altered ( $p < 0.05$ ) in NAFL between ethnicities with an additional 59 metabolites showing a  $p$ -value between 0.05 and  $< 0.1$ . However, none of these passed the FDR-based multiple comparisons adjustment. Although the probability of differences was low and the number of findings was close to that expected by random chance, due to the strong class-specific changes and the exploratory nature of this study, we proceeded with a characterization of metabolite differences between the groups.

The variable clustering approach reduced the data to 21 cluster components. To highlight the apparent ethnicity-specific metabolic differences between NAFL and HC groups, these cluster components were projected using a PLS-DA (Fig. 2). In CAU, 11 of the 21 clusters contributed to the discrimination of NAFL and HC in CAU with VIP scores  $> 1$ . These clusters were represented by ether-linked PL(32-40:0-5) (cluster 8 and 15), PE(18-36:0-1) and PC(34-36:0-3) (cluster 3) which were lower in NAFL-CAU, and PC(38:4-5) (cluster 20) which appeared higher. Also, NAFL-CAU showed higher abundance of short to medium length acylcarnitines (i.e. AC(2-14:0-2); (cluster 2 and 7) and in non-esterified FFAs (cluster 2), including the SFAs myristic acid (14:0) and margaric acid (17:0), oleic acid (18:1n9); the PUFAs linoleic acid (18:2n6) and  $\alpha$ -linolenic acid (18:3n3). Similar trends were observed for docosahexaenoic acid (22:6n3) and eicosapentaenoic acid (20:5n3) (cluster 21), but with VIP  $< 1$ . Also, NAFL-CAU showed higher levels of the intestinal microbiota-related, trimethylamine N-oxide (TMAO) and indole-3-acetate (cluster 5) and lower levels of the purine-related metabolites, adenosine and guanine (cluster 16 and 13).

The differences in ACs and in non-esterified FFAs were not evident in NAFL-HIS, as compared to corresponding HC. Instead, 9 of the 21 clusters contributed to the discrimination of NAFL and HC with VIP scores  $> 1$ . These clusters indicated lower levels of PC(40:6-7) (cluster 9) and higher levels of PC(38:4) (cluster 19) and ether-linked PL (36:1-4) (cluster 4 and 19). There was also evidence of higher abundance of metabolites related to purine metabolism, xanthine and hypoxanthine (cluster 11) and in the endocannabinoid-like stearoylethanolamide (cluster 17), with differences in multiple other organic compounds (cluster 6, 11, 12, 14, 16). Because the PLS-DA was generated using a reduced number of metabolites (with ethnicity interaction  $p < 0.1$ ), the VIP scores should not

be compared directly between the two models. Details on ANCOVA, variable clustering and PLS-DA results are shown in Table S3.

Together, results suggest metabolomic variation between NAFL and HC in CAU with alterations in PLs, ACs, non-esterified FFAs and some organic compounds, while in NAFL-HIS, changes were limited to PLs and some organic compounds. In addition, plasma FFA and AC profiles appear differentially altered with NAFL between ethnicity groups. These findings are depicted by the unsupervised PCA performed on cluster components (Fig. S1), showing complete separation of NAFL-CAU from HC-CAU, indicating these two groups are metabolically distinct, while there was a partial overlap between NAFL-HIS and HC-HIS, suggesting less metabolic variations between these groups.

#### **1.10. *High acylcarnitines, triglycerides and unsaturated fatty acids distinguish HIS from CAU in HC***

The limited differences seen between NAFL and HC in HIS may reflect metabolic dysregulations in lean healthy HIS. To examine this, we compared plasma metabolomic profile in HC between ethnicities. Chemical similarity analysis clearly showed that in lean healthy subjects, HIS presented with higher ACs, TGs and unsaturated FFAs (Fig 3 and Table S4). HC-HIS had higher level ( $p < 0.05$ ) of the FFAs, margaric acid (17:0), oleic acid (18:1n9), linoleic acid (18:2n6), with similar trends in a number of other fatty acids. In addition, HC-HIS presented higher TG(51-58:1-9), DG(36-38:2-6), AC(2-16:0-1), altered PLs profiles, lower levels of the amino acids, glycine and alanine and the purine-related metabolites, adenosine, and hypoxanthine (Table S5).

#### **1.11. *Ethnicity-specific alteration in hepatic FFAs profile characterizes NASH***

To examine differences in hepatic metabolomic profile associated with the progression to NASH, we stratified NAFL group into 0-NASH and NASH. Due to the limited sample size and breadth of current analysis, we first examined NASH-dependent changes in each ethnicity by chemical classes. Next, to examine ethnicity-specific metabolomic alterations in NASH, ANCOVA was performed with interaction (ethnicity x NASH) followed by variable clustering for data reduction, given the strong class-specific changes observed, the small sample size and the exploratory nature of this pilot.

Upon examining liver metabolomic profile, ChemRich analysis (Fig. 4) showed that NASH was associated with higher unsaturated FFAs in HIS, driven by heptadecenoic acid (17:1n7); lower unsaturated PCs concurrent with higher levels in unsaturated LPCs; lower levels of unsaturated PEs with an elevation in many ether-linked PLs; lower ACs with higher TGs and DGs. To a lesser impact, HIS-NASH showed alteration in organic compounds, including lower level of several amino acids and related derivatives and in purine nucleosides and adenosine (Table S6). NASH in CAU showed higher SFAs, mainly capric acid (10:0) and lauric acid (12:0); lower levels of many unsaturated FFAs, PE, phosphatidylserines and in organic compounds including trimethyl ammonium compounds and dipeptides (Table S7).

ANCOVA showed 26 liver metabolites, (2.8%) of detected metabolites being altered at a  $p < 0.05$  between ethnicities in case of NASH with an additional 33 metabolites showing a  $p$ -value between 0.05 and  $< 0.1$ . However, these did not survive FDR-correction. Regardless, we proceeded with the characterization of the composition of these metabolites and their distribution between the groups.

Variable clustering performed on metabolites with  $p < 0.05$  for the NASH effect within ethnicity groups and with  $p < 0.05$  for the ethnicity x NASH interaction collapsed the data into 32 cluster components. Comparison of cluster components between ethnicities (Fig. 5) suggested that with NASH, clusters 3, 4, 6, 7, 8, 16, 18, 22, 23, 24 were differentially altered with tendencies shown for cluster 2, 9, 13, 14, 26. Cluster descriptions, correlations, means and  $p$ -values for cluster components and individual metabolites are detailed in Table S8.

NASH appeared associated with differential changes in the hepatic FFA profiles between ethnicities. Among the altered clusters was cluster 18 ( $p < 0.05$  for interaction of ethnicity x NASH). This cluster is composed of the MUFAs, heptadecenoic acid (17:1n7), oleic acid (18:1n9) and eicosenoic acid (20:1n9); and the PUFAs, linoleic acid (18:2n6),  $\alpha$ -linolenic acid (18:3n3). These FFAs were higher with NASH in HIS with an opposite trend seen in CAU. Similar trends were observed for arachidonic acid (20:4n6) and eicosapentanoic acid (20:5n3) (cluster 14), however, this cluster showed tendency for interaction (ethnicity x NASH). The MUFAs and PUFAs in cluster 14 and 18 correlated with LPC(16:1) and LPC(20:5).

Hepatic LPC and LPE profiles appeared to be differentially altered between ethnicities in NASH with higher levels seen in HIS and lower levels in CAU and interaction shown for LPC(16-20:1-5) (clusters 18, 8, 25) and LPE(18-20:0-4) (cluster 16 and 23), and with tendency shown for LPC(16-22:1-6) (cluster 2, 14). For both ethnicities, NASH had lower levels of almost all hepatic PCs and PEs. This trend differed between ethnicities in HIS for PC(32-37:1-3) and PE(34-36:2-4) (cluster 4), with apparent alterations in some ether-linked PLs (cluster 9 and 23) and SM(d33-36:1-2) (cluster 4).

There also appeared to be a lower level of hepatic ACs in NASH cases. However, a differentially lower ACs with interaction (ethnicity x NASH) was shown in HIS for AC(10-18:0-2) (cluster 22, 6) with tendency for AC(2:0) (cluster 26). In both ethnicities, NASH showed higher hepatic TGs, with differentially higher ( $p < 0.05$  in NASH between ethnicities) seen for TG(44-58:0-2) (cluster 2) and tendency shown for TG(48-50:0) (cluster 7, 4) observed in HIS. Some organic compounds of unspecific classification (cluster 3, 13, 14, 8) were also differentially altered in NASH between ethnicities.

Collectively, these findings suggest ethnicity-related differences in hepatic metabolomic profile with the progression to NASH, with markedly increased hepatic FFAs, TGs; lower levels of ACs and changes in several PLs seen in NASH-HIS. A heatmap illustrating variations in plasma and liver FFAs profile with NASH is shown in Fig. 6. Additionally, we performed pathway analysis using hepatic metabolites seen to be different between ethnicity group in NASH (raw  $p < 0.05$ ). These results support our cluster analysis with pathways related to unsaturated fatty acid metabolism found altered (FDR-adjusted ( $p < 0.2$ ), reflecting alteration in linoleic acid (18:2n6), eicosapentaenoic acid (20:5), oleic acid (18:1n9) and several PLs (Fig 7 and Table S9).

### **1.12. *Ethnicity-specific alteration in plasma metabolites characterizing NASH***

When examining NASH-dependent changes by chemical classes in plasma and in comparison to 0-NASH groups, ChemRich analysis (Fig. 8) showed that NASH-HIS had higher unsaturated TGs and SMs (Table S10) and NASH-CAU had higher Cers and SMs (Table S11).

To examine ethnicity-specific metabolomic alterations in NASH, we performed ANCOVA with interaction (ethnicity x NASH) followed by variable clustering for data reduction. Results showed 18

(1.9%) of detected plasma metabolites appeared different at a  $p < 0.05$  in NASH between ethnicities, with 13 additional metabolites showing a  $p$ -value between 0.05 and  $< 0.1$ . These differences did not survive FDR-correction. Cluster analysis reduced data dimensionality into 25 clusters. Comparison of cluster components (Fig. 9) showed that clusters 4, 5, 17, 20, 25 were differentially altered with NASH between ethnicities with tendencies shown for cluster 7, 11, 12, 13, 16. Cluster descriptions, correlations, means and  $p$ -values for cluster components and individual metabolites are detailed in Table S12.

With NASH in HIS, the plasma TGs profile was differentially altered ( $p < 0.05$  for ethnicity x NASH interaction) with higher levels of TG(50-52:0-6) (cluster 4) and tendency for TG(54-56:1-2) (cluster 7). Compared to respective 0-NASH, plasma levels of CEs, PCs, and PEs were higher in NASH. Ethnicity-specific differences included CE(16:1) (cluster 11), which was higher in CAU; LPE(18:2) (cluster 4) and ether-linked PLs (cluster 5 and 25), which were higher in HIS.

Differences in FFA profiles were not observed in plasma between NASH and 0-NASH. Both ethnicities showed lower plasma AC(10-14:1-2) (cluster 22) with NASH, however, HIS had a differentially lower ( $p < 0.05$  for ethnicity x NASH interaction) 3-hydroxybutyric acid (cluster 5). NASH was also associated with specific plasma amino acid profile with interaction (ethnicity x NASH) seen in HIS with higher alanine (cluster 25). Also, differential or with tendency for interaction are alterations in some organic compounds (cluster 4, 7, 12, 13, 15, 16, 17, 20 and 25).

Together, these findings reveal that ethnicity-related differences associated with NASH in plasma mainly affected TGs and some PLs in HIS, with altered organic compounds seen in both ethnicities.

### **1.13. Correlations of metabolomic profiles with liver histology**

Correlation analyses were performed on hepatic metabolites with steatosis and lobular inflammation, two histological features relevant to NASH diagnosis. In NASH-CAU, lobular inflammation correlated positively with metabolites including the eicosanoid, 20-hydroxyarachidonic acid; and negatively with MUFA(16-18:1); TG(50:0) ( $r = -0.6$ , raw  $p < 0.05$ ). Hepatic steatosis correlated negatively with metabolites including MUFA(20-24:1); arachidonic acid (20:4n6); choline

and S-Adenosyl-L-homocysteine. It correlated positively some SFA(9-12:0), TG(49:0) ( $r > -0.6$ , raw  $p < 0.05$ ).

In NASH-HIS, hepatic inflammation correlated negatively with metabolites including AC(5-20:0-4); purine related metabolites, adenosine, inosine, hypoxanthine; SAME; Cer(d40:1-2), and PC(33-40:1-7). It correlated positively with DG(34-36:1-3); TG(44-60:0-4); the MUFA(17-24:1); PUFA,  $\alpha$ -linolenic acid (18:3n3), linoleic acid (18:2n6), eicosadienoic acid (20:2n6); and LPC(18-20:0-5) ( $r > 0.7$ , raw  $p < 0.05$ ). These metabolites retained significance after FDR-adjustments. Hepatic steatosis correlated positively with TG(48-58:2-8) and negatively with some organic compounds ( $r > 0.7$ , raw  $p < 0.05$ ) (Table S13). Conversely, hepatic steatosis and lobular inflammation scores correlated with many plasma metabolites, but these did not pass FDR-adjustment (Table S14).

#### 4. Discussion

Hispanics are impacted with higher prevalence and progression rate of NAFLD [6-11]. However, the biological background for this disparity is not clear. To investigate metabolic variations associated with NAFL in these groups, we examined plasma and liver metabolomic profiles with respect to ethnicity in a group of HIS and CAU subjects with obesity and liver biopsy-characterized NAFL. Results revealed several ethnicity-related metabolomic distinctions and the major findings are: 1) In NAFL, as compared to HC, the plasma FFAs and ACs profile are differentially altered between ethnicities; 2) HIS present with signs of metabolic perturbation independent of obesity; 3) In NASH, comparing to BMI and histology-matched NASH-free subjects, the hepatic profile was differentially altered between ethnicities with HIS showing higher abundance FFAs and lipotoxic lipids.

In NAFLD, peripheral insulin resistance contributes to elevated plasma FFAs as the insulin-mediated suppression of adipose tissue lipolysis is impaired [47,48]. In the current study, NAFL groups were obese with features of metabolic syndrome. However, our results show discrepancies in plasma profiles between ethnicities. In NAFL-CAU, there were higher plasma FFAs, as compared to HC. This is consistent with insulin resistance, increased adipose tissue efflux and is in line with previous lipidomic analysis in NAFLD subject [24,29,49]. NAFLD is also characterized by impaired metabolic flexibility and plasma ACs are reported to be altered [25,50]. In NAFL-CAU, we confirmed



an elevation in many ACs species, including short chain AC(2-5:0) and long chain AC(10-14:0-2). AC(3-5) are derived from amino acids, even-chain AC(4-20) reflect incomplete fatty acid  $\beta$ -oxidation and AC(2:0) is the product of complete  $\beta$ -oxidation and may originate from glucose metabolism [51]. Altered plasma ACs profile indicates dysregulations in substrate oxidation across all tissues.

Unexpectedly, elevations in plasma FFAs and in ACs profiles were not marked in NAFL-HIS, which can be explained by the higher ACs and unsaturated fatty acids seen in lean and healthy HIS, as compared to CAU counterparts. We also observed higher plasma TGs in HC-HIS, a feature often associated with insulin resistance and obesity [52]. Hypertriglyceridemia is reported to be more frequent in overweight and obese HIS, compared to other ethnicities [53-56]. However, our findings indicate that this derangement along with a higher FFAs, ACs, altered PLs and amino acids profiles are independent of obesity and suggest early signs of metabolic perturbation in HC-HIS. Given that NAFLD results from a complex interplay between environmental factors, host genetics, intestinal dysbiosis and comorbidities [13], it is possible that such metabolic derangements increase the predisposition of HIS to NAFLD and/or its associated risk factors and are worth further investigation.

Our findings also show lower ether-linked PLs in NAFL-CAU. Although these differences were not evident in NAFL-HIS, a lower abundance of many ether-linked PLs were observed in HC-HIS, compared to HC-CAU. In NAFLD, a reduction in ether-linked PLs correlated with disease severity [29]. Beside a role in maintaining bio membrane fluidity and integrity, ether-linked PLs are thought to ameliorate NAFLD by modulating fatty acid oxidation and an antioxidant capacity [57,58].

With the progression from NAFL to NASH, our findings show differences in hepatic lipidomic profile between ethnicities, despite comparable NAS scores. Remarkably, NASH-HIS subjects had higher levels of hepatic FFAs with ethnicity interaction ( $p < 0.05$ ) shown for the MUFA heptadecenoic acid (17:1n), oleic acid (18:1n9), eicosenoic acid (20:1n9); and in the PUFA,  $\alpha$ -linolenic acid (18:3n3), linoleic acid (18:2n6). Results from hepatic pathway analysis corroborate our metabolomic findings and show unsaturated fatty acid metabolism pathways differentially altered with NASH between ethnicities. These ethnicity- related alterations in hepatic FFAs suggest variations in

processes including hepatic uptake of FFAs, DNL, PLs turnover and hepatic unsaturated fatty acid metabolism, which are worth further examination.

Upregulated hepatic FFA clearance may explain the observed elevation of hepatic FFAs in NASH-HIS. In fact, tracer studies in NAFLD show that 60% of hepatic lipid content originates from adipose tissue lipolysis, indicating a major contribution of the liver's uptake to hepatic FFAs profile [59]. In support, in both animals and humans, the expression and membrane localization for fatty acid translocase CD36 are increased in NASH [60].

Hepatic TGs accumulation is thought to be a protective adaptive mechanism from the lipotoxic effect of FFAs [61-63]. However, this notion is questioned as in subjects with early NAFL and no histological evidence of inflammation, the expression of several hepatic inflammatory genes were upregulated [64]. In NASH, DNL was reported to be increased in comparison to NAFL [65]. This process generates SFA(14-16:0), which are converted to MUFA via stearoyl-CoA desaturase (SCD1, or  $\Delta$ -9 desaturase) and further esterified to form DGs and TGs [66]. In our study, NASH in both ethnicities showed no differences in the estimated hepatic  $\Delta$ -9 desaturase index (results not shown). NASH also had higher level of TGs, but more profound in HIS with a trend of higher DGs. The higher levels of TGs, DGs and MUFA observed in NAHS-HIS suggest increased DNL. In NASH-HIS, lobular inflammation correlated positively with TG(44-60:0-4) ( $r > 0.7$ ,  $p < 0.05$ ), DG(34-36:1-3) ( $r > 0.7$ ,  $p < 0.000$ ) and the MUFAs, heptadecenoic acid (17:1n7), oleic acid (18:1n9), eicosenoic acid (20:1n9), and nervonic acid (24:1n9) ( $r > 0.8$ ,  $p < 0.00$ ) suggesting an involvement of TGs, DGs, MUFAs with NASH in HIS. Interestingly, in NASH-CAU a negative correlation ( $r > -0.6$ ,  $p < 0.05$ ) was observed between hepatocellular inflammation and heptadecenoic acid (17:1n7), oleic acid (18:1n9), with tendency shown for palmitoleic acid (16:1n7). While, when tested individually, MUFAs are shown to be less lipotoxic compared than SFAs, it has been shown that treatment of HepG2 cells and human primary hepatocytes with a mixture of five SFAs and MUFAs as observed in NASH, exhibited higher toxicity compared to the mixture reported in normal liver and NAFL [21,24]. Therefore, the effect of MUFAs may be dependent factors including proportion and composition.

Also in our samples, plasma TGs were differentially higher in NASH-HIS, which suggests upregulated hepatic export or impaired peripheral clearance.

An upregulated PL turnover can contribute to elevated unsaturated fatty acids. In our results, the strong correlation found between the altered MUFAs, PUFAs and many lysophospholipid species (Table S8) suggests a shared biochemical pathway. As part of hepatic lipid remodeling, phospholipase A<sub>2</sub> catalyzes the breakdown of membrane PL to form lysophospholipids and release unsaturated fatty acids. In NASH, the transcript level of cytosolic phospholipases A<sub>2</sub> (*cPLA*<sub>2</sub>) is upregulated [67]. Also, NASH is markedly lower in hepatic PCs content and higher in LPCs [24,28,68]. Our results are in line with the decreased hepatic PCs and PEs profile seen in NASH in both ethnicities, with more marked reductions seen in NAHS-HIS. However, the hepatic LPC and LPE profile showed differential alterations by ethnicity with higher levels observed in HIS and lower levels in CAU. Together, the higher abundance of hepatic PUFA, lower level of PC and higher LPC seen in NASH-HIS support an upregulated hepatic PL turnover. The depletion in PC or alteration in PC to PE ratio disrupts the function and integrity of cellular, mitochondrial and lipid droplets bio-membranes and results in cellular stress, apoptosis and inflammation [69]. *In vitro* evidence shows a lipotoxic effect of LPC by altering mitochondrial function and activating apoptosis [23,70,71]. In HIS-NASH, lobular inflammation correlated positively with LPC(16-20:0-5) and the PUFA, linoleic acid (18:2n6),  $\alpha$ -linolenic acid (18:3n3) and eicosadienoic acid (20:2n6); and negatively with PC(32-40:1-7) and PE(34-38:2-6) ( $r > 0.8$ ,  $p < 0.006$ ), which are also in support of a role of upregulated PLs turnover in NASH pathogenesis.

A decrease in hepatic fatty acid desaturase-1 (FADS1,  $\Delta$ -5 desaturase) is reported with NASH [24]. This is thought to induce preferential increase in n6 PUFAs flux at the expense of n3 PUFAs. Accordingly, NAFLD progression is characterized by de-enrichment of long-chain PUFAs with a shift towards a higher n6 to n3 PUFAs ratio seen across multiple lipid classes [27,28]. In the current study, we estimated  $\Delta$ -5 desaturase and the relative ratio of n6 to n3 PUFAs from hepatic FFAs and results show no differences with NASH for both ethnicities (not shown).

Also, the progression to NASH was associated with reduction in most hepatic ACs in both ethnicities with differentially lower AC(12-18: 0-2) seen in HIS. We also found the hepatic AC(5-18:0-4) correlated negatively with lobular inflammation in NASH-HIS. In plasma, 3-hydroxybutyric acid was found differentially reduced in NASH-HIS. 3-hydroxybutyric (or  $\beta$ -hydroxybutyrate) is a liver-produced ketone body from acetyl-CoA derived from mitochondrial  $\beta$ -oxidation of fatty acid [72]. Together, these findings suggest a role of mitochondrial  $\beta$ -oxidation dysfunction in both ethnicities with NASH.

Alterations in hepatic amino acid, choline, methionine and SAME profiles were associated with NASH but not different between ethnicities. The dysregulations in hepatic unsaturated fatty acid metabolism associated with NASH progression were not reflected in plasma. This, along with the limited correlations of plasma metabolomic profile with liver histological scores, leads us to conclude plasma profile is not an optimal predictor of hepatic histological differences relevant to NASH.

Our data may be used for hypotheses generation. Diet is a modulator of PUFAs status [73]. In this study, we did not account for the role of diet or the treatment with lipid-lowering drugs to the ethnicity-related differences observed in NAFL and NASH. Since performing a liver biopsy without clinical indication is ethically questionable, we could not confirm that our HC subjects are free from liver pathology. It might have been interesting to genotype our subjects for *PNPLA3* as the G allele is robustly associated with NAFLD and the homozygous rs738409 [G] variant presents with high frequency in HIS [74-76]. Due to sample size, cross-sectional and proof-of-concept nature, our findings need to be confirmed in larger and mechanistic settings. In particular, based on selected metabolites with ethnicity interaction ( $p < 0.05$ ) (Table S15), the minimum sample size required to verify plasma findings in lean healthy subjects is 45 subjects per group. To verify alterations in hepatic lipidomic profile, a minimum of 24 and 12 subjects would be required for each arm in CAU and HIS, respectively.

To our knowledge, this is the first metabolomic profiling addressing ethnicity in NAFLD. Our NAFL patients are biopsy-characterized with comparable BMI, clinical and histological presentations; with almost all plasma and liver samples obtained from the same subjects. Our findings provide

preliminary evidence supporting ethnicity-related variations in NAFLD pathogenesis and highlight signs of metabolic perturbations in HIS independent of obesity and other components of metabolic syndrome. With the progression to NASH, our data suggest ethnicity-related alterations in hepatic unsaturated fatty acids metabolism and points toward potential involvement of lipotoxicity in its mechanisms. We postulate that such alterations predispose HIS to higher rate of NAFLD and/or add a “hit” component when coexisting with metabolic syndrome to act as a driver for the advanced NASH presentation seen in HIS.

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## 7. Tables:

**Table 1.** Demographic, clinical, and histological characteristics of study subjects.

	Hispanics		Caucasians		<i>p</i> -value		
	NAFL	HC	NAFL	HC	a	b	c
Liver, n (F/M)	7 (5/2)	-	10 (5/5)	-			
Plasma, n (F/M)	7 (5/2)	14 (6/8)	8 (4/4)	8 (4/4)			
Age (Yrs.)	45 ± 16	43 ± 14	50 ± 16	44 ± 12	0.818	0.413	0.55
BMI (Kg/m <sup>2</sup> )	47 ± 7	26 ± 2	42 ± 7	25 ± 3	<.0001	<.0001	0.28
DM, yes (%)	3 (42.9)	-	4 (40)	-	-	-	0.913
FBG (mmol/L)	93 ± 5	-	94 ± 13	-	-	-	0.88
Cholesterol(mg/dL)	168 ± 29	-	173 ± 33	-	-	-	0.952
TG (mg/dL)	112 ± 37	-	139 ± 65	-	-	-	0.42
HDL (mg/dL)	44 ± 7	-	41 ± 8	-	-	-	0.403
LDL (mg/dL)	102 ± 23	-	104 ± 33	-	-	-	0.855
HbA1c (%)	6.1 ± 0.7	-	6.2 ± 0.8	-	-	-	0.67
AST (U/L)	27 ± 12	-	31 ± 19	-	-	-	0.499
ALT (U/L)	34 ± 18	-	31 ± 10	-	-	-	0.752
Platelet	308 ± 58	-	292 ± 100	-	-	-	0.506
NAS	2.43 ± 2.40	-	3 ± 1.5	-	-	-	0.653
NASH, yes (%)	6 (60)	-	5 (50)	-	-	-	0.708
<b>Steatosis (%)</b>							
< 5%	3 (42.8)	-	2 (20)	-	-	-	
5 to ≤ 33%	2 (28.6)	-	5 (50)	-	-	-	
34 to ≤ 66 %	2 (28.6)	-	2 (20)	-	-	-	0.452
> 66%	0 (0)	-	1 (10)	-	-	-	
<b>Inflammation (%)</b>							
None	3 (42.9)	-	1 (10)	-	-	-	
Mild	1 (14.3)	-	6 (60)	-	-	-	
Moderate	2 (28.6)	-	3 (30)	-	-	-	0.763
Severe	1 (14.3)	-	0 (0)	-	-	-	
<b>Ballooning (%)</b>							
None	4 (57)	-	5 (50)	-	-	-	
Few	3 (42.9)	-	5 (50)	-	-	-	0.772
Many	0 (0)	-	0 (0)	-	-	-	
<b>Fibrosis (%)</b>							
None	7 (100)	-	9 (90)	-	-	-	
1A	0 (0)	-	1 (10)	-	-	-	
2	0 (0)	-	0 (0)	-	-	-	0.998
4	0 (0)	-	0 (0)	-	-	-	

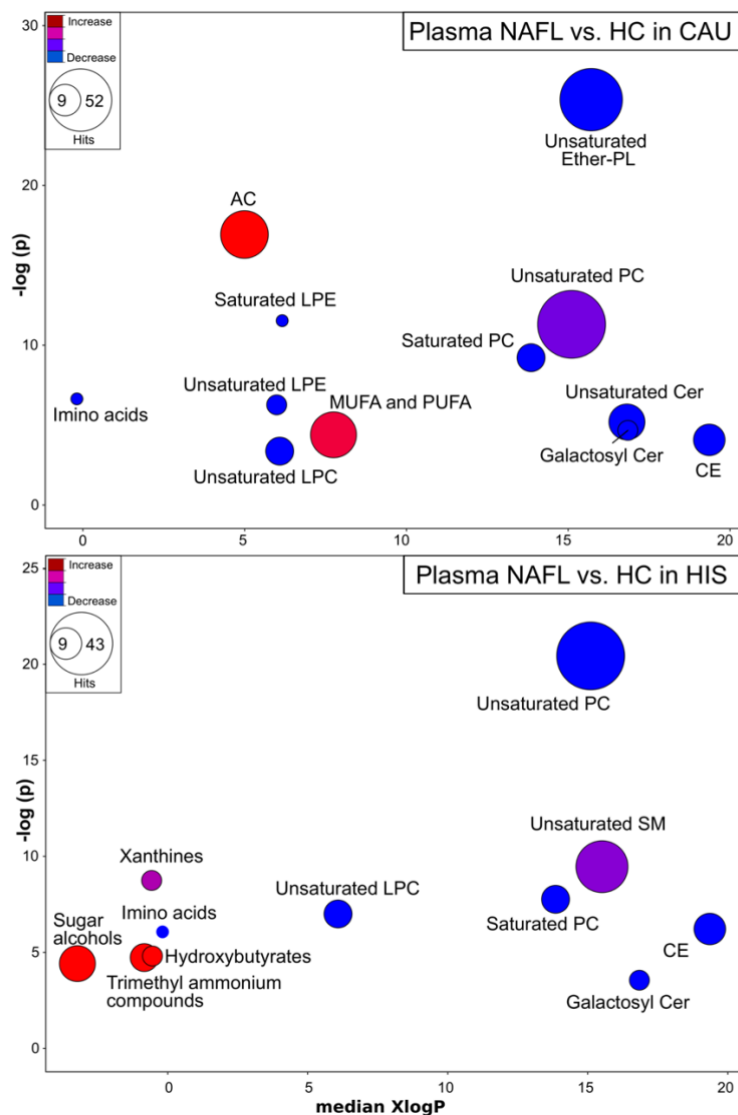
General characteristics are shown as percent (for categorical data) and mean ± SEM (for nominal data). Group comparisons were performed by chi-square test (categorical) or t- test (nominal). (a) NAFL-HIS vs. HC-HIS; (b) NAFL-CAU vs. HC-CAU; (c) NAFL-HIS vs. NAFL-CAU. ALT, alanine aminotransferase; AST, aspartate aminotransferase; BMI, body mass index; DM, diabetes mellitus; FBG, fasting blood glucose; HbA1c, hemoglobin A1c; HDL, high-density lipoprotein; LDL, low density lipoprotein; NAS, the NAFLD Activity Score; TG, triglycerides.

**Table 2.** Demographic, clinical, and histological characteristics of subjects with NASH.

	Hispanics		Caucasians		<i>p</i> -value	
	0 NASH	NASH	0 NASH	NASH	a	b
Liver, n (F/M)	4(3/1)	3(2/1)	5(3/2)	5(2/3)		
Plasma, n (F/M)	4(3/1)	3(2/1)	5(3/2)	3(1/2)		
Age (Yrs.)	45 ± 21	46 ± 10	54 ± 19	45 ± 14	0.872	0.405
BMI (Kg/m <sup>2</sup> )	47.4 ± 7.9	45.7 ± 6.7	39.9 ± 4.4	44.4 ± 3.8	0.787	0.406
FBG (mmol/L)	93 ± 5	94 ± 4	98 ± 15	90 ± 10	0.873	0.379
TG (mg/dL)	105 ± 39	121 ± 40	120 ± 80	157 ± 50	0.59	0.35
AST (U/L)	20 ± 3	36 ± 14	21 ± 3	40 ± 23	0.064	0.0276
ALT (U/L)	23 ± 9	48 ± 18	25 ± 2.2	38 ± 11	0.0431	0.0246
Steatosis	12 ± 19	22.7 ± 9.3	15.6 ± 15.5	32.2 ± 21.8	0.197	0.1474
NAS	0.75 ± 1.1	4.7 ± 0.6	1.8 ± 1	4 ± 1	0.004	0.017
<b>Inflammation (%)</b>						
None	3(75)	0(0)	1(20)	0(0)		
Mild	1(25)	0(0)	3(60)	3(60)	0.998	0.323
Moderate	0(0)	2(66.7)	1(20)	2(40)		
Severe	0(0)	1(33.3)	0(0)	0(0)		
<b>Ballooning (%)</b>						
None	4(100)	0(0)	5(100)	0(0)		
Few	0(0)	3(100)	0(0)	5(100)	<0.0001	<0.0001
Many	0(0)	0(0)	0(0)	0(0)		
<b>Fibrosis (%)</b>						
None	4(100)	3(100)	5(100)	4(80)		
1A	0(0)	0(0)	0(0)	1(20)		
2	0(0)	0(0)	0(0)	0(0)	1	0.998
3	0(0)	0(0)	0(0)	0(0)		
4	0(0)	0(0)	0(0)	0(0)		

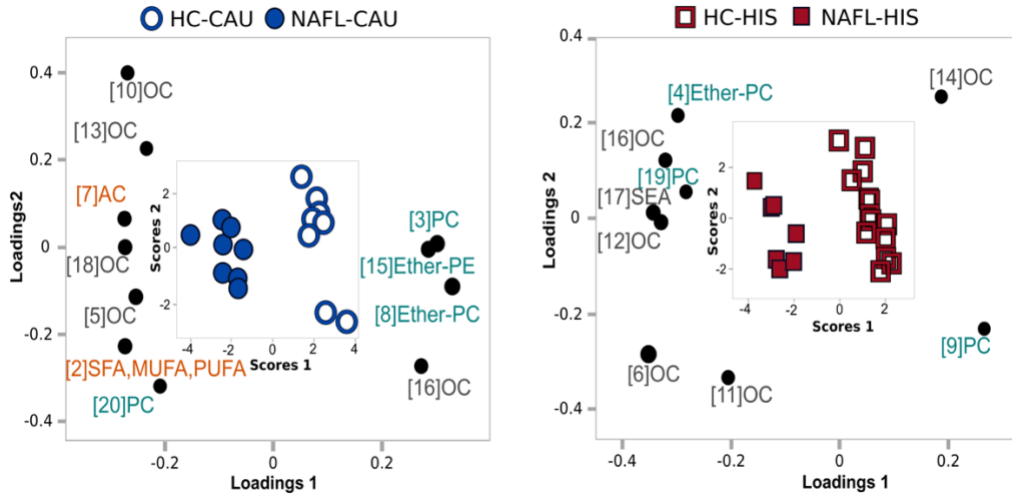
General characteristics are shown as percent (for categorical data) and mean ± SEM (for nominal data). Comparison was performed by *t*-test (nominal) or chi-square test (categorical). (a) NASH-HIS vs. 0-NASH-HIS; (b) NASH-CAU vs. 0-NASH-CAU. ALT, alanine aminotransferase; AST, aspartate aminotransferase; BMI, body mass index; FBG, fasting blood glucose; NAS, the NAFLD Activity Score; NASH, Nonalcoholic steatohepatitis; 0-NASH, Nonalcoholic steatohepatitis-free; TG, triglycerides.

## 8. Figures

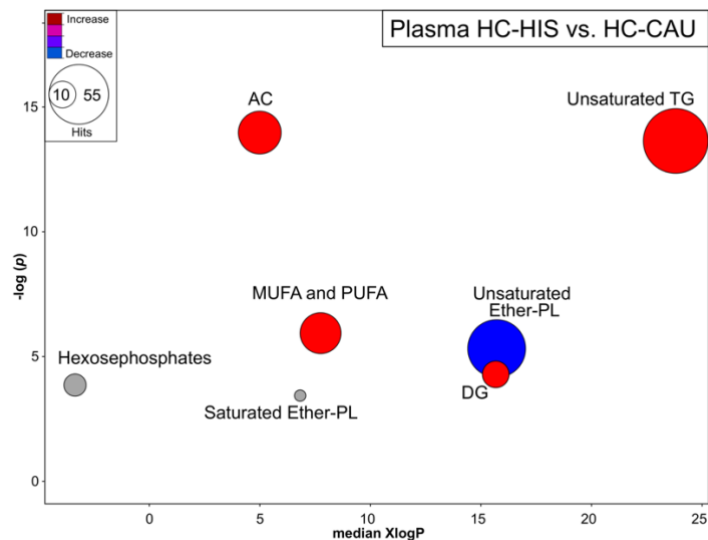


**Figure 1. Plasma metabolites altered by chemical class in NAFL, compared to HC in both ethnicities.**

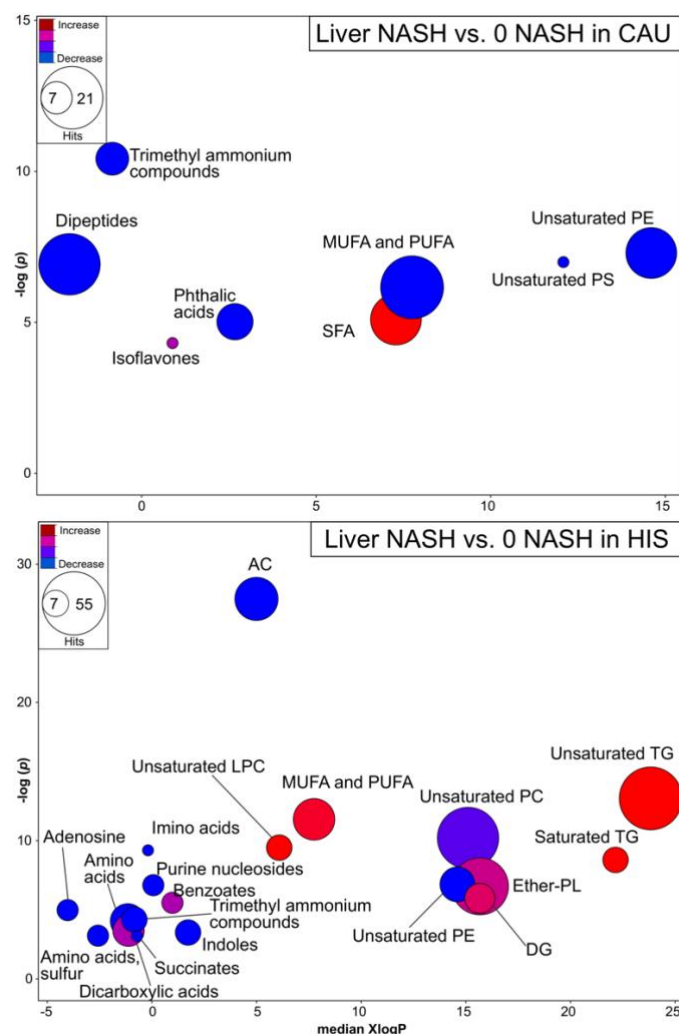
Chemical similarity enrichment analysis (ChemRICH) and enrichment statistics plot for NAFL vs. HC in CAU (top panel) and HIS (bottom panel). Each cluster represents altered chemical class of metabolites ( $p < 0.05$ ). Cluster sizes represent the total number of metabolites. Cluster's color represents the directionality of metabolite differences: red – higher in NAFL; blue – lower in NAFL. Colors in between refer to mixed population of metabolites manifesting both higher and lower levels in NAFL when compared to the control. The  $x$ -axis represents the cluster order on the chemical similarity tree. The plot  $y$ -axis shows chemical enrichment  $p$ -values calculated using Kolmogorov–Smirnov test. Only clusters with  $p < 0.05$  are shown. FDR-adjustment  $q = 0.2$ , and clusters with FDR-adjusted  $p \geq 0.2$  are shown in gray. ( $n$ , NAFL-HIS = 7, HC-HIS = 14; NAFL-CAU = 8, HC-CAU = 8). The detailed ChemRICH results are shown in (Table S1 and S2). AC, Acylcarnitines; CAU, White Caucasian; Cer, Ceramides; CE, Cholesteryl ester; DG, Diglycerides; Ether-PL, Ether-linked phospholipids; HIS, Hispanic; LPC, Lysophosphatidylcholine; LPE, Lysophosphatidylethanolamines; MUFA, Monounsaturated fatty acid; PC, Phosphatidylcholines; PUFA, Polyunsaturated fatty acids; SFA, Saturated fatty acids; SM, Sphingomyelins; NAFL, Steatosis; TG, Triglycerides.



**Figure 2. Supervised clustering model illustrating potential ethnicity-specific variations in plasma observed between NAFL vs. HC in both ethnicities.** Metabolites with  $p < 0.1$  for interaction (ethnicity x NAFL) from ANCOVA were clustered and cluster components were subjected to partial least square-discriminant analysis (PLS-DA) separately in each ethnicity. Only clusters of variable importance in projection (VIP) > 1 are illustrated. A combined loading and score plot for a) NAFL-CAU vs. HC-CAU; b) NAFL-HIS vs. HC-HIS. The model was validated with leave-one-out cross validation (LOOCV). The ( $Q^2$ ), ( $R^2X$ ) and ( $R^2Y$ ) is 0.817, 0.285 and 0.918; 0.816, 0.204 and 0.911 for CAU and HIS, respectively. The details on metabolites and clusters components are shown in (Table S3). AC, Acylcarnitines; CAU, White Caucasian; Ether-PC, Ether-linked phosphatidylcholines; Ether-PE, Ether-linked phosphatidylethanolamines; HC, Healthy control; HIS, Hispanic; MUFA, Monounsaturated fatty acid; OC, Organic compounds; PC, Phosphatidylcholines; PUFA, Polyunsaturated fatty acids; NAFL, Steatosis; SEA, Stearoyl ethanolamine; SFA, Saturated fatty acids.

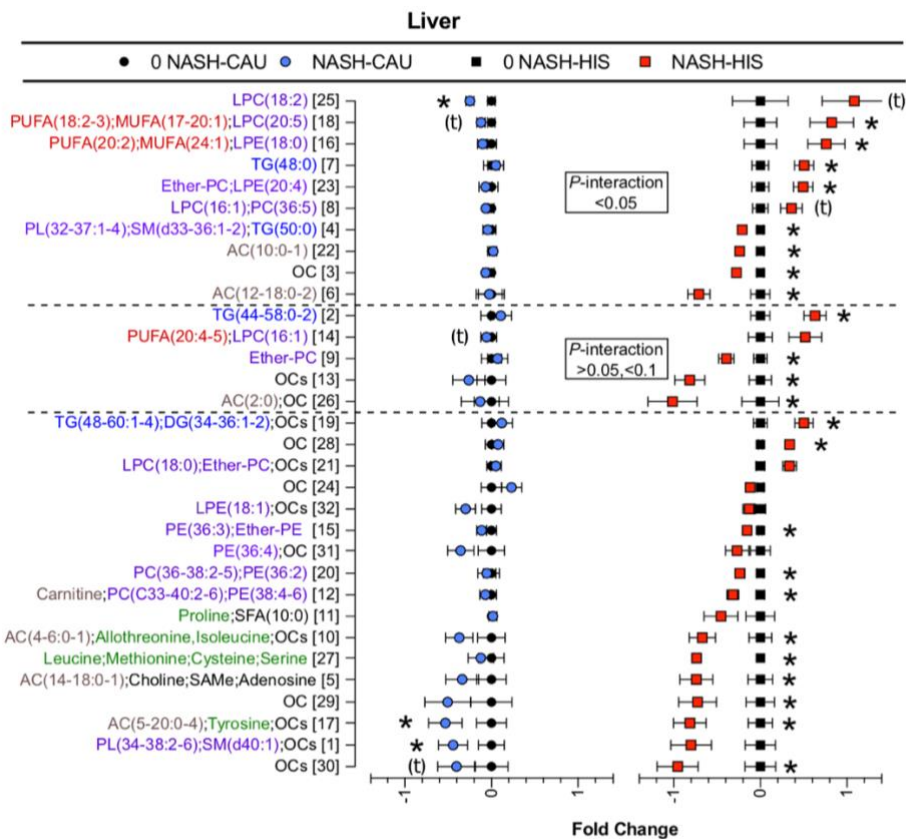


**Figure 3. Plasma metabolites altered by chemical class in lean healthy control subjects between ethnicities.** Chemical similarity enrichment analysis (ChemRICH) highlighting plasma metabolomic changes observed in HC-HIS, compared to HC-CAU. Each cluster represents altered chemical class of metabolites ( $p < 0.05$ ). Cluster sizes represent the total number of metabolites. Cluster color represents the directionality of metabolite differences: red – higher in HC-HIS; blue – lower in HC-HIS. Colors in between refer to mixed population of metabolites manifesting both higher and lower levels in HC-HIS when compared to the HC-CAU. The  $x$ -axis represents the cluster order on the chemical similarity tree. The plot  $y$ -axis shows chemical enrichment  $p$ -values calculated using Kolmogorov–Smirnov test. Only clusters with  $p < 0.05$  are shown. FDR-adjustment  $q = 0.2$ , and clusters with FDR-adjusted  $p \geq 0.2$  are shown in gray. ( $n$ , HC-HIS = 14, HC-CAU = 8) The detailed ChemRICH results are shown in (Table S4). AC, Acylcarnitines; CAU, White Caucasian; DG, Diglycerides; Ether-PC, Ether-linked phospholipids; HIS, Hispanic; MUFA, Monounsaturated fatty acid; PUFA, Polyunsaturated fatty acids; TG, Triglycerides.

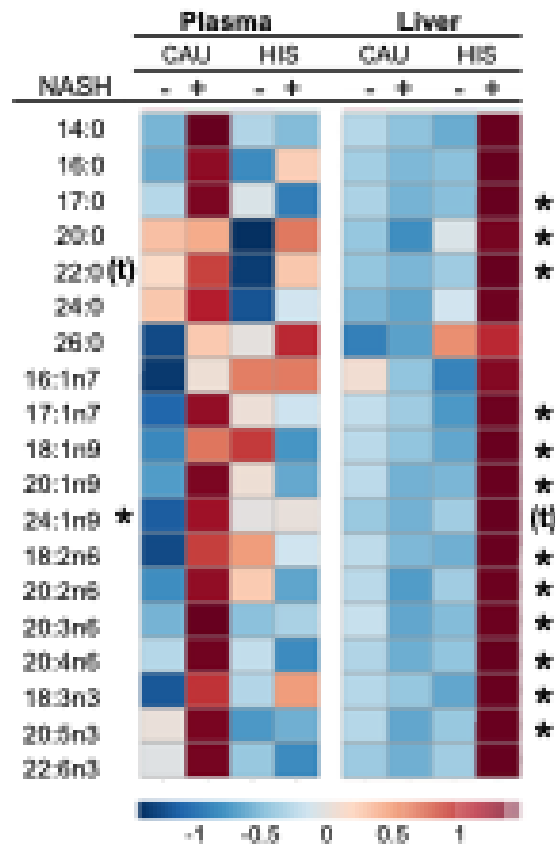


**Figure 4. Liver metabolites altered by chemical class in NASH, compared to NASH-free subjects, in both ethnicities.** Chemical similarity enrichment analysis (ChemRICH) illustrating hepatic metabolite class altered in NASH compared to 0-NASH in both ethnicities. ChemRICH enrichment statistics plot, illustrating liver alterations in NASH vs. 0-NASH in CAU (top panel) and HIS (bottom panel). Each cluster represents altered chemical class of metabolites ( $p < 0.05$ ). Cluster sizes represent the total number of metabolites. Cluster's color represents the directionality of metabolite differences: red – higher in NASH; blue – lower in NASH. Colors in between refer to mixed population of metabolites manifesting both higher and lower levels in NASH when compared to the 0-NASH. The  $x$ -axis represents the cluster order on the chemical similarity tree. The plot  $y$ -axis shows chemical enrichment  $p$ -values calculated using Kolmogorov–Smirnov test. Only clusters with  $p < 0.05$  are shown. FDR-adjustment  $q = 0.2$ , and clusters with FDR-adjusted  $p \geq 0.2$  are shown in gray. ( $n$ , 0 NASH-HIS = 4, NASH-HIS = 3; 0 NASH-CAU = 5, NASH-CAU = 5). The detailed ChemRICH results are shown in (Table S6 and S7). AC, Acylcarnitines; CAU, White Caucasian; Cer, Ceramides; CE, Cholesteryl ester; DG, Diglycerides; Ether-PL, Ether-linked phospholipids; HIS, Hispanic; LPC, Lysophosphatidylethanolamines; MUFA, Monounsaturated fatty acid; NASH, Nonalcoholic steatohepatitis; 0-NASH, Nonalcoholic steatohepatitis-free; PC, Phosphatidylecholine; PE, Phosphatidylethanolamine; PUFA, Polyunsaturated fatty acids; SFA, Saturated fatty acids; TG, Triglycerides.

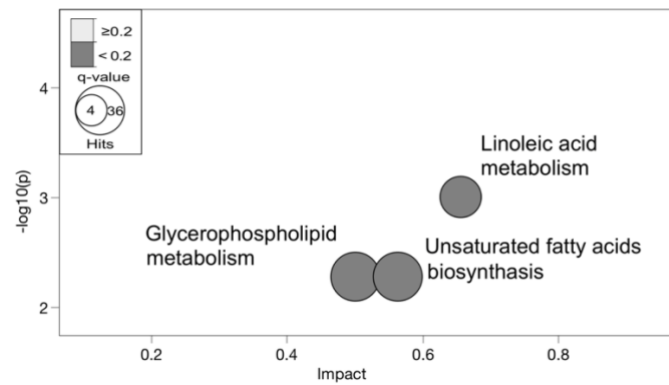




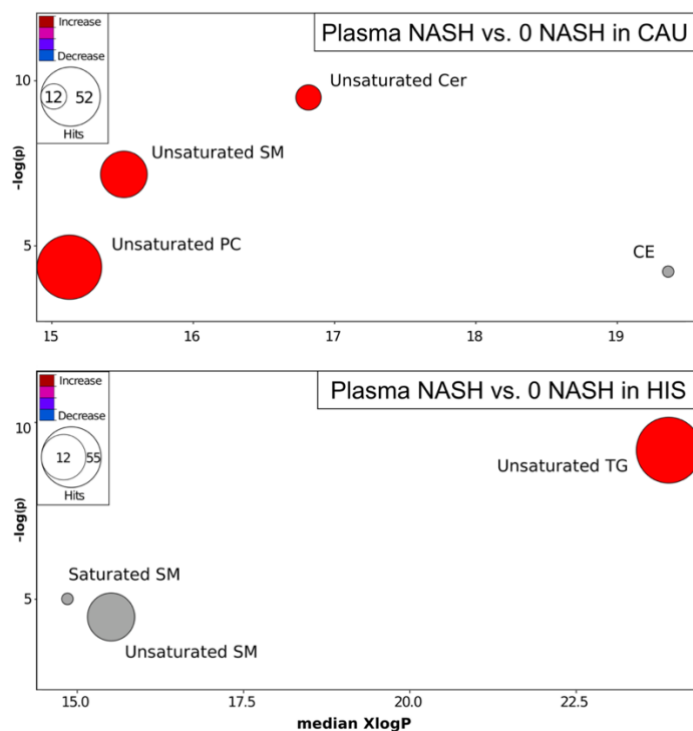
**Figure 5. Ethnicity-related variations in liver metabolomic profile in NASH vs. 0-NASH.** Results of *t*-test and ANCOVA (ethnicity x NASH) interaction comparison performed on plasma variable cluster components between NASH and 0-NASH in both ethnicities. Clustering was performed on metabolites that were different ( $p < 0.05$ ) within groups (NASH vs. 0-NASH) or between ethnicity groups (interaction (NASH x ethnicity)). Data are presented as the fold change from 0-NASH; error bars represent standard error. Metabolite clusters are ranked in order of  $p$ -value for (interaction (NASH x ethnicity) and labeled by a number and a description of representative metabolite. For complex lipids, lipid class is followed by number of (carbons, double bonds) of the fatty acyl moiety. Clusters with interaction ( $p < 0.05$ ) or tendency for interaction ( $p = 0.05$  to  $< 0.1$ ) are marked with the dashed line. Clusters showing ethnicity-related differences in NASH ( $p < 0.05$ ) or tendency for interaction ( $p = 0.05$  to  $< 0.1$ ) are marked with the dashed line. Clusters affected by NASH within ethnicity ( $p < 0.05$ ) are denoted with (\*); clusters with tendency ( $p = 0.05$  to  $< 0.1$ ) are denoted with (t). ( $n$ , 0 NASH-HIS = 4, NASH-HIS = 3; 0 NASH-CAU = 5, NASH-CAU = 5). The details on metabolites and clusters components are shown in (Table S8). AC, Acylcarnitines; CAU, White Caucasian; DG, diglycerides; Ether-PC, Ether-linked phosphatidylcholines; Ether-PE, Ether-linked phosphatidylethanolamines; HIS, Hispanic; MUFA, Monounsaturated fatty acid; NASH, Nonalcoholic steatohepatitis; 0-NASH, Nonalcoholic steatohepatitis-free; OC, Organic compounds; PC, Phosphatidylcholines; PE, Phosphatidylethanolamine; PL, Phospholipids; PUFA, Polyunsaturated fatty acids; NAFL, Steatosis; SAME, S-Adenosyl-L-methionine; SFA, Saturated fatty acids; SM, sphingomyelins; TG, triglycerides.



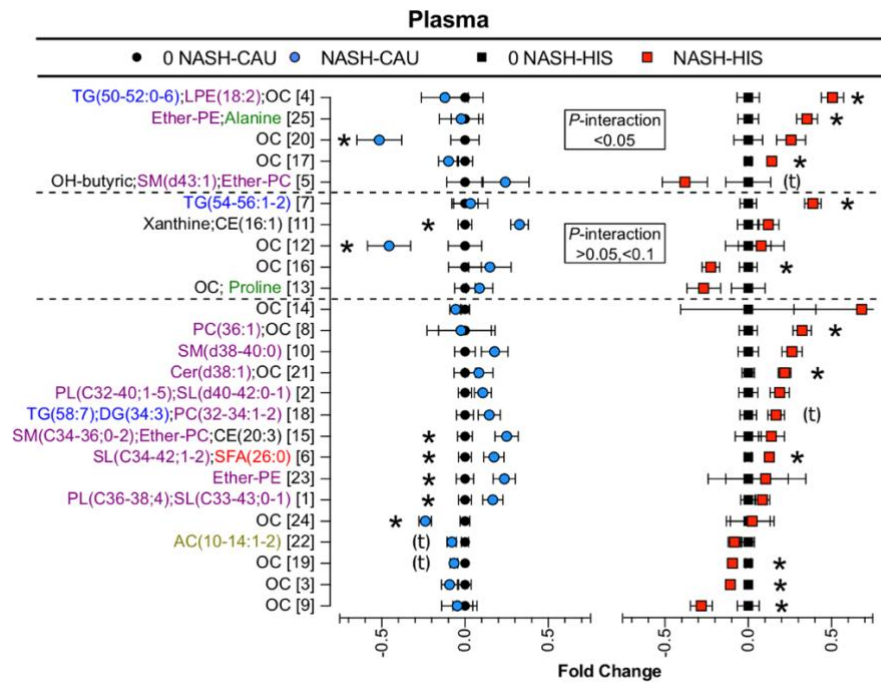
**Figure 6. Heat-map for plasma and liver free fatty acids with fold change and  $p$ -values in NASH vs. 0 NASH in both ethnicities.** Group means are shown with normalized data converted to z-scores. Fatty acids showing ethnicity-related differences ( $p < 0.05$  on interaction NASH x ethnicity) in are denoted by (\*), and with tendency for interaction ( $p = 0.05$  to  $< 0.1$ ) are denoted with (t). Mean direction of change is indicated by color and intensity, with red representing increased values, and blue representing decreased values. CAU, White Caucasian; HIS, Hispanics; NASH, Nonalcoholic steatohepatitis.



**Figure 7. Hepatic metabolic pathways differentially altered with NAHS between ethnicities.** Metabolites with differential alterations between ethnicity in NASH ( $p < 0.05$ ) were compared against pathway-associated metabolites sets from Kyoto Encyclopedia of Genes and Genomes (KEGG) [46]. Metabolic pathways significantly altered are shown as nodes. The (y-axis) represents the  $p$ -values as determined by Fisher's Exact test. The (x-axis) represents the impact of pathways as determined by the relative betweenness centrality-topology analysis. The size of the node represents the total hit number of hits. ( $n$ , 0 NASH-HIS=4, NASH-HIS=3; 0 NASH-CAU=5, NASH-CAU=5). Detailed pathway analysis statistics are shown in (Table S9).



**Figure 8. Plasma metabolites altered by chemical class in NASH, compared to NASH-free subjects, in both ethnicities.** Chemical Similarity Enrichment Analysis (ChemRICH) of illustrating plasma metabolite class altered in NASH compared to 0-NASH in both ethnicities. ChemRICH enrichment statistics plot, illustrating plasma alterations in NASH vs. 0-NASH in CAU (top panel) and HIS (bottom panel). Each cluster represents altered chemical class of metabolites ( $p < 0.05$ ). Cluster sizes represent the total number of metabolites. Cluster's color represents the directionality of metabolite differences: red – higher in NASH; blue – lower in NASH. Colors in between refer to mixed population of metabolites manifesting both higher and lower levels in NASH when compared to the 0-NASH. The  $x$ -axis represents the cluster order on the chemical similarity tree. The plot  $y$ -axis shows chemical enrichment  $p$ -values calculated using Kolmogorov–Smirnov test. Only clusters with  $p < 0.05$  are shown. FDR-adjustment  $q=0.2$ , and clusters with FDR-adjusted  $p \geq 0.2$  are shown in gray. ( $n$ , 0 NASH-HIS=4, NASH-HIS=3; 0 NASH-CAU=5, NASH-CAU=3). The detailed ChemRICH results are shown in (Table S10 and S11). CAU, White Caucasian; Cer, Ceramides; CE, Cholesteryl ester; HIS, Hispanic; SM, Sphingomyelins; NASH, Nonalcoholic steatohepatitis; PC, Phosphatidylcholine; TG, Triglycerides.



**Figure 9. Ethnicity-related differences in plasma metabolomic profile in NASH vs. 0-NASH.** Results of  $t$ -test and ANCOVA (ethnicity  $\times$  NASH) interaction comparison performed on plasma variable cluster components between NASH and 0-NASH in both ethnicities. Clustering was performed on metabolites that were different ( $p < 0.05$ ) within groups (NASH vs. 0-NASH) or between ethnicity groups (interaction (NASH  $\times$  ethnicity)). Data are presented as the fold change from 0-NASH; error bars represent standard error. Metabolite clusters are ranked in order of  $p$ -value for (interaction (NASH  $\times$  ethnicity) and labeled by a number and a description of representative metabolite. For complex lipids, lipid class is followed by number of (carbons, double bounds) of the fatty acyl moiety. Clusters showing ethnicity-related differences in NASH ( $p < 0.05$ ) or tendency for interaction ( $p = 0.05$  to  $< 0.1$ ) are marked with the dashed line. Clusters affected by NASH within ethnicity ( $p < 0.05$ ) are denoted with (\*); clusters with tendency ( $p = 0.05$  to  $< 0.1$ ) are denoted with (t). ( $n$ , 0 NASH-HIS=4, NASH-HIS=3; 0 NASH-CAU=5, NASH-CAU=3). The details on metabolites and clusters components are shown in (Table S12). AC, Acylcarnitines; CAU, White Caucasian; CE, cholesteryl ester; DG, diglycerides; Ether-PC, Ether-linked phosphatidylcholines; Ether-PE, Ether-linked phosphatidylethanolamines; HIS, Hispanic; MUFA, Monounsaturated fatty acid; NASH, Nonalcoholic steatohepatitis; 0-NASH, Nonalcoholic steatohepatitis-free; OC, Organic compounds; PC, Phosphatidylcholines; PL, Phospholipids; PUFA, Polyunsaturated fatty acids; NAFL, Steatosis; SFA, Saturated fatty acids; SM, sphingomyelins; TG, triglycerides.

## 9. Supplemental materials

**Table S1.** ChemRich enrichment statistics for plasma comparisons of obese with NAFL vs. lean healthy control in White Caucasian.

**Table S2.** ChemRich enrichment statistics for plasma comparisons of obese with NAFL vs. lean healthy control in Hispanic.

**Table S3.** Untargeted semi-quantification data table for comparisons of obese with NAFL (NAFL) vs. lean healthy control (HC) in Hispanic (HIS) and White Caucasian (CAU).

**Table S4.** ChemRich enrichment statistics for plasma comparisons of healthy control Hispanic vs. White Caucasian.

**Table S5.** Untargeted semi-quantification data table for comparisons of healthy control subjects between ethnicities.

**Table S6.** ChemRich enrichment statistics for liver comparisons of NASH vs. 0-NASH in Hispanic.

**Table S7.** ChemRich enrichment statistics for liver comparisons of NASH vs. 0-NASH in White Caucasians.

**Table S8.** Untargeted semi-quantification data table for comparisons of liver metabolomic profiles in NASH vs. 0-NASH in both ethnicities.

**Table S9.** Results from pathway analysis performed on liver metabolites of interaction with ethnicity in NASH. Metabolites with ( $p$ -value  $<0.05$ ) on (ethnicity x NASH) from ANCOVA were mapped against pathway-associated metabolites sets from Kyoto Encyclopedia of Genes and Genomes (KEGG).

**Table S10.** ChemRich enrichment statistics for plasma comparisons of NASH vs. 0-NASH in Hispanics.

**Table S11.** ChemRich enrichment statistics for plasma comparisons of NASH vs. 0-NASH in White Caucasian.

**Table S12.** Untargeted semi-quantification data table for comparisons for plasma metabolomic profiles in NASH vs. 0-NASH in both ethnicities.

**Table S13.** Spearman's rank correlation analysis performed on liver metabolites and histological features in NASH.

**Table S14.** Spearman's rank correlation analysis performed on plasma metabolites and histological features in NASH.

**Table S15.** The minimum sample size required to detect differences between group means with 80% power and 95% confidence level was calculated. Calculation is based on selected metabolites with ethnicity interaction ( $p <0.05$ ) for (a) Lean healthy comparison, (b) NASH comparison.

**Figure S1.** Natural clustering of study groups illustrating variations in plasma metabolomic profile

## **Chapter 3**

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### ***Targeted oxylipins and endocannabinoid profiling***

## 1. Introduction

Non-alcoholic fatty liver disease (NAFLD) is a chronic liver condition affecting one in four adults worldwide and this rate increases with coexisting components of metabolic syndrome [1]. Its histological presentation includes hepatocellular steatosis, or non-alcoholic fatty liver (NAFL) with a range of necroinflammation with or without fibrosis. When hepatocellular damage and ballooning are present, this is clinically defined as non-alcoholic steatohepatitis (NASH) [2]. The pathogenesis of NAFLD is not fully elucidated. Whereas its onset involves an interplay between genetics and environmental factors with coexisting comorbidities, the progression to NASH appears to be provoked by multiple or parallel hits including oxidative stress and inflammation [3,4]. Oxidative stress modulates insulin signaling, lipid metabolism, inflammation, and fibrogenesis, and many oxidative stress biomarkers have been associated with NAFLD severity [5,6]. In the U.S., the risk and severity of NAFLD vary among ethnic/racial groups, with Hispanics (HIS) being affected disproportionately and presenting more frequently with advanced inflammation and fibrosis compared to other ethnicities [7-9]. The metabolic drivers underlying this disparity are not clear.

Polyunsaturated fatty acid (PUFAs) are bioactive lipids and precursors to inflammatory lipid mediators including oxylipins (OXLs) and endocannabinoids (eCBs). OXLs are produced from PUFAs by mono- and dioxygenases, including lipoxygenases (e.g., 5-LOX, 12-LOXs, and 15-LOXs); cyclooxygenases (i.e., COX-1 and -2), and a variety of cytochrome P450s (CYPs) [10]. PUFAs can also undergo non-enzymatic oxygenation mediated by free radicals and the rate of this production is increased under oxidative stress [11]. In general, OXLs from n-3 PUFAs have anti-inflammatory or less pro-inflammatory effect compared to those derived from n-6 PUFAs [12,13]. The fatty acid ethanolamides (i.e., N-acylethanolamides), one class of eCB, are synthesized by complex interactions of lipases and fatty acid amide hydrolase from PUFAs and membrane associated precursors [14]. Collectively, these lipids work through receptor-mediated mechanisms and likely contribute to NAFLD by modulating processes including lipogenesis, inflammation, and mitochondrial  $\beta$ -oxidation [10,15].



Previous lipidomic analyses showed that NAFLD is associated with dysregulated PUFAs metabolism [16-20]. Alterations in circulating OXL and eCB profiles are reported in NAFLD and other liver pathologies. In fact, numerous lipid mediators have been shown to predict NAFL or NASH [18,21-26]. However, metabolomic profiling in NAFLD with regards to ethnicity is limited. Our prior semi-quantitative lipidomic profiling study indicated ethnicity-specific differences in plasma PUFA profiles in subjects with NAFL, with higher abundance of linoleic acid (LA) and  $\alpha$ -linolenic acid (ALA) seen in Caucasians (CAU) compared to ethnicity-matched lean subjects [27]. In the same study, the progression to NASH was characterized by ethnicity-specific differences in hepatic lipidomic profiles with higher levels of saturated and unsaturated fatty acids seen in NASH-HIS. Ethnicity was not previously addressed in OXL and eCB profiling efforts. Examining such lipidomic differences among ethnicities may shed light on potential mechanisms modulating the disparity in NAFLD prevalence and severity.

The objective of this “proof-of-concept” study is to examine ethnicity-related changes in PUFAs and their downstream inflammatory mediators in a group of subjects with obesity and biopsy-confirmed NAFL and NASH. We employed targeted lipidomic analysis of plasma PUFAs, OXLs, and the N-acyl ethanolamides class of eCBs to compare HIS and CAU subjects with medically complicated obesity to ethnicity-matched lean healthy controls (HC). Profiles in subjects diagnosed with NASH were also compared to ethnicity and BMI-matched participants without NASH (0-NASH). In addition, we conducted a secondary analysis including prospectively collected subjects to compare OXL profile between ethnicities in NASH.

## **2. Subjects and methods**

### **2.1. Subjects and samples**

In this retrospective/ prospective cohort study (Figure S4), all subjects self-reported ethnicity as either HIS or CAU. HC subjects ( $n = 22$ ) were recruited via public posts. Plasma and liver samples from bariatric surgery patients with medically complicated obesity were retrieved from the biobank repository of the Division of Gastroenterology and Hepatology, UC Davis Medical Center. The primary cohort ( $n = 18$ ) consisted of subjects with NAFL and various degrees of necroinflammation.

Only subjects with NASH were included in the secondary analysis ( $n = 9$ ) and this cohort was expanded with prospectively collected subjects diagnosed with NASH ( $n = 20$ ). Subject inclusion and exclusion criteria and details on data collection are described elsewhere [25]. Briefly, plasma samples were collected preoperatively after an overnight fast, and liver tissue samples were collected by biopsy performed during bariatric surgery. Liver histopathological evaluations were performed in a blinded fashion in the UC Davis Medical Center Department of Pathology, and samples were scored according to the NASH Clinical Research Network (NASH-CRN) histology system, The NAFLD Activity Score (NAS) and fibrosis scores were calculated [26]. NASH diagnosis was determined using a diagnostic algorithm based on steatosis, inflammation, and fibrosis scores [27]. All subjects were consented and the Institutional Review Board at the University of California, Davis approved the study protocol (# 856052).

## ***2.2. Plasma targeted lipidomic analysis***

Quantitative lipidomic profiling of PUFAs, OXLs and NAEs was performed by ultra-high-performance liquid chromatography-electrospray ionization-tandem mass spectrometry (UPLC-ESI-MS/MS) (S2), as previously described [28]. Briefly, plasma samples were enriched with deuterated surrogates, isolated by liquid/liquid extraction, and separated and quantified by UPLC-ESI-MS/MS. In the primary analysis, ESI-polarity switching facilitated the simultaneous detection of eCBs (positive mode) and oxylipins and PUFAs (negative mode) on an API 6500 QTRAP (AB Sciex, Framingham, MA, USA). Metabolites were quantified against authentic analytical standards with 6- to-10-point calibration curves and calculated concentrations were corrected for analytical surrogate recovery. This method detected 5 PUFAs and 66 lipid mediators, including 10 eCBs and 46 OXLs.

The secondary analysis was performed on an API 4000 QTrap (AB Sciex) and restricted to the negative mode electrospray ionization to increase the power of the OXLs discovery. This approach detected 46 OXLs and two nitrolipids. Details on the analysis protocols and reported data are available on the Metabolomics Workbench (<http://www.metabolomicsworkbench.org>, accessed on 06/13/2021), ID numbers (ST000977 and ST001845). Analyses were carried out at the UC Davis

West Coast Metabolomics Center. In this manuscript, abbreviations used for OXLs and eCBs follow standard consensus and are detailed with lipid identifiers in Table S6.

### 2.3. Statistical analysis

Statistical analyses were performed using JMP Pro 14.1 (SAS Institute Inc., Cary, NC; <http://www.jmp.com>, accessed on 03/10/2021). Outliers were identified and excluded using “robust Huber M test”. Lipids with >30% missing data were excluded. Missing data were imputed by “multivariate normal imputation”. Data normality was achieved by Johnson’s transformation. After data processing, and to determine if subjects with stage 4 fibrosis ( $n = 2$ ) are biological outliers, we employed principal component analysis (PCA). As a result, no outliers were detected (Figure S5).

Non-normalized data were used to calculate metabolite geometric means. Fold change (FC) was calculated for each ethnicity separately as  $(A - B)/B$  where A is the mean of (NAFL or NASH) and B is the mean of (HC or 0-NASH). A FC >0 indicates an increase and <0 indicates decrease and  $\pm 20\%$  FC was set as a threshold. Student’s *t*-test of Johnson normalized data was used to examine differences between (NAFL vs. HC) and (0-NASH vs. NASH) in each ethnicity. Full factorial analysis of covariates (ANCOVA) was employed to evaluate the interaction of ethnicity  $\times$  health status. This model included ethnicity (HIS or CAU), health status (NAFL or HC; 0-NASH or NASH), ethnicity  $\times$  health status interaction as fixed effects, with age and sex as covariates. To check any effect of fibrosis or advance NAS score on the differences observed, we repeated the analysis on a subset of histology-matched subjects ( $n = 5$  HIS and  $n = 5$  CAU). Pathways/network visualization with fold change and *p*-values were plotted using Cytoscape 3.8.2 (<https://cytoscape.org>, accessed on 05/22/2021). [29]. Mean differences were considered likely at  $p < 0.05$ . To adjust for false discovery rate (FDR), Benjamini-Hochberg FDR correction was performed [30]. A  $q = 0.2$  was set as a threshold, given the pilot nature and small sample size of the study.

For the secondary analysis, raw data were auto-scaled to correct for batch effect (Figure S6) [31]. Lipids affected by batch were excluded (three lipids) and data were normalized by Johnson’s transformation. Partial least square-discriminant analysis (PLS-DA) was performed to discriminate ethnicities in NASH subjects with leave- one-out cross validation (LOOCV) [32]. An  $R^2$  and  $Q^2 > 0.5$

are acceptable values to indicate reliability of the model in explaining differences between groups [33]. A variable importance in projection (VIP) score of  $>1.0$  was set as a threshold for variable selection. To check any effect of advanced fibrosis, we repeated the analysis after excluding subjects with fibrosis grade 3 and 4 ( $n = 3$  HIS and  $n = 4$  CAU).

### 3. Results

#### 3.1. Subject characteristics

The clinical and histological features of NAFL subjects from the primary cohort are presented in Table 1. The mean age in NAFL and HC, respectively, was  $47 \pm 15$  and  $43 \pm 14$  in HIS;  $50 \pm 18$  and  $44 \pm 12$  in CAU (n.s). The mean BMI in HIS was  $46 \pm 6$  in NAFL and  $26 \pm 2$  in HC ( $p$ -value  $< 0.05$ ); in CAU, the mean BMI was  $42 \pm 8$  in NAFL and  $25 \pm 3$  in HC ( $p$ -value  $< 0.05$ ). Within NAFL group, the mean NAS score was  $3 \pm 3$  and  $3 \pm 1$  for HIS and CAU, respectively (n.s). No difference in clinical and histological parameters was found between ethnicities. In subjects with NASH compared to 0-NASH, the mean NAS score was  $5 \pm 2$  and  $4 \pm 1$  for HIS and CAU, respectively (n.s) (data not shown).

The secondary cohort included NASH subject with various degrees of necroinflammation and fibrosis (Table 2). When comparing NASH-HIS and NASH-CAU, no difference was found with BMI and other clinical and histological parameters. The mean NAS score was  $5 \pm 2$  and  $5 \pm 1$  for NASH-HIS and NASH-CAU, respectively (n.s).

#### 3.2. Ethnicity-related alterations in plasma PUFAs and lipid mediator profiles characterize NAFL

We examined differences in plasma fatty acids and lipid mediators between NAFL and HC (Figure 1 and Table S1). Compared to corresponding HC, 25 (38% of total detected) and 7 (11%) lipid levels were different in NAFL-HIS and NAFL-CAU, respectively (FDR-adjusted  $p < 0.2$ ). Ethnicity-specific changes observed in NAFL, with interaction (ethnicity  $\times$  NAFL), include 8 lipids (15%) and 2 enzymatic ratios (raw  $p$ -Interaction  $< 0.05$ ) but did not survive FDR-correction ( $q = 0.2$ ). To rule out any effect of histological severity on the differences observed between ethnicities, the analysis was repeated on a subset of histology-matched subjects (Table S2). As a result, 12 lipids

(19%) and one enzymatic ratio were found altered (raw  $p$ -Interaction < 0.05), with 3 lipids, i.e., ALA, LA, and 9-hydroperoxyoctadecadienoic acid (-HpODE) surviving FDR correction.

When compared to HC, there were overlapping differences seen in NAFL for both ethnicities as well as ethnicity-specific differences (Figure S1). In both ethnicities, NAFL showed higher levels of several eCBs derived from PUFA and other fatty acids. The 18 carbon (C18) PUFAs, ALA and LA showed similar higher trend with higher levels of downstream fatty acid alcohols, hydroperoxide, ketones, epoxides, and vicinal diols. Specific to NAFL-HIS, there were differentially higher levels of LA-triols (i.e., trihydroxyoctadecaenoic acids (TriHOMEs) (raw  $p$ -Interaction < 0.05). On histology-matched analysis, higher TriHOMEs and LA-epoxide, 12(13)-epoxyoctadecenoic acid (-EpOME) levels were found significant (raw  $p$ -Interaction < 0.05). Of note, the n-6 to n-3 ratio was higher, however, with no ethnicity x NAFL interaction. In NAFL-CAU, there was differentially higher ALA and LA and its hydroperoxide, 9-HpODE (raw  $p$ -Interaction < 0.05). On histology-matched analysis, these lipids retained significance with LA, and 9-HpODE passing the FDR-threshold.

The 20 carbon (C20) and longer chain PUFAs (LC-PUFA) showed opposite trends with higher levels in NAFL-CAU and lower in NAFL-HIS. The ratio of docosahexaenoic acid (DHA)/eicosapentanoic acid (EPA) + ALA was found lower in both ethnicities (FDR-adjusted  $p$ -value). In HIS, alcohols, ketones, thromboxane derived from arachidonic acid (AA) were higher, however with no interaction (ethnicity x NAFL). DHA and its vicinal diol, 19,20-dihydroxydocosapentaenoic acid (-DiHDoPA), levels were differentially lower (raw  $p$ -Interaction < 0.05) with tendency shown for lower EPA. On histology-matched analysis, lower levels of these lipids were found significant (raw  $p$ -Interaction < 0.05). Specific to CAU, there was differentially higher AA and its vicinal diol, 14,15-dihydroxyeicosatrienoic acid (-DiHETrE) that remained significant after histology adjustment (raw  $p$  < 0.05). While these findings show common alterations seen in NAFL for both ethnicities, they also highlight ethnicity-specific changes. This includes a divergence in LC-PUFA profile, mainly with lower EPA and DHA seen in HIS. Although these differences did not pass FDR adjustment, histology-matched analysis yielded consistent and stronger differences, suggesting ethnicity-specific

differences characterized NAFL, independently of liver histology severity. It also suggests that fibrosis may weaken the differences between ethnicities.

### **3.3. Ethnicity-related differences in plasma PUFAs and lipid mediators' independent of obesity**

Ethnicity-specific differences in plasma lipidome within lean HC were examined (Figure S2 and Table S1). Among the differences observed, HIS had higher LA (raw  $p < 0.05$ ), ALA, 9-HpODE, and TriHOMEs levels (FDR-adjusted  $p$ -value), and lower AA-derived prostaglandin, PGE2 (FDR-adjusted  $p$ -value) levels. These findings indicate alterations in plasma PUFAs and lipid mediator profiles in HIS independent of obesity.

### **3.4. The progression to NASH is characterized by ethnicity-related alterations in plasma PUFAs and lipid mediator profiles**

We examined differences in plasma fatty acids and lipid mediators between 0-NASH and NASH (Figure 2 and Table S3). Compared to corresponding 0-NASH, 7 (11% of total detected) and 6 (9%) lipids were found different in NASH-HIS and NASH-CAU, respectively (raw  $p$ -value  $< 0.05$ ). None passed the FDR-correction threshold. There were differentially altered lipids by ethnicity group (raw  $p$ -Interaction  $< 0.05$ ), including 11 lipids (17%) and two enzymatic ratios. Three of these lipids and the two enzymatic ratios passed the FDR-correction threshold.

With the progression from 0-NASH to NASH, less marked differences in plasma PUFA profile were observed. Compared to 0-NASH, NASH-HIS showed a trend for lower plasma PUFAs, only affecting AA (raw  $p$ -value  $< 0.05$ ). There was a trend for higher C18-PUFA derived alcohols, triol, epoxides and vicinal diols, with TriHOMEs being differentially higher (raw  $p$ -Interaction  $< 0.05$ ). We also observed a trend for lower LC-PUFA derived lipid mediators, mainly affecting AA-alcohols, 5-hydroxyeicosatetraenoic acid (-HETE); thromboxane (TXB2); and prostaglandin (PGE2), with 5-HETE and TXB2 found differentially changed between ethnicities (raw  $p$ -Interaction  $< 0.05$ ). Also, the oleic acid (OA)-derived N-oleoyl glycine levels were lower with NASH (raw  $p$ -Interaction  $< 0.05$ ).

In NASH-CAU, there was a trend of higher C18, LC-PUFAs and downstream lipid mediators. Interaction (ethnicity  $\times$  NASH) was shown with higher 9-HpODE, TXB2, and in EPA-epoxide,

17(18)-epoxyeicosatetraenoic acid (-EpETE) (raw  $p$ -Interaction < 0.05). There was an opposite trend for C18-PUFA derived vicinal diols that were higher in HIS and lower in CAU, compared to corresponding 0-NASH, with interaction (ethnicity x NASH) shown for 12,13- and 15,16-dihydroxyoctadecadienoic acid (-DiHODE) (raw  $p$ -Interaction < 0.05). Multiple sEH enzymatic indices were higher in HIS and lower in CAU, including 9\_10-dihydroxyoctadecenoic acid (-DiHOME)/9(10)- epoxyoctadecenoic acid (-EpOME) and 9\_10-DiHODE)/9(10)- epoxyoctadecadienoic acid (-EpODE) (raw  $p$ -Interaction <0.05). Also, with NASH, there were higher levels of many eCBs, including dihomogamma-linolenylethanolamide, palmitoleylethanolamide, palmitoleylethanolamide, oleoyl-ethanolamide and N-oleoylglycine (raw  $p$ -Interaction < 0.05). Although PUFA changes are less marked in NASH, trends are consistent with changes seen in NAFL and support divergence in LC-PUFA profiles. It also highlights ethnicity-related differences in OXLs and eCBs associated with NASH progression. Given that NASH groups in both ethnicities had comparable NAS scores, this suggests the ethnicity-related differences observed with NASH are not likely driven by histological severity.

### **3.5. Plasma OXLs profile discriminates between ethnicities with NASH**

A supervised PLS-DA was performed including all profiled lipids to examine if plasma OXLs profile can discriminate between ethnicities with NASH. The model demonstrated separation between HIS and CAU with 22 (49%) contributing lipids having VIP > 1. This indicates differences in OXLs profile characterizes HIS and CAU with NASH (Figure S3 and Table S4). The  $Q^2$  and  $R^2$  for the model were 0.62 and 0.72, respectively, indicating a fair reliability of the model. Of note, an overlap between ethnic groups was observed and subjects within this area shared advanced fibrosis (grade 3 and 4), indicating that HIS and CAU subjects with NASH and advanced fibrosis share similar plasma OXLs profile. Also, it suggests that advanced fibrosis may be attenuating the multivariate model. Therefore, we repeated the analysis after excluding subjects with advanced fibrosis (Figure 3 and Table S4). As a result, the model exhibited complete separation between ethnicities in NASH with 20 (44%) lipids contributing to this difference (VIP > 1.0). The  $Q^2$ ,  $R^2$  were 0.99 and 0.98, respectively, indicating optimal prediction and reliability of the multivariate model.

In subjects with NASH and mild to moderate fibrosis, OXLs profiles showed opposite direction of change between ethnicities in some AA-derived mediators, with TXB<sub>2</sub>, 15-keto PGE<sub>2</sub>, 5-HETE and 5,6 DiHETrE being lower in HIS compared to CAU. Many OXLs derived via LOX pathway and/or auto-oxidative routes were lower in NASH-HIS, including TriHOMEs, 9- and 13-keto-octadecadienoic acid (-KODE), 9- and 13- hydroxyoctadecatrienoic acid (-HOTE), and 5-HETE. Some CYP-derived OXLs were lower in NASH-HIS, as 9(10)-EpOME, 12(13) EpOME and 12(13)-EpODE. Multiple sEH enzymatic indices were found higher in NASH-HIS, compared to NASH-CAU, including 12,13-DiHOME/12(13)-EpOME; 9,10-DiHOME/9(10)-EpOME; 17\_18-DiHETE/17(18)-EpETE along with higher levels of the vicinal diol, 14,15-DiHETrE. These findings further confirm lower AA-derived OXLs in HIS with NASH, which are also characterized by lower LOX and higher sEH-derived lipid mediators compared to CAU. They also indicate that plasma OXL profiles can discriminate between ethnicities in NASH.

#### **4. Discussion**

This study is the first to examine targeted plasma PUFA, OXL, and eCB profiles with regards to ethnicity in a group of HIS and CAU subjects with obesity and biopsy-diagnosed NAFL and NASH. Our findings indicate that: (1) NAFL and NASH are characterized by ethnicity-related differences in plasma PUFA profiles, independent of histological severity; (2) Ethnicity-related differences in plasma OXLs profiles characterize NASH, independent of histological scores; (3) Plasma PUFA profile is altered in apparently healthy HIS, independent of obesity.

The hepatic and serum/plasma PUFA profiles are dysregulated in NAFLD [16-20]. Our results expand on these findings and show ethnicity-related differences in plasma PUFA profile in NAFL and NASH. With NAFL, both ethnicities showed higher ALA and LA levels, which were pronounced in CAU but not in HIS. This can be attributed to differences in the levels of these PUFAs in lean and healthy subjects, as HIS showed higher levels compared to their CAU counterpart. There was also a divergence in LC-PUFA profiles between ethnicities. CAU showed higher levels mainly affecting AA, while HIS displayed lower levels mainly affecting DHA and EPA. Consistent trends were shown with the progression from 0-NASH to NASH with arachidonic almost reaching significance



( $p$ -Interaction = 0.07). This is in line with our previous untargeted profiling in NAFL done on the same subjects showing higher C18-PUFAs in CAU, and a trend for lower LC-PUFA with tendencies shown for DHA and EPA in HIS [27]. The lack of significant difference in LC-PUFA in our previous analysis may be due to the semi-quantitative nature and the clustering statistical approach. Also in agreement with our current finding is the lower serum/plasma DHA and EPA levels reported in obese HIS, compared to non-HIS [34,35]. Together, this implies diminished plasma LC-PUFA characterizes obese HIS with NAFL and NASH. As diet affects circulating and tissue PUFA levels [36], the ethnicity-dependent differences in dietary intake of n-3 PUFAs which is reportedly lower in HIS could be responsible for these observed changes [35,37]. While we did not account for diet, our findings suggest a possible etiological role for it as we observed higher linoleic and ALA levels independent of obesity in lean healthy HIS compared to CAU. Beside diet, genetic variants in cluster region of fatty acid desaturases (FADS) can predict LC-PUFA serum/blood levels [38,39]. Single nucleotide polymorphisms (SNP) in FADS1 and FADS2, which encode fatty acid desaturases, were robustly associated with NAFLD [40,41]. Lower  $\Delta$ -5 desaturase levels are reported in both NAFL and NASH [16,17,20]. Notably, SNPs in FADS that are associated with insufficient LC-PUFA biosynthesis present with high frequency in Amerindians, a subgroup of HIS [42]. However, genotype was not examined in current study, and both ethnicities had lower estimated  $\Delta$ -5 desaturase activity with NAFL. Therefore, diet and/or genetic factors may contribute to the observed ethnicity-related PUFA alterations but need further assessment.

Other key findings include the ethnicity-related differences in OXs and eCBs profiles. The COX pathway exerts pro-inflammatory effects as it catalyzes the conversion of AA to prostaglandin PGE<sub>2</sub>, thromboxane TXB<sub>2</sub>, and other fatty acid alcohols [10]. In animal models of NASH, the expression and activity of COX-2 were upregulated, and its inhibition ameliorated NAFL and NASH [43,44]. Previously, high TXB<sub>2</sub> and PGE<sub>2</sub> levels were reported in subjects with NAFL and NASH [22]. Findings in NASH-CAU from our secondary analysis are consistent with this literature, as TXB<sub>2</sub> and 15-Keto PGE<sub>2</sub> discriminated between ethnicities with NASH with higher levels in CAU and lower levels in HIS. When comparing within ethnicities, the progression from 0-NASH to NASH in

HIS was marked with a trend for lower AA, almost reaching statistical significance ( $p$ -Interaction = 0.07) and downstream OXLs with TXB2 being differentially lower ( $p$ -Interaction < 0.05). These findings suggest ethnicity-related alterations in AA metabolism and downstream COX-derived OXLs in NASH.

Animal studies indicate a role for LOX pathways in NAFL and inflammation [45,46]. LOX pathways lead to the synthesis of fatty acid alcohols, ketones, hydroperoxides, and the specialized pro-resolving mediators (SPMs). With possible exceptions, n-6 PUFA derived alcohols are pro-inflammatory [10]. Under oxidative stress, PUFAs can also undergo auto-oxidation to form alcohols, ketones, hydroperoxides [11]. Previous studies reported higher LOX and auto-oxidation metabolites in NAFL and increased AA metabolites via LOX with the progression to NASH [18,22,23,41]. In our results, compared to control groups, NAFL and NASH in both ethnicities presented higher alcohols and ketones derived from C18-PUFAs, indicating an upregulated LOX pathway(s). In NAFL, we observed a positive correlation between some fatty acid alcohols and the oxidative stress markers, F2-isoprostanes and 9-HETE (Table S5), implying a contribution of non-enzymatic auto-oxidation. Interestingly, our secondary analysis showed many LOX derived OXLs being higher in NASH-CAU compared to NASH-HIS, with a similar trend found for the oxidative stress marker, 9-HETE (VIP = 0.98). Together, while LOX and oxidative pathways are upregulated with NAFL in both ethnicities, the magnitude of these alterations is lesser in HIS with NASH, compared to CAU. Based on this finding, we reasoned that LOX, and possibly oxidative stress, may be pivotal for NASH severity in CAU, and to a lesser extent in HIS.

CYP enzymes catalyze the synthesis of fatty acids epoxides and alcohols. In general, fatty acid alcohols are pro-inflammatory, and epoxides are anti-inflammatory and transient, and are hydrolyzed by the action of sEH to form inactive or less active vicinal diols [10,47]. A role for sEH in NAFLD progression is indicated by animal studies, showing that sEH inhibition improves NAFL, NASH, and fibrosis [47]. In subjects with NASH, compared to NAFL, AA derived vicinal diols are higher [22]. Our results show, with the progression to NASH, an ethnicity-dependent opposite trend for vicinal diols derived from C18-PUFA, which were higher in HIS and lower in CAU. Some of these vicinal

diols and sEH enzymatic indices showed interaction (ethnicity  $\times$  NASH) and were found higher in NAHS-HIS and lower in NASH-CAU, compared corresponding 0-NASH. This may suggest higher activity of sEH in NASH-HIS. Our secondary analysis also shows higher ratios of multiple sEH enzymatic indices in HIS compared to CAU, and lower C18-PUFA epoxides possibly due higher hydrolysis rate. NASH-CAU showed higher levels of many PUFA epoxides, compared to NASH-HIS, indicating upregulated CYP pathway(s) and/or less hydrolysis. Together, our finding highlights ethnicity-related differences in sEH activity that was higher in HIS with NASH.

Extensive evidence from animal studies indicates a role for eCB system in NAFL, mitochondrial dysfunction and inflammation and fibrosis [48,49]. In NAFL, both ethnicities had higher levels of several eCBs. However, with the progression to NASH, many eCBs were higher in CAU and lower in HIS as compared to corresponding 0-NASH (raw *p*-Interaction < 0.05). We also observed levels of the OA-derived mediators N-oleoyl glycine, and oleoylethanolamide. These observations could not be examined in our secondary analysis as we detected limited numbers of eCBs and did not profile for fatty acids. Nevertheless, this may indicate ethnicity-related variations in eCBs profiles and OA metabolism with NAFLD in HIS that need to be further examined.

Our findings corroborate the epidemiological evidence indicating ethnicity as one variable affecting the association between PUFAs and cardiometabolic risks [29,45,46]. In fact, the observed ethnicity-related alterations may be relevant to NAFLD severity. EPA and DHA modulate hepatic fatty acid oxidation, de novo lipogenesis, redox balance and inflammation via direct interaction with nuclear receptors and transcription factors [50]. These LC-PUFAs are also precursors to potent SPMs which drive inflammatory resolution [10]. Also, the pro-inflammatory cascade of AA via COX is necessary for the biosynthesis of SPMs and initiating inflammatory resolution [13,51]. Therefore, a diminished level of these PUFAs may abolish anti-steatogenic and anti-inflammatory mechanisms. Likewise, a higher sEH activity may result in deactivation of anti-inflammatory PUFA epoxides [10,47]. Interestingly, our findings suggest that upregulated LOX pathway(s) may be imperative to NASH severity in CAU with a lesser extent in HIS. Collectively, we postulate that the observed ethnicity-related changes translate to the more advanced NASH histological presentation seen in HIS.

Of note, these changes are independent of fibrosis or NAS scores, in fact, histology adjustment resulted in stronger differences in both analyses, implying that subjects with advanced fibrosis may share similar lipidomic profile.

Our findings have clinical/diagnostic implications. Given liver biopsy risks and limitations [52], there is an ongoing search for noninvasive biomarker for NAFLD, with multiple biomarkers have been recently proposed including betatrophin and fetuin-A [53,54]. Also, several AA- derived OXLs were shown to predict NASH including higher levels of 5- and 15-HETE, PGE<sub>2</sub>, and some vicinal diols [18,22]. While our findings in NASH-CAU show trends consistent with current literature, findings in HIS indicate otherwise. Ethnicity-related differences in plasma metabolomic profile have been reported before in diabetes, Alzheimer's disease, and bladder cancer [55-57]. We propose that ethnicity-specific plasma signature may characterize NASH. In fact, utilizing ethnicity-related variations in plasma lipidomic profile may be instrumental for the enhanced precision of such diagnostic tools. If further verified, it will serve as a much-needed non-invasive tool aiding in clinical practice for early detection of NASH in both HIS and CAU populations. It can also pave the road for examination of ethnicity-specific lipidomic signatures in other ethnicities as the Asian and African American populations. On another note, a role of EPA and DHA supplementations in improving NAFLD and its risk factors is supported by clinical evidence [58,59]. Also, growing data indicate the utility of sEH inhibitors in NASH treatment [42,57,58]. Therefore, evaluating these interventions for NASH treatment seems warranted, particularly in the HIS population.

This "proof-of-concept" analysis is based on a small, single-center study. The limited sample size may have compromised the correction for multiple testing in the primary analysis. However, findings from the secondary analysis were consistent and the multivariate model is validated for overfitting and predictability. Other strengths include biopsy-characterized NAFL and NASH and analysis adjusted for BMI and histology. While NAFLD prevalence is reported to be higher in males compared to females [60-62], we could not examine sex differences due to small sample size. However, we did adjust for sex as a covariate.

In conclusion, we performed targeted lipidomic profiling for PUFAs and related lipid mediators with regards to ethnicity. Results show ethnicity-related divergence in LC-PUFA and downstream OXLs profiles with NAFL and NASH progression, independent of histological scores. Our secondary analysis indicates that in NASH and compared to CAU, HIS are characterized by lower levels of AA derived OXLs, lower LOX with an upregulated sEH pathway(s). These lipidomic differences may be relevant to the ethnicity-related disparity reported in NAFLD rate and severity and are worth further investigations. Our findings suggest ethnicity-specific lipidomic signature may characterize NASH. Although preliminary, these novel observations support the need for larger validation studies.

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## 7. Tables

**Table 1.** Demographic, clinical, and histological characteristics of study subjects in primary analysis.

	<b>NAFL-HIS</b>	<b>NAFL-CAU</b>	<b>p-Value *</b>
Plasma, <i>n</i> (F/M)	10 (7/3)	8 (4/4)	-
Age (Yrs.)	47 ± 15	50 ± 18	0.6
DM, yes (%)	4 (40)	4 (50)	1
FBG mmol/L	101 ± 14	94 ± 13	0.3
Cholesterol (mg/dL)	172 ± 28	166 ± 34	0.7
TG (mg/dL)	135 ± 79	129 ± 70	0.8
HDL (mg/dL)	44 ± 6	43 ± 8	0.7
LDL (mg/dL)	107 ± 24	99 ± 35	0.4
HbA1c (%)	6 ± 1	6 ± 1	0.7
AST (U/L)	31 ± 13	26 ± 9	0.6
ALT (U/L)	40 ± 27	31 ± 11	0.9
Platelet	280 ± 84	302 ± 110	0.8
NAS	3 ± 3	3 ± 1	0.7
<b>Steatosis (%)</b>			
<5%	4 (40)	1 (12.5)	
5 to ≤33%	3 (30)	5 (62.5)	0.9
34 to ≤66 %	2 (20)	2 (25)	
>66%	1 (10.0)	0 (0)	
<b>Inflammation (%)</b>			
None	3 (30)	1 (12)	
Mild	1 (10)	4 (50)	0.6
Moderate	4 (40)	3 (38)	
Severe	2 (20)	0 (0)	
<b>Ballooning (%)</b>			
None	4 (40)	5 (62)	
Few	5 (50)	3 (38)	0.3
Many	1 (10)	0 (0)	
<b>Fibrosis (%)</b>			
None	7 (70)	7 (88)	
1A	0 (0)	1 (12)	0.3
2	1 (10)	0 (0)	
4	2 (20)	0 (0)	

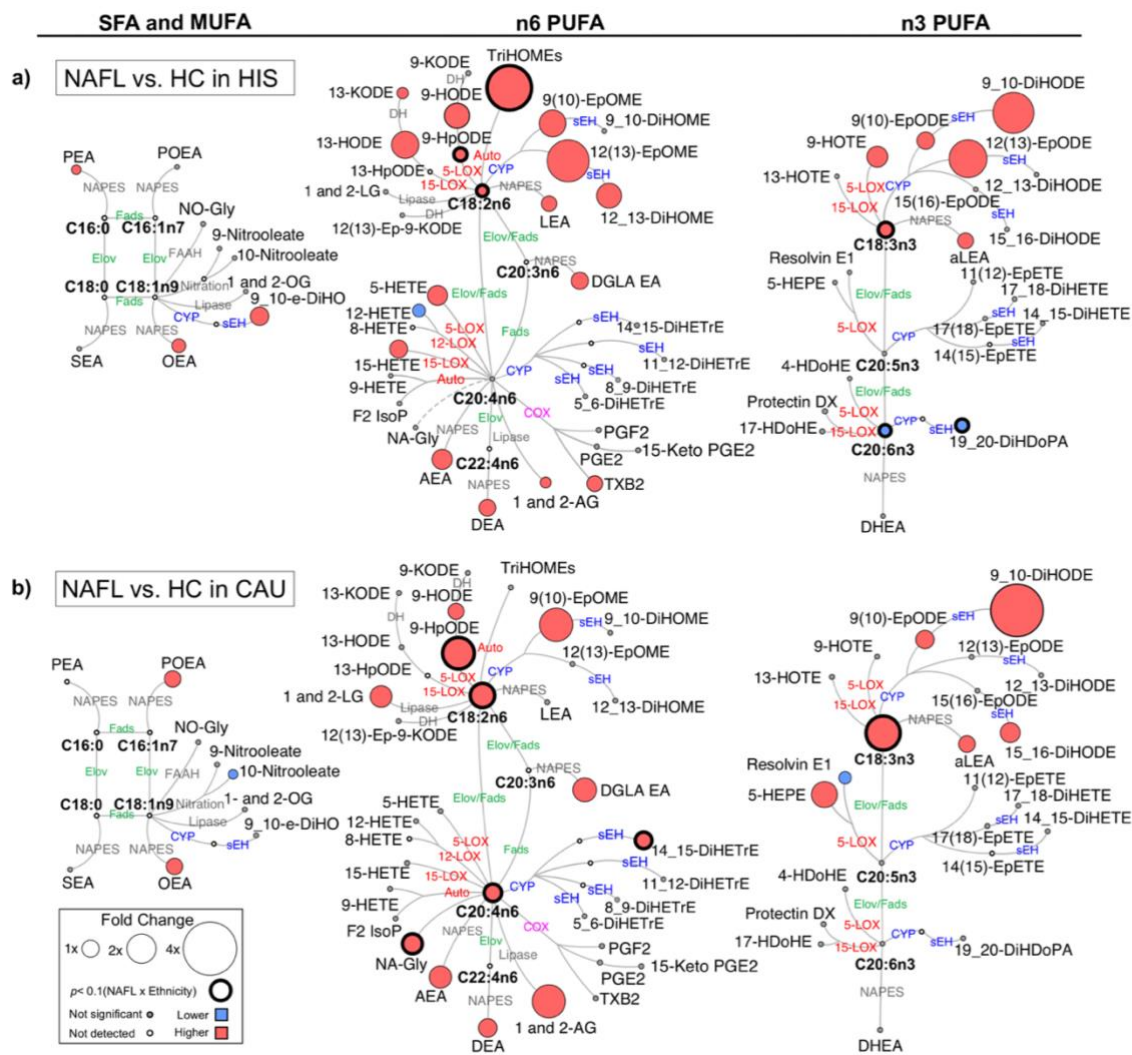
General characteristics of NAFL group in both ethnicities shown as percent (for categorical data) and mean ± SEM (for nominal data). Comparisons were performed by *t*-test (nominal) or chi-square test (categorical). (\*) NAFL-HIS vs. NAFL-CAU.

**Table 2.** Demographic, clinical, and histological characteristics of NASH subjects in secondary analysis.

	<b>NASH-HIS</b>	<b>NASH-CAU</b>	<b>p-Value *</b>
Plasma, <i>n</i> (F/M)	12 (9/3)	17 (11/6)	-
Age (Yrs.)	49 ± 8	50 ± 13	0.8
BMI (Kg/m <sup>2</sup> )	41 ± 8	37 ± 7	0.6
NAS	5 ± 2	5 ± 1	0.9
<b>Steatosis (%)</b>			
<5%	2 (17)	0 (0)	
5 to ≤33%	4 (33)	7 (41)	
34 to ≤66 %	3 (25)	4 (24)	0.4
>66%	3 (25)	6 (35)	
<b>Inflammation (%)</b>			
None	0 (0)	0 (0)	
Mild	2 (17)	3 (18)	
Moderate	6 (50)	13 (76)	0.1
Severe	4 (33)	1 (6)	
<b>Ballooning (%)</b>			
None	0 (0)	0 (0)	
Few	8 (67)	13 (76)	0.6
Many	4 (33)	4 (24)	
<b>Fibrosis (%)</b>			
None	5 (41)	4 (23)	
1a, b, c	2 (17)	6 (35)	
2	2 (17)	3 (18)	0.8
3	2 (17)	2 (12)	
4	1 (8)	2 (12)	

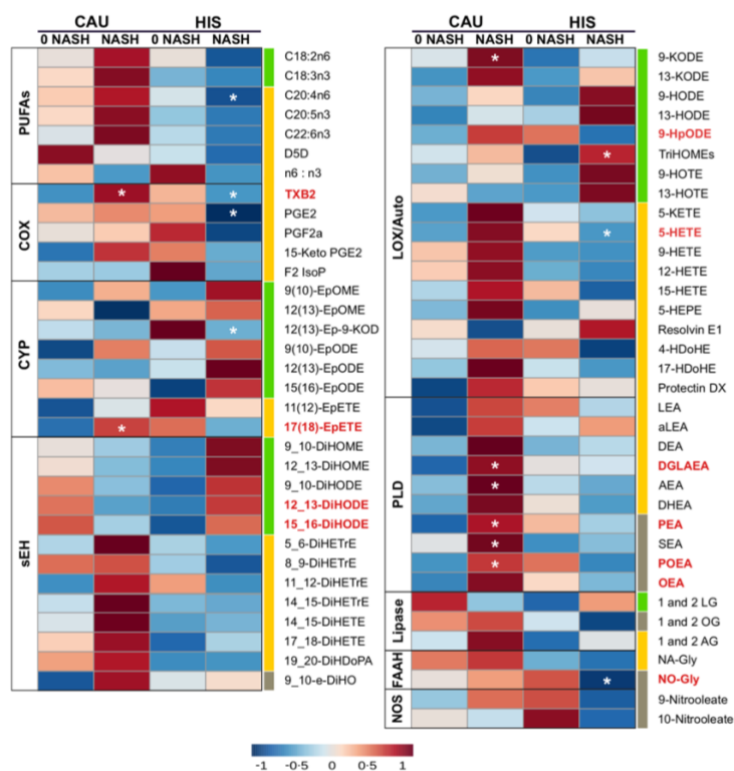
General characteristics of subjects included in the secondary analysis shown as percent (for categorical data) and mean ± SEM (for nominal data). Comparisons were performed by *t*-test (nominal) or chi-square test (categorical). (\*) NASH-HIS vs. NASH-CAU.

## 8. Figures

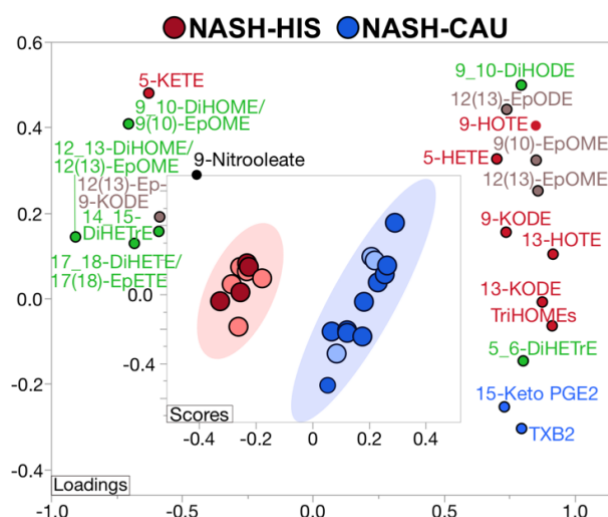


**Figure 1.** Differences in plasma polyunsaturated fatty acids (PUFAs) and lipid mediators between non-alcoholic fatty liver (NAFL) compared to healthy control (HC) in primary cohort. Metabolic network for (a) Hispanic (HIS); (b) Caucasian (CAU) illustrating saturated (SFAs), monounsaturated (MUFAs) and polyunsaturated fatty acids (PUFAs), including n-3 and n-6 PUFAs with pathways of oxylipins and endocannabinoids synthesis. Node size represents fold changes, calculated as  $(\text{HC} - \text{NAFL})/\text{HC}$ . Node's color represents the directionality of differences: higher in NAFL (red); lower in NAFL (blue); no change (grey). Shown are only lipids with differences between NAFL vs. HC ( $t$ -test raw  $p < 0.05$ ) and/or with interaction (ethnicity x NAFL) (ANCOVA raw  $p < 0.05$ ). Lipids with interaction (ethnicity x NAFL) (ANCOVA raw  $p < 0.05$ ) are marked with a solid circle. Means and  $p$ -values are detailed in Table S1. Fatty acids are described by number of carbons and double bounds of the fatty acyl moiety (i.e., C18:2n6). NAFL ( $n = 10$  HIS and 8 CAU); HC ( $n = 14$  HIS and 8 CAU). ADH, alcohol dehydrogenase; AEA, arachidonoyl ethanolamine; AG, arachidonoyl glycerol; DEA, docosatetraenyl ethanolamide; DGL EA, dihomogamma-linolenoyl ethanolamide; DH, dehydrogenase; DHEA, docosahexaenoyl ethanolamide; DiHDoPA, dihydroxydocosapentaenoic acid; DiHETE, dihydroyeicosatetraenoic acid; DiHETrE, dihydroyeicosatrienoic acid; DiHO, dihydroxyoctadecanoic acid; DiHODE, dihydroxyoctadecadienoic acid; DiHOME, dihydroxyoctadecenoic acid; Elov, fatty acid elongase; Ep-KODE, epoxyoctadecenoic acid; EpETE, epoxyeicosatetraenoic acid; EpODE, epoxyoctadecadienoic acid; EpOME, epoxyoctadecenoic acid; F2-IsoP, F2 isoprostanes; FAAH, fatty acid amide hydrolase; Fads, fatty acid desaturase; HDoHE, hydroxydocosahexaenoic acid; HEPE, hydroxyeicosapentaenoic acid; HETE, hydroxyeicosatetraenoic acid; HODE, hydroxyoctadecadienoic acid; HOTE, hydroxyoctadecatrienoic acid; HpODE, hydroperoxyoctadecadienoic acid; KETE, keto-eicosatetraenoic; KODE, keto-octadecadienoic acid;

LEA, Linoleyl ethanolamine; LG, linoleoylglycerol; LOX, lipoxygenase; NA-Gly, arachidonylglycine; NAPES, N-acylphosphatidyl ethanolamine-specific; NO-Gly; OEA, oleoyl ethanolamine; OG, oleoylglycerol; PEA, palmitoyl ethanolamine; PGE, prostaglandin E; PGF, prostaglandin F; POEA, palmitoleoyl ethanolamide; SEA, stearoyl ethanolamide; sEH, soluble epoxide hydrolase; TriHOME, trihydroxyoctadecaenoic acid; TXB, thromboxane.



**Figure 2.** Heatmap illustrating fold changes and differences in plasma polyunsaturated fatty acids (PUFAs) and lipid mediators between non-alcoholic steatohepatitis (NASH) compared to NASH-free (0-NASH) in primary cohort. Fold changes are indicated by color and intensity, with red indicating an increase, and blue indicating a decrease. Lipids different in NASH vs. 0-NASH (t-test raw  $p < 0.05$ ) are noted by (\*). Ethnicity-related differences, or interaction (ethnicity  $\times$  NASH) (ANCOVA raw  $p < 0.05$ ) are marked with bold red color. C18 PUFAs and related lipids are marked with “green”; long chain-PUFAs and related lipids are marked with “yellow”; saturated fatty acids (SFA) and monounsaturated fatty acid (MUFA) related lipids are marked with “grey”. Means and p-values are detailed in Table S3. Fatty acids are described by number of carbons and double bounds of the fatty acyl moiety (i.e., C18:2n6). NASH ( $n = 6$  Hispanic (HIS) and 3 Caucasian (CAU)); 0-NASH ( $n = 4$  HIS and 5 CAU). ADH, alcohol dehydrogenase; AEA, arachidonoyl ethanolamine; AG, arachidonoyl glycerol; DEA, docosatetraenyl ethanolamide; DGLEA, dihomo-gamma-linolenoyl ethanolamide; DH, dehydrogenase; DHEA, docosahexaenoyl ethanolamide; DiHDoPA, dihydroxydocosapentaenoic acid; DiHETE, dihydroxyeicosatetraenoic acid; DiHETrE, dihydroxyeicosatrienoic acid; DiHO, dihydroxyoctadecanoic acid; DiHODE, dihydroxyoctadecadienoic acid; DiHOME, dihydroxyoctadecenoic acid; Elov, fatty acid elongase; Ep-KODE, epoxyxooctadecenoic acid; EpETE, epoxyeicosatetraenoic acid; EpODE, epoxyoctadecadienoic acid; EpOME, epoxyoctadecenoic acid; F2-IsoP, F2 isoprostanes; FAAH, fatty acid amide hydrolase; Fads, fattyacididesaturase; HDoHE, hydroxydocosahexaenoic acid; HEPE, hydroxyeicosapentaenoic acid; HETE, hydroxyeicosatetraenoic acid; HODE, hydroxyoctadecadienoic acid; HOTE, hydroxyoctadecatrienoic acid; HpODE, hydroperoxyoctadecadienoic acid; KETE, keto-eicosatetraenoic; KODE, keto-octadecadienoic acid; LEA, Linoleyl ethanolamine; LG, linoleoylglycerol; LOX, lipoxygenase; NA-Gly, arachidonoylglycine; NAPES, N-acylphosphatidyl ethanolamine-specific; NO-Gly, oleoyl ethanolamine; OG, oleoylglycerol; PEA, palmitoyl ethanolamine; PGE, prostaglandin E; PGF, prostaglandin F; POEA, palmitoleoyl ethanolamide; SEA, stearoyl ethanolamine; sEH, soluble epoxide hydrolase; TriHOME, trihydroxyoctadecanoic acid; TXB, thromboxane



**Figure 3.** Supervised multivariate clustering model demonstrating ethnicity specific oxylipins profile discriminates Hispanic (HIS) and Caucasian (CAU) with non-alcoholic steatohepatitis (NASH) without advanced fibrosis. Score plot for NASH-HIS (red) vs. NASH-CAU (blue) when excluding stage 3 and 4 fibrosis. Light color represents subjects from primary cohort and dark color represents secondary cohort. The model was performed on all profiled lipids. Lipid mediators are colored according to metabolizing enzyme pathways, lipoxygenase, and autoxidation (red); cytochrome p450 epoxygenase (brown); and soluble epoxide hydrolase (green); cyclooxygenase (blue); other (black). The model was validated with leave-one-out cross validation. The  $Q^2$  and  $R^2$  are 0.99 and 0.98, respectively. Details on variable importance into the projection scores are shown in Table S4. NASH ( $n = 9$  HIS and 13 CAU). DiHETE, dihydroxyeicosatetraenoic acid; DiHETrE, dihydroxyeicosatrienoic acid; DiHODE, dihydroxyoctadecadienoic acid; DiHOME, dihydroxyoctadecenoic acid; Ep-KODE, epoxyoxooctadecenoic acid; EpETE, epoxyeicosatetraenoic acid; EpODE, epoxyoctadecadienoic acid; EpOME, epoxyoctadecenoic acid; HETE, hydroxyeicosatetraenoic acid; HOTE, hydroxyoctadecatrienoic acid; KETE, keto-eicosatetraenoic; KODE, keto-octadecadienoic; PGE, prostaglandin E; TriHOME, trihydroxyoctadecaenoic acid; TXB, thromboxane.



## 9. Supplementary materials

**Table S1:** Targeted quantification data table for comparisons of HIS and CAU obese subjects with NAFL vs. lean HC.

**Table S2:** Demographic, clinical, and histological characteristics of histology-matched subjects. **Table S3:** Targeted quantification data table for comparisons of HIS and CAU with NASH vs. 0-NASH.

**Table S4:** Targeted quantification data table for comparisons of HIS and CAU with NASH in the secondary analysis.

**Table S5:** Pearson's correlation analysis between LOX metabolites and markers of oxidative stress.

**Table S6:** Details on detected lipid class and identifiers.

**Figure S1:** Venn-Diagram illustrating overlapping and unshared differences in polyunsaturated fatty acids (PUFAs) and lipid mediators between non-alcoholic fatty liver (NAFL) compared to healthy control (HC) in both ethnicities.

**Figure S2:** Differences in plasma PUFA and lipid mediators between Hispanic (HIS) and Caucasian (CAU) in lean healthy subjects.

**Figure S3:** Supervised multivariate clustering model demonstrating ethnicity specific oxylipins profile discriminates Hispanic (HIS) and Caucasian (CAU) with non-alcoholic steatohepatitis (NASH) with advanced fibrosis.

**Figure S4:** Flow chart illustrating subject recruitment details for primary and secondary analysis. **Figure S5:** Principal component analysis (PCA) illustrating outliers before (left) and after (right) data normalization.

**Figure S6:** Principal component analysis (PCA) illustrating the unsupervised clustering of samples from primary (red) and secondary cohort (green) shown before (left) and after (right) batch correction.