

**Cytochrome P450 3A Activity and Expression in  
Non-Alcoholic Fatty Liver Disease**

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**List of Non-Standard Abbreviations:**

CYP3A4, cytochrome P450 3A4; HOMA IR, homeostatic model assessment of insulin resistance; Huh7, Huh7 human hepatoma cell line; LC-MS/MS, liquid chromatography-tandem mass spectrometry; MDZ, midazolam; NAFLD, non-alcoholic fatty liver disease; NAS, non-alcoholic fatty liver disease activity score; NASH, non-alcoholic steatohepatitis; SS, simple steatosis; 4 $\beta$ -OHC, 4 $\beta$ -hydroxycholesterol; NF- $\kappa$ B, kappa-light-chain-enhancer of activated B cells; PXR, pregnane x receptor

## ABSTRACT

Non-alcoholic fatty liver disease (NAFLD) is the leading cause of liver disease in the Western world given its association to obesity, type 2 diabetes and dyslipidemia. Medications are widely used in NAFLD to manage comorbid conditions, and there is significant interest in developing new drug therapies to treat the disease. Despite this, little is known about the effects of NAFLD on drug metabolism. We examined the activity and expression of the major drug metabolizing enzyme subfamily, cytochrome P450 3A (CYP3A) in subjects with NAFLD, and in mouse and cellular models. CYP3A activity was determined in healthy volunteers and subjects with biopsy-proven NAFLD by oral midazolam phenotyping and measurement of plasma 4 $\beta$ -hydroxycholesterol, an endogenous metabolic biomarker. *CYP3A4* transcriptional activity, metabolic activity and expression were also assessed in a mouse and cellular model of NAFLD. Subjects with non-alcoholic steatohepatitis (NASH) had 2.4-fold higher plasma midazolam levels compared to controls. Plasma 4 $\beta$ -hydroxycholesterol was 51% and 37% lower than controls in subjects with simple steatosis and NASH, respectively. Fibrosis was associated with 57% lower plasma 4 $\beta$ -hydroxycholesterol levels than controls. Furthermore, hepatic CYP3A4 mRNA expression in NASH was 69% lower than control livers. *CYP3A4* gene luciferase activity in the livers of NAFLD mice was 38% lower than that of controls. Lipid-loaded Huh7 cells had a 38% reduction in CYP3A4 activity and 80% lower CYP3A4 mRNA expression compared to control. CYP3A activity is reduced in human NAFLD in addition to mouse and *in vitro* cell models of the disease.

## INTRODUCTION

Non-alcoholic fatty liver disease (NAFLD) is the most common liver disease in the Western world, affecting 20-35% of the general adult population, and 70-90% of obese individuals (Browning et al., 2004; Bedogni et al., 2005). Given its close association with the metabolic syndrome and increased risk of cardiovascular disease, many NAFLD patients are prescribed a variety of medications to manage these associated conditions (Stepanova and Younossi, 2012). While the liver is the primary site of drug metabolism, little is known about the effect of NAFLD on this process. With the current lack of approved pharmacologic treatments for NAFLD, much of the current focus of therapy for this condition has been in managing comorbid conditions. If significant differences in drug metabolism are present in NAFLD, this may not only have implications for dosing and administration of currently used medications, but also for the development of new therapies targeting hepatic steatosis and fibrosis.

There is a paucity of information on the influence of NAFLD on the *in vivo* activity of major hepatic drug metabolizing pathways. A key pathway involves cytochrome P450 3A enzymes (CYP3A4 and CYP3A5), which act in the intestine and liver. CYP3A4 is responsible for the oxidative metabolism of more than 50% of all drugs including those widely prescribed in NAFLD such as HMGCo-A reductase inhibitors (statins), calcium channel blockers, thiazolidinediones and sulfonylureas (Guengerich, 1999). Inter-individual variability in hepatic CYP3A enzyme activity can reach 100-fold (Lin and Lu, 2001). This highly variable enzyme activity has been largely attributed to environmental

factors (Burk and Wojnowski, 2004; Wilkinson, 2005) and genetic polymorphisms including reduced activity *CYP3A4*\*22 (Wang et al., 2011) and the inactivating allele *CYP3A5*\*3 (Kuehl et al., 2001).

In the setting of cirrhosis, there is clear *in vivo* evidence for reduced hepatic CYP3A activity which contributes to decreased drug dose requirements (Verbeeck, 2008). However, in NAFLD with simple steatosis and NASH (non-alcoholic steatohepatitis), *in vivo* CYP3A activity has not been evaluated. A small number of *ex vivo* studies using archived livers have been published but findings are conflicting; reporting increased (Niemela et al., 2000), decreased (Donato et al., 2006; Donato et al., 2007), or no change (Kolwankar et al., 2007; Fisher et al., 2009) in hepatic CYP3A4 protein expression in NAFLD. Moreover, those studies that noted decreased CYP3A4 protein expression differed with respect to whether CYP3A4 mRNA was also reduced (Niemela et al., 2000; Fisher et al., 2009). In a study of donated human type 2 diabetic liver, where NAFLD has a prevalence of 50%, hepatic CYP3A4 expression was reduced (Dostalek et al., 2011). Taken together, a majority of studies to date suggest that NAFLD is associated with reduced hepatic CYP3A activity, however the data are heterogeneous and this finding has not yet been demonstrated *in vivo*.

In this study, we directly examined CYP3A drug metabolism activity in patients with biopsy-proven NAFLD as well as both mouse and cell culture models of hepatic steatosis. We demonstrate, for the first time, that *in vivo* CYP3A activity is decreased in NAFLD.

## MATERIALS AND METHODS

### *In Vivo CYP3A Activity Phenotyping*

The short-acting benzodiazepine, midazolam (MDZ), is oxidatively metabolized by CYP3A4 and CYP3A5 (Gorski et al., 1994). MDZ pharmacokinetic phenotyping is a widely used method to assess *in vivo* CYP3A activity (Lin et al., 2001). After an overnight fast, a group of 10 subjects with biopsy-proven NAFLD and a cohort of 20 healthy control subjects collected from previous studies reported by Woolsey *et al.* (submitted) and Gong *et al.* (Gong et al., 2012), received an oral microdose (100 µg) of MDZ (1 mg/mL, Sandoz, Boucherville, QC) as an aqueous solution. Blood was collected 3 hours after drug administration for plasma MDZ concentration analysis. 4β-hydroxycholesterol (4β-OHC) is a cholesterol metabolite formed by CYP3A4/CYP3A5 and an endogenous biomarker for *in vivo* CYP3A activity (Diczfalusy et al., 2012). Fasting plasma was obtained from the healthy control subjects (n=20) and subjects with biopsy-proven NAFLD (n=30) for 4β-OHC level analysis. Histologic NAFLD stage was categorized simple steatosis (SS) or NASH, according to the non-alcoholic fatty liver disease activity score (NAS), which includes steatosis (0-3), hepatic inflammation (0-3) and hepatocellular ballooning (0-2). Patients were categorized as having NASH if NAS was ≥3 with a ballooning score of ≥1. SS was determined as total NAS of <3 or ≤3 with a ballooning score of 0. Hepatic fibrosis was scored separately (0 – 4) (no fibrosis = 0 and fibrosis ≥ 1). Insulin resistance was calculated using the homeostasis model assessment (HOMA IR). These studies conformed to the ethical guidelines of the 1975 Declaration of

Helsinki and were approved by the Human Subjects Research Ethics Board at the University of Western Ontario. All study participants provided informed written consent.

### *Genotyping*

Single-nucleotide polymorphisms (SNPs) associated with altered CYP3A activity were genotyped by TaqMan allelic discrimination assay (Applied Biosystems, Foster City, CA) for *CYP3A4*\*22 (rs35599367), *CYP3A5*\*3 (rs776746), Peroxisome Proliferator Activating Receptor  $\alpha$  (PPAR $\alpha$ ; *NR1C1*, rs4253728) and Cytochrome P450 Oxidoreductase *POR*\*28 (rs1057868). Patatin-like phospholipase domain-containing protein 3 (*PNPLA3*, rs738409) gene variation associated with hepatic steatosis was similarly determined.

### *Human Liver Tissues*

Liver samples used for gene expression (mRNA) analyses were obtained by biopsy from subjects with NAFLD (n=17; mean age 46; 10 male, 7 female; 3 SS, 14 NASH) as reported by Beaton *et al.* (Beaton *et al.*, 2013) while normal human liver samples (n=9, mean age 45, 3 male, 6 female) were obtained through the Liver Tissue Cell Distribution System (Minneapolis, MN, Funded by NIH Contract #N01-DK-7-0004 / HHSN267200700004C). Control livers were chosen as those without hepatic steatosis after Oil Red O histological staining.

### *Drug, Metabolite and Endogenous Biomarker Analysis*

Plasma and samples from cell culture studies were analyzed for levels of MDZ and its CYP3A-catalyzed primary metabolite, 1-hydroxymidazolam, by liquid chromatography-

tandem mass spectrometry (LC-MS/MS) according to our previous report (Woolsey *et al.*, submitted). 4 $\beta$ -hydroxycholesterol (4 $\beta$ -OHC) levels in plasma were measured after picolinic acid derivatization and LC-MS/MS analysis according to the method of Honda *et al.* (Honda *et al.*, 2010) and detailed in our previous report (Woolsey *et al.*, submitted).

### *Animal Studies*

Female, 5 week old C57BL/6 mice were obtained from Jackson Laboratories (Bar Harbor, MA). Mice were fed a normal standard diet (2018 Teklad Global 18% protein rodent diet, Harlan Laboratories, Madison, WI) or a high-fat diet (TD.88137 adjusted calories diet 42% from fat, Harlan Laboratories,) for 4 weeks. Human CYP3A4 reporter gene activity in liver was determined in mice after hydrodynamic, tail-vein delivery (25  $\mu$ g of DNA in 2 mL saline administered over 10 sec) of a CYP3A4 gene luciferase plasmid (CYP3A4-XREM-Luc) or a promoterless reporter (pGL3 Basic, Promega, Madison, WI) with correction for transfection efficiency with a Renilla luciferase vector (2  $\mu$ g, pRL-CMV, Promega). The CYP3A4-XREM-Luc plasmid containing the proximal promoter (–362/+53) and distal xenobiotic response element (XREM; –7836/–7208) inserted in pGL3 Basic (Promega) was prepared previously (Tirona *et al.*, 2003). Twenty-four hours post-injection, livers were harvested and homogenized for analysis by Dual Luciferase Assay (Promega). Liver segments were fixed and embedded in paraffin for staining with Hematoxylin/Eosin and Trichrome or frozen in OCT for Oil Red O staining. This study protocol was approved by the University of Western Ontario Animal Use Subcommittee.



### *Cell Culture Studies*

Huh7 human hepatoma cells (Japan Health Sciences Foundation Tokyo, Japan) were cultured in high glucose Dulbecco's modified Eagle's medium (Lonza, Walkersville, MD) with 10% fetal bovine serum (Invitrogen, Carlsbad, CA), 2 mM L-glutamine, 50 U/ml penicillin (Invitrogen), 50 µg/ml streptomycin (Invitrogen) and incubated at 37°C in 5% CO<sub>2</sub>. Prior to experiments, Huh7 cells were grown 3 weeks post-confluence with media changed routinely every 2 to 3 days. To induce steatosis, Huh7 cells were treated with 600 µM fatty acids (2:1 ratio of oleic and palmitic acids, Sigma-Aldrich) in serum free media containing 1% fatty acid-free bovine serum albumin (Sigma-Aldrich) for 24 hours using a modified protocol (Sivertsson et al., 2010). Lipid accumulation was determined by Nile red staining and confocal fluorescence microscopy. Cell viability was assessed 24 hours after lipid loading using colorimetric MTT assay. To determine CYP3A4 metabolic activity, Huh7 cells were exposed to 1 µg/mL of MDZ (ThermoFisher Diagnostix) in Krebs Henseleit Bicarbonate buffer (KHB, pH 7.4) supplemented with 12.5 mM HEPES and 5 mM glucose. After a 3-hour incubation, cell culture media was collected for analysis of 1-hydroxymidazolam concentration by LC-MS/MS as described above.

### *Gene Expression Analysis*

RNA from liver samples and Huh7 cells was extracted using TRIzol (Invitrogen) and cDNA synthesized using Multiscribe reverse transcriptase (Applied Biosystems, Carlsbad, CA) with random hexamers. RNA quality and concentration was determined using Agilent Bioanalyzer (RNA 600 Nano kit, Agilent, Santa Clara, CA) and NanoVue Plus Spectrophotometer (GE Healthcare Life Sciences, Baie d'Urfe, QC). Relative mRNA

expression of CYP3A4, CYP2E1, mCyp2e1, and mCyp3a11 were determined by SYBR green-based quantitative PCR (ABI Prism 7700, Applied Biosystems). Primer sequences are: Human CYP3A4: 5'-CAGGAGGAAATTGATGCAGTTTT-3' (Forward) and 5'-TCAAGATACTCCATCTGTAGCACAGT-3' (Reverse); Human CYP2E1: 5'-CCCAATCACCTGTCAATTT-3' (Forward) and 5'-GACCACCAGCACAACTCTGA-3' (Reverse); Mouse Cyp2e1: 5'-CCTGGTGGAGGAGCTCAAAA-3' (Forward) and 5'-TGTTGAAGAGAATATCCGCAATGA-3' (Reverse); Mouse Cyp3a11: 5'-CTTTCCTTCACCCTGCATTCC-3' (Forward) and 5'-CTCATCCTGCAGTTTTTTCTGGAT-3' (Reverse). Reactions were performed in triplicate for each sample and gene expression was normalized to 18S ribosomal RNA (TaqMan Gene Expression Assay, Applied Biosystems).

### *Statistical Analysis*

Values are expressed as the mean  $\pm$  SEM or Tukey boxplot. Differences between experimental groups was evaluated using an unpaired, two-tailed, t-test or a one-way ANOVA with Dunnett Test. Differences were considered significant at the  $p < 0.05$  level. All analysis was performed using GraphPad Prism Version 5.0 (GraphPad, La Jolla, CA).

## **RESULTS**

### *CYP3A Activity and Expression are Decreased in NAFLD.*

We examined *in vivo* CYP3A activity using oral MDZ phenotyping and plasma 4 $\beta$ -OHC biomarker level analysis. Control subjects (n=20) were tested with both MDZ and 4 $\beta$ -

OHC tests. MDZ phenotyping and 4 $\beta$ -OHC plasma level was determined in 10 and 30 subjects with biopsy-proven NAFLD, respectively. Subject demographics are summarized in Table 1. Neither healthy control nor NAFLD study subjects were taking CYP3A4 interacting medications at the time of study participation (Supplemental Tables 1 and 2). All NAFLD subjects and 17 of 20 control subjects consented to genetic analysis. There were no significant differences in the frequencies of allele carriers associated with CYP3A activity, MDZ pharmacokinetics or plasma 4 $\beta$ -OHC levels among study groups (Table 1). We found mean MDZ concentrations were 2.4-fold greater ( $p < 0.0001$ ) in subjects with NASH ( $n=9$ ) in comparison to control subjects (Fig. 1A). The single subject with simple steatosis had 2.5-fold higher MDZ levels than controls (Fig. 1A). This result suggests that MDZ was not as readily metabolized in NASH due to a decrease in CYP3A activity. NAFLD and healthy control subjects were also phenotyped for CYP3A activity using fasting plasma 4 $\beta$ -OHC level. NAFLD subjects had significantly lower mean 4 $\beta$ -OHC levels in comparison to control subjects (Simple Steatosis, 51% lower than control,  $p < 0.001$ ; NASH 37% lower than control,  $p < 0.001$ ) (Fig. 1B), indicating decreased CYP3A activity. We separately examined the influence of hepatic fibrosis, *PNPLA3* genotype and HOMA IR on plasma 4 $\beta$ -OHC levels. There were lower 4 $\beta$ -OHC levels in the presence of NAFLD fibrosis in comparison to control subjects (43% of control,  $p < 0.0001$ ) (Fig. 1C). *PNPLA3* genotypes are associated with histological severity of NAFLD (Sookoian and Pirola, 2011) and susceptibility to NASH (Zain et al., 2012). In the NAFLD cohort, carriers of the risk *PNPLA3* (rs738409) G allele tended to have lower 4 $\beta$ -OHC concentrations, although the association was not statistically significant (Supplemental Figure 3A). Furthermore insulin resistance, as assessed by HOMA IR, was not associated

with plasma 4 $\beta$ -OHC levels among participants with NAFLD (Supplemental Figure 3B). CYP3A4 mRNA expression level was determined in NAFLD biopsy samples and histologically normal, non-steatotic archived livers. There was 69% lower CYP3A4 mRNA levels in NASH biopsies (n = 14) than control livers (n=9) (p = 0.059) (Fig 1D). The amount of CYP3A4 mRNA was 60% lower in biopsies with simple steatosis (n = 3) than control livers (n = 9), however this difference was not statistically significant (p = 0.34) (Fig. 1D). In composite, results from both the MDZ and 4 $\beta$ -OHC phenotyping tests demonstrate that *in vivo* CYP3A activity is reduced in NAFLD. Fibrosis is associated with lower CYP3A enzyme function. Reduced *in vivo* CYP3A activity is associated with decreased hepatic CYP3A4 mRNA levels.

#### *Reduced CYP3A4 Transcriptional Activity in a Mouse Model of NAFLD.*

Female C57BL/6 mice were fed a high fat diet for 4 weeks to induce NAFLD. Simple steatosis was observed after H&E, trichrome and Oil Red O lipid staining of livers of mice fed a high fat diet while steatosis was absent in animals fed a normal diet (Fig. 2A). The livers of mice were *in vivo* transfected with a CYP3A4-XREM-Luc reporter plasmid or a pGL3 Basic control plasmid in conjunction with a normalizing Renilla luciferase vector, by hydrodynamic tail vein injection method. Hepatic CYP3A4 luciferase activity in the NAFLD mouse model was lower by 60% in comparison to mice on a normal diet (Fig. 2C). These results demonstrate that hepatic steatosis causes reduced liver *CYP3A4* transcriptional activity in an *in vivo* model of NAFLD.

*CYP3A4 Activity and Expression are Decreased in a NAFLD Cell Culture Model.*

Huh7 human hepatoma cells were incubated with and without fatty acids to induce steatosis. Lipid accumulation was confirmed using the neutral lipid stain, Nile red (Fig. 3A, B). The fatty acid treatment did not cause cytotoxicity up to concentrations of 600  $\mu$ M as determined by MTT assay (Supplemental Figure 1). Incubation of cells with MDZ (1  $\mu$ g/mL) resulted in the appearance of the CYP3A metabolite, 1-hydroxymidazolam, in the culture media. The levels of 1-hydroxymidazolam in the fatty-acid treated Huh7 cells were lower by 38% in comparison to control cells (Fig. 3C), indicating reduced CYP3A enzyme activity in experimental steatosis. Furthermore, there was a significant decrease (reduction of 80%) in CYP3A4 mRNA expression in steatotic cells in comparison to control cells (Fig. 3D). These findings indicate that steatosis is associated with a reduction in CYP3A4 mRNA expression leading to decreased enzyme activity in a cell culture model of NAFLD.

## **DISCUSSION**

With the global prevalence of NAFLD rising (Loomba and Sanyal, 2013) it is expected that this disease will become the number one indication for liver transplant (Charlton et al., 2011). As such, the need for effective drug therapy to prevent disease progression is vital. Unfortunately, little is known about the effect of NAFLD on drug metabolism capacity, oral bioavailability, systemic exposure and therapeutic response. The strongest evidence supporting altered drug metabolism relates to the well-characterized induction of hepatic CYP2E1 expression and *in vivo* activity in NAFLD (Chalasani et al., 2003; Emery

et al., 2003). CYP2E1 induction has been associated with enhanced susceptibility to acetaminophen bioactivation (to its reactive metabolite) and hepatotoxicity (Michaut et al., 2014). In the present study we also observed significantly increased CYP2E1 mRNA expression in both human NAFLD subjects and the cell culture model. In the mouse model of NAFLD a trend toward increased *Cyp2e1* mRNA level was observed (Supplemental Figure 2). While there is evidence for CYP2E1 alterations in NAFLD, whether the expression and activity of the CYP3A subfamily are affected by NAFLD is not as clear. The *in vivo* activity of these primary drug metabolizing enzymes in NAFLD has not been previously reported. In this study we demonstrate that subjects with biopsy-proven NAFLD, phenotyped using an oral microdose of MDZ, have increased plasma MDZ concentrations in comparison to healthy control subjects (Fig. 1A). The validity of this simplified microdose and single time point sampling phenotyping strategy is supported by pharmacokinetic linearity of MDZ over a wide oral dose range (Halama et al., 2013) and strong correlation between the 3 hour plasma concentration with area under the concentration-time curve (Woolsey *et al.*, submitted) (Lin et al., 2001). The observed 2.4-fold higher midazolam exposure in NASH compared to healthy subjects indicates moderately reduced CYP3A activity given that the drug interaction with the potent CYP3A inhibitor, ketoconazole, results in a 16-fold increase in oral midazolam AUC (Tsunoda et al., 1999).

We further assessed *in vivo* CYP3A activity by measuring plasma concentrations of 4 $\beta$ -OHC, a product of CYP3A-mediated metabolism of cholesterol (Diczfalusy et al., 2012). NAFLD patients had significantly lower 4 $\beta$ -OHC levels than controls, again indicating a

decrease in CYP3A activity (Fig. 1B). Interestingly, CYP3A activity did not differ between NAFLD subjects with SS or NASH ( $p=0.4941$ ) despite studies demonstrating marked reduction in CYP3A4 expression and metabolic function in cultured human hepatocytes treated with inflammatory cytokines (Abdel-Razzak et al., 1993; Muntane-Relat et al., 1995). When examined independently from NAS, fibrosis, a marker of advanced NAFLD, was associated with significantly lower 4 $\beta$ -OHC levels when compared to control.

Plasma 4 $\beta$ -OHC levels are sensitive to the effects of CYP3A4 induction by drugs such as anticonvulsants (Bodin et al., 2001). However, the use of 4 $\beta$ -OHC as a biomarker for decreased CYP3A4 activity by enzyme inhibition with drugs may be limited due to the long half-life of this oxysterol, requiring weeks of inhibitor administration for reductions in plasma levels to become apparent (Josephson et al., 2008). In the context of disease effects on CYP3A4 activity, our results in NAFLD, as well as those reported for Crohn's disease (Iwamoto et al., 2013), show that 4 $\beta$ -OHC may be a valid biomarker of reduced metabolic activity for chronic conditions. Plasma 4 $\beta$ -OHC levels are a reflection of CYP3A4 activity in the liver as was demonstrated in a study of subjects treated with the enzyme inducer efavirenz (Meyer zu Schwabedissen et al., 2012). Systemic levels of this biomarker were increased while no changes in intestinal CYP3A4 expression were observed. Our results implicate changes in liver CYP3A4 levels however, the contribution of intestinal CYP3A4 activity to plasma 4 $\beta$ -OHC concentrations in NAFLD has not yet been formally evaluated.

There are some limitations to this study. Our findings of reduced CYP3A4 activity and expression in the mouse and cell culture models of NAFLD indicate that the observed increase in MDZ levels in NAFLD are at least partly a result of decreased hepatic activity. Larger pharmacokinetic studies using both oral and intravenous MDZ in NAFLD are required to define the metabolic changes that occur specifically in liver and intestine.

For ethical reasons, liver biopsies could not be obtained from the control group to confirm absence of NAFLD. In this group, we considered anthropometric and serum biochemical indices for inclusion of healthy subjects into the control group. The average age of the control group was approximately 7 years younger than that of NAFLD subjects (Table 1). In our previous study of healthy subjects we found that MDZ oral clearance was only reduced by 3% for every 10-year increase in age (Woolsey *et al.*, submitted), while others have reported no effect of age on clearance (Gorski *et al.*, 2003). We therefore do not consider the age difference between groups a significant contributor to the reduced CYP expression and activity.

To obtain further insight to the mechanisms of decreased *in vivo* CYP3A4 activity in NAFLD, additional experiments were performed in a diet-induced mouse NAFLD model. It is important to consider that CYP3A protein isoforms differ between rodents and humans. Specifically, mice express 8 different active Cyp3a genes (Cyp3a11, Cyp3a13, Cyp3a16, Cyp3a25, Cyp3a41, Cyp3a44, Cyp3a57 and Cyp3a58) while adult humans express only 2 forms (CYP3A4 and genetically polymorphic CYP3A5) (Nelson *et al.*, 2004). Furthermore, there are clear distinctions between mouse and human CYP3A gene



regulation (Martignoni et al., 2006). Given the species difference in the expression and regulation of CYP3A genes, we delivered a *CYP3A4* gene promoter firefly luciferase reporter into the livers of mice with experimental hepatic steatosis. The effectiveness and advantages of this strategy in an *in vivo* experimental model with intact liver to study *CYP3A4* gene regulation is well-documented (Schuetz et al., 2002; Tirona et al., 2003). Decreased liver CYP3A4 luciferase reporter activity in the mouse NAFLD model suggests that in the *in vivo* milieu of simple steatosis, there is reduced *CYP3A4* transcription (Fig. 2C). For comparison, we examined the expression of the predominant mouse hepatic Cyp3a11 enzyme in the simple steatosis model and found a trend toward lower ( $20\% \pm 6\%$ ,  $p = 0.10$ ) mRNA expression level in mice on HFD ( $n = 6$ ) than those on ND ( $n = 6$ ). In the context of previous reports, results in mouse models of NAFLD have been heterogeneous with some demonstrating decreased (Yoshinari et al., 2006; Ghose et al., 2011; Wahlang et al., 2014) or induced (Fisher et al., 2008; Spruiell et al., 2014) expression of Cyp3a11. Similarly, rat models of hepatic steatosis are conflicting with some reporting decreased Cyp3a expression (Leclercq et al., 1998) while others showing higher levels (Ghoneim et al., 2015).

Lastly, we examined CYP3A4 activity in a cultured human hepatoma cell model of steatosis. Huh7 cells were grown for weeks at confluence in these experiments because native expression and activity of CYP3A4 under these conditions is enhanced (Sivertsson et al., 2010). In fatty acid-induced steatotic Huh7 cells, we found a significant decrease in CYP3A4 activity similar to the results shown in NAFLD subjects *in vivo* (Fig. 3C). Reduced CYP3A4 activity was associated with decreased CYP3A4 mRNA levels (Fig.

3D), consistent with the findings of reduced CYP3A4 luciferase activity in the NAFLD mouse model.

A probable mechanism for reduced CYP3A4 activity in NAFLD are the effects of inflammation and associated cytokines on hepatic drug metabolism gene expression (Abdel-Razzak et al., 1993; Muntane-Relat et al., 1995; Pascussi et al., 2000; Jover et al., 2002). Indeed, inflammatory infiltration occurs in simple steatosis and NASH together with increased hepatic expression of inflammatory cytokines (Gadd et al., 2014). Inflammatory cytokines, acting through nuclear factor kappa-light-chain-enhancer of activated B cells (NF- $\kappa$ B), causes trans-repression of the pregnane X receptor (PXR), a central transcription factor regulating CYP3A4 expression (Gu et al., 2006; Zhou et al., 2006). Moreover, PXR is down-regulated by inflammatory cytokines (Pascussi et al., 2000) and its expression is reduced in human NASH (Bitter et al., 2014). Other mechanisms may be involved in the down-regulation of CYP3A4 in NAFLD.

The clinical importance and drug development relevance of the current findings of reduced CYP3A activity in NAFLD are potentially significant and remain to be further explored. While CYP3A-metabolized medications such as some statins which are commonly prescribed in patients with this condition are safe, our finding that *in vivo* CYP3A metabolic activity is reduced in NAFLD leads one to ponder whether current drug dosing recommendations may need to be reevaluated in this population in order to ensure the best possible clinical outcomes for NAFLD patients with metabolic comorbidities. Indeed, we have recently found plasma 4 $\beta$ -OHC concentrations are associated with of

atorvastatin plasma levels during routine clinical care (DeGorter et al., 2013). Future investigations to determine the importance of altered drug metabolism in NAFLD together with studies to elucidate the molecular mechanisms involved will be required to provide additional insights into therapies and management of this important cause of liver disease.

## **AUTHORSHIP CONTRIBUTIONS**

Participated in research design: Woolsey, Kim, Tirona and Beaton

Conducted experiments: Woolsey, Mansell, Tirona and Beaton

Performed data analysis: Woolsey and Tirona

Wrote or contributed to the writing of the manuscript: Woolsey, Kim, Tirona and Beaton

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## FOOTNOTES

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## FIGURE LEGENDS

**Figure 1.** CYP3A4 activity and expression in NAFLD. (A) Plasma MDZ concentrations 3 hours post oral MDZ microdose (100  $\mu$ g) in healthy control (n=20) and biopsy-proven NAFLD subjects (Simple Steatosis, SS, n=1; NASH, n=9). Shown as Tukey boxplots with median (line), 25 to 75 percentile (box) and minimum / maximum values (whiskers). Statistical analysis by two-tailed t-test (control vs. NASH). (B) Fasting, plasma 4 $\beta$ -OHC concentrations in control (n=20) and NAFLD subjects (Simple Steatosis, SS, n=7; NASH, n=23). Statistical analysis by one-way ANOVA followed by Dunnett test. (C) Plasma 4 $\beta$ -OHC concentrations in healthy controls (n=20) and NAFLD subjects according to histological assessment of fibrosis (No Fibrosis, n=6; Fibrosis, n=24). Statistical analysis by one-way ANOVA followed by Dunnett test. (D) CYP3A4 mRNA expression in archived normal liver tissue (n=9) and NAFLD liver biopsy samples (Simple Steatosis, SS, n=3; NASH, n=14) compared using one-way ANOVA followed by Dunnett test. Bars represent mean with standard error of mean. Gene expression was normalized to a commercial normal pooled human liver RNA sample. \*\*\*p<0.0001; \*\*\*p<0.001.

**Figure 2.** CYP3A4 transcriptional activity in NAFLD mouse model. (A) Representative H&E, Trichrome and Oil Red O staining of liver sections from adult mice fed a normal diet (ND) or high fat diet (HFD) for 4 weeks. Scale = 20  $\mu$ m (B) Hepatic CYP3A4 luciferase reporter activity in mice after a normal diet (n=9) or high fat diet (n=5). Values are presented as mean and standard error of mean. \*p<0.05 (two-tailed t-test).

**Figure 3.** CYP3A4 activity and expression in a cultured human hepatoma cell (Huh7) NAFLD model. (A) Localization and accumulation of lipids in control and 24 hour, free fatty acid treated (600  $\mu$ M; oleate:palmitate, 2:1) Huh7 cells using Nile Red lipid fluorescent stain. Scale = 50  $\mu$ m. (B) Quantitative analysis of lipid accumulation within control and fatty acid (FA) treated Huh7 cells by image analysis (ImageJ). (C) Accumulation of 1-hydroxymidazolam in the cell culture media after a 3 hour incubation with the midazolam (1  $\mu$ g/mL) in control (n=6) and fatty acid (FA) treated cells (n=6). (D) Relative CYP3A4 mRNA expression in control (n=9) and fatty acid (FA) treated Huh7 cells (n=9). Values are presented as mean and standard error of mean: \*\*\*p<0.0001; \*\*p<0.001 (two tailed t-test).

**TABLES**

**Table 1.** Subjects phenotyped for CYP3A activity with MDZ and 4 $\beta$ -OHC tests.

Characteristic	Control	NAFLD	NAFLD
	MDZ/4 $\beta$ -OHC (n=20)	MDZ (n=10)	4 $\beta$ -OHC (n=30)
Age (Range)	43 (28-58)	51 (27-63)	49 (27-69)
Sex			
Male	7	5	19
Female	13	5	11
BMI (Range)	24 (19-30)	35 (28-45)	33 (23-45)
HOMA IR (Range)	-	3.5 (1.7-6.5)	3.1 (1-9.6)
NAFLD Stage <sup>1</sup>			
Simple Steatosis	-	1	7
NASH	-	9	23
Fibrosis <sup>2</sup>			
No Fibrosis	-	1	6
Fibrosis	-	9	24
Allele Carrier Status <sup>3</sup>			
CYP3A4*22	(17/0/0)	(9/1/0)	(24/6/0)
CYP3A5*3	(0/1/16)	(0/2/8)	(0/7/23)
PPAR $\alpha$ (rs4253728)	(12/5/0)	(6/4/0)	(16/12/2)
POR*28	(10/6/1)	(5/5/0)	(13/14/3)
PNPLA3 (rs738409)	-	(2/7/1)	(9/14/7)

<sup>1</sup> NASH was defined as NAS score [steatosis (0-3), lobular inflammation (0-3) and hepatocellular ballooning (0-2)]  $\geq$  3 plus a hepatocellular ballooning score  $\geq$  1; Simple Steatosis was defined as NAS  $<$  3 or NAS  $\leq$  3 with a ballooning score of 0.

<sup>2</sup> Degree of fibrosis was categorized by histologic fibrosis score (0-4); No fibrosis = 0; Fibrosis  $\geq$  1.

<sup>3</sup> Number of non-carriers/heterozygous carriers/homozygous carriers. For Control group, genotype was of available for 17 of 20 subjects.

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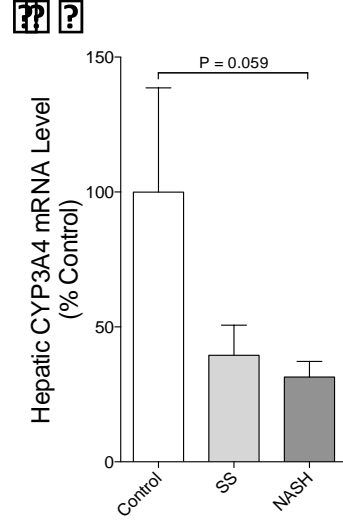
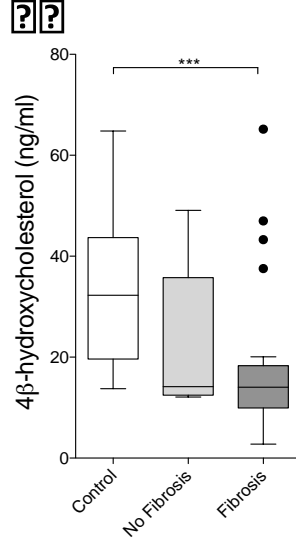
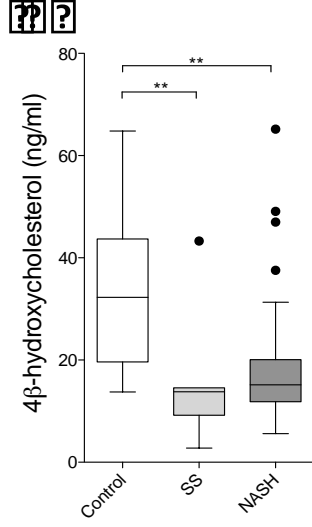
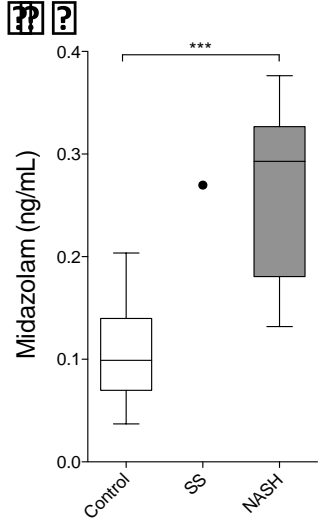




Figure 1

Figure 2

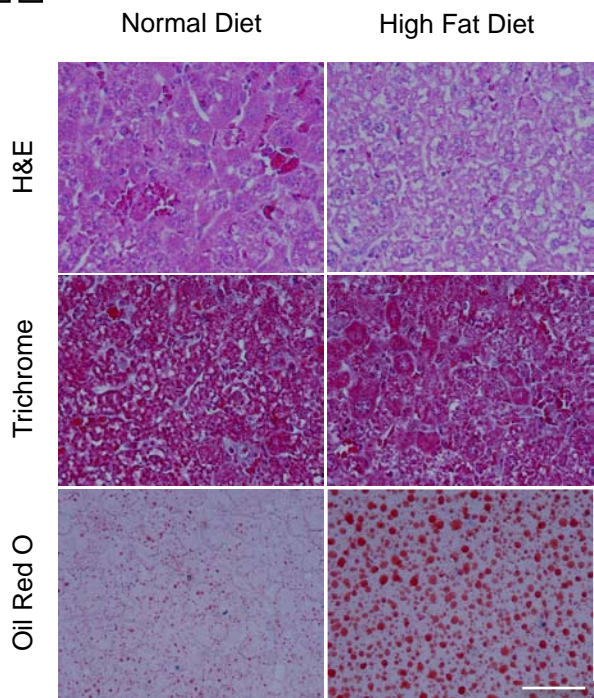
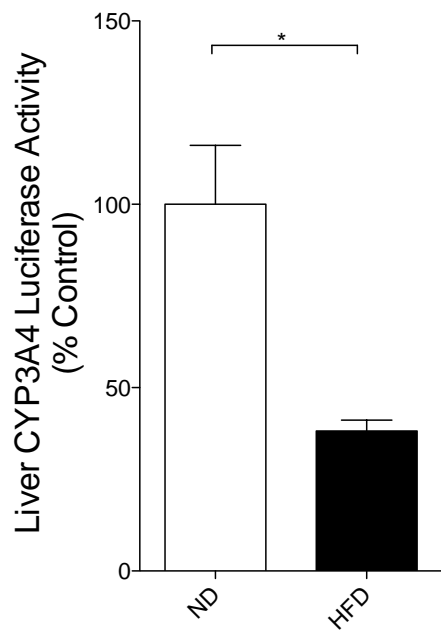


Figure 3



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