Hepatic lipid accumulation: cause and consequence of dysregulated glucoregulatory hormones

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Abstract
Fatty liver can be diet, endocrine, drug, virus or genetically induced. Independent of cause, hepatic lipid accumulation promotes systemic metabolic dysfunction. By acting as peroxisome proliferator-activated receptor (PPAR) ligands, hepatic non-esterified fatty acids upregulate expression of gluconeogenic, beta-oxidative, lipogenic and ketogenic genes, promoting hyperglycemia, hyperlipidemia and ketosis. The typical hormonal environment in fatty liver disease consists of hyperinsulinemia, hyperglucagonemia, hypercortisolemia, growth hormone deficiency and elevated sympathetic tone. These endocrine and metabolic changes further encourage hepatic steatosis by regulating adipose tissue lipolysis, liver lipid uptake, de novo lipogenesis (DNL), beta-oxidation, ketogenesis and lipid export. Hepatic lipid accumulation may be induced by 4 separate mechanisms: (1) increased hepatic uptake of circulating fatty acids, (2) increased hepatic de novo fatty acid synthesis, (3) decreased hepatic beta-oxidation and (4) decreased hepatic lipid export. This review will discuss the hormonal regulation of each mechanism comparing multiple physiological models of hepatic lipid accumulation. Nonalcoholic fatty liver disease (NAFLD) is typified by increased hepatic lipid uptake, synthesis, oxidation and export. Chronic hepatic lipid signaling through PPARgamma results in gene expression changes that allow concurrent activity of DNL and beta-oxidation. The importance of hepatic steatosis in driving systemic metabolic dysfunction is highlighted by the common endocrine and metabolic disturbances across many conditions that result in fatty liver. Understanding the mechanisms underlying the metabolic dysfunction that develops as a consequence of hepatic lipid accumulation is critical to identifying points of intervention in this increasingly prevalent disease state.

Introduction
Fatty liver is common to a wide range of human conditions. Nonalcoholic fatty liver disease (NAFLD) is the most frequent chronic liver disease in developed countries and its increased prevalence parallels the rise in obesity, type 2 diabetes and metabolic syndrome in recent decades (Tuyama & Chang 2012, Yki-Jarvinen 2016). NAFLD encompasses hepatic steatosis driven by factors other than excessive alcohol consumption and is estimated to affect 25% of the global population (Zhu et al. 2015). While NAFLD most commonly refers to
fatty liver resulting from overnutrition and consumption of a western diet, NAFLD may also be induced by endocrine disorders, viral infections or side effects of pharmacological therapies.

The prevalence of alcoholic fatty liver disease (AFLD) in the general population is approximately 8% (Kotronen et al. 2010, Kim et al. 2014b). Like NAFLD, the prevalence of AFLD is expected to rise (Toshikuni et al. 2014). While both AFLD and NAFLD have similar histology and disease progression, AFLD also induces molecular and clinical changes that are attributed to high alcohol consumption, and not as a result of hepatic lipid accumulation (Toshikuni et al. 2014, Rasineni et al. 2016). Interestingly, both AFLD and NAFLD are strongly associated with metabolic syndrome and type 2 diabetes (Kotronen et al. 2010), suggesting that fatty liver, independent of origin, promotes systemic metabolic dysfunction.

The severity of fatty liver disease is directly related to classic components of the metabolic syndrome including central obesity, insulin resistance, hyperinsulinemia, hypertriglyceridemia and hyperglycemia (Bedogni et al. 2005, Wainwright & Byrne 2016). In fact, 60–70% of type 2 diabetics and 65–85% of obese patients (BMI ≥ 30) are comorbid with NAFLD (Schindhelm et al. 2007, Fabbrini et al. 2010, Chon et al. 2016). Postprandial hyperinsulinemia is present in 100% of NAFLD cases independent of diabetes status (Manchanayake et al. 2011). Furthermore, sympathetic nervous system activity and circulating norepinephrine concentrations are commonly elevated in obesity and fatty liver disease (Patley et al. 1995, Thorp & Schlaich 2015). Nearly all nonalcoholic steatohepatitis (NASH) patients display insulin resistance independent of body weight (Chitturi et al. 2002). In fact, peripheral insulin resistance is now considered a better predictor of hepatic injury in NAFLD than visceral adiposity or the commonly used fibrosis scoring system (Erçin et al. 2015, Rosso et al. 2016).

Dysregulated glucagon secretion and signaling is also associated with fatty liver disease. NAFLD patients both with and without type 2 diabetes display fasting hyperglucagonemia (Bersmeier et al. 2014, Junker et al. 2016). In fact, the suppression of plasma glucagon in response to a meal or hyperglycemia is impaired or eliminated in prediabetic and diabetic individuals (Müller et al. 1970, Unger et al. 1972, Rohrer et al. 2012, Foghsgaard et al. 2016). Glucose-mediated inhibition of glucagon secretion from pancreatic alpha cells occurs indirectly and relies on paracrine signaling from insulin secreting beta cells (Le Marchand & Piston 2010).

Loss of this paracrine inhibition in diabetes promotes hypersecretion of glucagon, and the hyperglycemia and hyperketonemia of diabetes classically thought to be a consequence of blunted insulin signaling are mediated, in part, by excess glucagon (Brand et al. 1996, Lee et al. 2011, Unger & Cherrington 2012). Therefore, abnormal alpha-cell function and an increased glucagon:insulin ratio are central to the pathology of fatty liver disease.

Hepatic lipid accumulation occurs transiently as a metabolic adaptation to fasting. In this review, fasting is defined by an increase in circulating ketone bodies and hepatic glucose output attributed to continuous food deprivation. In mice, this occurs between 4 and 8h of food deprivation, while in humans, this corresponds to 12–24h without food intake (Katz & Tayek 1998, Browning et al. 2012, Geisler et al. 2016). Early in a fast, hepatic glucose output is derived both from gluconeogenesis and glycogenolysis. In conjunction with a robust reduction of hepatic glycogen stores, which occurs by 12 and 40h of fasting in mice and humans, respectively (Rothman et al. 1991, Geisler et al. 2016), total hepatic glucose output declines as gluconeogenic flux remains constant (Katz & Tayek 1998). In order to meet the systemic energy demands during a fast, hormonal signals stimulate adipose tissue to release non-esterified fatty acids (NEFA) into circulation at a rate which exceeds clearance by non-hepatic tissues (Patel et al. 2002, Djurhuus et al. 2004). Additionally, depression of hepatic glycogen stores during fasting further stimulates adipose tissue lipolysis, indicating that in addition to external hormonal signals, internal liver-derived signals regulate systemic energy metabolism and promote lipid mobilization (Izumida et al. 2013). To better clear circulating fatty acids, the liver upregulates expression of the hepatic fatty acid transporter Cd36 (Xu et al. 2013). In the mouse, significant accumulation of hepatic NEFAs and triglycerides occurs within 4 and 12h fasting, respectively (Geisler et al. 2016). These hepatic lipids spare the oxidation of gluconeogenic amino acids and serve as substrates to generate ketones. Prolonged (>50h) fasting in humans also results in insulin resistance, which develops after the accumulation of hepatic lipids and prevents glucose clearance by non-glucose obligate tissues (Hoeks et al. 2010, Browning et al. 2012, Hanssen et al. 2015). Thus, fasting shares a metabolic profile common to hepatic lipid accumulation including systemic insulin resistance and activation of hepatic gluconeogenesis and ketogenesis.

Given that hormonal signals are integral to hepatic lipid accumulation during fasting, it may be expected that endocrine disorders commonly result in
NAFLD. Hypogonadism, polycystic ovarian syndrome, hypothyroidism, growth hormone deficiency, hypercortisolemia, hyperaldosteronism and hyperpro-lactemia are all associated with a higher prevalence of NAFLD and insulin resistance (Hazlehurst & Tomlinson 2013, Marino & Jornayvaz 2015). In one cohort of growth hormone-deficient patients, 77% presented with NAFLD (Nishizawa et al. 2012). Conversely, individuals with NAFLD were found to have significantly lower growth hormone levels than controls (Xu et al. 2012). Cushing’s syndrome is present in 0.00025% of the general population, yet exists in 1.4% of type 2 diabetics with 3.4% displaying hypercortisolemia (Steffensen et al. 2016). Daily hydrocortisone dose is positively associated with hepatic lipid accumulation in humans, and exogenous corticosterone treatment in rats induces hepatic steatosis (D’Souza A et al. 2012, Auer et al. 2016). Furthermore, NAFLD patients have chronic hypothalamic–pituitary–adrenal (HPA) axis hyperactivity and subclinical hypercortisolemia (Targher et al. 2006). Dysfunction of a number of hormonal systems can contribute to NAFLD pathogenesis, as correction of underlying endocrine disorders alleviates hepatic steatosis (Marino & Jornayvaz 2015).

Hepatic steatosis in humans can also be virus or drug induced. Hepatitis B, C and HIV infection are all mechanistically linked to hepatic lipid accumulation, and hepatic steatosis occurs in 40–50% of HIV-infected patients (Lemoine et al. 2006, Macias et al. 2014, Matthews et al. 2015, Wu et al. 2016). The common HIV therapeutic, highly active antiretroviral therapy (HAART), encourages lipodystrophy and can itself induce hepatic steatosis (Vallet-Pichard et al. 2012). Cancer therapeutics including tamoxifen, irinotecan and cisplatin are additionally known to promote fatty liver (Satapathy et al. 2015, Pan et al. 2016).

In this review, we aim to compare multiple models of hepatic lipid accumulation (diet, drug, genetic and hormone induced) to better isolate the specific phenotypes that accompany hepatic steatosis. Accordingly, we will discuss how hepatic lipids function as signaling molecules and regulators of hepatic metabolic activity to potentiate systemic metabolic dysfunction. Finally, we will compare the metabolic adaptation in models with hepatic lipid accumulation resulting from (1) increased mobilization of adipose tissue lipid stores and accumulation in the liver, (2) increased hepatic de novo lipogenesis (DNL), (3) decreased hepatic beta-oxidation and ketogenesis, or (4) decreased export of lipids from the liver in very low density lipoproteins (VLDL).

Hepatic lipids as signaling molecules

Hepatic fatty acids act as endogenous ligands that activate peroxisome proliferator receptor alpha (PPARα) regulated pathways to produce metabolic products required to meet whole body nutritional demands while fasting (Kersten et al. 1999). Fatty acid binding to nuclear PPARα allows for PPARα activation and binding to the PPAR response element (PPRE) in the promoter of many genes (Ellinghaus et al. 1999, Elholm et al. 2001). During a fast, PPARα expression is increased in response to glucagon signaling and by fatty-acid-induced PPARα-mediated self-upregulation (Pineda Torra et al. 2002, Berglund et al. 2010). This increased expression ensures that PPARα availability is not limiting to the signal generated by hepatic lipid accumulation.

PPARα signaling increases transcription of target genes in gluconeogenesis (phosphoenolpyruvate carboxykinase; PEPCK, glucose 6-phosphatase; G6Pase), beta-oxidation (carnitine palmitoyltransferase I; CPT1) and ketogenesis (hydroxy-3-methyl glutaryl CoA synthase 2; HMGCS2) (Rodriguez et al. 1994, Pineda Torra et al. 2002, Napal et al. 2005, Tachibana et al. 2005, Im et al. 2011). PPARα transcriptional activity is further enhanced by the coactivator peroxisome proliferator-activated receptor gamma coactivator 1alpha (PGC-1α) (Vega et al. 2000, Song et al. 2010). As evidence for the central role of PPARα in coordinating the hepatic adaptation to fasting, fasted PPARα null mice are hypoglycemic and fail to become ketotic (Kersten et al. 1999, Leone et al. 1999). Additionally, PPARα null mice exhibit impaired gluconeogenesis from lactate, pyruvate and glycerol (Le May et al. 2000, Xu et al. 2002, Patsouris et al. 2004). Furthermore, blunted G6Pase upregulation in fasted PPARα null mice directs glucose 6-phosphate toward glycogen synthesis rather than hepatic export (Bandsma et al. 2004). PPARα-mediated upregulation of lipid oxidative genes also encourages maximal hepatic glucose output during fasting, since acetyl-CoA serves as an ample source of carbons for oxidation in the TCA cycle, which allows for flux of gluconeogenic substrates toward gluconeogenesis and away from TCA cycle oxidation (Pettit et al. 1975, Tutwiler & Dellevigne 1979, Chow et al. 1990, Gonzalez-Manchon et al. 1992). In response to a fast, PPARα null mice also develop more severe hepatic steatosis than controls. By encouraging flux through beta-oxidation and ketogenesis, PPARα signaling limits the hepatic accumulation of lipids (Aoyama et al. 1998, Hashimoto et al. 2000). This prevents hepatic oxidative stress that results from the generation of reactive oxygen species.
species and lipid peroxidation products in response to excess hepatic lipid accumulation (Pawlak et al. 2015). Thus, under periods of food deprivation, PPARα promotes hepatic glucose and ketone production and prevents lipotoxicity.

Glucoregulatory gene expression is upregulated in response to elevated circulating NEFA (Massillon et al. 1997). Like in fasting, the elevation of glucoregulatory enzyme expression in NAFLD is dependent upon PPARα (Im et al. 2011). Hepatic PPARα expression and transcriptional activity are induced by high-fat diet feeding (Kim et al. 2004, Patsouris et al. 2006), and elevated hepatic glucose output in diabetes is a dominant factor underlying abnormal glucose homeostasis (Consoli 1992). However, diet-induced obesity does not increase hepatic glucose production or result in hyperglycemia in mice that lack PPARα (Guerre-Milo et al. 2001, Cha et al. 2007). Interestingly, the PPARα agonist-mediated increase in G6Pase and PEPCK mRNA expression is exacerbated by dexamethasone (Lemberger et al. 1996, Bernal-Mizrachi et al. 2007), suggesting that the hypercortisolemia observed in both obesity and fasting is important in enhancing the response to PPARα signaling generated from hepatic lipid accumulation. Glucagon and glucocorticoids upregulate the expression of PGC-1α, the PPARα coactivator, and glucocorticoid-induced gluconeogenesis is dependent upon PPARα signaling (Yoon et al. 2001, Bernal-Mizrachi et al. 2007). In fact, decreased local glucocorticoid production impairs the hepatic induction of PEPCK and G6Pase during fasting and prevents diet-induced hyperglycemia (Kotelevtsev et al. 1997). Because of reduced hepatic glucose production, mice that lack PPARα maintain glucose tolerance and insulin sensitivity when challenged with high-fat diet (Guerre-Milo et al. 2001, Cha et al. 2007).

PPARα is also essential for the upregulation in flux through beta-oxidation and ketogenesis in response to diet-induced hepatic lipid accumulation. PPARα knockout reduces fasting-stimulated hepatic beta-oxidation and HMGCS2 upregulation (Le May et al. 2000). Glucagon and glucocorticoids induce HMGCS2 expression (Hegardt 1999), possibly depending upon PPARα signaling. The PPARα target and major stimulator of ketone production in mice, fibroblast growth factor 21 (FGF21), is required for the increase in beta-oxidation and ketone synthesis common to fatty liver disease (Badman et al. 2007, Xu et al. 2009b, Fisher et al. 2014). However, despite a similar obesity-induced rise in FGF21 in mice and humans, FGF21, which rises only in response to an extended 7-day fast, does not appear to drive ketogenesis in the human (Dushay et al. 2010, Fisher et al. 2010, Fazeli et al. 2015).

PPARα signaling in fatty liver disease promotes lipid catabolism and ketone production. Interestingly, PPARα signaling also upregulates expression of UCP2 (Kelly et al. 1998). UCP2 separates electron transport chain activity from ATP synthesis, leading to the decline in hepatic ATP in fatty livers. Under conditions of abundant substrate availability (e.g., hepatic lipid accumulation), this uncoupling allows for continued oxidation of fatty acids beyond that required to meet cellular energy requirements (Chavin et al. 1999). In fact, despite increased TCA cycle activity, hepatic ATP depletion is a consistent finding in hepatic steatosis (Chavin et al. 1999, Koliaki & Roden 2013, Patterson et al. 2016). In fatty liver disease, hepatic lipid accumulation, hyperglucagonemia and hypercortisolemia synergistically increase PPARα activity and upregulate gluconeogenic, beta-oxidative and ketogenic gene expression. By increasing the potential for hepatic glucose output, lipid catabolism and ketone production, PPARα-induced changes in gene expression limit the lipotoxicity of hepatic lipid accumulation. In both alcohol- and methionine-choline-deficient models of hepatic lipid accumulation, elimination of PPARα signaling increases the resulting hepatic lipid accumulation (Ip et al. 2003, Li et al. 2014). Accordingly, PPARα agonist treatment in fatty liver models consistently decreases hepatic steatosis (Ide et al. 2004, Larner et al. 2012, Barbosa-da-Silva et al. 2015, Souza-Mello 2015).

Several models of fatty liver disease have reported increased expression of both PPARα and peroxisome proliferator-activated receptor gamma (PPARγ) (Memon et al. 2000, Lopez-Soldado et al. 2015). PPARγ expression is mainly limited to the adipocyte, but under conditions of chronic hepatic lipid accumulation, the liver expresses considerable amounts of PPARγ (Vidal-Puig et al. 1996, Pettinelli & Videla 2011, Schultz et al. 2013, Barbosa-da-Silva et al. 2015). Both PPARα and PPARγ recognize the same fatty acids and eicosanoids ligands (Xu et al. 1999). In fact, liver fatty acid-binding protein (L-FABP), which is upregulated in diabetes and obesity, transports fatty acids into the nucleus for both PPARα and PPARγ activation (Wolfrum et al. 2001, Atshaves et al. 2010). However, the metabolic influences of each differ dramatically. PPARα is integral to limiting hepatic lipid accumulation by upregulating pathways that allow for fatty acid oxidation, ketogenesis and fatty acid export (Rakhshandehroo et al. 2007), while PPARγ encourages fatty acid storage by upregulating lipogenic genes including fatty acid transporters and enzymes in fatty liver.
acid and triglyceride synthesis (Schadinger et al. 2005). However, in fatty liver disease, PPARg can also upregulate traditionally PPARa target genes (Patsouris et al. 2006, Moran-Salvador et al. 2011). Hepatic-specific PPARg knockout protects high-fat diet-fed mice from hepatic lipid accumulation, improves glucose tolerance and prevents upregulation of lipogenic, beta-oxidative and gluconeogenic genes (Moran-Salvador et al. 2011). Thus, induction of both PPARg and PPARa by hepatic lipid accumulation directs hepatic metabolic flux toward hepatic glucose and ketone production.

PPARg is a master transcriptional regulator of adipogenesis and is required for adipocyte differentiation (Takahashi et al. 2008, Hamza et al. 2009). High-fat diet feeding elevates hepatic expression of many classically adipocyte-specific genes, making fatty livers more functionally and histologically similar to adipose tissue (Pan et al. 2015). Therefore, upregulated PPARg signaling in hepatic steatosis may promote expression of an adipogenic gene profile. This suggests that while hepatocytes adapt to chronic lipid accumulation by increasing lipid oxidation and ketogenesis, hepatocytes additionally adapt by promoting long-term storage of lipids in a manner similar to adipocytes.

**Mechanisms of hepatic steatosis—Influence of glucoregulatory hormones**

An increase in hepatic lipid content can be generated through *de novo* fatty acid synthesis or influx of diet or adipose-tissue-derived fatty acids, while beta-oxidation and lipoprotein secretion decrease hepatic lipid content. The typical hormonal environment in fatty liver disease is characterized by hyperinsulinemia, hyperglucagonemia, elevated sympathetic tone, hypercortisolemia and growth hormone deficiency. This hormonal milieu alters whole body lipid metabolism and can promote the progression of more severe hepatic steatosis.

**Adipose tissue lipolysis and hepatic lipid uptake**

When energy demand exceeds metabolic energy from the diet, NEFAs are mobilized from white adipose tissue (WAT). Insulin and catecholamines are the dominant inhibitory and stimulatory regulators, respectively, of adipose lipolysis (Fig. 1). During fasting and exercise, insulin levels are low, allowing norepinephrine, cortisol and growth hormone to synergistically stimulate lipolysis and increase systemic fatty acid availability (Marcus et al. 1994, Djurhuus et al. 2004). Similarly, hepatic lipid accumulation induces endocrine changes that dysregulate adipose tissue lipolysis, including insulin resistance, increased sympathetic tone and HPA axis activity (Pratley et al. 1995, Ward et al. 1996, Targher et al. 2006, Armstrong et al. 2014, Thorp & Schaich 2015). The lipolytic hormone profile along with increased adipose tissue mass results in more adipose-tissue-derived fatty acids entering circulation in obese than in normal-weight individuals (Mittendorfer et al. 2009, Howe et al. 2011).

Hormonally regulated lipolysis depends on the activity of the lipolytic enzyme, hormone-sensitive lipase (HSL).
Insulin and catecholamines modulate HSL activity by decreasing and increasing adipocyte cAMP concentrations, respectively (Meijssen et al. 2001, Watt et al. 2006, Nishino et al. 2007). Sympathetic nervous system activity also stimulates cortisol release (Pacak et al. 1995), and may underlie the hypercortisolemia common in NAFLD. Cortisol differentially regulates adipose tissue metabolism depending on insulin signaling. When insulin is low, as would occur during a fast, cortisol stimulates lipolysis and inhibits lipogenesis in WAT (Djurhuus et al. 2004, Gathercole et al. 2011). Yet, in the presence of elevated insulin, cortisol synergistically stimulates lipogenesis (Fig. 1) (Ottosson et al. 1994, Wang et al. 2004). The metabolic response of adipose tissue to glucocorticoids also depends on the duration of exposure. There is not an acute lipolytic response to glucocorticoids, yet, chronically elevated glucocorticoids stimulate lipolysis in adipocytes (Xu et al. 2009a). This chronic induction of lipolysis is transcriptionally regulated, as glucocorticoids upregulate HSL expression and downregulate phosphodiesterase 3B expression, which increases HSL activity by limiting cAMP degradation (Xu et al. 2009a). Glucocorticoids also increase catecholamine-induced AMP signaling by enhancing beta-adrenergic receptor expression, resulting in a more robust elevation in adenylyl cyclase and PKA activity (Lamberts et al. 1975, Lacasa et al. 1988). In line with the catabolic response to glucocorticoid exposure, hypercortisolemia decreases insulin-induced adipose tissue glucose clearance (Hasni Ebou et al. 2016). Moreover, chronic hypercortisolemia, obesity and NAFLD increase adipose tissue expression of 11beta-hydroxysteroid dehydrogenase type 1 (11beta-HSD1), an enzyme that catalyzes the production of cortisol from cortisone (Candia et al. 2012, Wang et al. 2015). In fact, transgenic overexpression of adipose specific 11beta-HSD1 in lean mice results in visceral obesity and insulin-resistant diabetes (Masuzaki et al. 2001). Thereby, enhanced local cortisol synthesis at adipose tissue in obesity promotes adipose tissue insulin resistance.

Excessive lipolysis and adipose tissue fatty acid release into circulation results in ectopic accumulation of lipids. Hepatic lipid accumulation is limited in mice that lack HSL and thus have muted adipose tissue lipolytic capacity. These HSL null mice have improved insulin sensitivity and systemic glucose clearance (Girousse et al. 2013, Wang et al. 2016b). Fasting and NAFLD are characterized by a rise in sympathetic activity and adipose tissue lipolysis (Migliorini et al. 1997, Grassi et al. 2005, Thorp & Schlaich 2015). The lipolytic response to obesity depends on the adipose tissue depot, with decreased lipolytic capacity in subcutaneous adipose tissue and increased lipolysis from visceral adipose tissue (Jensen et al. 1989, Busetto et al. 1993). Adipose triglyceride lipase primarily mediates basal lipolysis, while HSL mediates catecholamine-stimulated lipolysis, and the lipolytic capacity of subcutaneous adipose tissue is largely determined by HSL expression (Large et al. 1998, Langin et al. 2005). In subcutaneous adipose tissue, obesity decreases HSL expression, limiting sensitivity to beta3-adrenoceptor-induced lipolysis is increased in obesity (Hoffstedt et al. 1996). Thus, catecholamine-stimulated lipolysis depends on the regional adipose tissue depot.

Despite increased adipose tissue lipolysis, skeletal muscle lipid clearance is decreased in obese, type 2 diabetics (Kelley & Simonneau 1994, Turpeinen et al. 1999, Blaak et al. 2000, Blaak 2003, Goossens et al. 2016). The combination of increased fatty acid release from adipose tissue and decreased clearance by skeletal muscle results in hyperlipidemia and increased reliance on the liver to clear fatty acids (Lewis et al. 2002, Jonkers et al. 2013, Janssens et al. 2015). Hepatic expression of Cd36, a fatty acid transporter, is increased with alcohol or high-fat feeding in mice and in NAFLD (Miquirena-Colina et al. 2011, Clugston et al. 2014). Hyperinsulinemia alone can stimulate hepatic Cd36 expression, and is suggested as a primary mechanism driving hepatic lipid accumulation (Steneberg et al. 2015). Hepatic-specific knockout of Cd36 protects mice from high-fat diet-induced fatty liver and insulin resistance, supporting the hypothesis that increased hepatic lipid uptake is critical for the development of hepatic triglyceride accumulation (Wilson et al. 2016). Hepatic lipoprotein lipase (LPL) expression and activity are also increased in high-fat diet-fed mice and obese individuals, offering another mechanism for increased hepatic lipid uptake in fatty liver disease (Pardina et al. 2009, Ahn et al. 2011). These data support that dysregulated adipose tissue lipolysis and hepatic clearance are integral for the development of fatty liver in obesity.

Lipodystrophy disorders, characterized by impaired adipocyte triglyceride storage, also result in hepatic steatosis and insulin resistance (Rochford 2014). Genetic mouse models of lipodystrophy develop markedly depleted adipose stores, severe fatty liver disease and systemic insulin resistance (Saha et al. 2004, Softic et al. 2016). Due to limited adipose tissue lipid storage, patients with lipodystrophy frequently develop NAFLD and are at an increased risk for developing hypertriglyceridemia.
and diabetes (Safar Zadeh et al. 2013, Akinci et al. 2015). Antiretroviral therapy (HAART) for HIV infection commonly results in lipodystrophy. This is a consequence of adipocyte apoptosis, impaired adipogenesis and increased lipolysis, leading to hepatic lipid accumulation and insulin resistance (Nerurkar et al. 2001, Giralt et al. 2010, Goulibourne & Vaux 2010, Kumar et al. 2015, Mandal et al. 2016). Common phenotypes between NAFLD, fasting and alcohol-induced fatty liver, and lipodystrophy patients point to the importance of hepatic lipid accumulation in driving metabolic dysregulation.

Through the multiple models of increased adipose tissue lipolysis that result in hepatic lipid accumulation (i.e. fasting, diet-induced obesity, chronic alcohol consumption and lipodystrophies), it is evident that increased fatty acid availability can drive hepatic lipid accumulation, insulin resistance and impaired glucose clearance. Moreover, hepatic lipid accumulation appears to feed forward to further increase adipose tissue lipolysis by limiting insulin sensitivity, increasing HPA axis activity and increasing catecholaminergic tone.

**De novo lipogenesis**

Although an influx of fatty acids from adipose tissue robustly and quickly increases hepatic lipid content, hepatic steatosis may also occur as a result of increased de novo fatty acid synthesis. Under normal physiological conditions, an elevation in circulating glucose upregulates lipogenic enzyme expression to encourage hepatic glucose clearance and storage of the carbons as fatty acids and triglycerides. Blood glucose enhances DNL through two signaling pathways. First, by increasing circulating insulin, glucose stimulates sterol response element-binding protein 1c (SREBP1c) signaling. Second, glucose can directly activate the carbohydrate response element-binding protein (ChREBP) (Iizuka et al. 2004). Both SREBP1c and ChREBP upregulate lipogenic enzymes such as acetyl-CoA carboxylase 1 (ACC1) and fatty acid synthase (FAS). Hyperinsulinemia increases SREBP1c and ChREBP expression and further promotes hepatic DNL by inhibiting FoxO1, which normally downregulates SREBP1c expression and promotes ChREBP degradation (Deng et al. 2012, Ido-Kitamura et al. 2012, Zhang et al. 2006). This coordinated response stimulates storage of excess dietary energy as triglycerides for future oxidation under energy-deplete conditions. However, chronic overconsumption of carbohydrates, a diet high in fructose, hepatic PPAR signaling, alcohol and hypercholesterolemia all activate the lipogenic pathways resulting in hepatic lipid accumulation.

While a single exposure to fructose has minimal effects of hepatic lipid metabolism, a diet rich in fructose can increase flux through DNL by increasing lipogenic substrate and by promoting lipogenic gene expression. The importance of fructose as a lipogenic substrate results from the outsized role of the liver in fructose clearance. In the first pass through the liver sequesters 71% of dietary fructose, while only clearing 13% of dietary glucose (Muratoglu et al. 1986). In addition to providing the carbons necessary for fatty acid synthesis, fructose also induces signaling pathways that encourage lipogenesis. Fructose potentiates glucose-stimulated insulin secretion (Kyriazis et al. 2012), increasing insulin-mediated SREBP1c signaling in the hepatocyte. Fructose also increases SREBP1c expression and activity independent of insulin. In liver-specific insulin receptor null mice, fructose stimulates SREBP1c expression, nuclear localization and the expression of target lipogenic enzymes (Haas et al. 2012). Without altering ChREBP nuclear localization, a diet rich in fructose increases ChREBP binding to DNA nearly 4 fold (Koo et al. 2009). Interestingly, dietary fructose more robustly induces DNL in patients with fatty liver disease (Lambert et al. 2014). Thus, dietary fructose contributes to the development of NAFLD through increased DNL and NAFLD feeds forward to increase DNL from fructose.

Increased DNL is also a key factor in alcohol-induced fatty liver. Acute ethanol consumption only modestly stimulates DNL with 5% of consumed alcohol entering lipogenesis (Silet et al. 1999). However, ethanol induces transcriptional changes that encourage DNL. Ethanol inhibits hepatic 5‘ adenosine monophosphate-activated protein kinase (AMPK), simultaneously inhibiting beta-oxidation and activating fatty acid synthesis. This decrease in AMPK is integral to the increased SREBP1c and ACC activity induced by ethanol (You et al. 2004). The SREBP1c-induced increase in ACC activity directly increases fatty acid synthesis, while suppressing fatty acid oxidation. SREBP1c also upregulates lipin-1 expression and localization to the cytosol (Hu et al. 2012). Within the cytosol, lipin-1 acts as a phosphatidate phosphatase, enzymatically converting phosphatidate to diacylglycerol and promoting triglyceride synthesis. In the nucleus, lipin-1 acts as a PPARa coactivator and facilitates the upregulation of beta-oxidative genes while suppressing lipogenic gene expression (Finck et al. 2006). By increasing lipin-1 expression and cytosolic localization, while reducing nuclear lipin-1 localization, ethanol...
simultaneously enhances triglyceride synthesis while limiting the nuclear action of lipin-1 to stimulate beta-oxidation (Bi et al. 2015). Chronic alcohol consumption induces hepatic steatosis and robustly elevates expression of PPARg, inducing the adipocyte-like gene expression profile commonly observed in NAFLD (Zhang et al. 2016).

Abnormal glucocorticoid signaling is implicated in the pathology of numerous metabolic disorders, and hepatic glucocorticoid signaling stimulates hepatic lipogenesis (Krausz et al. 1981). Glucocorticoids directly upregulate lipin-1 expression (Mannontri et al. 2008), representing an intriguing mechanism driving hepatic steatosis by simultaneously decreasing lipid oxidation and increasing DNL and triglyceride esterification. By removing hairy enhancer of split 1 (Hes1), a negative regulator of PPARg expression, hepatic glucocorticoid signaling enhances PPARg expression (Revollo et al. 2013, Wu et al. 2015). In obese db/db mice, transgenic overexpression of Hes1 prevents PPARg upregulation and corrects fatty liver (Lemke et al. 2008). Although systemic glucocorticoid concentrations are often normal in NAFLD patients, elevated adipocyte expression of 11beta-HSD1 and cortisol production induced either by obesity or genetic overexpression result in hypercortisolemia in the hepatic portal circulation, exposing the liver to excess glucocorticoids (Masuzaki et al. 2001, Candia et al. 2012). Similar to adipose tissue, hepatic expression of 11beta-HSD1 and local cortisol synthesis may be more metabolically relevant than circulating cortisol levels. Interestingly, obesity is initially characterized by a decrease in hepatic 11beta-HSD1 expression in mice and humans (Ahmed et al. 2012, Candia et al. 2012). This may serve as a protective mechanism to limit local glucocorticoid production in the face of increased hepatic glucocorticoid delivery. However, progression of hepatic steatosis to NASH is accompanied by increased hepatic 11beta-HSD1 mRNA expression and activity (Ahmed et al. 2012). Hepatic 11beta-HSD1 expression has clear systemic metabolic consequences as mice that overexpress 11beta-HSD1 have excess local hepatic glucocorticoid production, increased hepatic triglyceride accumulation and overexpress FAS (Paterson et al. 2004). Despite no change in body weight or adipose tissue mass, these mice are hyperinsulinemic and insulin resistant. Conversely, hepatic-specific knockdown of 11beta-HSD1 in mice protects against western-type diet-induced hepatic steatosis by reducing hepatic lipogenesis and increasing fatty acid oxidation (Li et al. 2011). Similarly, pharmacological 11beta-HSD1 inhibition in NAFLD patients decreases hepatic lipid accumulation (Stefan et al. 2014). Thus, the elevated glucocorticoid signaling, common in fatty liver, encourages hepatic DNL.

Unlike cortisol and insulin, glucagon, norepinephrine and growth hormone inhibit hepatic DNL (Fig. 1) (Stark and Keller 1987, Cordoba-Chacon et al. 2015, Wang et al. 2016a). Growth hormone deficiency in NAFLD may contribute to hepatic steatosis by removing GH-mediated suppression of DNL. In liver-specific growth hormone knockout mice, increased hepatic DNL is driven by enhanced glycolytic flux, supplying more substrate to enter the lipogenic pathway (Cordoba-Chacon et al. 2015). Although liver PPARg is upregulated in this model, PPARg is a consequence, not a cause, of steatosis, as knockout of hepatic PPARg does not prevent development of hepatic steatosis in the absence of growth hormone signaling (Kineman et al. 2016).

Insulin-resistant NAFLD patients have markedly upregulated hepatic lipogenic gene expression and DNL flux (Schwarz et al. 2003, Eissing et al. 2013). In fact, hyperinsulinemic obese subjects have higher rates of hepatic DNL following a high-fat meal than normoinsulinemic obese or lean subjects (Schwarz et al. 2003). Increased DNL represents an important mechanism driving hepatic triglyceride accumulation in fatty liver disease.

Beta-oxidation and ketogenesis

In fatty liver disease, hepatic beta-oxidation and ketogenesis are upregulated (Sunny et al. 2010, Mannisto et al. 2015). Hepatic beta-oxidation in response to lipid accumulation prevents lipotoxicity and supports gluconeogenesis and ketogenesis. Mice that are unable to normally upregulate lipid oxidative genes during fasting have severe hepatic steatosis, do not display ketosis and are hypoglycemic (Kersten et al. 1999, Leone et al. 1999). Similarly, individuals with mitochondrial fatty acid oxidation disorders (MFAOD), conditions that affect ~1 in 10,000 people, are sensitive to fasting and high-fat diets and present with hypoketotic hypoglycemic episodes (Pollitt 1995, Rector et al. 2008).

Hepatitis C infection impairs hepatic lipid oxidation by decreasing expression of the mitochondrial trifunctional protein (MTP), an enzyme that catalyzes the last 3 steps in mitochondrial beta-oxidation (Amako et al. 2015). Mouse models with genetically or pharmacologically induced deficits in beta-oxidation develop fatty liver disease. Mice heterozygous for MTP (MTP+/−) have a 50% reduction in hepatic
beta-oxidation, hepatic steatosis and systemic insulin resistance (Ibdah et al. 2005, Rector et al. 2013). Hepatic microRNA-107, upregulated in metabolic syndrome, inhibits the expression of the MTP alpha subunit. Exogenous miR-107 induces hepatic lipid accumulation, hyperglycemia and decreases glucose tolerance (Bhatia et al. 2016). Further, hepatic carnitine deficiency limits entry of fatty acids into the mitochondria, impairing beta-oxidative flux and inducing a more robust hepatic triglyceride accumulation as a result of high-fat diet (Du et al. 2013). Together, these models establish that limiting beta-oxidation severely exacerbates hepatic lipid accumulation. Moreover, they propose that the PPARα-mediated increase in beta-oxidative gene expression is key to muting hepatic lipid accumulation during a fast.

Interestingly, the hepatic lipid accumulation resulting from dietary fructose also involves PPARα signaling. Chronic (>2 weeks) fructose feeding downregulates hepatic PPARα expression and activity, reducing the expression of PPARα-targeted beta-oxidative enzymes. Of note, PPARα agonists limit hepatic steatosis and improve systemic insulin sensitivity by stimulating beta-oxidation in this fructose consumption model (Nagai et al. 2002, Roglans et al. 2007). Although enhanced DNL is commonly blamed for the steatosis resulting from dietary fructose, the inhibition of beta-oxidation may be equally important. Fructose acutely inhibits CPT1 activity and beta-oxidation through a resulting increase in malonyl-CoA synthesis and chronically downregulates the expression of beta-oxidative genes.

Increased hepatic uptake of either diet or adipose-derived fatty acids stimulates hepatic beta-oxidation (Reed et al. 1991). Like fasting-induced hepatic lipid accumulation, high-fat diet feeding elevates hepatic CPT1 activity and beta-oxidative capacity (Stefanovic-Racic et al. 2008, Sunny et al. 2010, Zhang et al. 2014, Geisler et al. 2016). The acetyl-CoA derived through beta-oxidation can either be oxidized through the TCA cycle or enter ketogenesis. Accordingly, diet-induced obesity increases HMGCS2 mRNA expression, increasing flux through ketogenesis (Guo et al. 2013, Darkhal et al. 2015). Finally, to regenerate NAD+ and maintain maximal beta-oxidation, obesity increases expression of UCP2 (Chavin et al. 1999). Rodents with hepatic steatosis from diets rich in fructose or sucrose also aberrantly overexpress hepatic UCP2 mRNA (Ruiz-Ramirez et al. 2011, Schultz et al. 2015). These data recommend that transcriptional changes are central to the upregulation of beta-oxidation and ketogenesis in the adaptation to hepatic lipid accumulation.

The increased ketogenesis in obesity depends on increased flux through beta-oxidation which results in increased substrate (acetyl-CoA) availability. Activity of HMGCS2, the enzyme-regulating flux through ketogenesis, is decreased by acetylation and succinylation, and increased by phosphorylation (Quant et al. 1990, Shimazu et al. 2010, Grimsrud et al. 2012). HMGCS2 is phosphorylated by PKA, a downstream glucagon signaling molecule, and hyperphosphorylation of HMGCS2 occurs in obese rodents (Grimsrud et al. 2012). Therefore, hyperglucagonemia in fatty liver increases HMGCS2 activity and ketone production. Although increased hepatic ketone synthesis is integral to the development of ketosis in obesity, insulin resistance also decreases clearance of beta-OH butyrate (Nosadini et al. 1985). In turn, beta-OH butyrate has been shown to decrease peripheral insulin-stimulated glucose uptake, and may contribute to the development of insulin resistance in fatty liver disease (Tardif et al. 2001, Yamada et al. 2010). As evidenced, the individual metabolic and hormonal perturbations common to hepatic lipid accumulation are intertwined, making it difficult to isolate the response to changes in a single pathway.

The interplay of DNL and beta-oxidation

Diminished beta-oxidative capacity resulting from genetic disorders or viral infections establishes the central role of beta-oxidative flux in limiting steatosis. Accordingly, fasting and hypercaloric diets that increase hepatic lipid accumulation induce changes in gene expression that encourage fatty acid oxidation and ketone production. However, despite enhanced lipid catabolism and ketogenic capacity resulting from increased enzyme expression and hormonal changes that promote increased enzyme activity, each of these models still develop hepatic steatosis and insulin resistance. Hepatic DNL contributes directly to the development of steatosis in NAFLD. However, the inhibition of beta-oxidative flux, an indirect response to elevated DNL may more robustly encourage steatosis.

Fatty acid flux through beta-oxidation is inhibited by hepatic DNL. The production of malonyl-CoA inhibits activity of CPT1, limiting the mitochondrial entry of fatty acids for oxidation (Morillas et al. 2002). This interaction prevents newly synthesized fatty acids from undergoing oxidation and avoids futile nutrient cycling. Malonyl-CoA production is regulated by ACC1 and ACC2, while degradation is dependent upon the activity of malonyl-CoA decarboxylase (MCD). ACC1

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expression and activity increases in fatty liver disease, while ACC2 expression is independent of hepatic lipid accumulation (Yahagi et al. 2005, Kennedy et al. 2007, Kohijima et al. 2007). This increase in total ACC activity increases malonyl-CoA synthesis, hepatic malonyl-CoA concentration and flux through fatty acid synthesis (Zhao et al. 2009). The increase in hepatic malonyl-CoA would be expected to inhibit CPT1 and beta-oxidative flux. However, in fatty liver, both fatty acid synthesis and beta-oxidation can be simultaneously increased as a result of the subcellular distribution of ACC activity. ACC1 is located in the cytosol, while ACC2 is tethered to the outer mitochondrial membrane (Abu-Elheiga et al. 2000). Accordingly, ACC2 produces malonyl-CoA in close proximity to CPT1 and is therefore the enzyme more responsible for the inhibition of beta-oxidation. In fact, ACC2 deletion prevents hepatic lipid accumulation and increases fatty acid oxidation, while simultaneously preventing the diet-induced insulin resistance and glucose intolerance (Abu-Elheiga et al. 2003). The activity of ACC2 is inhibited by AMPK, a cellular energy sensor regulated by AMP, glucagon and insulin (Jeon et al. 2012). AMPK activity increases with a decrease in cellular energy. Accordingly, insulin inhibits AMPK to increase ACC2 activity and malonyl-CoA production (Witters et al. 1988, Shaw 2013, Valentine et al. 2014). This increase in malonyl-CoA production limits fatty acid oxidation. In contrast, glucagon increases AMPK activity to depress ACC2 activity and malonyl-CoA production, which encourages fatty acid oxidation (Geelen et al. 1978, Berglund et al. 2009, Cyphert et al. 2014).

In addition to altering the enzymes involved in malonyl-CoA synthesis, AMPK simultaneously alters malonyl-CoA breakdown. MCD catalyzes the conversion of malonyl-CoA to acetyl-CoA, relieving CPT1 inhibition (Dyck et al. 2000). A genetic model of hepatic MCD overexpression establishes that decreasing hepatic malonyl-CoA concentrations increases beta-oxidative flux, improves whole body insulin sensitivity and prevents hyperinsulinemia on a high-fat diet (An et al. 2004). Hepatic MCD expression is increased by PPARα agonism, representing another mechanism by which hepatic lipid-induced PPARα signaling accelerates fatty acid oxidation. (Lee et al. 2004). AMPK activates MCD (Sambandam et al. 2004). Through modulating AMPK signaling, glucagon increases MCD activity, promoting conversion of malonyl-CoA to acetyl-CoA and relieving CPT1 inhibition, while insulin inhibits MCD activity and reduces CPT1 activity (Dyck et al. 2000). Thus, as evidenced by the ACC2 knockout and MCD overexpression models, malonyl-CoA-mediated inhibition of CPT1 depresses maximal beta-oxidative capacity in fatty liver disease. However, given the subcellular distribution and divergent regulation of hepatic lipid accumulation on ACC expression, simultaneous stimulation of lipogenic and beta-oxidative flux can occur.

This concurrent flux through fatty acid synthesis and oxidation occurs normally in non-hepatic tissue as an adaptive mechanism to promote substrate utilization and increase cellular metabolic rate (Solinas et al. 2004, Mottillo et al. 2014, O’Sullivan et al. 2014). Like in fatty liver, this simultaneous induction of lipogenesis and oxidation is proposed to be dependent upon diminished ACC2-generated malonyl-CoA and submaximal CPT1 inhibition (Yu et al. 2002). In adipose tissue, PPARγ-dependent DNL upregulation enhances glucose clearance and utilization, allowing adipocytes to act as a glucose sink to maintain euglycemia (Marcelino et al. 2013). Increased hepatic DNL in fatty liver disease may similarly serve as a mechanism to minimize hyperglycemia, while increased beta-oxidation allows energy dissipation and protects against lipotoxicity. The upregulation of PPARγ and lipogenic gene expression in response to chronic hepatic lipid accumulation drives the increase in DNL in fatty liver disease (Matsusue et al. 2003), and supports the simultaneous induction of lipogenesis and beta-oxidation. The onset of this nutrient cycling represents another mechanism by which hepatocytes adopt metabolic characteristics of adipocytes to accommodate long-term lipid accumulation.

**Hepatic lipid export and extrahepatic lipid clearance**

Hepatocytes distribute lipids to peripheral tissues by exporting VLDL. Impaired VLDL export limits hepatic disposal of triglycerides and induces hepatic steatosis. Chronic ethanol consumption decreases VLDL synthesis and secretion, enhancing the development of fatty liver (Simpson et al. 1990, Kharbanda et al. 2009). However, since ethanol consumption increases DNL, inhibits hepatic beta-oxidation and increases adipose tissue lipolysis, the isolated response to inhibiting VLDL secretion can be better understood in genetic models with inhibited lipoprotein synthesis and release. Inhibited lipoprotein transfer increases steatosis without decreasing insulin sensitivity. Knockout of hepatic
Hepatic lipid accumulation can result from excessive lipid influx or impaired lipid efflux. In response to elevated hepatic lipid uptake, as occurs in response to fasting, high-fat diet feeding or lipodystrophies, hepatocytes activate metabolic pathways (beta-oxidation, ketogenesis and VLDL export) to minimize lipotoxicity. Still, hepatic steatosis develops when lipid influx overwhelms these protective mechanisms. In numerous models of hepatic steatosis, including overconsumption of fat, fructose or ethanol, and genetic lipodystrophy and MFAOD conditions, fatty liver is accompanied by systemic insulin resistance. Thus, independent of origin, hepatic lipid accumulation is associated with peripheral metabolic dysfunction.

Altered hepatic metabolite flux as a consequence of hepatic lipid accumulation can affect systemic insulin signaling. Elevated circulating beta-OH butyrate concentrations, a result of upregulated ketogenesis, interfere with insulin-stimulated skeletal muscle glucose uptake, while increased hepatic glucose output exacerbates hyperglycemia and further promotes hyperinsulinemia. Enhanced VLDL secretion contributes to hypertriglyceridemia and encourages extrahepatic lipid uptake, which further impairs insulin-stimulated skeletal muscle glucose uptake. Thus, metabolic activity induced by hepatic lipid accumulation contributes to the dysregulated glucose homeostasis, which occurs in fatty liver disease.

NAFLD and insulin resistance are highly linked comorbidities. Although fatty liver develops in response to a wide diversity of physiological perturbations, these perturbations result in a similar metabolic phenotype that includes insulin resistance, hyperglucagonemia, hypertriglyceridemia, hyperglycemia and hyperketonemia. Of note, mouse models that lack hepatic lipid accumulation retain insulin sensitivity during obesity (Chen et al. 2002, Franckhauser et al. 2002, Haemmerle et al. 2006, Montgomery et al. 2013). Similarly, metabolically healthy obese humans are insulin sensitive with significantly less liver fat accumulation than obese, insulin resistance individuals (Stefan et al. 2008,
Samocha-Bonet et al. 2012). Thus, understanding the mechanisms that result in hepatic lipid accumulation and underlie the metabolic dysfunction resulting from fatty liver is critical to identifying points of intervention to treat this increasingly prevalent disease state.

Declaration of Interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of this review.

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