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Strategies, models and biomarkers in experimental non-alcoholic fatty liver disease research

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Abstract

Non-alcoholic fatty liver disease encompasses a spectrum of liver diseases, including simple steatosis, steatohepatitis, liver fibrosis and cirrhosis and hepatocellular carcinoma. Non-alcoholic fatty liver disease is currently the most dominant chronic liver disease in Western countries due to the fact that hepatic steatosis is associated with insulin resistance, type 2 diabetes mellitus, obesity, metabolic syndrome and drug-induced injury. A variety of chemicals, mainly drugs, and diets is known to cause hepatic steatosis in humans and rodents. Experimental non-alcoholic fatty liver disease models rely on the application of a diet or the administration of drugs to laboratory

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animals or the exposure of hepatic cell lines to these drugs. More recently, genetically modified rodents or zebrafish have been introduced as non-alcoholic fatty liver disease models. Considerable interest now lies in the discovery and development of novel non-invasive biomarkers of non-alcoholic fatty liver disease, with specific focus on hepatic steatosis. Experimental diagnostic biomarkers of non-alcoholic fatty liver disease, such as (epi)genetic parameters and ‘-omics’-based read-outs are still in their infancy, but show great promise. . In this paper, the array of tools and models for the study of liver steatosis is discussed. Furthermore, the current state-of-art regarding experimental biomarkers such as epigenetic, genetic, transcriptomic, proteomic and metabonomic biomarkers will be reviewed.

Keywords

Non-alcoholic fatty liver disease; steatosis; models; drugs; biomarkers

1. Introduction

Non-alcoholic fatty liver disease (NAFLD) covers a spectrum of chronic liver diseases, ranging from hepatic steatosis or fatty liver to non-alcoholic steatohepatitis (NASH), liver fibrosis, liver cirrhosis and eventually hepatocellular carcinoma (HCC). It is estimated that 1 billion people currently suffer from any form of NAFLD [1]. Liver steatosis, marked as the first stage of NAFLD, is closely associated with obesity, type 2 diabetes mellitus, insulin resistance (IR) and drug-induced liver injury [2]. This is substantiated by the fact that NAFLD is the most dominant chronic liver disease with a prevalence of 20-30 % in Western countries, 30-50 % in patients with type 2 diabetes mellitus and 80-90 % in obese adults [3-6]. Steatosis is considered as a benign reversible event, while NASH has the potential to lead to cirrhosis and HCC. As much as 10-25 % of liver steatosis patients progress to NASH and 2-3 % of NASH patients develop liver cancer [3, 7]. Hence, liver steatosis is of major concern for worldwide health, especially since sedentary lifestyle, modern Western nutrition, genetic predispositions, a variety of pharmacological agents and hepatitis B and C infection have been identified as critical causes of NAFLD [2, 3, 7-12]. At present, 70.000 Europeans are fatally affected by chronic liver disease every year [13]. Furthermore, HCC incidence increased tremendously over the past 25 years [14] and was responsible for the death of 21.670 patients in the United States in 2013 [15]. The economic burden imposed by chronic liver disease and its causes is considerable. Indeed, in the United States, 160 to 300 billion Dollars are spent every year on obesity, which constitutes 10 % of overall health care costs [16]. So far, the only curative therapy for acute and chronic liver failure is liver transplantation, with a cost in Europe of about 100.000 Euro the first year and 10.000 Euro yearly thereafter [17].

Liver steatosis is featured by the accumulation of fat in at least 5 % of hepatocytes. These fatty or lipid droplets, typically present in the cytosol, are composed of aggregated triglycerides (TGs) engulfed by a phospholipid monolayer [18]. In physiological conditions, these lipids generate energy and serve as a substrate for membrane synthesis, though in excess, this can lead to hepatocellular damage. Four pathogenic mechanisms are thought to be responsible for the accumulation of TG-based lipid droplets (Figure 1), namely (*i*) the

increased uptake of free fatty acids (FFAs) from high-fat food or adipocytes in body fat, (ii) the increased synthesis of FFAs in the liver from glucose or acetate by IR, (iii) the decreased mitochondrial β -oxidation of FFAs caused by a multitude of drugs and (iv) the decreased secretion of TGs in very low density lipoproteins from the liver [11, 19]. The progression from steatosis to NASH is presented in the so-called “two-hit” hypothesis [20]. TG accumulation by IR, increased fatty acid influx, decreased fatty acid oxidation and/or decreased TG transport can be considered as the “first hit”, making the liver more sensitive to a “second hit”, such as oxidative stress, lipoapoptosis and increased production of inflammatory cytokines. This can ultimately result in the development of NASH [7, 20, 21]. Being associated with obesity and type 2 diabetes mellitus, IR plays a key role in the origin and maintenance of hepatic steatosis. Increased peripheral lipolysis and downregulation of tissue glucose uptake results in an increase of FFAs in hepatocytes and thus creates the basis for TG production. Together with decreased apolipoprotein synthesis, TG secretion, in the form of very low density lipoproteins, is inhibited. The resulting excess of FFAs induces a rise in mitochondrial β -oxidation, production of reactive oxygen species and oxidative stress as well as elevated lipid peroxidation, all which are hallmarks of the injury observed in the liver of obese patients suffering from steatosis [22-24]. Additionally, hyperinsulinemia and hyperglycemia, both caused by increased insulin secretion by pancreatic β -cells, trigger the transformation of FFAs to glucose and inhibit β -oxidation, resulting in the accumulation of TGs in the cytosol of hepatocytes. Collectively, these triggers induce the production of proinflammatory cytokines *via* release of tumor necrosis factor α , which leads to the development of NASH [11, 25-28]. The development of liver steatosis is also closely related to the metabolic syndrome. In this respect, liver steatosis patients show one or more features of the metabolic syndrome, such as IR, glucose intolerance, obesity, hypertriglyceridemia and elevated blood pressure [29]. Additionally, pharmacological agents targeting mitochondria are known to cause oxidative stress or liver steatosis (Figure 2).

Histologically, no distinction can be made between alcoholic fatty liver disease and NASH, since both conditions have an identical histological pattern. This emphasizes the importance of excluding significant alcohol intake (*i.e.* more than 20 gram per day) in patients when diagnosing NASH. The latter is characterized by the presence of steatosis, mixed inflammatory cell infiltration, hepatocyte ballooning, necrosis, glycogen nuclei, Mallory’s bodies and fibrosis [30]. Two types of steatosis can be recognized, namely macrovesicular steatosis and microvesicular steatosis. Both present the accumulation of TGs in the cytosol of hepatocytes. However, in case of macrovesicular steatosis, large lipid droplets which displace the cytoplasmic content and nucleus are observed, while in microvesicular steatosis small well-circumscribed lipid droplets that do not displace the nucleus are seen (Figure 3) [31].

Steatosis is often accompanied by phospholipidosis, implying the intracellular accumulation of phospholipids. As such, phospholipidosis is a lysosomal storage disorder and is considered as a reversible side effect [32]. Phospholipidosis will not be further discussed in this paper. Rather, focus will be put on strategies to experimentally mimic the pathological features of NAFLD induced by drugs, diets or dietary ingredients combined with rodents, zebrafish and genetic modified animals as well as with liver-based *in vitro* models. The

clinical diagnosis of liver steatosis and NAFLD is based on a number of read-outs, including clinical chemistry parameters (*e.g.* cholesterol and transaminase levels), histopathological examination of liver biopsies and specific physical tests (*e.g.* computed tomography and nuclear magnetic resonance) [33]. These clinical read-outs will not be considered in this paper. Instead, particular attention will be paid to more experimental diagnostic biomarkers of NAFLD, such as (epi)genetic parameters and ‘-omics’-based read-outs.

2. Strategies in NAFLD research

2.1. Drug treatment

2.1.1. Valproic acid—With its anticonvulsive activity being discovered in 1963, valproic acid (VPA), or its sodium valproate derivative, is currently the most commonly prescribed anti-epileptic drug worldwide. In addition to its anticonvulsant properties, VPA is also used for the treatment of bipolar disorders [34-36], clinical depression [37], absence seizures [38], tonic-clonic seizures [39], complex partial seizures [40] and juvenile myoclonic epilepsy [41]. More recently, VPA has been characterized as a histone deacetylase inhibitor [42] with therapeutic potential in the cancer field. Although VPA is considered as a drug with a relatively safe profile, adverse reactions, such as encephalopathy, hypersensitivity syndrome and teratogenicity, have been reported in patients receiving VPA [43]. One of the most alarming side effects is hepatotoxicity, in particular microvesicular steatosis, caused by impairment of mitochondrial β -oxidation. Indeed, upon sequestration with coenzyme A (CoA) to valproyl-CoA in the cytosol of hepatocytes, VPA can enter mitochondria. This results in the inhibition of mitochondrial fatty acid oxidation, since VPA undergoes oxidation to several products and hereby competes with endogenous lipids for enzymes in the oxidation pathway [44-46]. The development of microvesicular steatosis typically occurs in mice given doses of VPA ranging from 100 mg/kg/day for 2 weeks to 1000 mg/kg/day for 24 hours [47, 48]. The first step in the bioactivation pathway of VPA is the dehydrogenation by cytochrome P450 (CYP) 2C9 and CYP2A6 enzymes, forming 4-ene-valproate. This triggers an additional mechanism of β -oxidation inhibition. *In vivo* and *in vitro* studies have shown that 4-ene-valproate is a more steatogenic and cytotoxic compound compared with the parent drug [49-51]. Furthermore, 4-ene-valproate is transformed to 2,4-diene-valproyl-CoA, which may inactivate β -oxidation enzymes [52, 53]. VPA also acts as an anionic uncoupler by translocating protons in the mitochondrial matrix. This protonophoric effect can slightly uncouple mitochondrial respiration and may induce opening of the mitochondrial permeability transition pore, serving as another stimulus of VPA-induced cell death [54]. Recently, a new mechanism of VPA-induced hepatic steatosis has been described, namely inhibition of carnitine palmitoyl transferase 1, which transfers FFA into the mitochondria, by VPA-CoA. This results in decreased mitochondrial uptake of FFA and thus leads to a rise in TG accumulation [55].

2.1.2. Amiodarone—Amiodarone is a large amphiphilic drug used for the treatment of atrial and ventricular arrhythmias. Long-term therapy with amiodarone is limited by a multitude of extracardiac side effects, such as pulmonary toxicity [56], skin hyperpigmentation [57], thyroid dysfunction [58] and liver failure [59] due to the inhibition of mitochondrial β -oxidation [60-62]. Hepatic steatosis usually occurs in mice at a dose of

150 mg/kg/day when treated for 4 to 7 days [63]. In its unprotonated form, amiodarone can easily move across the outer mitochondrial membrane. Upon protonation, it diffuses through the inner mitochondrial membrane. Inside the relatively alkaline mitochondrial matrix, amiodarone loses its protonated status, which as such decreases the membrane potential [60, 64]. Furthermore, amiodarone equally inhibits microsomal triglyceride transfer protein [65], able to transfer TGs and assemble them into very low density lipoproteins and chylomicrons [66]. Dronedarone, an amiodarone-like anti-arrhythmic drug, was proposed as an alternative for amiodarone for the treatment of atrial fibrillation and was alleged to be less hepatotoxic. Nevertheless, it has been demonstrated that dronedarone has at least the same potential to inhibit the mitochondrial respiratory chain and β -oxidation [67].

2.1.3. Tetracyclines—The tetracyclines, a family of broad-spectrum antibiotics, are widely used in the therapy of human and animal infections due to their activity against gram-positive and gram-negative bacteria and atypical organisms such as *chlamydiae* and mycoplasmas [68]. Tetracyclines were among the first drugs found to induce microvesicular steatosis, typically becoming manifested 4 to 10 days after the first intravenous administration of high doses [69, 70]. In mice, microvesicular steatosis is caused by doses of 100 to 200 mg/kg/day [71, 72]. The main mechanism responsible for the development of hepatic steatosis relies on decreased evacuation of TGs by inhibition of mitochondrial triglyceride transfer protein, as tetracyclines are rapidly taken up by mitochondria *in vitro* and *in vivo* [70, 73, 74]. Different cases of fatal hepatotoxicity during tetracycline or minocycline therapy [75, 76] together with the development of oral alternatives and the emergence of resistance strains of bacteria in the last decades have led to a decrease in the use of intravenous tetracyclines [77].

2.1.4. Tamoxifen—Tamoxifen is the golden standard in the treatment of estrogen-related breast cancer in women. It is a selective estrogen receptor modulator and can act both agonistic and antagonistic, executing a multitude of beneficial and detrimental effects, including downregulated low density lipoprotein levels [78], an increase in bone mineral density [78], promoted cardioprotection [79] and a higher risk for the development of endometrial cancer [80]. Tamoxifen is an estrogen receptor antagonist in breast tissue and therefore can block estrogen signaling leading to a decrease in breast cancer death rate [81]. Another well-known side effect of tamoxifen includes the occurrence of liver steatosis [82-84]. This is found in mice treated with 150 mg/kg tamoxifen for 24 hours or for 2 weeks with 40 mg/kg/day tamoxifen [85, 86]. Like amiodarone, tamoxifen is an amphiphilic drug that is protonated in the intermembrane space and unprotonated in the matrix of mitochondria following transportation over the inner membrane. The subsequent release of protons uncouples oxidative phosphorylation. In fact, tamoxifen compromises the electron transport chain and decreases the regeneration of oxidized cofactors, such as nicotinamide adenine dinucleotide and flavin adenine dinucleotide [87, 88].

2.1.5. Non-steroidal anti-inflammatory drugs—The analgesic, antipyretic and anti-inflammatory drug acetylsalicylic acid is known to cause Reye's syndrome [89], an often fatal complication in children characterized by vomiting, high fever, encephalopathy and hepatic failure [90]. The latter is accompanied by accumulation of lipid droplets in

hepatocytes and is mostly due to salicylate, the main toxic metabolite of acetylsalicylic acid. Salicylate causes mitochondrial swelling, uncoupling of oxidative phosphorylation, impairment of mitochondrial respiration and inhibition of adenosine triphosphate (ATP) synthesis [91-93]. Other non-steroidal anti-inflammatory drugs, such as ibuprofen and pirofen, were also found to interfere with mitochondrial β -oxidation and to produce microvesicular steatosis. Both enantiomers of ibuprofen inhibit β -oxidation and oxidative phosphorylation [94], but only the *R*-enantiomer can sequester CoA and may stereoselectively inhibit the uptake and oxidation of fatty acids [95]. By contrast, pirofen suppresses mitochondrial triglyceride transfer protein activity [96]. Furthermore, both diclofenac and nimesulide have the potential to inhibit oxidative phosphorylation and to induce mitochondrial permeability transition pore opening [97]. Acetaminophen damages mitochondrial DNA, is able to open the mitochondrial permeability transition pore and inhibits oxidative phosphorylation [98-100].

2.1.6. Miscellaneous drugs—Methotrexate is a drug used for the treatment of rheumatoid arthritis, psoriasis, psoriatic arthritis, inflammatory bowel disease and Crohn's disease [101, 102]. It acts through the inhibition of folic acid production, a key regulator in the synthesis of RNA and DNA. Methotrexate can enter the cell *via* the organic anion-transporting polypeptide 1B1 [103] and inhibits the respiratory chain [104]. Patients displaying risk factors, such as obesity and diabetes, are more prone to the hepatotoxic characteristics of methotrexate and may develop steatohepatitis-like histological patterns [105]. Irinotecan is a topoisomerase 1 inhibitor and a very active antineoplastic drug. It is a component of modern chemotherapy regimens for lung and colorectal cancer treatment. Irinotecan use has been associated with the development of NASH [106]. Amineptine and tianeptine, both tricyclic antidepressant drugs, impair β -oxidation and cause microvesicular steatosis in mice in large doses [107, 108]. Besides the direct inhibition of FFA oxidation, both drugs also negatively affect mitochondrial triglyceride transfer protein activity [96]. The antiretroviral nucleoside reverse-transcriptase inhibitors stavudine and zidovudine constitute important drugs in the therapy of human immunodeficiency virus-infected patients. They can cause hepatic steatosis by depleting mitochondrial DNA [109], a mechanism equally reported for didanosine and zalcitabine [110]. Perhexiline is a prophylactic anti-anginal agent that inhibits oxidative phosphorylation [64] and carnitine palmitoyl transferase 1 [111]. Patients taking perhexiline maleate show mild to moderate fatty changes in the liver together with steatohepatitis [112]. Cycloheximide, which impedes the binding of tRNA to mRNA, induces liver steatosis in rats [113]. Several studies have demonstrated that this may be caused by enhanced hepatic FFA uptake, disturbed balance between FFA oxidation and esterification and inhibition of very low density lipoproteins secretion [114, 115]. Recently, cycloheximide has been shown to decrease hepatic lipid secretion due to acute apolipoprotein B reduction, a lipoprotein responsible for the packaging of very low density lipoproteins [116]. Other drugs altering mitochondrial functions (see Figure 2) include disulfiram (*i.e.* mitochondrial permeability transition pore opening and inhibition of mitochondrial respiratory chain reaction) [117-119], fialuridine (*i.e.* inhibition of mitochondrial DNA synthesis) [120], alpidem (*i.e.* mitochondrial permeability transition pore opening) [121], nilutamide (*i.e.* inhibition of mitochondrial respiratory chain reaction) [122], troglitazone (*i.e.* damaging of mitochondrial DNA and

mitochondrial permeability transition pore opening) [123, 124], tacrine (*i.e.* impairment of oxidative phosphorylation and inhibition of mitochondrial DNA synthesis) [125, 126], buprenorphine (*i.e.* inhibition of oxidative phosphorylation and mitochondrial respiratory chain reaction) [127], orotic acid [128], clozapine [129] and thioacetamide [130].

2.2. Diet treatment

2.2.1. High-fat diet—A high-fat diet (HFD), consisting typically of 30 to 60 % fat, is commonly used to experimentally induce human-relevant NAFLD in rodents. However, the amount of fat, the composition of the HFD and the duration of the diet regime may cause different responses with respect to obesity, impaired glucose tolerance, dyslipidemia, increased lipogenesis, production of proinflammatory cytokines and oxidative stress depending on the species, strain and gender [131, 132]. In this respect, a diet containing high quantities of unsaturated fat leads to more pronounced hepatic lipid peroxidation as well as a higher expression of chemokines and cytokines compared to saturated fat-based diets [133]. Furthermore, a lard-rich HFD has much more impact on hepatic insulin sensitivity than a palm oil-rich HFD in mice [134]. The HFD most closely resembles the human pathology of NAFLD, as it is associated with IR, obesity and a similar histological pattern of liver steatosis.

2.2.2. Methionine-choline-deficient diet—Methionine and choline play a role in hepatic β -oxidation and the production and secretion of very low density lipoproteins [135]. They cannot be *de novo* synthesized and therefore must be included in the diet. A methionine-choline-deficient (MCD) diet consists of 40 % sucrose and only 10 % fat, and lacks methionine and choline. Feeding mice an MCD diet results in the onset of hepatic steatosis after 1 or 2 weeks due to increased uptake of fatty acids and altered secretion of very low density lipoproteins [135]. Subsequently, NASH is developed and is accompanied by oxidative stress [136], production of cytokines and adipocytokines [137], and fibrosis [136]. Although NAFLD is developed very rapidly, these mice lack IR and do not display overweight, which mirrors less the human pathology of NAFLD. In fact, several studies showed a severe weight loss in mice on MCD diet [138]. Although these animals abundantly present inflammation, oxidative stress and fibrosis, the response of the MCD diet may vary depending on species, strain and gender [139]. Compensating the lack of weight gain and IR can be done by feeding rodents a choline-deficient L-amino acid diet, which also causes NAFLD [140].

2.2.3. Lipogenic methyl-deficient diet—Mice fed a methyl-deficient diet for 6, 12 or 18 weeks develop liver injury similar to NASH, characterized by the presence of steatosis, inflammation and hepatocellular degeneration. These liver effects are progressive with duration of the diet, being most severe in the DBA/2J mice fed a methyl-deficient diet for 18 weeks. Moreover, the level of triglycerides in DBA/2J mice was greater than in C57BL/6J mice. Feeding mice a methyl-deficient diet resulted in a change in DNA methylation and profound alterations in histone modification patterns [141, 142].

2.2.4. Fructose-rich diet—Fructose is one of the most important sugars in human diet and is a major inducer of hepatic steatosis in rodents. It is taken up into the portal system

and further by hepatocytes *via* glucose transporter members 2 and 5. Thereafter, fructose is metabolized in the glycolytic and lipogenic pathways. Fructose is known to harm the liver and to cause IR, oxidative stress, increased cytokine and adipocytokine levels and obesity [143, 144]. Thus, rats fed a 70 % fructose diet for 5 weeks produce macrovesicular steatosis, inflammation and high TG concentrations in the liver [145]. Likewise, after 16 weeks of high-fructose diet in mice, increased lipogenic proteins, increased serum transaminases, mixed macrovesicular and microvesicular steatosis as well as NASH are observed [146].

2.2.5. Fast food diet—A Western style diet or fast food diet is a combination of fat, cholesterol and sugar, which are acknowledged risk factors for the development of obesity. Hence, this diet can be used in rodents to induce NAFLD. When feeding mice a fast food diet consisting of 40 % fat and 2 % cholesterol combined with fructose-rich drinking water for 6 months, overweight, IR and NASH are produced [147]. Similarly, mice fed a liquid fast food diet for 6 weeks show massive hepatic steatosis and inflammation [132].

2.2.6. Dietary fatty acids—Oleic acid, a naturally occurring mono-unsaturated fatty acid, is one of the most common fatty acids in human diet [148-155]. It is indispensable for the formation of the plasma membrane and acts as an energy source. Fatty acids are metabolized in the mitochondria and serve as suppliers of ATP in the mitochondrial respiratory chain. Despite this critical physiological role, oleic acid is the most dominant fatty acid observed in liver steatosis patients [156]. The uptake of fatty acids, including oleic acid and palmitic acid, by hepatocytes takes place after dissociation from serum albumin. The main plasma membrane transporters that underlie this process are fatty acid-binding protein, cluster of differentiation 36 (CD36)/fatty acid translocase, fatty acid transport protein and caveolins [157-161]. After cytosolic fatty acid conjugation with acyl-CoA, the fatty acids can be transferred inside the mitochondria by means of carnitine palmitoyl transferase 1 [162, 163]. Under physiological conditions, intracellular fatty acid levels are low as a result of mitochondrial β -oxidation or esterification to triglycerides [164-166]. Oleic acid and palmitic acid are often used in *in vitro* to induce fat accumulation in cultured cells, with the former acting more potent than the latter [163, 167]. Common concentrations of oleic acid and palmitic acid used can range from 0.05 to 2 mM, depending on the duration of exposure [163, 168-170].

3. Models in NAFLD research

3.1. Animal models

3.1.1. Rodents—Rodents are currently the most routinely used *in vivo* models in liver steatosis research. Nevertheless, major differences exist in the development of mitochondrial injury, the progression of liver steatosis and the production of inflammatory markers and TGs between species, strains and genders. Thus, male rats fed an MCD diet or HFD produce more steatosis, and have a higher liver lipid content and serum alanine aminotransferase quantities than female rats. Male and female Wistar rats show higher liver lipid amounts, serum alanine aminotransferase levels and liver mass-body mass ratios compared to Long-Evans and Sprague Dawley counterparts. Male C57/BL6 mice show more inflammatory foci, products of lipid peroxidation and mitochondrial injury, but less steatosis and lower

hepatic TG levels than Wistar rats [171, 172]. Unlike Sprague Dawley rats that exhibit macrovesicular steatosis accompanied by fibrosis, Lewis rats present microvesicular steatosis after receiving a HFD for 3 weeks. Also, lower cholesterol, TGs and leptin levels are measured in female Lewis rats compared to male rats of the same strain [172].

The induction of steatosis by VPA associated with microvesicular fat deposition in the liver was first shown in male Crl Swiss mice [173]. Sprague Dawley rats repeatedly exposed to VPA produce liver steatosis correlating with lipid accumulation, preferably in the perivenous zone [174]. In contrast, daily administration of VPA to male Sprague Dawley results in combined macrovesicular and microvesicular steatosis located in the periportal area [175]. ICR mice develop microvesicular steatosis after receiving tetracycline [71], and a time-dependent and dose-dependent increase in TGs is seen after treatment with VPA [47, 176]. Female Sprague Dawley rats daily fed tamoxifen display a rise in hepatic TG levels by more than 50 % after 14 days. However, activities and mRNA levels of enzymes involved in β -oxidation, ketogenesis and uptake of lipids from liver are unaffected, whereas the uptake of fatty acids is decreased [86]. Furthermore, female Wistar rats and jvs mice show extensive microvesicular and focal macrovesicular steatosis after repeated VPA administration [48, 177]. Male C57BL/6 mice have been used in a number of studies, whereby hepatic fat accumulation in the liver was observed following administration of tamoxifen [85] or amiodarone [63]. Swiss male mice treated with irinotecan manifest steatosis, lobular neutrophil infiltration and ballooning, portal neutrophil infiltration, interleukin-1 β and fibrosis in liver tissue [178].

3.1.2. Zebrafish—In recent years, the zebrafish model for studying lipid metabolism has gained tremendous popularity because of the relatively low cost, ease of genetic manipulation, molecular homology with humans and rapid development of liver pathology. Zebrafish express adiponectin receptors [179] and the 3 peroxisome proliferator-activated receptor (PPAR) isoforms (α , β , γ) [180], all of which are essential to lipid homeostasis. Injection of thioacetamide in zebrafish 3 times a week for 2 weeks causes an increase of hepatic lipid content. However, serum TGs are not significantly increased, while tumor necrosis factor α and adiponectin receptor 2 mRNA expression is elevated and downregulated, respectively [130]. When adding thioacetamide to the rearing water of zebrafish embryos, necrotic fatty hepatocytes are observed. This is associated with strong transcriptional upregulation of adiponectin and mild to moderate upregulation of peroxisomal thiolase (*i.e.* β -oxidation related gene), CCAAT/enhancer binding protein α and β (*i.e.* transcription factors which play a role in adipogenesis) and sterol regulatory element-binding protein 1c (*i.e.* transcription factor that regulates lipid synthesis) [181]. Zebrafish *larvae* exposed to tunicamycin develop hepatomegaly and hepatic steatosis. In this model, hepatic stellate cells become activated, suggesting the onset of liver fibrosis [182]. Daily feeding of zebrafish with *Artemia* results in obesity characterized by an increase in body weight, plasma TGs and blood glucose after 2 weeks [183, 184]. Similarly, fructose-treated zebrafish *larvae* develop liver steatosis [185].

3.1.3. Genetically modified rodents and zebrafish—Leptin is a key regulator of lipid storage by adjusting the sensation of hunger. Leptin-deficient or *ob/ob* mice are

hyperphagic, extremely obese, develop IR with hyperinsulinemia and hyperglycemia, and have a fatty liver [186]. However, they do only develop NASH upon a “second hit”, such as the administration of lipopolysaccharide [187] or feeding a HFD or MCD diet. A similar model is the *db/db* mouse, carrying a mutation in the leptin receptor gene. *Db/db* mice develop steatosis, are obese and diabetic and also need a “second hit” to develop NASH [188]. Attenuated P2 diphtheria toxin A-transgenic mice are hyperphagic, have low leptin levels, and show hyperlipidemia, hyperglycemia and IR [189]. Mice deficient in the melanocortin 4 receptor, a regulator of food intake and lipid metabolism, present NASH, but need a HFD to progress to liver fibrosis and HCC. Likewise, mice in which the expression of sterol regulatory-element binding protein 1a, a determinant of fatty acid synthesis and regulation of lipogenic genes, is overexpressed have an enlarged steatotic liver [190, 191], are hyperphagic because of low leptin levels and develop hepatic steatosis, IR and increased TG levels [192]. CD36-null mice exhibit increased plasma fatty acids and TG levels [193]. Recently, liver-specific overexpression of insulin-like growth factor 2 mRNA binding protein 2-2 p62 was shown to induce steatosis in mice receiving regular chow diet. Additionally, NASH-induced fibrosis was amplified in p62-transgenic mice fed a MCD diet.

In both models, hepatic cholesterol and monounsaturated fatty acids were increased in comparison with wild-type animals [194]. This is in line with other studies exhibiting the role of p62 in human HCC [195] and steatosis [196, 197]. A multitude of studies confirmed the association between a sequence polymorphism in patatin-like phospholipid domain-containing protein 3 (PNPLA3) on the 148M allele and the full spectrum of NAFLD [198]. After being fed a high-fructose diet, PNPLA3/148M-transgenic mice exhibit TG accumulation in the liver [199]. Furthermore, apolipoprotein E2 knock-in mice were found to be hyperlipidaemic. When fed a HFD, female apolipoprotein E2 knock-in mice show higher expression of lipogenic, cholesterol-synthesizing, inflammatory and cell-stress genes in comparison with female wild-type mice or male apolipoprotein E2 knock-in mice [200]. Several other genetically modified mice have been described, all which are pertinent to liver steatosis research. Their characteristics are summarized in Table 1.

Guanosine monophosphate synthetase mutant zebrafish *larvae* develop liver steatosis characterized by an accumulation of lipid droplets and increased TG levels. *De novo* guanosine monophosphate synthesis is required to prevent hepatic steatosis and inhibition of Rac1 activity in hepatocytes induces liver steatosis [201]. Cannabinoid receptor 1-transgenic zebrafish show hepatic lipid accumulation, while the expression of sterol regulatory element-binding protein 1c, acetyl-CoA carboxylase-1 and fatty acid synthase is upregulated [202]. Moreover, ying yang 1-transgenic zebrafish present also hepatic lipid accumulation. This indicates that ying yang 1, a transcription factor belonging to the GLI-Kruppel class of zinc finger proteins, promotes lipid accumulation. Important lipogenic factors such as PPAR γ , sterol regulatory element-binding protein 1c and CCAAT/enhancer-binding protein α , and key lipogenic enzymes, like acetyl-CoA carboxylase 1 and diglyceride acyltransferase, are upregulated in this steatotic transgenic zebrafish model [203]. Gankyrin, a proteasome-interacting protein, is known to be overexpressed in HCC and causes increased lipid content in the liver of transgenic zebrafish. Since hepatocellular endoplasmic reticulum stress recently has been associated with IR in diabetes, obesity and NAFLD [204],

zebrafish with mutant phosphatidylinositol, being an important regulator of calcium homeostasis, membrane trafficking, secretory pathways and signal transduction, exhibit revocation of *de novo* phosphatidylinositol synthesis and NAFLD features in hepatocytes, characterized by macrovesicular steatosis, ballooning and necroapoptosis. In addition, an increase of endoplasmic reticulum stress response genes is observed in hi559 mutants, supporting the role of endoplasmic reticulum stress in the development of NAFLD [205].

3.2. *In vitro* models

3.2.1. Monolayer cultures of primary hepatocytes—Cultures of primary hepatocytes are considered the most relevant *in vivo*-like liver-based *in vitro* models. Primary hepatocytes are typically isolated from freshly removed liver tissue by means of the two-step collagenase perfusion technique [206]. A disadvantage of cultures of primary hepatocytes is that they progressively lose their liver-specific functionality and morphology in culture. Nevertheless, they can be of value to experimental liver steatosis research. Cultures of primary C57BL/6 mouse hepatocytes simultaneously exposed to oleic acid and palmitic acid preferably take up the former and show intracellular lipid droplets [167, 207]. When mixed, more steatosis is observed compared to oleic acid and palmitic acid alone [163, 208, 209]. Interestingly, the addition of interleukin-17, a pro-inflammatory cytokine, exacerbated the accumulation of lipid droplets in hepatocytes [207]. Isolated hepatocytes from Sprague Dawley rats accumulate lipid droplets upon incubation with VPA, amiodarone, tetracycline or tamoxifen [210]. The use of primary human hepatocytes faces many challenges, including availability, phenotypic instability and limited lifespan [211]. Moreover, triglyceride accumulation causes a downregulation of CYP enzymes in cultures of human primary hepatocytes, which may affect the metabolism of administered drugs [212]. Nevertheless, human hepatocytes supplemented with oleic acid or eicosapentaenoic acid have an increased presence of TG-based lipid droplets and VLDL secretion without a change in apolipoprotein B abundance [213], which makes them a suitable *in vitro* model for the study of liver steatosis.

3.2.2. Monolayer cultures of liver-based cell lines—Hepatocarcinoma-derived cell lines present some advantages and disadvantages over primary hepatocytes. Their high availability, easy handling and unlimited life span make cell lines attractive models. However, genetic instability and a phenotype that strongly differs from that of primary hepatocytes are drawbacks of these systems [214]. HepG2 cells originate from human HCC and retain several biochemical functions of liver parenchymal cells [215], including the potential to secrete lipoproteins [216]. Consequently, the HepG2 cell line is a suitable model for studying human lipid metabolism. HepG2 cells exposed to different concentrations of oleic acid or palmitic acid exhibit intracellular accumulation of lipid droplets and TGs [163, 168-170, 208, 217]. Similarly, tamoxifen causes an increase of lipid droplets in the cytosol of HepG2 cells [218]. It should be mentioned, however, that HepG2 cells lack CYP activity, important for xenobiotic metabolism. Therefore, a number of subclones, such as HepG2/C3A cells, have been developed, which express functional CYP activity and that display accumulation of TGs after exposure to oleic acid either alone or combined with palmitic acid [219]. The HepaRG cell line stems from a female suffering from HCC. When seeded at low density, HepaRG cells quickly recover bipotent progenitors and actively

divide until they reach confluence. Subsequently, they differentiate into hepatocyte-like and biliary-like cells. HepaRG cells express major liver-specific functions, including CYP activity, are functionally stable at confluency and have an indefinite growth potential [211]. HepaRG cells have great potential in *in vitro* liver steatosis research, as they accumulate lipid droplets following exposure to stearic acid, palmitic acid, oleic acid, linoleic acid, eicosapentaenoic acid, docosahexaenoic acid and amiodarone [220, 221]. This also holds true for Huh-7 cells, a well-differentiated HCC cell line, which is able to pile up lipid droplets when treated with oleic acid either alone or together with palmitic acid [163, 222, 223].

3.2.3. Co-cultures—Culturing hepatocytes and non-parenchymal cells together modulates cell growth and hepatocyte morphology and increases functionality [224]. Also, co-cultures of hepatocytes with Kupffer cells or fibroblasts provide improved hepatocyte viability and function [225, 226]. Co-cultures of Huh-7 cells and LX-2 hepatic stellate cells, exposed to a mixture of oleic acid and palmitic acid, were found to accumulate intracellular fat. In these co-cultures, stellate cells became activated, assessed by alpha-smooth muscle actin expression. Furthermore, a time-dependent increase of tissue inhibitor metalloproteinase-2 protein has been observed, suggesting enhanced collagen biosynthesis [227]. Similarly, matrix-metallo-proteinase-2 and other profibrogenic genes, such as tissue inhibitor of metallo-proteinase-1 and transforming growth factor β were upregulated in a co-culture of primary human hepatocytes, which were treated with palmitic acid, and human hepatic stellate cells [228]. Micropatterned co-cultures allow the development of heterogeneous surfaces on which control over cell-cell interactions is possible in the micrometer range. This enables modulation of the phenotype of liver cells *in vitro* [229]. Co-cultures of primary human hepatocytes and murine embryonic fibroblasts have shown to maintain morphology, gene expression and functionality up to six weeks [230]. Additionally, the use of micropatterned co-cultures delivers a higher sensitivity in the prediction of drug toxicity outcomes in comparison with conventional twodimensional cultures [231]. In this context, a microscale model of primary human hepatocytes and stromal fibroblasts was established and proved to be a robust model for the study of glucose metabolism, which is closely associated with NAFLD. This was possible for several weeks and thus would allow the study of the effects of drugs in diabetes [232].

3.2.4. Sandwich cultures—To partly overcome the rapid decline in functionality and morphology of primary hepatocytes in monolayer culture established in plastic dishes, sandwich cultures are often used. Here, primary hepatocytes are cultivated in a confluent monolayer between two layers of collagen type one [233]. This set-up decreases the functional decline and allows the application of a more time-consuming experimental set-up [234]. Hepatocytes isolated from lean Zucker rats cultivated in a collagen sandwich configuration developed microvesicular and macrovesicular steatosis upon exposure to a mix of oleic acid and linoleic acid after three and six days, respectively [235]. Additionally, primary human hepatocytes in sandwich culture treated with chlorpromazine showed changes in the genetic signature related to fibrosis, inflammation, necrosis and steatosis after short-term and long-term chlorpromazine treatment [236]. Primary rat hepatocytes, cultured

between two layers of collagen, showed lipid droplets following incubation with VPA, amiodarone, tetracycline or tamoxifen [237].

3.2.5. Spheroid cultures—Planar culture systems do not represent the complex architecture of hepatic tissue *in vivo*. Culture of hepatocytes into spheroids may improve some of their functions due to the establishment of cell-cell contacts and presence of extracellular matrix components within and around the aggregates [234]. Today, the use of spheroid models is limited in experimental NAFLD research. H35 rat hepatoma cells in spheroid configuration have been exposed to free fatty acids, leading to increased fatty acid uptake and increased intracellular TG accumulation. In turn, this decreased DNA content, reduced proliferation and increased intracellular reactive oxygen species [238]. Oleic acid-treated HepG2 spheroids have also been proven useful *in vitro* tools for studying hepatic steatosis. These spheroids were surprisingly less susceptible to cytokine and pro-oxidant damage *via* an adaptive mechanism dependent on adenosine monophosphate-activated protein kinase activity [239]. Additionally, a spheroid model of primary hepatocytes from male Sprague Dawley rats shows higher intracellular glycogen content, glucose consumption, and gluconeogenesis, and a more *in vivo*-like sensitivity to insulin and glucagon in comparison with monolayer cultures. Finally, the exposure of primary hepatocytes to high levels of glucose induced toxicities, including alteration of mitochondrial membrane potential, lipid accumulation and reactive oxygen species formation [240].

3.2.6. Precision-cut liver slices—Precision-cut mice liver slices can act as valuable tools for the study of lipid metabolism, especially since they are considered to closely reflect the *in vivo* situation. In these systems, all cell types are present, thus maintaining overall cell-cell and cell-extracellular matrix interactions [241]. Although liver slices are promising *in vitro* models, they have not been used extensively in NAFLD research [242]. Liver slices exposed to VPA, amiodarone and tetracycline have been used to identify genes altered by steatogenic drugs. Microarray analysis shows that amiodarone and VPA upregulate lipid metabolism, whereas processes associated with extracellular matrix remodeling and inflammation were downregulated. Tetracycline causes a downregulation of mitochondrial functions, lipid metabolism and fibrosis [243]. Liver slices from *ob/ob* mice showed a reduced VLDL secretion in CD36-deficient mice, which highlights the importance of CD36 and VLDL in the development of NAFLD [244].

4. Biomarkers in NAFLD research

4.1. Epigenetic biomarkers

Genes involved in lipid and glucose metabolism, development of fibrosis and liver tissue remodeling are known to be regulated by DNA methylation [245]. Thus, DBA/2J mice fed a lipogenic methyl-deficient diet show DNA demethylation in liver, which is less pronounced compared to C57BL/6J counterparts. This is associated with a loss of cytosine methylation at repeated sequences, such as major and minor satellites, long interspersed nuclear elements, short interspersed nuclear elements and intracisternal A-particle elements [142]. Significantly altered genes encoding chromatin-remodeling enzymes, including jumonji C-

domain-containing histone demethylases, which regulate histone H3K9 and H3K4 trimethylation, have been observed in livers of steatotic hAPOE2 mice. This is accompanied by modified expression of genes related to PPAR α and hepatic lipid catabolism [246]. In NASH patients, mitochondrial nicotinamide adenine dinucleotide dehydrogenase 6 gene methylation was found to be increased, whereby the degree of methylation was linked to the severity of NAFLD. This goes hand in hand with decreased production of mitochondrial nicotinamide adenine dinucleotide dehydrogenase 6 and increased DNA methyltransferase I expression [247]. The DNA methylation status of the PPAR α coactivator 1 α gene positively correlates with plasma fasting insulin levels and IR in NAFLD patients, while the inverse holds true for the mitochondrial transcription factor A gene [248]. In the last few years, circulating microRNAs (miRs) gained quite some interest as possible diagnostic biomarkers of NAFLD.

MiR-122, an miR species highly expressed in liver, was shown to be an important regulator in cholesterol metabolism [249], HCC [250] and hepatitis C infection [251]. MiR-122 expression is downregulated in NASH patients [252, 253], partly evidenced by the elevated production of some of the miR-122 targets, such as sterol regulatory element-binding protein 1c, fatty acid synthase and 3-hydroxy-3-methyl-glutaryl-CoA reductase [252]. By contrast, serum levels of miR-122, miR-21, miR-34a and miR-451, all which control liver cholesterol and fatty acid homeostasis, were found to be increased in NAFLD patients, with miR-122 levels being associated with liver steatosis [254, 255]. MiR-122 knock-out mice exhibit accumulation of TGs caused by upregulation of enzymes involved in the synthesis and storage of TGs in the liver. These animals display inflammation, fibrosis and HCC [256]. Furthermore, a wide array of miRs is altered in animal models of NAFLD. In this regard, miR-29 (*i.e.* a potential therapeutic target in NAFLD in mice) [257], miR-34a (*i.e.* a regulator of apoptosis), miR-155 (*i.e.* a tumor suppressor regulator) and miR-200b (*i.e.* targets transcriptional repressors of E-cadherin) are positively affected upon feeding of C57BL/6J and DBA/2J mice a methyl-deficient diet [258]. Along the same line, downregulation of miR-122, miR-451 and miR-27 and upregulation of miR-200a, miR-200b and miR-429 occur in steatotic Sprague Dawley rats [259]. In HFD-fed Sprague Dawley rats, downregulation of enhancer of zeste homolog 2, a protein which controls the epigenetic silencing of specific genes and/or miRs by trimethylating lysine²⁷ on histone H3, is inversely correlated with lipid accumulation [260]. Hepatic miR-34a levels are elevated in dietary and leptin-deficient *ob/ob* obese mice [261, 262]. MiR-34a plays a role in the regulation of gene encoding silent mating type information regulation 2 homolog, a nicotine adenine dinucleotide-dependent deacetylase that is implicated in the prevention of many age-related diseases, including metabolic disorders associated with steatosis, inflammation and glucose intolerance [263].

4.2. Genetic biomarkers

Genome-wide association studies have been instrumental for the detection of specific genetic changes in the pathology of NAFLD. These studies equally allowed the identification of steatosis biomarkers across genomes. A mutation in the patatin-like phospholipase domain containing family member A3, also named adiponutrin, on chromosome 22 is strongly associated with increased hepatic fat levels and hepatic

inflammation in steatosis patients [264]. This mutation is phenotypically associated with steatosis, portal inflammation, lobular inflammation, Mallory-Denk bodies and fibrosis [265] as well as with HCC [266] in NAFLD patients. Recently, a single nucleotide polymorphism in transmembrane 6 superfamily member 2, a gene of unknown function on chromosome 19, has been linked to NAFLD [267]. It is well-known that Toll-like receptor 4 plays an important role in the pathogenesis of NAFLD. Interestingly, allelic variants of Toll-like receptor 4 (*i.e.* Asp299Gly and Thr399IleTLR4) in humans may prevent NAFLD, since the number of subjects with the heterozygous mutation (*i.e.* Asp299Gly) is significantly lower in NAFLD patients than in the control group [268]. Additionally, sterol regulatory element-binding factor 1c polymorphism reflects an increased risk of developing NAFLD with more severe liver histology and derangement in glucose and lipoprotein metabolism [269]. A common variant in the glucokinase regulatory gene and MTP-493G>T polymorphism was found to be associated with a higher NAFLD incidence [270, 271], along with more severe liver fibrosis and higher serum TG levels [272]. Furthermore, thymine-cytosine, cytosine-cytosine and thymine-thymine genotypes of apolipoprotein C3 (*i.e.* -455T>C) polymorphism are more susceptible to NAFLD. The cytosine-cytosine genotype is more prone to IR than the thymine-thymine genotype, while the cytosine-cytosine genotype presents a significantly higher risk of hypertension, hypertriglyceridemia and low levels of high-density lipoprotein [273].

4.3. Transcriptomic biomarkers

Transcriptomics studies the expression level of mRNAs at genome-wide level. This enables characterization of transcriptomic signatures of specific diseases. The major tool in transcriptomics is the microarray [274]. By using this technology, genes related to fatty acid metabolism, such as CYP4A14, and to cell proliferation and differentiation, like fibroblast growth factor 21 and CYP4A10, have been found upregulated in VPA-administered ICR mice, while the genes encoding glucose-6-phosphatase and protein phosphatase 2, regulatory subunit B, δ , a protein involved in cell growth are downregulated [47, 176]. Similarly, tamoxifen-treated C57BL/6 mice display hepatic transcriptional upregulation of androgen receptor, nuclear receptor subfamily 2 group F member 1, hepatocyte nuclear factor α 4 and retinoic acid receptor-related orphan receptor 1 α all related to lipid and carbohydrate metabolism [85]. Furthermore, male ICR mice exposed to tetracycline show overexpression of several genes involved in phospholipid metabolism, including choline kinase α , elongation of very long chain fatty acids, insulin-induced gene 2 and genes related to carbohydrate metabolism, such as protein phosphatase 1, regulatory subunit 3C, and prostaglandin D2 synthase [71]. Transcriptomics analysis of liver tissue of apolipoprotein E-deficient mice fed a Western-type diet enriched with linoleic acid reveals an upregulation of lymphocyte antigen 6D, genes associated with adipocyte differentiation, like fat-specific protein 27, genes related to fatty acid metabolism, such as stearoyl-CoA desaturase-1 and CD36, and a concomitant downregulation of genes involved in bile acid biosynthesis, such as CYP7B1 (cytochrome P450, 7b1) as well as genes related to steroid hormone biosynthesis, like 3-ketosteroid reductase [275]. Decorin, a proteoglycan produced by monocytes and macrophages at sites of inflammation, is known to be upregulated in adipose tissue of obese human patients. This suggests a role of decorin in the development of inflammation in NASH. This is further substantiated by the observation that decorin

production is increased in the liver of *ob/ob*, *db/db* and C57BL/6J mice fed a HFD. Other upregulated genes include endothelial membrane protein 1, a peripheral myelin protein suggested to modulate cell-matrix and cell-cell interactions, and I κ B kinase β -interacting protein, which links the transcription factor NF- κ B to the apoptotic signaling pathway in the endoplasmic reticulum. Reduction of the former decreases cytokine expression, suggesting a protective role against IR [276]. Protein tyrosine phosphatases fulfill an important function in regulating insulin action and hepatic glucose metabolism protein tyrosine phosphatase 6 knock-out mice fed a HFD are protected from IR, but are more prone to hepatic steatosis and show an upregulation of the PPAR γ gene [277]. Liver tissue of human liver steatosis patients presents enhanced gene expression of evolutionarily conserved signaling intermediate in Toll pathway (*i.e.* an adapter protein of the Toll-like and interleukin-1 receptor signaling pathway involved in the assembly of mitochondrial nicotinamide adenine dinucleotide), Toll-interacting protein and single immunoglobulin interleukin-1-related molecule. This overexpression can be attributed to the activation of Kupffer cells or hepatocytes releasing interleukins that act on hepatic stellate cells [278]. mRNA quantities of keratin type I cytoskeletal 23, a protein related to metabolism, and aldo-keto reductase family 1 member B10, a protein involved in the control of cytoarchitecture, are upregulated in steatohepatitis compared to steatosis and normal liver, and hence have been proposed as potential biomarkers for steatohepatitis as well as for HCC progression [279]. An overview of transcriptomics biomarkers in models of liver steatosis is displayed in Table 2.

4.4. Proteomic biomarkers

Compared to the genome, the proteome can provide a more dynamic and accurate reflection of both the intrinsic genetic program of the cell and the impact of environmental factors. Gene expression changes do not always accurately predict protein levels because proteins can undergo posttranslational modifications, including phosphorylation and glycosylation [280]. Proteomics techniques, such as tandem liquid chromatography-mass spectrometry and two-dimensional gel electrophoresis, can be used to study changes in proteins at large-scale, *in casu in vitro* and *in vivo* models of liver steatosis (see Table 3). Using such approaches, it has been found that hamsters fed a high-fructose diet abundantly produce many proteins, including fatty acid binding protein, carbamoyl-phosphate synthase, apolipoprotein A1, protein disulfide isomerase, proteins involved in anti-oxidation, such as peroxiredoxin 2 and heat shock protein 70, fructose-1,6-biphosphatase and glycerol kinase [281]. Upon feeding male C57BL/6J mice a HFD enhanced protein production of cytokeratine 8 and 18, vimentin and apolipoprotein E, but decreased quantities of glutathione peroxidase are observed [282]. Furthermore, major urinary protein 2 is overexpressed in apolipoprotein E-null mice. It has been suggested that this may represent a compensatory, protective response triggered in the liver. In turn, this could play a role in plasma lipid homeostasis, since another subunit of major urinary protein 2, namely major urinary protein 1, enhances mitochondrial biogenesis and decreases lipid accumulation in the liver of *db/db* mice [283]. Also, mitochondrial antioxidant expression is increased in apolipoprotein E-null mice, in particular peroxiredoxin-4, thioredoxin-dependent peroxide reductase and glutathione peroxidase 1, due to an increase in reactive oxygen species [284]. Liver tissue of female C57BL/6N mice fed a HFD exhibits increased protein expression of methylenetetrahydrofolate dehydrogenase 1, while translational levels of glucose transporter 1, methylthioadenosine

phosphorylase and methionine adenosyltransferase 1 α are decreased [285]. Likewise, *db/db* mice show a number of overexpressed proteins, including annexin 5 (*i.e.* a well-known apoptotic marker), cadherin 2 (*i.e.* a protein involved in insulin signaling), transporter 2, 24-dehydrocholesterol reductase (*i.e.* a protein related to inflammation and possibly to insulin signaling) and guanosinetriphosphate-binding protein SAR1 gene homolog B, whereas other are underexpressed, such as epidermal growth factor, six-transmembrane epithelial antigen of prostate 4 and translocation protein SEC62 [286]. Heat shock proteins are significantly downregulated in liver of rats fed HFD [287]. Such steatosis-related protein changes have also been observed in human patients. Thus, fatty acid binding protein 1 is overexpressed in livers of steatosis patients, but is downregulated during different stages in NASH progression [288]. Moreover, protein analysis of lipid droplets in human steatotic liver samples revealed a yet unidentified lipid droplet-associated protein which is upregulated upon fat accumulation. Interestingly, its protein expression has been validated in *db/db* mice and HFD-fed mice [289].

4.5. Metabonomic biomarkers

Among all ‘-omics’, metabonomics is the most stable, most closely represents the phenotype and most appropriately mirrors the activities of the cell. The main methodologies used for metabonomics analysis are mass spectrometry and nuclear magnetic resonance spectroscopy [290]. By applying such techniques, it has been found that PPAR α knock-out mice exhibit a decrease in glucose and glycogen content, and a concomitant increase in linoleic acid, oleic acid and di-homo- γ -linolenic acid in liver [291]. In a similar study, an increase in TGs, free and esterified cholesterol, oleic acid, leucine, valine, lysine and methionine and a decrease in arachidonic acid, eicosapentaenoic acid, docosahexaenoic acid and carnitine were observed in liver of low density lipoprotein knock-out mice fed a cholesterol-rich diet [292]. Rats administered aflatoxinB1 develop hepatic steatosis associated with elevated levels levels of glucose, amino acids, choline, phosphocholine, and glycerophosphocholine, and decreased lipid amounts in blood. Simultaneously, aflatoxinB1 increases quantities of lipids, tyrosine, histidine, phenylalanine, leucine, isoleucine, valine, choline, inosine, adenosine, and uridine, but decreases glycogen and glucose in liver [293]. HFD-fed C57BL/6J mice show high levels of oxidized glutathione, choline, taurine, sarcosine and downregulated amounts of reduced glutathione, methionine, serine, glycine, ethanolamine and phosphoethanolamine [294]. When these animals additionally receive leucine through drinking water, a marked improvement in hepatic steatosis, inflammation in adipose tissue, glucose tolerance and insulin signaling was noticed, suggesting that leucine acts as an important future adjunct in the management of obesity-related IR [295]. The liver of paraoxonase-1-deficient mice fed a HFD contains high levels of methionine sulfoxide, taurine, fructose, glucose and 1,3-dihydroxyacetone, but low levels of glycine, glutamate, cysteine, hypotaurine, methionine, homocysteine, glutathione, 3-phosphoglycerate, phosphoenolpyruvate, lactate, citrate, *cis*-aconiate, succinylcarnitine, fumarate, malate and phosphate [296]. In serum of male C57BL/6NCr mice fed an MCD diet, abundant e oleic acid, linoleic acid, non-esterified fatty acids, tauro- β -muricholate, taurocholate and 12-hydroxyeicosatetraenoic acid and low production of stearyllysophosphatidylcholine, oleoyllysophosphatidylcholine and palmitoyllysophosphatidylcholine have been described, all which points to alterations in phospholipid and bile acid metabolism [297, 298]. Similarly, taurochendeoxycholate and

taurocholate are upregulated, while glycochendeoxycholate and glycocholate are downregulated in the serum of tetracycline-treated male C57BL/6NCr mice. These findings indicate that perturbation of bile acid homeostasis is an early event in drug-induced liver steatosis and that these metabolites may represent sensitive and early biomarkers for diagnosis of liver steatosis [299]. Four metabolites in the liver of mice fed a HFD are also altered in liver samples of steatosis and NASH patients, namely glucose, glutamate/glutamine, lactate and taurine, which again suggests a role as clinically relevant read-outs [300]. Metabolites upregulated in human liver steatosis and NASH patients include glutamyl dipeptides, glutamyl valine, glutamyl leucine, glutamyl phenylalanine, glutamyl tyrosine, free carnitine, butyrylcarnitine, glutamate, lysine, tyrosine and isoleucine, whereas cysteine-glutathione disulfide, caprate, 10-undecenoate and 1-oleoylglycerophosphocholine are downregulated [301]. Moreover, human NASH livers exhibit increased levels of taurine, taurocholic acid and taurodeoxycholic acid with concomitant decreased presence of cholic acid and glycodeoxycholic acid [302]. In addition, increased production of glycerophosphocholine, glycerylphosphorylethanolamine, taurine and glycine conjugates were found in liver tissue of steatosis patients, indicating disturbances in lipid and bile acid homeostasis and mitochondrial dysfunction. Furthermore, these patients also display elevated levels of hypoxanthine, creatinine, glutamate, glutamine, glutathione and ATP, suggesting alterations in energy metabolism and amino acid metabolism [303]. A detailed summary of metabolomic biomarkers in models of liver steatosis is shown in Table 4.

5. Conclusions and perspectives

As evidenced by epidemiological studies, NAFLD is currently a worldwide health problem [1, 13]. Hepatic steatosis, the first stage in the NAFLD spectrum, is related to type 2 diabetes mellitus, obesity and drug-induced liver injury [2, 304]. At present, histopathological examination of liver tissue is considered the golden standard for diagnosing. This procedure requires biopsy, which is not without risk. In fact, the ideal diagnostic biomarker of hepatic steatosis would be a non-invasive marker suitable for early detection of the disease and able to reflect the severity of the disease [305]. Great promise lies with metabolomic, proteomic and transcriptomic biomarkers, as they provide mechanistic information. In a similar way, the ideal liver steatosis model should fully reproduce the human pathology. To date, however, not a single *in vivo* model encompasses the spectrum of human disease progression. Rather, these models imitate particular characteristics of human NAFLD. Among those, the HFD model still most closely resembles clinical NAFLD, as it is associated with obesity, IR and type 2 diabetes mellitus as well as with a human-relevant histopathological pattern in liver [306]. *In vitro* models, especially cultures of primary hepatocytes and hepatic cell lines, are also valuable in liver steatosis research. Nevertheless, a combination of different models could be the most effective strategy in NAFLD research. Given the blossoming of stem cell-based *in vitro* models in the last few years, it can be expected that hepatocyte-like cells generated from stem cells will join in as *in vitro* liver steatosis test systems in near future [307]. It is of critical importance that researchers are aware of the power, but especially the shortcomings, of the experimental models in order to ensure scientifically sound conclusions and appropriate extrapolation to the human situation. When appropriately used, these models,

together with the various drug-based and diet-based strategies as well as with the relevant read-outs for evaluation, will continue to be indispensable tools in liver steatosis research. This, in turn, will undoubtedly result in new clinical approaches for the diagnosis and therapy of liver steatosis and NAFLD.

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Glossary

ACS	acyl-coenzyme A synthase
adipoR	adiponectin receptor
ADP	adenosine diphosphate
AP2diph	attenuated P2 diphtheria toxin
AOX	acyl-coenzyme A oxidase
ApoE	apolipoprotein E
ATP	adenosine triphosphate
CBS	cystathionine- β -synthase
CD36	cluster of differentiation 36
CoA	coenzyme A
CPT1	carnitine palmitoyl transferase 1
CYP	cytochrome P450
DNA	deoxyribonucleic acid
FAD	oxidized flavin adenine dinucleotide
FADH2	reduced flavin adenine dinucleotide
FFAs	free fatty acids
FXR	farnesoid x receptor
Gal	galectin
HCC	hepatocellular carcinoma
HFD	high-fat diet
IL-6	interleukine-6
IMS	intermembrane space
IR	insulin resistance
LDL	low density lipoprotein

LDs	lipid droplets
MA	macrovesicular steatosis
MAT	methionine adenosyl transferase
MC4	melanocortin 4
MCD	methionine and choline-deficient diet
MI	microvesicular steatosis
(micro)RNA	(micro)ribonucleic acid
MPT	mitochondrial permeability transition
MRC	mitochondrial respiratory chain
MTP	mitochondrial trifunctional protein
MTTP	mitochondrial triglyceride transfer protein
NAD	oxidized nicotinamide adenine dinucleotide
NADH	reduced nicotinamide adenine dinucleotide
NAFLD	non-alcoholic fatty liver disease
NASH	non-alcoholic steatohepatitis
PC	phosphatidylcholine
PECAM	platelet endothelial cell adhesion molecule
PNPLA	patatin-like phospholipid domain containing protein
PPAR	peroxisome proliferator-activated receptor
PTEN	hepatocyte-specific phosphatase and tensin homologue
SREBP	sterol regulatory-element binding protein
TGs	triglycerides
VLDL	very low density lipoproteins
VPA	valproic acid

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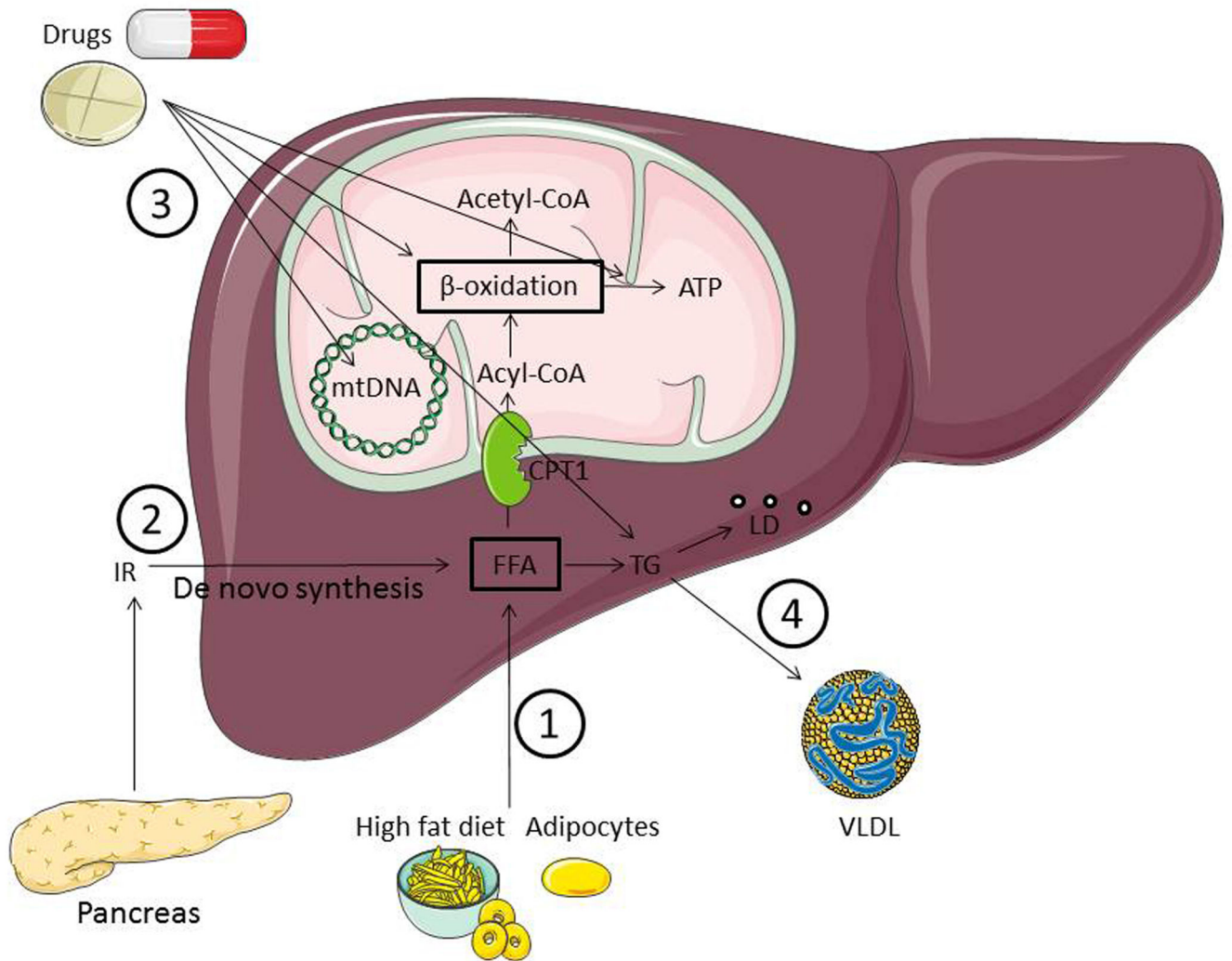


Figure 1. Pathogenesis of steatosis

Four pathogenic mechanisms can be responsible for the accumulation of TG-based lipid droplets, namely 1) increased uptake of FFAs from high-fat food or from adipocytes in body fat, 2) increased synthesis of FFAs in the liver from glucose or acetate by IR, 3) decreased mitochondrial β -oxidation of FFAs caused by a multitude of drugs, and 4) decreased synthesis or secretion of very low density lipoproteins, the principal route for elimination of lipids from the liver. (ATP, adenosine triphosphate; CoA, coenzyme A; FFA, free fatty acids; LDs, lipid droplets; IR, insulin resistance; TGs, triglyceride; VLDL, very low density lipoproteins).

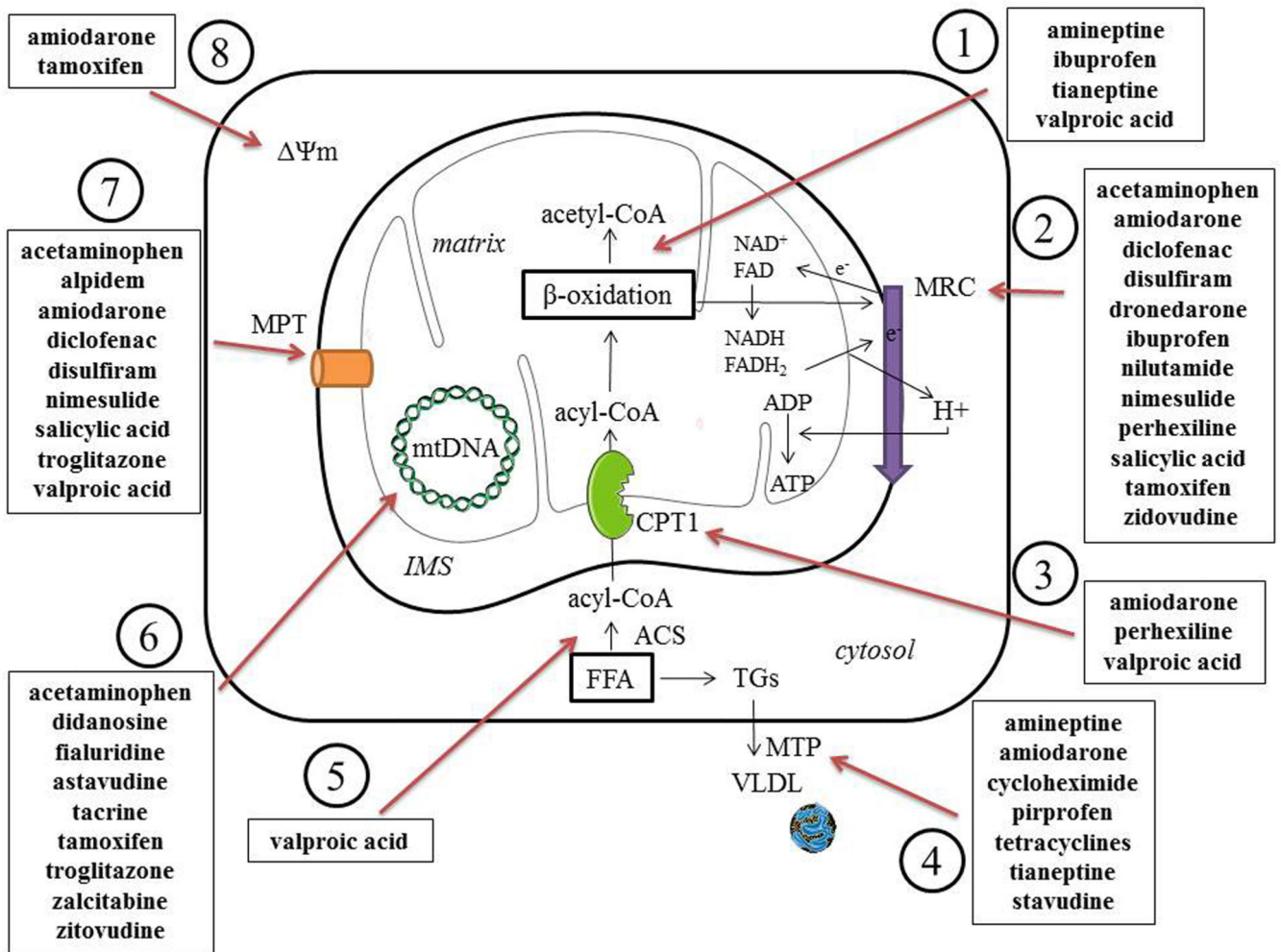


Figure 2. Mechanisms of drug-induced liver steatosis

Drugs may induce liver steatosis by a plethora of mechanisms associated with mitochondrial impairment, including 1) inhibition of enzymes involved in mitochondrial FFA oxidation leading to a direct alteration in β -oxidation function, 2) direct inhibition of the mitochondrial respiratory chain reaction or alteration of oxidative phosphorylation, 3) decreased uptake of acyl-CoA due to the inhibition of carnitine palmitoyl transferase 1, 4) reduction in triglyceride excretion by inhibition of microsomal triglyceride transfer protein, 5) impaired entrance of fatty acids in mitochondria due to the inhibition of acyl-CoA synthase, 6) depletion of mitochondrial DNA, encoding for mitochondrial proteins, which leads to impairment of MRC, 7) induction of the mitochondrial permeability transition pore opening, 8) alteration of mitochondrial membrane potential. (ACS, acyl-coenzyme A synthase; ADP, adenosine diphosphate; ATP, adenosine triphosphate; CoA, coenzyme A; CPT1, carnitine palmitoyl transferase 1; FAD, oxidized flavin adenine dinucleotide; FADH₂, reduced flavin adenine dinucleotide; FFA, free fatty acids; IMS, intermembrane space; MRC, mitochondrial respiratory chain; MPT, mitochondrial permeability transition; MTP, microsomal triglyceride transfer protein; NAD, oxidized nicotinamide adenine

dinucleotide; NADH, reduced nicotinamide adenine dinucleotide; TG, triglyceride; VLDL, very low density lipoproteins).

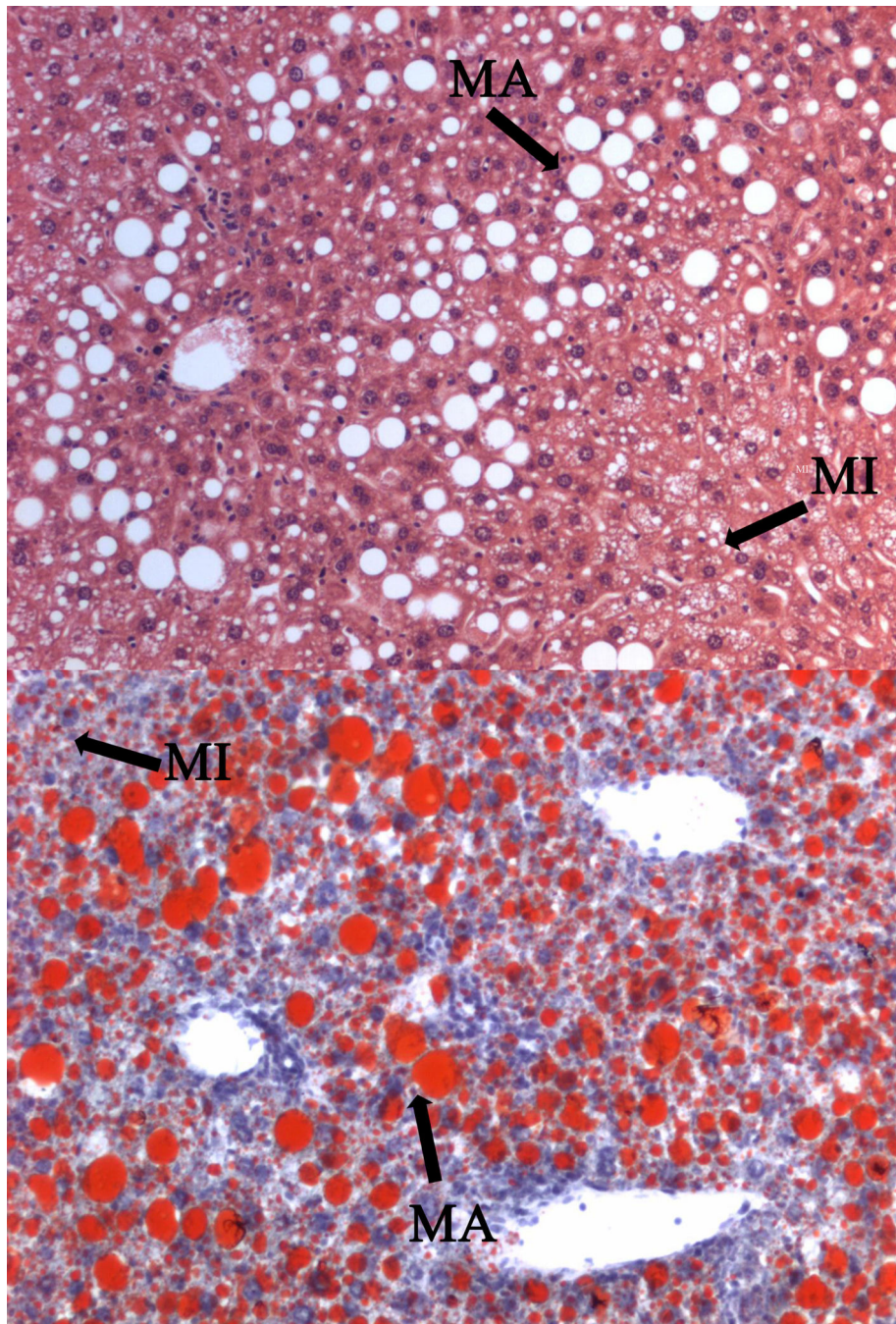


Figure 3. Histological patterns of liver steatosis

Hematoxylin and eosin (upper panel) and Oil Red (lower panel) stained liver slice from C57BL/6 mice fed a high-fat choline-deficient diet for 8 weeks developing mixed macrovesicular and microvesicular steatosis. Both pictures depict the accumulation of TGs in the cytosol of hepatocytes. However, in case of macrovesicular steatosis, large lipid droplets are observed, which displace the cytoplasmic content and nucleus, while in

microvesicular steatosis, small lipid droplets that do not displace the nucleus are seen (MA, macrovesicular steatosis; MI, microvesicular steatosis).

Table 1
Genetically altered animal models of NAFLD

AdipoR, adiponectin receptor; AOX, acyl-coenzyme A oxidase; AP2diph, Attenuated P2 diphtheria toxin A; ApoE, apolipoprotein E; CBS, Cystathionine- β -synthase; CBR, cannabinoid receptor; CD36, cluster of differentiation 36; CDIPT, CDP-diacylglycerol- inositol 3-phosphatidyltransferase; FXR, farnesoid x receptor; Gal, galectin; GMPS, guanosine monophosphate synthetase; HCC, hepatocellular carcinoma; HFD, high-fat diet; IL-6, interleukine-6; IR, insuline resistance; LDL(r) nicotinamide adenine dinucleotide (receptor), low density lipoprotein; MC4, melanocortin 4; MAT, methionine adenosyl transferase; MTP, mitochondrial trifunctional protein; NASH, non-alcoholic steatohepatitis; PPAR, peroxisome proliferator-activated receptor; PECAM, platelet endothelial cell adhesion molecule; PNPLA, patatin-like phospholipid domain containing protein; PTEN, hepatocyte-specific phosphatase and tensin homologue; SREBP, sterol regulatory-element binding protein; YY, ying yang.

Species	Model	Characteristics	Remarks	Reference
Mouse	Leptin-deficient: <i>ob/ob; db/db</i>	- Hyperphagia - Obesity - IR - Hyperinsulinemia - Hyperglycemia - Fatty liver	- Require "second hit" for evolution to NASH	[186-188]
	AP2diphA +/+	- Hyperphagia - Hyperlipidemia - Hyperglycemia - IR		[189]
	CD36 -/-	- Increased plasma fatty acids and TGs		[193]
	MC4 -/-	- NASH - Obesity - IR - Dyslipidemia	- HFD to progress to liver fibrosis and HCC	[304]
	SREBP1a +/+	- Steatosis		[190]
	SREBP1c +/+	- Hyperphagia - Steatosis - IR - Increased TG levels		[192]
	PPAR α -/-	- Severe steatosis	- After fasting	[305]
	Gal3 -/-	- Fatty changes		[306]
	MTPa -/-	- Steatosis		[307]

Species	Model	Characteristics	Remarks	Reference
	MTPa +/-	- Steatosis - IR		[308]
	AOX -/-	- Microvesicular steatosis - NASH		[309]
	PTEN -/-	- Steatosis - NASH - HCC		[310]
	MAT1A -/-	- Steatosis - NASH - HCC		[311]
	AdipoR1 -/-	- Mild IR		[312]
	AdipoR2 -/-	- Mild IR		
	AdipoR1 -/-/R2 -/-	- Increased TGs - Oxidative stress - Steatosis		[313]
	IL6 -/-	- Obesity - Steatosis - NASH - IR		[314]
	FXR -/-	- Altered lipid and cholesterol metabolism		[315]
	LDLr -/-	- Macrovesicular steatosis	- Need to be fed a HFD	[315]
	LDLr -/-/FXR -/-	- Macrovesicular steatosis - Inflammation		[315]
	PECAM1 -/-	- Microvesicular steatosis		[316]
	CBS +/- CBS -/-	- Inflammation - Fibrosis - Steatosis		[317]
	p62 +/+	- Elevated hepatic cholesterol - Increased monounsaturated fatty acids		[194]
	PNPLA3/148M variant	- Increased TG levels	Need to be fed a high-fructose diet	[199]
	ApoE2 +/+	- Hepatic steatosis		[200]
Rat	<i>fa/fa</i> Zucker rat	- Obesity - Fatty liver		[318]

Species	Model	Characteristics	Remarks	Reference
		- IR		
		- Hyperglycemia		
Zebrafish	GMPS mutant	- Increased TGs		[201]
	CBR1 +/+	- Lipid accumulation		[202]
	YY1 +/+	- Lipid accumulation		[203]
	CDIPT -/-	- Macrovesicular steatosis		[205]
		- Ballooning		
		- Necroapoptosis		

Table 2
Transcriptomic biomarkers of NAFLD

CoA, coenzyme A; CYP, cytochrome P450; CD36, cluster of differentiation; HFD, high-fat diet; PPAR, peroxisome proliferator-activated receptor; PTPN, tyrosine-protein phosphatase non-receptor; VPA, valproic acid.

	Species	Upregulated genes	Downregulated genes	Reference
Human	Steatotic liver	- Single immunoglobulin domain-containing IL1R-related molecule - Likely ortholog of mouse signaling intermediate in Toll pathway- evolutionarily conserved - Toll interacting protein		[253]
	Steatotic liver	- Aldo-keto reductase family 1 member B10 - Keratin, type I cytoskeletal 23		[254]
Mouse	VPA-induced liver steatosis	- CYP4A14 - CYP4A10	- Glucose-6-phosphatase - Protein phosphatase 2, regulatory subunit B, δ	[47]
	VPA-induced liver steatosis	- CYP4A14 - Fibroblast growth factor 21 - Glutathione S-transferase A2	- Flavin containing monooxygenase 3	[176]
	Tamoxifen-induced liver steatosis	- Androgen receptor - Nuclear receptor subfamily 2 group F member 1 - Hepatocyte nuclear factor α 4 - Retinoic acid receptor-related orphan receptor 1 α		[85]
	Linoleic acid isomer-induced liver steatosis in ApolipoproteinE-deficient mouse	- Lymphocyte antigen 6D - Fat-specific protein 27 - Aquaporin 4 - Uridine kinase 1 - Stearoyl-CoA desaturase-1 - CD36	- CYP7B1 - Trefoil factor 3 intestinal - Synaptotagmin 1 - 3-ketosteroid reductase	[250]
	Tetracycline-induced liver steatosis in mouse	- Choline kinase α - CYP2A12 - CYP2C38 - Elongation of very long chain fatty acids - Phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 γ - Insulin induced gene 2		[71]

Species	Upregulated genes	Downregulated genes	Reference
Liver of C57BL/6J mice fed a HFD, <i>ob/ob</i> mice and <i>db/db</i> mice	- Protein phosphatase 1, regulatory subunit 3C) - Prostaglandin D2 synthase 21kDa - Decorin - Epithelial membrane protein 1 - IκB kinase β interacting protein		[251]
Liver of Ptpn6 knock-out mice	- PPARγ		[252]

Table 3
Proteomic biomarkers of NAFLD

HFD, high-fat diet.

	Species	Validated upregulated proteins	Validated downregulated proteins	Reference
Human	Liver of steatosis patients	- Fatty acid binding protein		[263]
	Liver of steatosis patients	- 17 β -HSD13		[264]
Hamster	Liver of hamsters fed a fructose diet	- Fatty acid binding protein	- Heat shock protein 70	[256]
		- Apolipoprotein A1	- Senescence marker	
		- Protein disulfide isomerase	- Protein 30 - Chaperonin GroEL	
Mouse	Liver of mice fed a HFD	- Cytokeratin 8	- S-adenosylhomocysteine hydrolase	[257]
		- Cytokeratin 18		
		- Vimentin		
		- Apolipoprotein E		
	Liver of ApolipoproteinE-knock-out mice	- Major urinary protein 2	- Glutathione peroxidase 1	[259]
	Liver of mice fed a fat-sucrose diet		- Heat shock protein 70	[262]
Liver of mice fed a cholesterol diet	- Methylenetetrahydrofolate dehydrogenase 1	- Glucose transporter 1	[260]	
	- Lactate dehydrogenase A	- Methylthioadenosine		
		- Phosphorylase		
		- Methionine		
		- Adenosyltransferase 1 α		
Liver of <i>db/db</i> mice	- Annexin A5	- Epidermal growth factor receptor	[261]	
	- Dehydrocholesterol reductase - transporter 2	- Six-transmembrane epithelial antigen of prostate 4		
	- Cadherin 2	- Translocation protein SEC62		
	- Guanosinetriphosphate-binding protein SAR1b			

Table 4
Metabonomic biomarkers of NAFLD

HFD, high-fat diet; MCD, methionine-choline-deficient diet; PC, phosphatidylcholine; PPAR, peroxisome proliferator-activated receptor.

	Species	Upregulated metabolites	Downregulated metabolites	Reference
Human	Liver from steatosis patients	- Glutamyl dipeptides	- Cysteine-glutathione disulfide	[276]
		- Glutamyl valine	- Caprate	
		- Glutamyl leucin	- 10-undecenoate	
		- Glutamyl phenylalanine	- OleoyllysoPC	
		- Glutamyl tyrosine		
		- Carnitine		
		- Butyrylcarnitine		
		- Glutamate		
		- Lysine		
		- Tyrosin		
	- Isoleucine			
	Liver of steatosis patients	- GlyceroPC	- Oxidized and reduced glutathione	[278]
- Glycerolphosphorylethanolamine		- Glutamate		
- Taurine		- Adenosine triphosphate		
- Glycine conjugates		- Creatine		
Liver of NASH patients	- Taurine	- Cholic acid	[277]	
	- Taurocholic acid	- Glycodeoxycholic acid		
	- Taurodeoxycholic acid			
Serum of steatosis patients	- Lactate		[275]	
	- Glutamate			
	- Taurine			
Mouse	Plasma of rosiglitazone-treated mice		- Phosphatidylcholine	[298]
			- Triacylglyceride	
			- Cholesterol	
			- Leptin	
			- Insulin	
			- Glucose	
Liver of mice subjected to starvation	- Free cholesterol	- PC	[299]	
	- Triacylglycerols			
	- Cholesterol esters			
Liver of PPAR α knock-out and age-related steatotic mice	- Linoleic acid	- Glucose	[266]	
	- Oleic acid	- Glycogen		
	- Di-homo- γ -linolenic acid			

Species	Upregulated metabolites	Downregulated metabolites	Reference
Liver of LDLr knock-out mice fed a cholesterol-rich diet	- Triglycerides - Free and esterified cholesterol - Oleic acid - Leucine - Valine - Lysine - Methionine	- Arachidonic acid - Eicosapentaenoic acid - Docosahexaenoic acid - Carnitine	[267]
Liver of mice fed a HFD	- Oxidized glutathione - Choline - Taurine - Sarcosine	- Reduced glutathione - Methionine - Serine - Glycine - Ethanolamine - Phosphoethanolamine	[269]
Serum of mice fed a MCD	- Lactate - Glutamate - Taurine		[275]
Liver of mice fed a HFD	- Fructose - Sorbitol - α -hydroxybutyrate	- Leucine - Fumarate - Malate - Cholesterol - Nicotinamide adenine dinucleotide - Tryptophan	[270]
Serum of mice fed a MCD	- Tauro- β -muricholate - Taurocholate - 12-hydroxyeicosatetraenoic acid	- StearoyllysoPC - OleoyllysoPC - PalmitoyllysoPC	[272]
Liver of paraoxonase-1-deficient mice fed a HFD	- Methionine sulfoxide - Taurine - Fructose - Glucose - 1,3-dihydroxyacetone	- Glycine - Glutamate - Cysteine - Hypotaurine - Methionine - Homocysteine - Glutathione - 3-phosphoglycerate - Phosphoenolpyruvate - Lactate - Citrate - Cis-aconiate - Succinylcarnitine - Fumarate	[271]

Species	Upregulated metabolites	Downregulated metabolites	Reference
		- Malate - Phosphate	
Serum of mice fed a MCD	- Oleic acid - Linoleic acid - Non-esterified fatty acid		[273]
Plasma of mice of tetracycline-induced steatosis	- Taurochendeoxycholate - Taurocholate	- Glycochendeoxycholate - Glycocholate	[274]
Rat Liver of aflatoxin B1-treated rats	- Lipids - Tyrosine - Histidine - Phenylalanine - Leucine - Isoleucine - Valine - Choline - Inosine - Adenosine - Uridine	- Glucose - Glycogen	[268]