

## Genetically modified mouse models for the study of nonalcoholic fatty liver disease

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### Abstract

Nonalcoholic fatty liver disease (NAFLD) is associated with obesity, insulin resistance, and type 2 diabetes. NAFLD represents a large spectrum of diseases ranging from (1) fatty liver (hepatic steatosis); (2) steatosis with inflammation and necrosis; to (3) cirrhosis. The animal models to study NAFLD/nonalcoholic steatohepatitis (NASH) are extremely useful, as there are still many events to be elucidated in the pathology of NASH. The study of the established animal models has provided many clues in the pathogenesis of steatosis and steatohepatitis, but these remain incompletely understood. The different mouse models can be classified in two large groups. The first one includes genetically modified (transgenic or knockout) mice that spontaneously develop liver disease, and the second one includes mice that acquire the disease after dietary or pharmacological manipulation. Although the molecular mechanism leading to the development of hepatic steatosis in the pathogenesis of NAFLD is complex, genetically modified animal models may be a key for

the treatment of NAFLD. Ideal animal models for NASH should closely resemble the pathological characteristics observed in humans. To date, no single animal model has encompassed the full spectrum of human disease progression, but they can imitate particular characteristics of human disease. Therefore, it is important that the researchers choose the appropriate animal model. This review discusses various genetically modified animal models developed and used in research on NAFLD.

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**Key words:** Nonalcoholic fatty liver disease; Steatosis; Steatohepatitis; Knockout; Animal models

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### INTRODUCTION

Nonalcoholic fatty liver disease (NAFLD) represents a histological spectrum of liver disease associated with obesity, diabetes and insulin resistance that extends from isolated steatosis to steatohepatitis and cirrhosis. Besides being a potential cause of progressive liver disease, steatosis has been shown to be an important cofactor in the pathogenesis of many other liver diseases. Mouse models have been developed and the different mouse models can be classified in two major groups. The first one includes genetically modified (transgenic or knockout) mice that spontaneously develop liver disease, and the second one

includes mice that acquire the disease after dietary or pharmacological manipulation. NAFLD and nonalcoholic steatohepatitis (NASH) are increasing due to the prevalence of the metabolic syndrome linked to visceral adiposity, insulin resistance, dyslipidemia and type two diabetes. In this context, research has been undertaken using animal models for human steatosis and NAFLD to NASH disease progression. Most of the animal models develop a fatty liver and many develop aspects of steatohepatitis. However, spontaneous development of fibrosis is very rare. Because it is highly unlikely that NAFLD in the human population is monogenic, study of animals with deletion or over-expression of a single gene may not mimic etiology of the human disease at the molecular level. Likewise, choice of experimental diet may not mimic the human diets associated with development of NAFLD in man. Although rodent models of hepatic steatosis and/or insulin resistance do not always perfectly reproduce the human pathology of NAFLD, the use of transgenic, knockout, and knockdown mouse models have helped over the past years to better our understanding of the molecular determinants of NAFLD. This literature review describes different genetically modified mouse models that exhibit histological evidence of hepatic steatosis or, more variably, steatohepatitis.

## GENETIC MODELS FOR NAFLD

### *ob/ob* mice

The *ob/ob* mice carry a spontaneous mutation in the leptin gene (leptin-deficient). These mice are hyperphagic, inactive, extremely obese and are severely diabetic, with marked hyperinsulinemia and hyperglycemia. *ob/ob* mice develop NASH spontaneously<sup>[11]</sup>, but unlike human NAFLD, *ob/ob* mice do not spontaneously progress from steatosis to steatohepatitis. *ob/ob* mice require a 'second hit' to be administered in order to trigger progression to steatohepatitis. This may be provided by exposure to small doses of lipopolysaccharide (LPS) endotoxin, ethanol exposure or hepatic ischemia-reperfusion challenge which all provoke a severe steatohepatitis and frequently acute mortality<sup>[2-5]</sup>. *ob/ob* mice require other stimuli such as a methionine choline deficient (MCD) diet or a high fat diet to trigger progression to steatohepatitis. The effects of leptin deficiency on several aspects of physiology increase the complexity of studies while using this strain<sup>[6]</sup>. Similarly, the limited fibrotic capacity of a leptin-deficient model means that it is best suited to studies investigating the mechanisms behind the development of steatosis and the transition to steatohepatitis. Recent work demonstrates that the apparent flaws in this model can be turned to advantage, providing new insights into stellate cell function and the progression to fibrosis.

### *db/db* mice

The *db/db* mice have a natural mutation in the leptin receptor (*Ob-Rb*) gene<sup>[7]</sup>. These mice are obese with insulin resistance, and are able to develop macrovesicular he-

patic steatosis. These mice readily develop symptoms of NASH upon induction with a second hit, such as feeding with an MCD diet<sup>[8]</sup>. These mice have normal or elevated levels of leptin but are resistant to its effects. Studies have shown that the *db* gene encodes the leptin receptor (OB-R) which is structurally similar to a class I cytokine receptor<sup>[9,10]</sup>. There are two isoforms; the short OB-Ra isoform has not been shown to have any signaling activity. In contrast, the OB-Rb isoform has a long intracytoplasmic region that contains signal transduction motifs which activate the JAK/STAT protein kinase signal transduction cascade<sup>[11]</sup>. *db/db* mice carry a sequence insertion at the 3' end of the mRNA transcript exactly where the OB-Ra and OB-Rb transcripts diverge. This insertion contains a stop codon that leads to the premature termination of the OB-Rb long intracellular signaling domain, loss of function and consequently leptin resistance<sup>[12]</sup>.

### *Yellow-obese agouti (Ay)* mice

KK-*A<sup>y</sup>* mice are a cross-strain of diabetic KK mice<sup>[13]</sup> and lethal yellow (*A<sup>y</sup>*) mice, which carry mutation of the agouti(a) gene on mouse chromosome 2<sup>[14]</sup>. KK-*A<sup>y</sup>* mice develop maturity-onset obesity, dyslipidemia, and insulin resistance, in part because of the antagonism of melanocortin receptor-4 by ectopic expression of the agouti protein<sup>[14]</sup>. Importantly, these mice present hyperleptinemia and leptin resistance without defects in the *ObR* gene, and the expression of adiponectin is conversely down-regulated<sup>[15,16]</sup>. The phenotype of KK-*A<sup>y</sup>* mice, including altered adipokine expression, quite resembles metabolic syndrome in humans indicating the potential usefulness of this strain as a model of metabolic syndrome NASH<sup>[17,18]</sup>. In fact, KK-*A<sup>y</sup>* mice are more susceptible to experimental steatohepatitis induced by MCD diet.

### *CD36<sup>-/-</sup>* mice

A valuable model for the study of the effects of alteration in fatty acid (FA) utilization on insulin responsiveness is the recently generated CD36-deficient mouse<sup>[19,20]</sup>. CD36, also known as fatty acid translocase (FAT)<sup>[21]</sup>, is a multispecific, integral membrane glycoprotein<sup>[22,23]</sup> that has been identified as a facilitator of FA uptake. Its function in binding and transport of FA was documented *in vitro* by affinity labeling with FA derivatives and by cell transfection studies<sup>[23,24]</sup>. The CD36-deficient mouse exhibits greater than 60% decrease of FA uptake and utilization by heart, skeletal muscle, and adipose tissues and thereby increases FA delivery to liver and exhibits increased plasma free fatty acid (FFA) and triglyceride (TG) levels<sup>[20]</sup>. The pathogenic role of FAT/CD36 in hepatic steatosis in rodents is well-defined<sup>[25]</sup>.

### *Phosphoenolpyruvate carboxykinase-sterol regulatory-element binding protein 1a-mice*

Sterol regulatory-element binding protein (SREBP) family members have been established as transcription factors regulating the transcription of genes involved in cholesterol and FA synthesis. *In vivo* studies have demonstrated that

SREBP-1 plays a crucial role in the dietary regulation of most hepatic lipogenic genes<sup>[26,27]</sup>. Physiological changes of SREBP-1 protein in normal mice by dietary manipulation such as placement on high carbohydrate diets, polyunsaturated FA-enriched diets, and fasting-refeeding regimens has been reported<sup>[28,29]</sup>. SREBP-1a transgenic mice, under the control of liver specific Phosphoenolpyruvate carboxykinase promoter (TgSREBP-1a), show a massively enlarged liver and atrophic peripheral white adipose tissue, and develop steatosis<sup>[30]</sup>.

#### **aP2-NSREBP-1c mice**

Leptin has similar effects in lipodystrophic rodents, most notably in aP2-nSREBP-1c transgenic mice. These animals express a truncated, constitutively active form of the SREBP-1c transcription factor under the control of the adipose tissue specific aP2 promoter and develop lipodystrophy with very low plasma leptin levels. These mice are also hyperphagic and have massive fat accumulation in peripheral tissues with hyperglycemia and hyperinsulinemia<sup>[31,32]</sup>. This mouse model has markedly reduced body fat and develops liver steatosis, profound insulin resistance, and increased levels of triglycerides<sup>[31,32]</sup>.

#### **aP2-diphtheria toxin mice**

The aP2/DTA mice have low serum leptin levels and are hyperphagic. These mice when fed a control diet are hyperlipidemic, hyperglycemic, and have hyperinsulinemia indicative of insulin-resistant diabetes. These mice are born normally and initially lack any distinguishing phenotypic features, but develop atrophy and necrosis of the adipose tissue at five to six months resulting in the complete absence of subcutaneous or intra-abdominal adipose tissue at eight to nine months of age<sup>[33]</sup>. This late onset of adipose tissue loss is associated with reduced leptin levels, increased food consumption, hyperlipidemia, hyperglycemia and insulin resistance. Monosodium glutamate-treated aP2/DTA mice develop gross hepatomegaly as a result of severe fatty changes in the liver<sup>[33]</sup>.

#### **A-ZIP/F-1 mice**

The A-ZIP/F-1 mice express a dominant negative version of the C/EBP $\alpha$  leucine zipper domain that potently interferes with adipocyte differentiation<sup>[34]</sup>. The A-ZIP/F-1 mouse (*A-ZIPTg/+*) is a model of severe lipotrophic diabetes and is insulin resistant, hypoleptinemic, hyperphagic, and shows severe hepatic steatosis. This mouse has essentially no white adipose tissue, reduced brown fat and severe metabolic phenotype with a reduced life span. These mice display massive hepatomegaly causing increased body weight, liver steatosis, severe diabetes (hyperglycemia, hyperinsulinemia, hyperphagic, polydipsia and polyuria), and are hypertensive<sup>[35]</sup>. They have increased triglycerides and FFA levels, alveolar foam cells and reduced leptin levels. These mice are unable to sustain glucose levels during fasting. The insulin resistance and much of the liver steatosis in the A-ZIP/F-1 mice can be reversed by transgenic over-expression

of leptin<sup>[36]</sup> or by transplanting normal adipose tissue<sup>[37]</sup>. By contrast, transplantation of adipose tissue from *ob/ob* mice did not reverse the phenotype of the A-ZIP/F-1 mice indicating that leptin deficiency strongly contributes to the metabolic complications in lipodystrophy<sup>[38]</sup>.

#### **Peroxisome proliferator-activated receptor alpha<sup>-/-</sup> mice**

Peroxisome proliferator-activated receptor alpha (PPAR $\alpha$ ) is expressed in the liver and other metabolically active tissues including striated muscle, kidney and pancreas<sup>[39,40]</sup>. Many of the genes encoding enzymes involved in the mitochondrial and peroxisomal FA beta-oxidation pathways are regulated by PPAR $\alpha$ . In wild-type mice, peroxisome proliferators are compounds that induce lipid catabolism and an associated intracellular increase in peroxisome number and enzymatic activity. PPAR $\alpha$  mutated mice exhibit alterations of intracellular lipid processing, particularly in response to peroxisome proliferators. Mice deficient in PPAR $\alpha$  exhibit severe hepatic steatosis when subjected to fasting for 24-72 h, indicating that a defect in PPAR $\alpha$ -inducible FA oxidation accounts for severe FA overload in liver, causing steatosis, in contrast to the wild-type mice<sup>[41,42]</sup>.

#### **Galactin-3 knockout mice**

Galectin-3, a beta-galactoside-binding animal lectin, is a multifunctional protein. Galectin-3 plays a role in the regulation of hepatic stellate cell (HSC) activation *in vitro* and *in vivo*, thereby identifying galectin-3 as a potential therapeutic target in the treatment of liver fibrosis. This model plays a role in investigating liver carcinogenesis based on a natural history of NAFLD<sup>[43]</sup>. Previous studies have also suggested that galectin-3 may play an important role in inflammatory responses. The livers of *gal3(-/-)* male mice at six months of age displayed mild to severe fatty change. The liver weight per body weight ratio, serum alanine aminotransferase levels, liver triglyceride levels, and liver lipid peroxide in *gal3(-/-)* mice were significantly increased compared with those in *gal3(+/+)* mice. Furthermore, the hepatic protein levels of advanced glycation end-products (AGE), receptor for AGE, and PPAR $\gamma$  were increased in *gal3(-/-)* mice relative to *gal3(+/+)* mice<sup>[43,44]</sup>.

#### **Acetyl CoA oxidase<sup>-/-</sup> mice**

Acyl-coenzyme A oxidase (AOX) is the rate-limiting enzyme in peroxisomal FA  $\beta$ -oxidation for the preferential metabolism of very long-chain FAs. AOX null (*AOX(-/-)*) mice have defective peroxisomal  $\beta$ -oxidation and exhibit steatohepatitis. Microvesicular fatty change in hepatocytes is evident at 7 d. At 2 mo of age, livers show extensive steatosis and they have clusters of hepatocytes at periportal areas with abundant granular eosinophilic cytoplasm rich in peroxisomes. At 4-5 mo there is increased PPAR $\alpha$ , cytochrome P450, Cyp 4a10, and Cyp4a14 expression. By 6 to 7 mo, however, there is a compensatory increase in FA oxidation and reversal of hepatic steatosis resulting from hepatocellular regenera-

tion<sup>[45,46]</sup>. The *AOX*<sup>-/-</sup> mice proceed to develop adenomas and carcinomas by 15 mo of age<sup>[46,47]</sup>.

### **Aromatase (CYP 19)-deficient mice**

Aromatase P450 (CYP19) is an enzyme catalysing the conversion of androgens into estrogens<sup>[48]</sup>. These models present dyslipidemia, central obesity, hypercholesterolemia, hyperinsulinemia, hyperleptinemia, and hypertriglyceridemia<sup>[49]</sup>, and importantly the male mice have hepatic steatosis. Aromatase knockout (ArKO) mice have a similar phenotype to that of estrogen receptor null mice with increased gonadal fat pad weight<sup>[50]</sup>. Only ArKO males have elevated hepatic triglyceride levels leading to hepatic steatosis partly due to an increase in expression of enzymes involved in *de novo* lipogenesis and transporters involved in FA uptake<sup>[51-53]</sup>.

### **MTP<sup>-/-</sup> mice**

Mitochondrial  $\beta$ -oxidation of FAs is the major source of energy for skeletal muscle and the heart, and it plays an essential role in intermediary metabolism in the liver and impairment of mitochondrial  $\beta$ -oxidation in pathogenesis of NAFLD. The fetuses of *Mtpa*<sup>-/-</sup> mice accumulate long chain FA metabolites and have low birth weight compared with the *Mtpa*<sup>+/-</sup> and *Mtpa*<sup>+/+</sup> littermates. *Mtpa*<sup>-/-</sup> mice suffer neonatal hypoglycemia and sudden death 6-36 h after birth. Analysis of the histopathological changes in the *Mtpa*<sup>-/-</sup> pups revealed rapid development of hepatic steatosis after birth and, later, significant necrosis and acute degeneration of the cardiac and diaphragmatic myocytes. However, studies by Ibdah *et al*<sup>[54]</sup> indicated that aged but not young *MTPA*<sup>+/-</sup> mice developed hepatic steatosis with elevated alanine aminotransferase (ALT), basal hyperinsulinemia, and increased insulin compared with *MTPA*<sup>+/+</sup> littermates. Significant hepatic steatosis and insulin resistance developed concomitantly in the *MTPA*<sup>+/-</sup> mice at 9-10 mo of age. The cause resides in heterozygosity for  $\beta$ -oxidation defects that predisposes to NAFLD and insulin resistance in aging mice<sup>[55]</sup>.

### **Phosphatase and tensin homologue -/- mice**

Phosphatase and tensin homologue (PTEN) is a multifunctional phosphatase whose substrate is phosphatidylinositol-3,4,5-triphosphate and which acts as a tumor suppressor gene that downregulates phosphatidylinositol kinases<sup>[56,57]</sup>. Hepatocyte-specific PTEN-deficient mice spontaneously develop steatosis, steatohepatitis, and hepatocellular carcinoma<sup>[58,59]</sup>. By 10 wk of age, these mice have increased concentrations of triglyceride and cholesterol esters, and a histological analysis displays micro- and macrovesicular lipid vacuoles. At 40 wk of age, they have macrovesicular steatosis, Mallory bodies, ballooning degeneration, and sinusoidal fibrosis<sup>[59-60]</sup>. Mice that are homozygous for this allele are viable, fertile, and normal in size and do not display any gross physical or behavioral abnormalities. When crossed to a strain expressing Cre recombinase in liver, this mutant mouse

strain may be useful in studies of fatty liver and insulin signaling. Piguet *et al*<sup>[61]</sup> have investigated the effects of hypoxia in the PTEN-deficient mouse, a mouse model that develops NAFLD. The authors also showed that a short period (7 d) of exposure to hypoxia aggravates the NAFLD phenotype, causing changes in the liver that are in keeping with NASH, with increased lipogenesis and inflammation.

### **Methionine adenosyl transferase 1A -/- mice**

Mice deficient in methionine adenosyl transferase 1A (the enzyme responsible for SAM synthesis in the adult liver) have a decrease in hepatic SAM levels and spontaneously develop steatosis, NASH, and hepatocellular carcinoma (HCC)<sup>[62]</sup>. By three months of age, these mice have hepatomegaly with macrovesicular steatosis. These mice also have increased mRNA levels of CYP2E1 and UCP2, and levels of glutathione. Also, these mice have changes in the expression of genes involved in cell proliferation of lipid and carbohydrate metabolism<sup>[63]</sup>. These mice are predisposed to liver injury and have impaired liver regeneration after partial hepatectomy<sup>[64]</sup>.

### **Adiponectin null mice**

Adiponectin is an adipokine abundantly produced from adipocytes<sup>[65,66]</sup>. Adiponectin is an anti-inflammatory adipocyte-derived plasma protein known to alleviate steatosis and inflammation in NAFLD<sup>[65-67]</sup>. Two adiponectin receptors (adipoR1 and adipoR2) have been identified and found to be expressed in various tissues<sup>[68]</sup>. AdipoR1 is abundantly expressed in skeletal muscles, whereas adipoR2 is present predominantly in the liver, suggesting a role of adipoR2 in hepatic adiponectin signaling<sup>[68,69]</sup>. The physiological roles of adipoR1 and adipoR2 have recently been investigated by several laboratories in *adipoR1/2* knockout mice. Both *adipoR1* and *adipoR2* knockout mice exhibit mild insulin resistance<sup>[70]</sup>. In *adipoR1/R2* double knockout mice the binding and actions of adiponectin are abolished, resulting in increased tissue triglyceride content, inflammation oxidative stress<sup>[70-73]</sup> and mice exhibit impaired liver regeneration and increased hepatic steatosis.

### **Bid null mice**

The protein Bid is a participant in the pathway that leads to cell death (apoptosis), mediating the release of cytochrome from mitochondria in response to signals from "death" receptors known as tumor necrosis factor (TNF) receptor 1/Fas on the cell surface. Genetic inactivation of Bid, a key pro-apoptotic molecule that serves as a link between these two cell death pathways, significantly reduced caspase activation, adipocyte apoptosis, prevented adipose tissue macrophage infiltration, and protected against the development of systemic insulin resistance and hepatic steatosis independent of body weight<sup>[74,75]</sup>. These mice can be used in research based on adipocyte apoptosis which is a key initial event that contributes to macrophage infiltration into adipose tissue, insulin resistance, and hepatic steatosis associated with obesity.

**Fas adipocyte-specific (AfasKO) null mice**

Fas (CD95), a member of the TNF receptor super family, is a major contributor to apoptosis in many cells. Fas activation may contribute to obesity-induced insulin resistance, since mice lacking Fas in adipocytes were partly protected from developing insulin resistance. In particular, Fas activation led to increased release of pro-inflammatory cytokines, and reduced insulin-stimulated glucose uptake in 3T3-L1 adipocytes<sup>[75]</sup>. Fas-deficient (Fas-def) mice show increased insulin-stimulated glucose incorporation when compared to wild type (WT) with higher expression levels of Akt<sup>[76,77]</sup>.

**Interleukin-6 KO mice**

Interleukin-6 (IL-6) is an adipocytokine associated with NAFLD and obesity that is secreted in larger amounts by visceral fat compared to subcutaneous fat in obese adults<sup>[78]</sup>. Increased systemic IL-6 is associated with increased inflammation and fibrosis in NAFLD patients<sup>[79]</sup>. Expression of IL-6, a major proinflammatory cytokine, is increased in animal models of NAFLD. Hepatic IL-6 production may also play an important role in NASH development, as well as in systemic insulin resistance and diabetes. IL-6 is elevated in the plasma and peripheral blood monocytes of patients with fatty diseases, including alcoholic liver disease and non-alcoholic steatohepatitis, and elevation of IL-6 correlates with the progression and severity of liver disease, suggesting that IL-6 may be involved in the pathogenesis of fatty liver disease<sup>[80,81]</sup>. Studies using *Il6*<sup>-/-</sup> mice show these animals display obesity, hepatosteatosis, liver inflammation and insulin resistance when compared with control mice on a standard chow diet<sup>[82]</sup>.

**TNF alpha KO mice**

TNF- $\alpha$  appears to play a central role in the development of hepatic steatosis. TNF- $\alpha$ , by mechanisms not completely defined, is over expressed in the liver of obese mice and is an important mediator of insulin resistance in both diet-induced and *ob/ob* models of obesity<sup>[83,84]</sup>. Data from animal and clinical studies indicate that TNF- $\alpha$  mediates not only the early stages of fatty liver disease but also the transition to more advanced stages of liver damage<sup>[85,86]</sup>. Mice homozygous for the TNF targeted mutation are viable and fertile. Further, male mutant mice at 28 wk old display lower insulin, triglyceride, and leptin levels compared to wild type controls.

**NEMO<sup>LPC-KO</sup> mice**

The I $\kappa$ B kinase (IKK) subunit NEMO/IKK $\gamma$  is essential for activation of the transcription factor nuclear factor kappa B (NF- $\kappa$ B), which regulates cellular responses to inflammation. NEMO-mediated NF- $\kappa$ B activation in hepatocytes has an essential physiological function to prevent the spontaneous development of steatohepatitis and hepatocellular carcinoma. These mice were generated with liver parenchymal cell-specific knockout of these subunits (*NEMO*<sup>LPC-KO</sup>, *IKK2*<sup>LPC-KO</sup>) by crossing mice carrying loxP-

flanked *Nemo*<sup>[87]</sup> or *Ikk2*<sup>[88]</sup> alleles with Alfp-cre transgenic mice that mediate efficient Cre recombination in liver parenchymal cells, including hepatocytes and biliary epithelial cells, but not in endothelial or Kupffer cells<sup>[89]</sup>. *NEMO*<sup>LPC-KO</sup> mice were born and reached weaning age at the expected Mendelian frequency<sup>[90]</sup>. These mice showed efficient ablation of the respective proteins in whole-liver extracts and NF- $\kappa$ B activity in the liver was completely abolished<sup>[91,92]</sup>. Hepatocytes are LPS sensitive. When fed a high-fat diet, mice had reduced  $\beta$ -oxidation and upregulated PPAR- $\gamma$ , SREBP1 and FA synthase causing increased *de novo* lipid synthesis and macrovesicular steatosis with increased HCC occurrence<sup>[91,92]</sup>.

**Jun N-terminal kinase 1 null mice**

Jun N-terminal kinase (JNK) 1 null mice have less hepatic inflammation and fibrosis when fed a choline-deficient, l-amino acid-defined (CDAA) diet due to the absence of JNK1 in immune cells. As JNK is activated by oxidants and cytokines and regulates hepatocellular injury and insulin resistance, this kinase may mediate the development of steatohepatitis. JNK promotes the development of steatohepatitis as MCD diet-fed *JNK* null mice have significantly reduced levels of hepatic triglyceride accumulation, inflammation, lipid peroxidation, liver injury, and apoptosis compared with wild-type and *JNK2*<sup>-/-</sup> mice<sup>[93,94]</sup>. Hence JNK1 is responsible for JNK activation that promotes the development of steatohepatitis in the MCD diet model<sup>[93]</sup>. *JNK1* KO produces lean, male *JNK1* KO mice which have decreased body weights, fasting blood glucose levels, and fasting blood insulin levels compared to their wild-type controls<sup>[94]</sup>. This model can be used to study a combination of genetic and dietary challenges that constitute the disease etiology for NASH development and mimic more closely the pathogenesis of human NAFLD/NASH.

**Toll-like receptor 9 KO mice**

Development of NASH involves the innate immune system and is mediated by Kupffer cells and HSCs. Toll-like receptor 9 (TLR9) is a pattern recognition receptor that recognizes bacteria-derived cytosine phosphate guanine-containing DNA and activates innate immunity. Mice deficient in TLR9 have reduced steatohepatitis and fibrosis<sup>[95]</sup>. Hence this model can be used to study NAFLD involving innate immunity.

**LDLR KO and farnesoid X receptor KO mice**

Farnesoid X receptor (FXR) is essential for regulating bile-acid synthesis and transport. Mice with FXR deficiency have severe impairment of bile-acid homeostasis and manifest systemic abnormalities including altered lipid and cholesterol metabolism features known to be associated with the metabolic syndrome and NASH. Kong *et al*<sup>[96]</sup> studied LDL receptor knockout (*LDLR*<sup>-/-</sup>) mice fed with a high-fat diet for 5 mo, and checked whether FXR deficiency contributed to NASH development. Both high-fat diet and FXR deficiency increased

serum ALT activity, whereas only FXR deficiency increased bile-acid and ALP levels. FXR deficiency and high-fat feeding increased serum cholesterol and triglycerides. Although high-fat diet led to macrosteatosis and hepatocyte ballooning in livers of mice regardless of genotype, no inflammatory infiltrate was observed in the livers of *LDLR*<sup>-/-</sup> mice. In contrast, in the livers of *LDLR*<sup>-/-</sup>/*FXR*<sup>-/-</sup> mice, foci of inflammatory cells were observed when they were fed with control diet and were greatly increased when fed with the high-fat diet<sup>[96,97]</sup>. This model can be used to study a combination of genetic and dietary challenges that constitute the disease etiology for NASH development and mimic more closely the pathogenesis of human NAFLD/NASH.

### **Myd88 KO mice**

Chemokines, strongly induced by TLR stimulation, play an important role in the development of metabolic syndrome including NAFLD. TLR4- and MyD88-deficient mice, which are resistant to metabolic syndrome, show reduced chemokine production compared with WT mice<sup>[98,99]</sup>. MyD88 is a key molecule in the development of metabolic syndrome including NAFLD<sup>[98,99]</sup>. MyD88, an adaptor protein for all TLRs except for TLR3, is required for the expression of various inflammatory cytokines and chemokines<sup>[100]</sup>. MyD88-deficient mice are protected from metabolic syndrome as well as atherosclerosis<sup>[98,99]</sup> and from liver injury induced by bile duct ligation or carbon tetrachloride<sup>[101,102]</sup>. Miura *et al*<sup>[100]</sup> demonstrated that MyD88-deficient mice on a CDAA diet show less steatohepatitis with less insulin resistance compared with wild type mice. Inflammatory cytokines and fibrogenic factors are also significantly suppressed in MyD88-deficient mice compared with wild type mice fed a CDAA diet<sup>[100]</sup>.

### **Fatty liver dystrophy knockout mice**

Fatty liver dystrophy (*fld*) is a spontaneous point mutation in *Lpin1* which occurred on C3H/HeJ in 1994. An unstable gait and tremor at 3 wk of age was initially observed in these mice. The pups from these mice have a fatty liver before reaching weaning age. Mice carrying mutations in the *fld* gene have features of human lipodystrophy, a genetically heterogeneous group of disorders characterized by loss of body fat, fatty liver, and hypertriglyceridemia and insulin resistance<sup>[103]</sup>. Homozygous *fld* mice have an enlarged, fatty liver and hypertriglyceridemia that resolve to normal during the weaning transition. However, decreased overall size, decreased lipid in the fat pads and a peripheral neuropathy persist throughout the lifespan. This peripheral neuropathy manifests as a tremor and an unsteady gait shortly after 10 d of age and worsens with age. As with the original mutation of *fld*, homozygous females will breed and raise their litters but homozygous males do not breed.

### **Platelet endothelial cell adhesion molecule-1 null mice**

Platelet endothelial cell adhesion molecule-1 (PECAM-1)

is a 130-kDa transmembrane glycoprotein expressed on blood and vascular cells. Goel *et al*<sup>[104]</sup> demonstrated that genetic deficiency of PECAM-1 potentiates the development and progression of NASH. After 3 wk on an atherogenic diet, these mice developed mild microvesicular steatosis predominantly in hepatic parenchymal cells in the centrilobular region. At 9 and 18 wk on the atherogenic diet, more severe steatosis with lobular and sinusoidal inflammation developed in the livers, which are consistent with the typical histological features of steatohepatitis<sup>[104]</sup>.

### **ApolipoproteinB 38.9 mutant mice**

Fatty liver is prevalent in apolipoproteinB (apoB)-defective familial hypobetalipoproteinemia (FHBL). Similar to humans, mouse models of FHBL produced by gene targeting (*apoB*+/*38.9*) manifest low plasma cholesterol and increased hepatic TG even on a chow diet due to impaired hepatic VLDL-TG secretive capacity. These mice will be useful to study the genetic and molecular mechanism of apoB defects and lipid metabolism/liver fat accumulation, the relationship between hepatic steatosis and insulin resistance, and the progression of advanced NAFLD and atherosclerosis<sup>[105]</sup>.

### **Cystathionine-synthase deficient mice**

Cystathionine-synthase (CBS) deficiency causes severe hyperhomocysteinemia, which confers diverse clinical manifestations, notably liver disease. Robert *et al*<sup>[106]</sup> reported that CBS-deficient mice showed inflammation, fibrosis, and hepatic steatosis. These mice also had pathological resemblance to steatohepatitis and a pattern of perivenous and pericellular hepatic fibrosis around lipid-laden hepatocytes. CBS KO mice develop hepatic steatosis more tardily than inflammation and fibrosis at 8-32 wk old.

In addition to the above KO animals, Postic *et al*<sup>[107]</sup> has demonstrated a few animal models modulating enzymes in FA synthesis.

### **Acc2KO mice**

Acetyl-CoA carboxylase (ACC) catalyzes the synthesis of malonyl-CoA, the metabolic intermediate between lipogenesis<sup>[108]</sup> and  $\beta$ -oxidation<sup>[109]</sup>; this lipogenic enzyme has garnered significant attention over recent years. In mammals, two ACC isoforms exist, each with distinct tissue distribution and physiological roles: ACC1 is highly expressed in liver and adipose tissue, whereas ACC2 is predominantly expressed in heart and skeletal muscle and, to a lesser extent, in liver<sup>[110]</sup>. It is believed that only ACC1, but not ACC2, is committed to *de novo* lipogenesis in liver. Targeting ACC has beneficial effects on both hepatic steatosis and insulin resistance. ACC1-knockout mice (*Acc1*<sup>-/-</sup> mice and *ACC2*<sup>-/-</sup> mice) have been developed to study the effect.

### **SCD KO mice**

SCD1 has recently become a target of interest for the reversal of hepatic steatosis and insulin resistance<sup>[111]</sup>.

**Table 1** Potential candidate genes in fatty liver disease

Category of genes	Examples
Genes affecting insulin resistance	ADIPOQ, AKT2, ENPP1, IRS1, PPARG, HFE, resistin
Genes affecting hepatic lipid synthesis and uptake	DGAT2, SLC25A13, ACC, ELOVL6, SCD1, GPAT, SREBP1
Genes affecting hepatic lipid uptake	APOC3
Genes affecting hepatic triglyceride hydrolysis	PNPLA2, CGI-58, LIPA
Genes affecting hepatic lipid export	APOB, MTTP, PEMT
Genes affecting hepatic oxidative stress	GCLC, NOS2, SOD2, HFE, UCP2, MAT1A, GST, GSH-Px
Genes affecting immune regulation	ADIPOQ, ADIPOR1, ADIPOR2, STAT3, TNF $\alpha$ , IL10, IL6, CTLA-4, IL-4, IL-18
Genes influencing disease progression and fibrosis	TGF- $\beta$ 1, 3, PPAR $\alpha$ , DDX5, CPT1A, angiotensin II
Genes influencing response to endotoxin	CD14, TLR4, NOD2

ADIPOQ: Adiponectin; AKT: Beta serine/threonine-protein kinase; ENPP1: Ectonucleotide pyrophosphatase/phosphodiesterase 1; IRS-1: Insulin receptor substrate 1; PPARG: Peroxisome proliferator-activated receptor gamma; HFE: Hemochromatosis gene; DGAT2: Diacylglycerol acetyltransferase-2; SLC25A13: Solute carrier family 25 Member 13 (citrin); ACC gene: Acetyl-CoA carboxylase alpha; ELOVL6: Elongation of very long chain fatty acids; SCD1 gene: Stearoyl-CoA desaturase gene; GPAT: Glycerol-3-phosphate acyltransferase; SREBP1: Sterol regulatory element-binding transcription factor 1; APOC3: Apolipoprotein C-III; PNPLA2: Patatin-like phospholipase domain containing 2; CGI58: Comparative gene identification-58; LIPA: Lipase A; APOB: Apolipoprotein B; MTTP: Microsomal triglyceride transfer protein; PEMT: Phosphatidylethanolamine N-methyltransferase; GCLC: Glutamate-cysteine ligase, catalytic subunit; NOS2: Nitric oxide synthases2; SOD2: Superoxide dismutase-2; UCP2: Uncoupling protein 2; MAT1A: Methionine adenosyltransferase I alpha; GST: Glutathione S-transferase; ADH: Alcohol dehydrogenase; ALDH: Aldehyde dehydrogenase; CTGF: Connective tissue growth factor; CTLA-4: Cytotoxic T-cell associated antigen-4; GSH-Px: Glutathione peroxidase; STAT3: Signal transducer and activator of transcription 3; IL: Interleukin; PPAR: Peroxisomal proliferator activated receptor; SCD-1: Stearoyl CoA desaturase-1; TLR: Toll-like receptor; TNFR: TNF- $\alpha$  receptor; DDX5: DEAD box protein 5; CPT1A: Carnitine palmitoyltransferase 1A (liver); NOD2: Nucleotide-binding oligomerization domain containing 2.

SCD1 catalyzes the synthesis of monounsaturated FAs, particularly oleate (C18:1n-9) and palmitoleate (C16:1n-7), which are the major components of membrane phospholipids, TGs, and cholesterol esters. Mice with SCD1KO (*Scd1*<sup>-/-</sup> mice) show decreased lipogenic gene expression and increased  $\beta$ -oxidation and are protected from diet-induced obesity and insulin resistance when fed a HC/HF diet<sup>[112,113]</sup>. Inhibition of SCD1 using an ASO strategy (targeting SCD1 in both liver and adipose tissues) prevents many of the HF/HC-diet metabolic complications, including hepatic steatosis and postprandial hyperglycemia<sup>[114,115]</sup>.

### ELOVL6 KO mice

*Elovl6*<sup>-/-</sup> mice are protected against the development of hepatic insulin resistance when fed a HF/HC diet, despite the accumulation of palmitate concentrations. Improvement in insulin signaling (as evidenced by the restoration in insulin-mediated Akt phosphorylation)

occurred despite hepatic steatosis and marked obesity in *Elovl6*<sup>-/-</sup> mice<sup>[116]</sup>. While these results are somewhat surprising given the role of palmitate as a potent inducer of insulin resistance (at least in primary cultures of hepatocytes)<sup>[117]</sup>, they are also interesting since they indicate that the hepatic FA composition, and particularly the conversion of palmitate to stearate, is crucial for insulin sensitivity. It should be noted that the reduced SCD1 expression observed in livers of *Elovl6*<sup>-/-</sup> mice could have also contributed to the amelioration of insulin resistance in these mice<sup>[116]</sup>.

### ChREBP knockdown mice

ChREBP knockdown led to the expected inhibition of L-PK, ACC, FAS and SCD1 as well as GPAT. While a carbohydrate-response element was previously identified in the promoter region of the *GPAT* gene<sup>[118]</sup>, its expression was found to be unaffected in the liver of ChREBP-knockout mice upon refeeding<sup>[119]</sup>. It is possible that the nutritional regulation of GPAT may be more sensitive to insulin *via* SREBP-1c than to glucose *via* ChREBP. Nevertheless, following ChREBP knockdown, a resultant decrease in lipogenic rates was observed in shChREBP-RNA-treated *ob/ob* mice, leading to a 50% reduction in hepatic and circulating TG concentrations<sup>[120]</sup>. ChREBP knockdown not only affected the rate of *de novo* lipogenesis but also had consequences for  $\beta$ -oxidation. Therefore, similarly to the liver-specific knockout of SCD1 (LKO mice)<sup>[121]</sup>, the coordinated modulation in FA synthesis and oxidation in liver led to an overall improvement of lipid homeostasis in ChREBP-deficient mice. The decrease in lipogenic rates observed in LKO mice was at least partially attributed to a decrease in ChREBP nuclear protein content<sup>[122]</sup>. Clearly, ChREBP needs now to be considered as a key determinant of the molecular regulation of the lipogenic pathway.

## CLASSIFICATION OF SOME ANIMAL MODELS WITH DISRUPTION OF GENES INVOLVED IN NAFLD

Table 1 presents a number of candidate genes that are involved in the pathogenesis of NAFLD and a few are discussed below.

### Genes affecting lipid metabolism

**Pemt KO animals:** *Pemt*<sup>-/-</sup> mice have two selectively disrupted alleles of the *Pemt-2* gene at exon 2<sup>[123]</sup>, which encode PEMT, and do not express any PEMT activity in liver. Therefore these mice completely depend on dietary choline intake to meet daily choline requirements. When fed a diet deficient in choline and insufficient in methionine, *Pemt*<sup>-/-</sup> mice develop decreased PtdCho concentrations in hepatic membranes, leading to severe liver damage and death; a choline supplemented diet prevents this<sup>[124]</sup> and, if provided early enough, can reverse hepatic damage.

**DGAT2 mice:** DGAT2, an isoform of the enzyme acylCoA: diacylglycerol acyltransferase, catalyses the final stage of triglyceride synthesis in the liver<sup>[125]</sup>. Overexpression of DGAT2 in mice led to a 2.4-fold increase in hepatic triglyceride content, but no effect on production of VLDL triglyceride or apoB<sup>[126]</sup>. In addition, mice on a high-fat diet that overexpress DGAT develop fatty liver but not glucose or insulin intolerance<sup>[127]</sup>, showing that hepatic steatosis can occur independently of insulin resistance. Interestingly, antisense therapy reducing DGAT improves hepatic steatosis, but not insulin sensitivity<sup>[128]</sup>.

**Apolipoprotein C-III:** Apolipoprotein C-III (apoC-III) is the most abundant C apolipoprotein in human plasma, where it is present as an 8.8-kDa mature protein on chylomicrons, VLDL and HDL. ApoC-III is synthesized in the liver and in minor quantities by the intestine<sup>[129]</sup>. Several lines of evidence have implicated apoC-III as contributing to the development of hypertriglyceridemia in the human population. Investigation in *apoC3*<sup>-/-</sup> mice supports the concept that apoC-III is an effective inhibitor of VLDL TG hydrolysis and reveals a potential regulating role for apoC-III with respect to the selective uptake of cholesteryl esters<sup>[130]</sup>.

#### Genes affecting insulin resistance/sensitivity

**IRS 1:** Studies on mice with targeted disruption of the *Irs* genes lend some support to both situations. *Irs1* knockout (*Irs1*<sup>-/-</sup>) mice show significant embryonic and postnatal growth retardation, suggesting that IRS-1 plays a key role in relaying the growth-stimulating effects of insulin and insulin-like growth factor. IRS-1-deficient mice also have insulin resistance and mild glucose intolerance, but do not develop diabetes<sup>[131,132]</sup>.

**Ecto-nucleotide pyrophosphate phosphodiesterase:** Ecto-nucleotide pyrophosphate phosphodiesterase (ENPP1) has been shown to negatively modulate insulin receptor and to induce cellular insulin resistance when over-expressed in various cell types. Systemic insulin resistance has also been observed when ENPP1 is over-expressed in multiple tissues of transgenic models and is largely attributed to tissue insulin resistance induced in skeletal muscle and liver. In the presence of a high fat diet, ENPP1 over-expression in adipocytes induces fatty liver, hyperlipidemia and dysglycemia, thus recapitulating key manifestations of the metabolic syndrome<sup>[133]</sup>.

**Transcription factor 7-like 2:** Transcription factor 7-like 2 (TCF7L2) is a receptor for  $\beta$ -catenin and regulates the expression of a multitude of genes involved in cellular metabolism and growth. Various studies<sup>[134-136]</sup> have linked TCF7L2 variation with impaired insulin secretion and risk of diabetes, possibly mediated by altered  $\beta$ -cell glucose response. In addition, it regulates adipokine secretion and triglyceride metabolism through effects on PPAR- $\gamma$ , CCAAT/enhancer-binding protein, and lipoprotein lipase; TCF7L2 SNPs are associated with serum

triglyceride concentrations in familial hyperlipidemia<sup>[137]</sup>.

#### Genes affecting oxidative stress

**Glutamate-cysteine ligase:** Glutamate-cysteine ligase (GCLC) is the first and rate-limiting enzyme in the synthesis of glutathione, the major antioxidant in the liver. Liver-specific deletion of GCLC in mice rapidly leads to hepatic steatosis and progressive severe parenchymal damage<sup>[138]</sup>.

**Nitric oxide synthase:** Yoneda *et al.*<sup>[139]</sup>, who studied associations of PPAR $\gamma$ C1 $\alpha$ , also examined the influence of SNPs in the inducible nitric oxide synthase (*NOS2*) gene on their NAFLD cohort. iNOS is expressed as part of the inflammatory response and in the presence of superoxide radicals forms peroxynitrite, which can cause endoplasmic reticulum stress and cell death<sup>[140]</sup>. iNOS-deficient mice develop NASH with high fat diets<sup>[141]</sup>.

**Superoxide dismutase-2:** Elevated hepatic reactive oxygen species play an important role in pathogenesis of liver diseases, such as alcohol-induced liver injury, hepatitis C virus infection, and nonalcoholic steatohepatitis. Satoshi *et al.*<sup>[142]</sup> observed significant increases in lipid peroxidation and TG in the liver of *Sod1* KO and double KO mice but not in the liver of *Sod2* KO mice.

#### Genes affecting immune regulation

**Signal transducer and activator of transcription 3:** Signal transducer and activator of transcription 3 (STAT3) is an acute-phase transcription factor; after hepatic necrosis it activates pathways associated with liver regeneration and acute inflammation<sup>[143]</sup>. STAT3 is also implicated in nutrient metabolism and developing metabolic syndrome. Transgenic mice with hepatic deficiency of STAT3 develop insulin resistance and disturbed glucose homeostasis; whereas the constitutive liver specific expression of STAT3 in diabetic mice reduces blood glucose and plasma insulin concentrations and downregulates gluconeogenic gene expression<sup>[144]</sup>.

## CONCLUSION

Inbred strains of mice provide convenient tools to study the pathogenesis of NAFLD because they provide the opportunity to control genetic and environmental factors that might influence the natural history of NAFLD. Various genetic alterations or environmental stressors producing a similar phenotype prove that many different immunological, neuronal and hormonal factors are involved in the pathogenesis of NAFLD<sup>[145,146]</sup>. Transgenic mouse models also represent gene mediation to NAFLD. Therefore, any one of these animal models could be used to clarify how altered cross talk among immune cells, neurons and endocrine cells promote NAFLD. In contrast to human genetic studies, animal studies have found genes that consistently produce disease-like phenotypes, and the underlying genetic basis for the phenotypes in these models have often been



elucidated. Animal studies on NAFLD frequently reveal significant single-locus effects that can be reproduced across species and/or strains. Such “disease genes” in animal models can be found relatively easily using linkage mapping techniques in crossed inbred lines. Similarly, transgenic animals or genetically manipulated animals for NAFLD can reveal significant effects of candidate alleles in well-defined genetic backgrounds. This review has explored some of the advantages and disadvantages of a few genetically modified mouse models of NAFLD that would be useful in understanding the connections between lipid metabolism, host defences, environmental triggers, genetic variability, inflammatory recruitment, and fibrogenesis. These models will also serve as important platforms for assessing therapeutic strategies, which is an essential area of study.

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