

Causes and Metabolic Consequences of Fatty Liver

Norbert Stefan, Konstantinos Kantartzis, and Hans-Ulrich Häring

Department of Internal Medicine, Division of Endocrinology, Diabetology, Nephrology, Vascular Disease and Clinical Chemistry, University of Tübingen, D-72076 Tübingen, Germany

Type 2 diabetes and cardiovascular disease represent a serious threat to the health of the population worldwide. Although overall adiposity and particularly visceral adiposity are established risk factors for these diseases, in the recent years fatty liver emerged as an additional and independent factor. However, the pathophysiology of fat accumulation in the liver and the cross-talk of fatty liver with other tissues involved in metabolism in humans are not fully understood. Here we discuss the mechanisms involved in

the pathogenesis of hepatic fat accumulation, particularly the roles of body fat distribution, nutrition, exercise, genetics, and gene-environment interaction. Furthermore, the effects of fatty liver on glucose and lipid metabolism, specifically via induction of subclinical inflammation and secretion of humoral factors, are highlighted. Finally, new aspects regarding the dissociation of fatty liver and insulin resistance are addressed. (Endocrine Reviews 29: 939–960, 2008)

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I. Introduction

THE EPIDEMICS OF obesity, metabolic syndrome, type 2 diabetes, and atherosclerosis are increasing worldwide (1). Nonalcoholic fatty liver disease (NAFLD), for a long time unnoted in the metabolic field, is becoming recognized as a condition possibly involved in the pathogenesis of these diseases. Support for this hypothesis emerges from studies revealing that NAFLD precedes the manifestation of the metabolic derangements (2–4). Today, with a prevalence of about 34% in the United States among adults (5), NAFLD is the most common cause of chronic liver disease, constituting a major risk factor for progression to liver failure, cirrhosis, and hepatocellular carcinoma (6–8). Particularly alarming are the data showing that NAFLD has become the most common cause of liver disease in children (9). Therefore, and because the prevalence of the metabolic syndrome as well as type 2 diabetes continuously rises in children (10–12), a concerted effort of the academic disciplines is requested to study the pathophysiology of fatty liver. Furthermore, the consequences of fatty liver for metabolism need to be carefully investigated. Novel findings from the research in this field may help to implement intervention strategies aimed at preventing and reversing fat accumulation in the liver, as well as its complications.

II. Prevalence and Diagnosis of Fatty Liver

A. Prevalence of fatty liver

The term NAFLD is used to describe a condition of fat accumulation in the liver in the absence of excessive alcohol consumption (less than 20 g/d) and specific causes of hepatic steatosis. Among them, nutritional (e.g., malnutrition, rapid weight loss), metabolic (e.g., abetalipoproteinemia, lipodystrophy), and drug-induced (e.g., glucocorticoids, methotrexate) causes as well as other conditions (e.g., jejunal diverticulitis with bacterial overgrowth, inflammatory bowel disease) are relevant.

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Abbreviations: ADIPOR1, Adiponectin receptor-1; AMPK, AMP-activated protein kinase; BMI, body mass index; ChREBP, carbohydrate response element-binding protein; CLOCK, circadian locomotor output cycles protein kaput; CoA, coenzyme A; CRP, C-reactive protein; CT, computed tomographic; CYP7A1, cytochrome P450 cholesterol 7 α -hydroxylase; D2, type 2 iodothyronine deiodinase; DGAT2, diacylglycerol acyltransferase 2; DNL, *de novo* lipogenesis; ER, endoplasmic reticulum; FACoA, fatty acyl CoA; FFA, free fatty acid; FGF, fibroblast growth factor; FXR, farnesoid X receptor; HDL, high-density lipoprotein; ¹H-MRS, proton magnetic resonance spectroscopy; IFN, interferon; IRS, insulin receptor substrate; JNK, c-Jun N-terminal kinase; LDL, low-density-lipoprotein; LXR, liver X receptor; MR, magnetic resonance; MTP, microsomal transfer protein; NAFLD, nonalcoholic fatty liver disease; NASH, nonalcoholic steatohepatitis; NF- κ B, nuclear factor κ B; NK, natural killer; PGC-1 α , PPAR γ coactivator 1 α ; PPAR, peroxisome proliferator-activated receptor; RBP4, retinol binding protein 4; ROS, reactive oxygen species; SNP, single nucleotide polymorphism; SOCS, suppressor of cytokine signaling; SREBP-1c, sterol-regulatory binding protein 1c; VAT, visceral adipose tissue; VLDL, very low-density lipoprotein.

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A number of epidemiological studies converge in raising the prevalence of fatty liver, measured by proton magnetic resonance spectroscopy ($^1\text{H-MRS}$), to more than 30% of the adult general population (5, 13). Fatty liver is more frequent among obese subjects (75%) compared with controls (16%) (14) and among patients with type 2 diabetes (34–74%), whereas it is an almost universal finding in obese patients with type 2 diabetes (15). The prevalence of fatty liver is increasing with age. Nevertheless fatty liver is found even in children and that with increasing rates. Recent data indicate a doubling of the prevalence from 2.6% a decade ago (16) to 5% of normal-weight children, 38% of obese children (17), and 48% of children with type 2 diabetes (18). This makes fatty liver the most common chronic liver disease in westernized societies (15). In particular, males and certain ethnic groups, *e.g.*, Hispanics (5) and Asian-Indians (19), tend to have higher rates of fatty liver.

B. Imaging techniques and histology

The American Association for the Study of Liver Diseases (AASLD) set the limit for the diagnosis of NAFLD at fat accumulation in the liver of at least 5–10% by weight. For practical use, NAFLD is estimated as the percentage of fat-laden hepatocytes observed by light microscopy in liver biopsy (20). Because $^1\text{H-MRS}$, which is considered the most accurate noninvasive method for measuring liver fat, is more often applied, the cutoff limit has been set to 5.56% (hepatic triglyceride level of 55.6 mg/g), corresponding to the 95th percentile of the distribution of liver fat in 345 healthy subjects with no or minimal alcohol consumption (13). Furthermore, computed tomographic (CT) scanning for the low-density hepatic parenchyma, which is produced by the fat infiltration of the liver, can be used to estimate the amount of fat accumulation in the liver (7). Ultrasonography, the method that is most widely used, allows detecting moderate and severe steatosis with a fair sensitivity and specificity only when fat on liver biopsy exceeds 33% (21). Histologically, the liver of patients with NAFLD displays predominantly macrovesicular and microvesicular fat accumulation in hepatocytes. More severe states involving mononuclear cell infiltration and hepatocyte necrosis constitute steatosis with inflammation [nonalcoholic steatohepatitis (NASH)]. NASH may particularly advance to liver fibrosis, cirrhosis, and hepatocellular carcinoma (7, 22). NAFLD and NASH represent advanced stages of hepatic steatosis that are associated with metabolic diseases. However, findings from studies using very precise imaging techniques such as $^1\text{H-MRS}$, which allows detection of fat accumulation in the liver in early stages of steatosis, suggest that already moderate hepatic fat accumulation is associated with multiple metabolic phenotypes (5). Thus, a “low-grade fatty liver syndrome” may exist.

C. Laboratory and clinical findings

Up to 70% of patients with fatty liver do not show laboratory abnormalities (5, 7, 21–23). An increase in serum levels of liver alanine aminotransferase, which correlates with liver fat independently of adiposity, and to a lesser degree aspar-

tate aminotransferase can be found (24, 25). Serum alkaline phosphatase and γ -glutamyltransferase are also associated with liver fat independent of adiposity (26). However, they are not more helpful than aminotransferases for diagnosing steatosis or NASH (7). In general, elevation of liver enzymes can only be used as a crude estimate of the presence of fatty liver. Most patients with liver steatosis or NASH are asymptomatic and have no signs of liver disease at the time of diagnosis. When present, symptoms and findings are nonspecific and do not correlate well with the severity of the disease. Most commonly, fatigue or malaise and a right upper quadrant pain or sensation of fullness are reported. In addition, hepatomegaly can be found in physical examination (7, 27). Other findings relate to the presence of overweight or obesity and other features of the metabolic syndrome. Acanthosis nigricans, which was earlier found in the context of severe insulin resistance (28, 29), is present almost only in children (27, 30). Finally, cirrhosis exhibits signs and symptoms of decompensated liver disease, independent of the original cause. Altogether the diagnosis of fatty liver can be established with a combined approach involving clinical assessment including a careful history and physical examination, laboratory evaluation, imaging techniques, and liver biopsy. More specifically, when clinical, routine laboratory, or anthropometrical findings show abnormalities that are often associated with fatty liver, ultrasonography and specific laboratory tests are commonly used to diagnose liver diseases. Regarding fatty liver, other causes need to be excluded. CT scan, magnetic resonance (MR) tomography, $^1\text{H-MRS}$, and to a lesser extent ultrasonography allow the noninvasive diagnosis of fatty liver. When there are additional findings suggesting NASH or fibrosis (age > 45 yr, alanine aminotransferase/aspartate aminotransferase ratio > 1, visceral obesity, high triglycerides), a liver biopsy to estimate the severity and the prognosis of the disease, as well as to monitor the effectiveness of an intervention, may be useful.

Regarding the treatment of NAFLD, patients should avoid alcohol and other hepatotoxins. The goal of treatment is to reduce steatosis and prevent the development of fibrosis, which may lead to cirrhosis and its complications. Because the progression of NAFLD to more severe clinical conditions may be affected by obesity, the metabolic syndrome, and insulin resistance, these states have been the focus of treatment. In particular, moderate lifestyle intervention is considered the first-line therapy (15, 31, 32). Numerous clinical trials with pharmaceutical agents have been undertaken in the last few years; however, there is no final consensus on the effectiveness of such a treatment (33, 34). Agents affecting redistribution of body fat (thiazolidinediones), insulin sensitivity (thiazolidinediones and metformin), lipid oxidation and food intake (cannabinoid receptor-1 antagonists), and hepatoprotective drugs (ursodeoxycholic acid, betaine, vitamin E) have been tested. Particularly, thiazolidinediones were found to be effective in the treatment of NAFLD and NASH (35). Pilot studies further reveal a potential role of the nonselective phosphodiesterase inhibitor pentoxifylline, which reduces transcription of the TNF gene, in the treatment of NASH (36, 37).

III. Causes of Fatty Liver

A. Body fat composition, hepatic lipid supply, and adipokines

It is widely accepted that behavioral factors are involved in the pathophysiology of fatty liver. In this aspect, an increased energy intake is considered to represent a major player. In addition, diet composition was found to be relevant. Furthermore, studies showed that a sedentary lifestyle with reduced physical activity, independent of diet, represents another determinant for fatty liver. Although these risk factors may successfully be modified by moderate lifestyle interventions, the existence of other risk factors most probably may necessitate more intense treatment. Among them, a disproportionate fat distribution, particularly with increased visceral adiposity releasing humoral factors regulating liver fat, are relevant. Finally, impaired hepatic lipid oxidation as well as dysregulated lipogenesis, factors that are affected by genetics, may be of pathophysiological relevance (Fig. 1).

Liver fat measured by $^1\text{H-MRS}$ is closely and positively correlated with measures of total adiposity such as body mass index (BMI) or percentage body fat. Furthermore, the correlation of liver fat with visceral adiposity, measured as waist circumference, is particularly strong. In most studies, the latter association remains statistically significant after adjustment for BMI and is stronger than the relationship between liver fat and BMI (38–40). Even stronger are the correlations between liver fat and visceral adipose tissue (VAT) mass, quantified by means of computed (41) or MR tomography and $^1\text{H-MRS}$ (24, 42, 43). Of note, in multivariate analyses with gender, age, waist-to-hip ratio, and VAT as independent variables, only VAT is significantly correlated with liver fat (42). Both, in univariate and multivariate anal-

yses, the respective correlation coefficients generally range between 0.54 and 0.65, suggesting that 30 to 40% of the variation in liver fat content can be explained by the variability in VAT (44). The impact of other body fat compartments, as sc abdominal fat or fat of the extremities, remains to be studied.

A mechanism possibly explaining the relationship of overall and visceral obesity with liver fat is inflammation of hypertrophic adipose tissue. When adipose tissue expands, it becomes infiltrated by macrophages and overflows with proinflammatory cytokines and probably, therefore, is insulin resistant (45–47). The impairment of insulin-mediated suppression of lipolysis then results in an increased release of free fatty acids (FFAs) from adipose tissue (48, 49). In this aspect, VAT is of special importance because it is metabolically more active than sc adipose tissue (50, 51). The increased lipolysis in VAT is thought to result in an elevated flux of FFAs directly into the portal vein and the liver, a process that is commonly referred to as the “portal hypothesis” (48). FFAs are then taken up by the hepatocytes and are bound to coenzyme A (CoA). The fatty acyl CoAs (FACoAs) can react to form hepatic triglycerides but can also interfere with insulin signaling (52). Furthermore, FACoAs can induce intracellular inflammation by stimulating the nuclear factor κB (NF- κB) (53). Moreover, FFAs are ligands of the membrane-bound toll-like receptor 4 and can induce insulin resistance and inflammation virtually by the same intracellular mechanisms, without being converted to FACoAs (54–56).

Hepatic inflammation was previously considered to promote steatosis (57); however, this concept is not supported by other studies (58, 59). In mice selectively expressing active inhibitor κB kinase, which stimulates nuclear translocation and expression of NF- κB and NF- κB target genes, liver fat is not increased but is reduced (59).

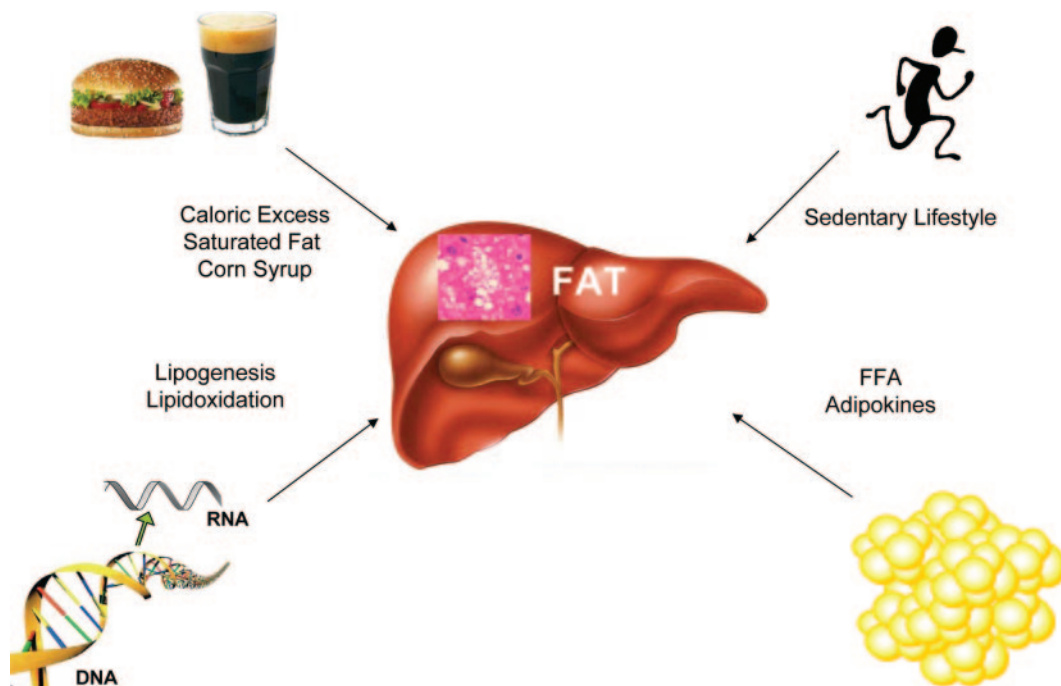
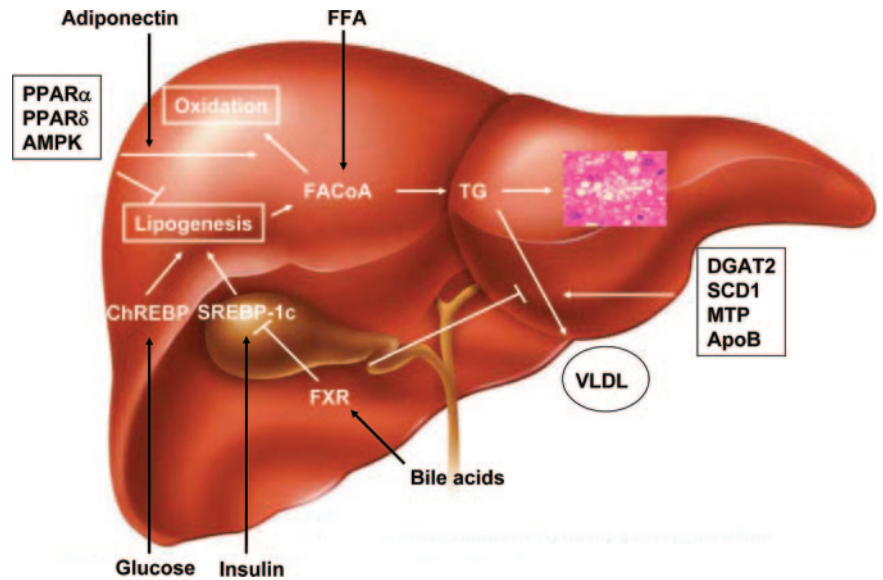


FIG. 1. Major determinants of fatty liver.

FIG. 2. Pathophysiology of fatty liver. Among the mechanisms involved in the pathophysiology of fatty liver, hyperglycemia and hyperinsulinemia are considered to induce lipogenesis via ChREBP and SREBP-1c, respectively, thereby increasing the hepatic pool of FAcCoA. This pool is also increased by increased delivery of FFA through either the diet or lipolysis in adipose tissue. FAcCoAs are assembled to triglycerides (TG) that remain in the liver or are secreted in the form of VLDLs. The latter pathway is regulated by several factors, among them the two enzymes stearoyl-CoA-desaturase (SCD) and acyl:CoA:D-GAT2, as well as the MTP and the availability of apolipoprotein B. FAcCoAs can also be oxidized in the liver, involving the transcription factors PPAR α and PPAR δ . In addition, the AMPK is involved. The adipokine adiponectin stimulates fatty acyl oxidation via AMPK activation and PPAR α induction. AMPK is also involved in the suppression of lipogenesis. Furthermore, bile acids activate the FXR that inhibits SREBP-1c. The role of insulin signaling in the pathophysiology of fatty liver needs to be elucidated further.



The “portal hypothesis” was challenged when the contribution of VAT lipolysis to the pool of FFAs drained into the liver, measured by isotope dilution and arteriovenous sampling methods, was found to be only 5–10% in normal-weight subjects and only up to 25% in viscerally obese individuals (60). The main origin of the FFAs in the systemic plasma pool in the fasting state is considered to be sc fat (60, 61). Whereas in the fasting state hepatic fatty acids originate predominantly from the systemic plasma FFA pool (62), the portal FFA supply to the liver may be substantially increased postprandially (63). Nevertheless, irrespectively of the origin of the FFAs, increased hepatic lipid supply is most probably contributing to hepatic fat accumulation (31, 49) (Fig. 2). This hypothesis is further supported by studies showing that exogenous lipid infusion and high-fat diet increase liver fat content and hepatic insulin resistance, whereas low-fat diets and treatment with fatty acid-lowering medication have the opposite effects (32, 49).

Furthermore, inflamed adipose tissue in obesity secretes high amounts of proinflammatory cytokines as TNF- α and ILs, particularly IL-6 (45–47), which suppress the production of the insulin-sensitizing adipokine adiponectin (64, 65). The imbalance in the secretion pattern of these adipocytokines is considered to represent another link between obesity and fatty liver (49). Although plasma levels of TNF- α and IL-6 are increased in obesity (47, 66, 67), they are low compared with their tissue concentrations (68, 69). In particular, TNF- α is likely to have predominantly paracrine effects in terms of increasing insulin resistance in the adipose tissue (31, 47). In contrast, circulating adiponectin closely correlates with liver fat content (43, 70) and hepatic insulin resistance (70). Furthermore, treatment with thiazolidinediones, which increase circulating adiponectin, results in a decrease in liver fat content (35). In addition, genetic variability in the adiponectin receptor gene affects hepatic fat accumulation (71), supporting the important role of adiponectin signaling in the pathophysiology of fatty liver in humans. Mechanisms of adiponectin action include increase in lipid oxidation in liver and skeletal muscle via activation of AMP-activated protein

kinase (AMPK) and induction of peroxisome proliferator-activated receptor (PPAR)- α (65, 72, 73). Furthermore, adiponectin decreases the activity of enzymes involved in fatty acid synthesis as acetyl-CoA carboxylase and fatty acid synthase (74).

Leptin is considered another important regulator of liver fat, although the mechanisms of the protective effect of this adipokine are not fully understood. Besides the hypothalamic effects of leptin in the regulation of food intake, it most probably has direct antisteatotic effects by enhancing lipid oxidation and inhibiting lipogenesis in tissues (75). This hypothesis is supported by data from studies with administration of recombinant adenovirus-receptor constructs containing the normal leptin receptor in obese Zucker diabetic fatty rats. Because most of the infused adenovirus-receptor construct is taken up by the liver, the reduction in hepatic triglycerides under treatment is thought to be predominantly mediated by direct antisteatotic effects of endogenous leptinemia (75). However, effects of this intervention on other tissues cannot be ruled out.

In line with findings from studies on lipoatrophy (76), both aforementioned hypotheses, the hepatic FFA oversupply and altered adipokine release, suggest that fat distribution may strongly be involved in the pathogenesis of hepatic steatosis. More specifically, it is hypothesized that when sc adipose tissue is absent or deficient, the excess of calories cannot be stored in this insulin-sensitive tissue. Thus, expansion of visceral fat mass, as well as ectopic fat accumulation in liver and skeletal muscle results from the inability of the body to adequately store energy, a state that is driven by insulin resistance of sc adipose tissue (77). Fatty liver would then rather be secondary to peripheral insulin resistance.

Whether hyperinsulinemia is only an innocent bystander, resulting from skeletal muscle insulin resistance-mediated hyperglycemia and thus, insulin hypersecretion from the β -cells, or whether it may also contribute to the pathogenesis of liver fat accumulation has been a matter of discussion. Insulin is a potent activator of sterol-regulatory binding protein 1c (SREBP-1c), a transcription factor regulating the ex-

pression of enzymes involved in the synthesis of fatty acids in the liver (31, 49, 78, 79) (Fig. 2). At first view, it seems contradictory that in hepatic insulin resistance, which is strongly associated with hepatic steatosis (44, 49, 80), insulin may still be able to stimulate lipogenesis. However, in the presence of profound insulin resistance in animals, insulin does stimulate hepatic SREBP-1c transcription. This is associated with increased rates of *de novo* lipogenesis (DNL) (81, 82), possibly mediated by a mechanism involving Foxa2 signaling (83–85). Alternatively, as discussed by Biddinger *et al.* (86), DNL may also become insulin resistant but may be stimulated by other factors such as carbohydrates.

In this aspect, glucose activates carbohydrate response element-binding protein (ChREBP), which exerts, similarly to SREBP-1c, stimulatory effects on the expression of genes involved in lipogenesis and triglyceride synthesis (79, 87, 88). ChREBP also stimulates pyruvate kinase, thus increasing the glycolysis of glucose into pyruvate, which forms acetyl-CoA and then malonyl-CoA, which is required for FFA synthesis (89). The activities of both transcription factors (ChREBP and SREBP-1c) are increased in animal models of fatty liver (81, 90) (Fig. 2).

Support from data in humans showing that hyperinsulinemia alone is not a major driving force for fat accumulation in the liver comes from a study in patients with type 2 diabetes. In that study, 7 months of insulin therapy resulting in systemic hyperinsulinemia actually was found to decrease liver fat content (91). Furthermore, a study addressing the effect of high-fat, low-carbohydrate *vs.* low-fat, high-carbohydrate diets on hepatic DNL in lean, obese insulin-sensitive and obese insulin-resistant subjects shows a major effect of carbohydrate intake on lipogenesis (92). On the high-fat diet, DNL increases only in obese, insulin-resistant subjects (but not in obese, insulin-sensitive subjects), supporting the finding that hyperinsulinemia is involved in DNL in humans. Moreover, and of particular importance, on the high-carbohydrate diet DNL is highest in lean insulin-sensitive subjects, and hyperinsulinemia has no additional effect on DNL. Altogether, these human data support, first, that hepatic DNL is up-regulated in insulin resistance; and second, that intake of carbohydrates has a more profound effect than hyperinsulinemia. Certainly, further studies are needed to precisely clarify the magnitude of these effects in human metabolism.

B. Nutrition

Nutritional factors affect the hepatic fatty acid pool in several ways. Dietary fatty acids enter the liver either through the uptake of intestinally derived chylomicron remnants or in the form of FFA from chylomicrons hydrolyzed at a rate in excess of what can be taken up by tissues (spillover) (62, 79). Dietary glucose, as mentioned above, and fat are important regulators of DNL via activation of ChREBP and SREBP-1c (79, 87, 88). Postprandially, both dietary fat supply to the liver and DNL increase and can provide more than 50% of the FFAs entering the liver (63). In the fasting state, DNL accounts for less than 5% of hepatic fatty acids in healthy subjects (93), but lipogenesis may substantially increase in subjects with fatty liver (62, 94). Moreover, it is likely that the fatty acid

pattern modulates the activity of ChREBP and SREBP-1c, with saturated and trans-unsaturated FFAs increasing and mono- as well as polyunsaturated FFAs decreasing their expression and activity (95–98).

In human studies, individuals with fatty liver have higher intake of calories as well as saturated fat and cholesterol compared with healthy controls. They also have lower intake of polyunsaturated fat, fiber, and antioxidant vitamins such as vitamin C and E (99–101). In trials with only caloric restriction in severely obese individuals, an improvement in liver enzymes and in liver steatosis is found in those subjects who lost weight (102, 103). Furthermore, a low-calorie diet is associated with improvement in liver histology in overweight patients with NASH (104). In intervention studies investigating the effect of fat intake, high-total fat diets cause an increase in liver fat content. In contrast, low-fat diets result in a decrease in liver fat content as well as in markers of insulin resistance. These effects occur under isocaloric (105) as well as hypocaloric diets (106–108). The restriction of saturated fat intake is particularly effective (108, 109). Many of these studies are relatively small and do not assess the effects of such diets on the improvement in liver fat content using precise measurement techniques such as histology, ¹H-MRS, or CT scans. Nevertheless, strategies aimed at weight reduction by restriction of total and saturated fat intake, combined with an increase in physical exercise, are now considered to constitute the most appropriate initial treatment for fatty liver (15, 32). A moderate weight loss by 5–10% of baseline weight or 0.5–1.5 kg/wk is recommended (31, 34). This is important because rapid weight loss was found to deteriorate liver histology, possibly due to increased lipolysis (15, 31, 110).

There are also human studies supporting the findings in animals regarding the role of dietary carbohydrates in the pathophysiology of fatty liver (111–113). A low-carbohydrate, ketogenic diet (<20 g/d) is associated with a greater weight loss, a better lipid profile, and clearly improved steatosis and inflammation in liver biopsies after 6 months than low-fat diets (113). Among the carbohydrates, fructose appears to have the strongest effects on lipogenesis (114, 115). In a study in seven young healthy males, a high-fructose diet for 6 d was found to increase the fractional hepatic DNL 6-fold as well as hepatic insulin resistance and plasma triglycerides. Interestingly, fish oil supplementation reversed dyslipidemia and tended to reduce DNL (116). However, in another study a 4-wk high-fructose consumption (1.5 g/kg·d) resulted in an increase in plasma triglycerides, but not in hepatic fat content, suggesting that the excess of triglycerides formed in the liver was exported as very low-density lipoprotein (VLDL) triglycerides (117). Because consumption of high-fructose corn syrup has tremendously increased in the last decades in the westernized world, it may have contributed to the respective increase in the incidence of fatty liver disease (118).

Other nutritional factors may also be of importance in the pathophysiology of hepatic steatosis and hepatosteatitis. Antioxidant vitamins, because of their ability to prevent oxidative stress and inflammation, may have beneficial effects particularly in the pathogenesis of steatohepatitis and fibrosis. In support of this hypothesis, obese patients with NASH

were found to consume less antioxidant vitamins C and E compared with obese controls (100). In addition, vitamin E supplementation as add-on treatment of NASH reduces liver fat content (119, 120). However, these are rather small trials, and the magnitude of the effect of vitamin supplementation on liver fat still remains to be clarified.

Furthermore, agents regulating bile acid metabolism may be important in the regulation of fat accumulation in the liver. Bile acids, by binding to the G protein-coupled receptor TGR5, or mBAR, induce PPAR γ coactivator 1 α (PGC-1 α) transcription, thereby increasing mitochondrial activity and β -oxidation (121). Furthermore, bile acids via G protein-coupled receptor increase cAMP production and activate the cAMP-protein kinase A pathway, resulting in an increase of cAMP-dependent thyroid hormone activating enzyme type 2 iodothyronine deiodinase (D2) activity. This enzyme converts T₄ to T₃, which binds to thyroid hormone receptor and uncouples electron transfer in the respiratory chain from oxidative phosphorylation. Thus, this bile acid-TGR5-cAMP-D2 signaling pathway increases energy expenditure and oxygen consumption and finely regulates energy homeostasis. These mechanisms are operative in the most thermogenically important tissues in rodents (brown adipose tissue) and humans (skeletal myocytes) (121, 122). Whether such a mechanism also takes place in the human liver, thereby possibly contributing to an increased oxidation of fatty acids and reducing liver fat, is unknown.

In addition, bile acids are the major ligands of the farnesoid X receptor (FXR) (Fig. 2), a nuclear receptor that plays a key role in protecting the liver and the intestine against bile acid toxicity (123, 124). In this context, FXR down-regulates cytochrome P450 cholesterol 7 α -hydroxylase (CYP7A1) gene expression and thus, bile acid synthesis via up-regulation of the atypical nuclear receptor small heterodimer partner (SHP) (121, 125, 126). Another pathway leading to suppression of CYP7A1 involves bile acid-mediated activation of FXR of the ileum, which induces the local expression of fibroblast growth factor (FGF)-19 (FGF15 in rodents) (127, 128). FGF19 is absorbed in the bloodstream and is able to activate FGF receptor isotype 4 in hepatocytes. Activated FGF receptor isotype 4 represses CYP7A1 expression via a c-Jun N-terminal kinase (JNK) pathway (127, 129–131). Liver FXR also down-regulates expression of polypeptides acting as bile acid import pumps, up-regulates bile acid export pumps, and inhibits intestinal reabsorption of bile acids (121, 127).

Furthermore, FXR has significant effects in modulating postprandial energy metabolism and particularly lipoprotein metabolism (130). A natural FXR agonist, chenodeoxycholic acid, has been known for several decades to reduce plasma triglycerides in humans (132). In animals, both this natural agonist (133) and the synthetic FXR agonist GW4064 reduce plasma triglycerides and the rate of VLDL production, as well as blood glucose (134). Although the mechanism of bile acid sequestrants (resins)-induced hypertriglyceridemia was unknown for a long time, recent findings indicate that a reduction in FXR ligands is involved. The reduction of triglycerides is, at least partially, attributed to the down-regulation of SREBP-1c (133, 135) and up-regulation of PPAR α , leading to a reduced hepatic fatty acid and trigly-

eride synthesis and an increased fatty acid oxidation (121). The latter effect may also be mediated by bile acid-induced production of FGF19 (136). Another mechanism includes induction of apolipoprotein C-II expression, which is a co-activator of lipoprotein lipase, the enzyme that hydrolyzes serum triglycerides (127, 137).

In addition, activation of FXR is associated with a decrease in blood glucose. This effect is thought to be mediated by suppression of hepatic gluconeogenic genes (130, 138). Therefore, it is reasonable to assume that an FXR agonist could decrease liver fat as well as plasma triglycerides and possibly glucose levels (139). On the other hand, an antagonist of FXR would be expected to lower low-density-lipoprotein (LDL) cholesterol by promoting conversion of cholesterol into bile acids (140). Furthermore, FXR activation seems to decrease high-density lipoprotein (HDL) cholesterol levels and regulate HDL remodeling. Possible mechanisms include repression of apolipoprotein A-I gene, up-regulation of hepatic scavenger receptor B1 (stimulation of hepatic HDL uptake), and up-regulation of the phospholipid transfer protein (125, 130, 139, 141, 142) and the cholesterol ester transfer protein (121) genes. These data derive principally from animal studies but are in line with the known moderate HDL cholesterol-increasing effect of bile acid sequestrants. In any case, the precise effects of FXR on LDL and HDL remain to be elucidated.

Liver X receptor (LXR, isoforms α and β) is another nuclear receptor that is an attractive target for new drugs. LXR in macrophages and in the liver plays a critical role for cholesterol reverse transport (the transport of cholesterol from macrophages to HDL particles and into the liver). Therefore, agonists of LXR are emerging as drugs potentially reducing atherosclerosis. However, they increase hepatic steatosis and plasma triglyceride levels, possibly by up-regulating SREBP-1c (125). It needs to be investigated whether selective hepatic LXR antagonists could have favorable effects on liver fat without accelerating atherosclerosis.

C. Exercise and mitochondrial function

It is still a matter of discussion whether there is a positive direct effect of exercise on liver fat (108, 109, 143, 144). Habitual physical activity is negatively associated with liver fat, independent of BMI (145, 146) but not independent of visceral adiposity (145). These data suggest that exercise intensity is not an independent determinant of liver fat. In contrast, mitochondrial function, which can be estimated by measurement of aerobic fitness, may be involved in the pathophysiology of hepatic steatosis. The association of maximal aerobic capacity with liver fat was investigated in three cross-sectional studies. In a relatively small study, no significant difference in maximal aerobic capacity between subjects with high *vs.* low liver fat was found (147). Two larger studies showed a close relationship of aerobic fitness, both with liver fat (148) and the prevalence of fatty liver (39). In 170 subjects, we found a strong predictive effect of high fitness at baseline on the reduction in liver fat during a lifestyle intervention (149). This effect was not only larger than the impact of total or visceral fat on change in liver fat, but it was also independent of these parameters, supporting

the hypothesis that aerobic fitness and hepatic lipid metabolism have a common background. In agreement with this assumption, in a recent study involving a cohort of 2603 adults that were followed up for a mean of 12 yr, fitness and BMI predicted mortality, independent of several established risk factors. Most notably, the effect of fitness was independent of total and abdominal adiposity (150). As discussed the effect of fitness on mortality may have been mediated by liver fat (151).

Mechanisms explaining the relationship between fitness and liver fat possibly include factors regulating hepatic lipid oxidation (152–156). Fitness is associated with enlargement of and increase in mitochondria in skeletal muscle and the generation of type I fibers (157). These effects may be regulated by genetics (152). Indeed, genetic variability in PGC-1 α and PPAR δ genes regulate mitochondrial function and the response of fitness to physical activity (153). Moreover, the same single nucleotide polymorphism (SNP) in the PPAR δ gene (PPARD) is associated with change in liver fat (158). Mitochondria play an important role in hepatocyte metabolism, representing the primary site for the oxidation of fatty acids and oxidative phosphorylation. Hepatocytes are rich in mitochondria, occupying about 18% of the liver cell volume (159). Thus, the aforementioned findings strongly suggest that mitochondrial function is a major regulator of liver fat. In addition, when mitochondrial function is impaired or even when an excess of substrate (FFA) is available, as is often the case in fatty liver, reactive oxygen species (ROS) can arise leading to oxidative stress, which is thought to be important for the progress to NASH and fibrosis (83). In fact, multiple functional abnormalities and even morphological changes have often been observed in mitochondria of patients with NASH (160, 161).

D. Genetics

The role of genetics in the pathogenesis of body fat distribution has been elegantly described in animal models (162). So far, there is not much information about the genetics of fat distribution in humans. Beyond that, there is little information about the impact of genetics, independent of body fat distribution, in the pathophysiology of fatty liver. A study in monozygotic twins even revealed that liver fat was different among the siblings; however, the twins also displayed different levels of total and visceral adiposity (163). On the other hand, the fact that the prevalence of fatty liver is different between ethnic groups, *e.g.*, higher in Hispanics compared with European Americans and African-Americans (5), suggests that the disease has a genetic component.

In recent years, microarray and PCR techniques for analyzing differential expression of genes in fatty liver and controls were widely used. Several genes involved in pathways of fatty acid metabolism in the liver such as uptake, *de novo* synthesis, and oxidation of fatty acids as well as synthesis and secretion of VLDL have been identified as candidates. However, the results thus far are largely inconsistent and are not replicated in large studies (164–170).

In contrast to the microarray approach determining merely expression of genes in fatty liver, the investigation of SNPs in candidate genes may be more promising in the

search for the impact of genetics. In this respect, the G/T SNP at position –493 of the promoter of the gene encoding microsomal triglyceride transfer protein (MTP), a protein critical for the synthesis and secretion of VLDL, was found to be associated with hepatic steatosis (171). Among factors affecting fatty acid oxidation, adiponectin serum levels and adiponectin signaling are of particular importance (64, 65). We found that variants in the genes encoding adiponectin receptor-1 (*ADIPOR1*) are associated with insulin sensitivity and liver fat content, both in cross-sectional and longitudinal analyses (71). The data on the impact of genetic variants of *ADIPOR1* on metabolism are supported by two other studies showing an association of SNPs of *ADIPOR1* with type 2 diabetes and the metabolic syndrome (172, 173). Such associations were not found in a study including relatively lean subjects (174). In agreement with the data showing that gene-environment interaction is important for adiponectin signaling in mice (175, 176), human studies suggest that the relationship of adiponectin and adiponectin signaling with insulin sensitivity and liver fat are stronger with increasing adiposity (43, 177–179).

As discussed above, mitochondrial dysfunction, which in skeletal muscle is implicated in the pathogenesis of insulin resistance and type 2 diabetes (180), could be a fundamental abnormality in the process of liver fat accumulation (83, 159). Mitochondrial biogenesis and activity are, among others, transcriptionally regulated by PGC-1 α and PGC-1 β (181, 182). Expression of PGC-1 α and PGC-1 β is low under normal conditions but is up-regulated under fasting conditions, thereby activating fatty oxidation by induction of PPAR α expression (183). Furthermore, PPAR δ is considered to interact with PGC-1 α in regulating fatty acid oxidation. In a recent study, the rs2267668 A/G SNP in *PPARD* was found to be a determinant of mitochondrial function in cultured myotubes and, together with the Gly482Ser SNP in the PGC-1 α gene (*PPARGC1A*), to be associated with the effect of aerobic exercise training to increase aerobic fitness, an effect probably mediated by mitochondrial function (153). In agreement with the aforementioned hypothesis, the SNP in *PPARD* was also associated with liver fat (158).

Among polymorphisms of other genes involved in fatty acid oxidation, SNPs in the gene encoding the hepatic isoform of carnitine palmitoyltransferase were recently investigated. This enzyme regulates the transport of long-chain fatty acids into mitochondria. However, no associations of the SNPs with liver fat or type 2 diabetes were found (185).

Furthermore, hepatic lipase plays a central role in hepatic lipid metabolism (186). In the hepatic lipase gene (*LIPC*), the –514C/T SNP in the promoter is associated with decreased activity of the enzyme (187) and with the plasma lipid profile (188, 189). Carriers of the T allele of this SNP have higher liver fat and insulin resistance, independent of established risk factors for these disorders (190). Furthermore, this SNP displays gene-gene interactions with the common Pro12Ala SNP of *PPARG* (190), which is well known to be involved in the pathogenesis of type 2 diabetes and lipid metabolism (191), and with the upstream transcription factor *usf1s2* G/A SNP (192), which is associated with familial combined hyperlipidemia and atherosclerosis (193, 194).

Another interesting candidate gene for fatty liver is the

circadian locomotor output cycles protein kaput (CLOCK) gene. *Clock* mutant mice display hyperphagia, obesity, the metabolic syndrome, and hepatic steatosis. In agreement with the animal data, in humans, SNPs in the CLOCK gene are associated with fatty liver and histological severity of liver damage (195). Furthermore, the phosphatidyl-ethanolamine N-methyl-transferase gene (*PEMT*) catalyzing hepatic *de novo* synthesis of phosphatidylcholine (196) may be involved in the regulation of fat accumulation in the liver in humans. *PEMT* knockout mice develop fatty liver under a choline-deficient diet (197), and in humans a functional SNP (V175M) is associated with fatty liver (198).

In summary, the genetic effects observed so far are rather small. Once available genome-wide association studies, similar to those that occurred in the field of type 2 diabetes (199) and atherosclerosis (200), may reveal new and possibly more important genes. Such efforts, however, are still limited by the relatively small existing databases containing precise measurements of liver fat and information about the diagnosis of NASH.

IV. Metabolic Consequences of Fatty Liver

A. Dyslipidemia

It has been shown convincingly that fatty liver is associated with insulin resistance, atherosclerosis, and the metabolic syndrome (15, 44, 49, 201–204). Furthermore, fatty liver predicts future cardiovascular events (3, 201). It is thought that a pro-atherogenic serum lipid profile, which is commonly observed in subjects with fatty liver, is in part responsible for these relationships. This profile consists of low HDL cholesterol and high triglyceride levels, small, dense LDL particles, and high apolipoprotein B100 levels (4, 78, 205–208). An increased rate of hepatic triglyceride synthesis and VLDL particle production, which secondarily results in low HDL cholesterol and increased LDL particle density (78, 209, 210), is considered to be causative for this type of dyslipidemia. Furthermore, a decrease in lipoprotein lipase activity may also be involved (211, 212). Although there is evidence that insulin resistance is a strong underlying mechanism for this dyslipidemia (78, 207, 209, 210, 213–215), other studies suggest that fat accumulation in the liver may also have an independent effect on dyslipidemia. In the study by Toledo *et al.* (206), plasma insulin was higher in subjects with steatosis compared with controls, but insulin was much weaker correlated with serum triglycerides than hepatic steatosis. However, in that study hepatic insulin resistance was not measured, leaving the question open whether liver fat correlated with triglycerides also independent of hepatic insulin resistance. Regarding HDL, not only quantitative, but also qualitative and compositional alterations are related to its antiatherogenic properties (216–219). Circulating HDL₂ was particularly found to protect from atherosclerosis (220, 221). We could recently show that fatty liver correlates more strongly with circulating HDL₂ and the HDL₂/HDL₃ ratio than with total HDL (222). Moreover, the correlation of liver fat with HDL₂ and the HDL₂/HDL₃ ratio remains statistically significant even after adjustment for whole-body insulin resistance and circulating adiponectin that is associated

with both dyslipidemia and liver fat (64, 65). In agreement with the data from Toledo *et al.* (206) and with the limitation that hepatic insulin resistance was not directly measured, these findings suggest that there may be a direct link between fatty liver, dyslipidemia, and thus atherosclerosis.

B. Inflammation

Besides its metabolic functions, the liver is involved in immune responses (47, 223). Although the hepatocytes represent approximately two thirds of the total cells in the liver, other cell types are biliary epithelial cells, sinusoidal endothelial cells, Kupffer cells, stellate cells, dendritic cells, and lymphocytes (224, 225). The Kupffer cells and lymphocytes are the main cell types involved in the hepatic immune response. Kupffer cells represent the largest group of fixed macrophages in the body and account for about 20% of nonparenchymal cells in the liver (226). They are derived from circulating monocytes that arise from bone marrow progenitors (227). In the liver, Kupffer cells clear endotoxins (lipopolysaccharides) from the passing blood, and phagocyte debris and microorganisms. Furthermore, they are in close contact with blood lymphocytes and other resident antigen-presenting cells.

Kupffer cells produce cytokines that play a key role in cell differentiation and cell proliferation. This process is modulated by the membrane-bound bile acid receptor TGR5/mBAR (228). Kupffer cell-derived IL-12 and IL-18, for example, regulate natural killer (NK) cell differentiation and promote the local expansion of cytotoxic NK cell subpopulations that express large amounts of antiviral interferon (IFN)- γ (229). Other Kupffer cell-derived cytokines such as IL-1 β , IL-6, TNF- α , and leukotrienes promote the infiltration and antimicrobial activity of neutrophils (230). Because NK T cells are capable of releasing IFN- γ and IL-4 (231), they are thought to modulate the local and systemic adaptive immune responses to either a proinflammatory type I (IFN- γ , TNF- α) or an antiinflammatory type II (IL-4, IL-10, IL-13) profile (224, 225). The increased production of TNF- α is considered to have a particularly major role in the pathogenesis of hepatic insulin resistance (232, 233).

In this aspect, the gastrointestinal tract may be important for hepatic inflammation and the pathophysiology of NASH. This is supported by data from animal studies (234) and from jejunoileal bypass surgery for morbid obesity in humans showing that NASH and fibrosis are encountered as a complication of this procedure (235, 236). Furthermore, small intestinal bacterial overgrowth was more frequently found in patients with NASH than in controls (237). Such derangement of the gut flora, which plays an important role in the prevention and treatment of infections as well as in immune functions, is also thought to be mediated by the consumption of manipulated and processed foods, *e.g.*, high amounts of refined sugar and saturated fat and a decrease in fiber, vitamins, and antioxidants (238). Small intestinal bacterial overgrowth results in the production of ethanol in animals (239) and humans (240–242) as well as in the release of bacterial lipopolysaccharides (243). Both ethanol and lipopolysaccharides activate TNF- α production in Kupffer cells, thereby, inducing hepatic inflammation (244). In agreement

with this hypothesis, antibiotics (245) and probiotics (246) targeting the gut flora positively affect hepatic inflammation in animals as well as in humans (235, 247).

Furthermore, hepatic inflammation is induced by hepatic steatosis. Hotamisligil (47) and Shoelson *et al.* (223) hypothesize that hepatic steatosis might induce a subacute inflammatory response in liver that is similar to the adipose tissue inflammation, after adipocyte lipid accumulation. Part of this process is considered to be attributed to endoplasmic reticulum (ER) and oxidative stress. The ER is a membranous network responsible for the processing and folding of newly synthesized proteins. Besides hypoxia, toxins, infections, and other insults, nutrient fluctuations and excess lipids pose stress on the ER that is accompanied by accumulation of unfolded or misfolded proteins (248). ER stress in liver and adipose tissue is generated in mice with genetic or diet-induced forms of obesity. This is largely mediated by activation of JNK resulting in impairment of insulin signaling (249). Furthermore, ER stress is associated with activation of multiple stress responses and with the specific activation of CREBP, a hepatocyte-specific bZip transcription factor that may have an important role in hepatic acute-phase response such as the induction of transcription of the serum amyloid P-component and C-reactive protein (CRP) genes (250).

In addition, the ER is involved in the generation of ROS and, consequently, oxidative stress (251). Furthermore, ROS are formed in the mitochondria by impaired mitochondrial respiratory chain capacity. Particularly an increase in cytosolic fatty acids results in increased fatty acid oxidation and, thus, ROS production (252, 253). In agreement, in humans with NASH, increased levels of by-products of lipid peroxidation are found, suggesting increased oxidative stress (254). Finally, under conditions of oxidative stress, NF- κ B and JNK pathways are activated, representing a link between oxidative stress and insulin resistance (47, 223, 255).

Altogether, the close interaction of immune cells with the metabolically active hepatocytes (47, 223) may trigger local but also systemic subclinical inflammation, a process that is strongly regulated by PPAR α (256). Systemic subclinical inflammation can be estimated by measurement of circulating CRP. The plasma levels of this acute-phase protein are very low under healthy conditions but increase in response to a pathological inflammatory process. Because of its relatively low half-life of 18 h, CRP represents a useful, early nonspecific marker of inflammation (257). Plasma CRP is produced predominantly by hepatocytes and is under transcriptional control by IL-6 and other proinflammatory cytokines. However, other sites of local CRP synthesis and possibly secretion have also been suggested (258). Circulating CRP is positively correlated with liver fat (259–262). Moreover, CRP levels are higher in patients with histologically proven NASH compared with simple steatosis (262). Of interest, circulating CRP most probably is not merely an indicator of systemic inflammation but is also involved in the pathogenesis of atherosclerosis (257). These data suggest that fat accumulation in the liver may be involved in the pathophysiology of atherosclerosis via induction of systemic inflammation.

C. Insulin resistance

Fatty liver and obesity are strongly associated with insulin resistance (263, 264), the condition that plays a predominant role in the pathophysiology of type 2 diabetes (47, 255, 264–266) and cardiovascular disease (67, 267–270). Animal studies reveal that fat accumulation in the liver inhibits insulin signaling in hepatocytes. In particular, hepatic insulin resistance can be attributed to impaired insulin-stimulated insulin receptor substrate (IRS)-1 and IRS-2 tyrosine phosphorylation resulting in increased gluconeogenesis (263, 271, 272). In humans, a strong relationship exists between fat accumulation in the liver and whole-body insulin resistance (4, 71, 80, 106, 146, 190, 273–285) (Fig. 3). More importantly, liver fat correlates with insulin resistance independent of visceral adiposity (147, 286), a major regulator of both liver fat and insulin resistance (77, 287). Euglycemic, hyperinsulinemic clamp studies with tracer methods to measure the suppression of endogenous glucose production, an estimate of hepatic insulin sensitivity, show that liver fat is particularly strongly correlated with hepatic insulin sensitivity (41, 106, 147, 280, 288, 289).

Interestingly, hepatic steatosis is also associated with myocardial insulin resistance. In patients with type 2 diabetes, liver fat measured by $^1\text{H-MRS}$ is the strongest predictor of insulin-stimulated myocardial glucose uptake, compared with other determinants such as visceral fat mass and whole-body glucose uptake (290). Moreover, liver fat is also strongly associated with myocardial perfusion, which is affected by coronary artery function (290). It needs to be determined whether fat accumulation in the liver induces myocardial insulin resistance via humoral mechanisms, as recently discussed (291), and/or mainly reflects myocardial steatosis and abnormal cardiac metabolism, parameters that strongly correlate with liver fat content (292).

It has not been determined whether fatty liver is mainly a result of insulin resistance of adipose tissue and skeletal muscle or whether fatty liver may also develop independent of the aforementioned conditions. Animal studies provided the first evidence that the latter could also be the case. Insulin resistance can be induced *in vivo* by overexpression of suppressor of cytokine signaling (SOCS)-1 or -3 in liver (293). SOCS proteins attenuate insulin signaling by binding to the insulin receptor and reducing its ability to phosphorylate IRS proteins (294–296). This hepatic overexpression of SOCS proteins is associated with an increase in SREBP-1c and hepatic steatosis (293). Conversely, suppression of SOCS-1, SOCS-3, or both in liver partially rescues impaired insulin sensitivity and ameliorates hyperinsulinemia in diabetic *db/db* mice. More importantly, suppression of SOCS proteins, especially SOCS-3, markedly improves hepatic steatosis. In summary, these findings suggest that fatty liver may also develop by alteration of hepatic insulin signaling and/or by direct effects of SOCS proteins on SREBP-1c in the liver (293, 297, 298). Thus, fatty liver may develop independent of skeletal muscle and adipose tissue insulin resistance.

Furthermore, there are human data showing that fatty liver may even have a primary role in the pathophysiology of skeletal muscle insulin resistance. In patients with type 2 diabetes, the PPAR γ agonist rosiglitazone, as well as met-

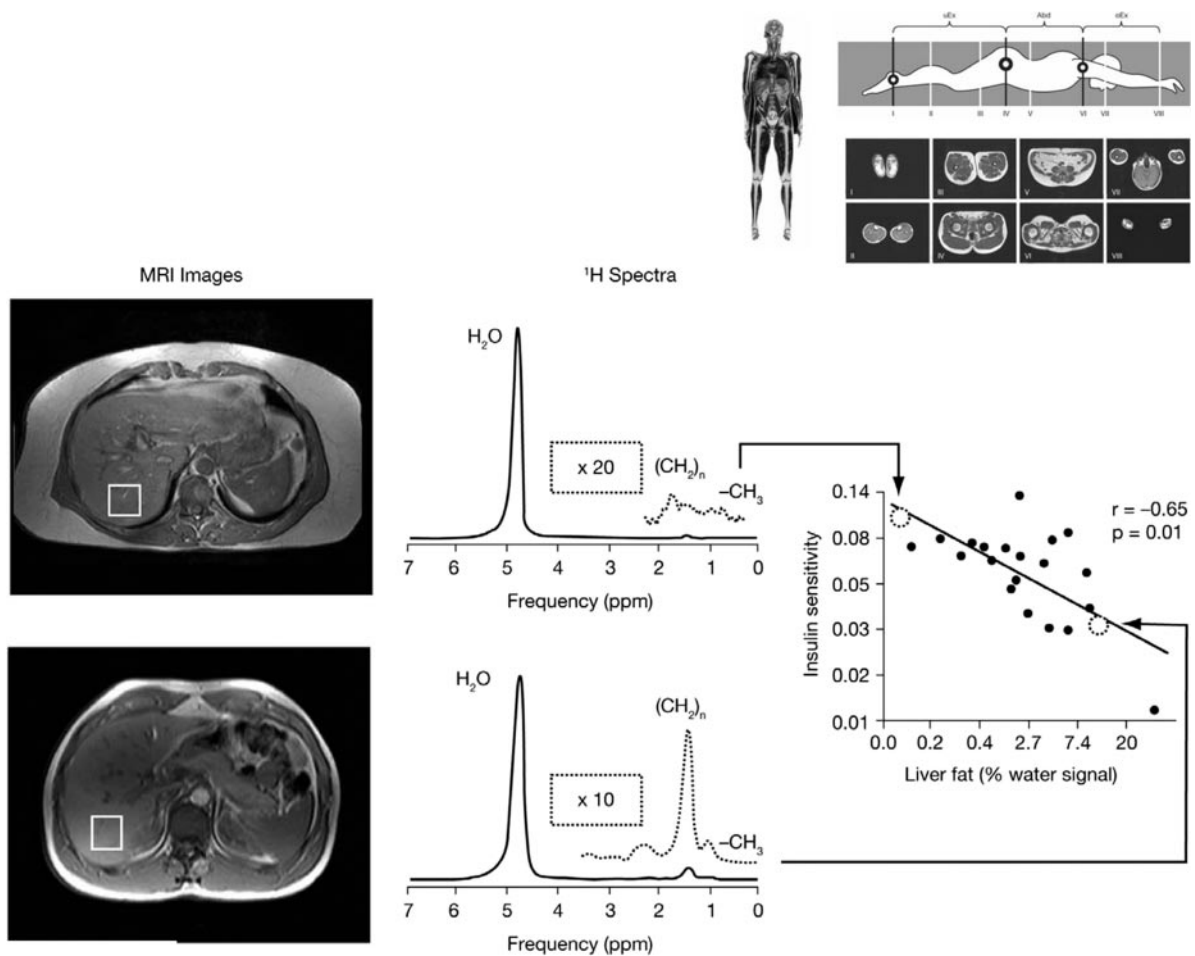


FIG. 3. Relationship of liver fat, measured by ^1H -MRS, to insulin sensitivity. Liver fat content was quantified by localized ^1H -MRS using a 1.5-T whole-body imager. Although there is no clear difference in gray shade in the liver between the individuals, the signal from the ^1H -MRS shows that liver fat content is obviously different. These two individuals also behaved differently when insulin sensitivity was measured during the euglycemic-hyperinsulinemic clamp. The individual with higher liver fat content had lower insulin sensitivity. To correct this relationship for the confounding factors total body fat and body fat compartments, whole-body MR imaging for quantification of these parameters (*inset*) is a precise technique. [Adapted from N. Stefan *et al.*: *Horm Res* 64(Suppl 3):38–44 (285), with permission from S. Karger AG.]

formin, increases hepatic insulin sensitivity via activation of AMPK (299). However, a decrease in liver fat is only seen in subjects receiving thiazolidinediones. More importantly, insulin sensitivity of glucose disposal increases only in the thiazolidinedione group (300). Because skeletal muscle is not a major target of PPAR γ action (301), these data support the notion that the increase in skeletal muscle insulin sensitivity in the thiazolidinedione group may be mediated by the decrease in liver fat.

A study by Hwang *et al.* (289), with quantification of fat in liver and skeletal muscle by ^1H -MRS and measurement of visceral fat by MRT and of endogenous glucose production and insulin sensitivity of glucose disposal by tracer methods, further supports a role of hepatic fat accumulation in the pathophysiology of skeletal muscle insulin resistance. In that study, the negative correlation between liver fat content and skeletal muscle insulin sensitivity is exceptionally tight (289). The authors discuss the fact that their data, together with previous studies (302–304), suggest that the liver releases factors that regulate insulin sensitivity in skeletal muscle.

Fetuin-A [former name for the human protein, α_2 -Heremans-Schmid glycoprotein (AHSG)] may represent one of these factors. Fetuin-A is predominantly expressed in the liver, and to a lesser degree in the placenta and the tongue (305). Because placental expression is only relevant during pregnancy and the tongue is not an organ with endocrine activity, the liver is the only organ regulating circulating fetuin-A levels. This protein is a natural inhibitor of the insulin receptor tyrosine kinase in liver and skeletal muscle (306–310). Furthermore, mice deficient for the gene encoding fetuin-A display improved insulin signaling (311), suggesting that fetuin-A may play a major role in the regulation of insulin sensitivity in animals. In humans, SNPs in the fetuin-A gene (*AHSG*) are associated with type 2 diabetes (312). However, the role of this protein in the natural history of type 2 diabetes was unknown for a long time. Of note, severe liver damage as in cirrhosis, acute viral hepatitis, and cancer is associated with a decrease and not an increase in circulating fetuin-A (313). Thus, no liver dysfunction was known to be associated with elevated fetuin-A production in humans. Recently, fetuin-A mRNA expression was found to be in-

creased in fatty liver in mice (281), which is in agreement with previous data from rats (314). In addition, circulating fetuin-A correlates positively with liver fat in humans in cross-sectional and longitudinal analyses. Circulating fetuin-A also correlates negatively with insulin sensitivity (281, 315). Moreover, high fetuin-A plasma levels predict change in insulin sensitivity, measured by the euglycemic, hyperinsulinemic clamp in prospective analyses (281) and are associated with incident type 2 diabetes (316, 317). In agreement with the notion that circulating fetuin-A is increased in fatty liver and insulin resistance, plasma fetuin-A is associated with the metabolic syndrome and correlates positively with CRP levels (316). Furthermore, fetuin-A promotes cytokine expression in monocytes and adipocytes and represses the production of the insulin-sensitizing adipokine adiponectin (317). Thus, these data support the hypothesis that fetuin-A may be one of the factors that mediate effects of fatty liver to other tissues. Such factors may be referred to as “hepatokines.”

Another protein that is preferentially produced by the liver is FGF21 (318). It has beneficial effects on lipid metabolism, as well as insulin sensitivity and pancreatic β -cell function (319–321). These effects of FGF21 on metabolism in animal models are not accompanied by changes in body weight (319). This finding is interesting because a profound synergy between the effects of FGF21 and the thiazolidinedione rosiglitazone, which induces weight gain, exists in stimulating glucose uptake in 3T3-L1 adipocytes (322). In addition, FGF21 regulates hepatic steatosis. FGF21 expression in the liver in the fasted state is induced by PPAR α . Accordingly, FGF21 expression in the livers of fasted mice is absent in PPAR α -deficient animals. These animals have fatty liver and serum hypertriglyceridemia (323–326). Furthermore, a decrease in endogenous FGF21 expression by RNA interference induces fatty liver and hyperlipidemia (323). So far, there is little information on the relationship of FGF21 with metabolic traits in humans. In a cross-sectional study in 200 subjects, circulating FGF21 levels correlated positively with components of the metabolic syndrome, but not with insulin sensitivity estimated from fasting serum glucose and insulin levels, independent of obesity (327). Whether hepatic FGF21 expression and production are affected by hepatic steatosis needs to be investigated.

Another very interesting protein, retinol binding protein 4 (RBP4), is expressed in adipose tissue and in the liver and is secreted into circulation (328). The first evidence that RBP4 has major effects on metabolism was found in adipose-specific knockout of glucose transporter 4 mice (329) that display insulin resistance in skeletal muscle, liver, and adipose tissue (330). In these animals, expression of *Rbp4* in adipose tissue and serum RBP4 levels are increased. In addition, increase in serum RBP4 concentrations by transgenic overexpression or by injection of purified RBP4 protein into wild-type mice causes insulin resistance (329). Furthermore, *Rbp4* knockout mice display enhanced insulin sensitivity, and lowering of serum RBP4 with the synthetic retinoid fenretinide improves insulin sensitivity and glucose tolerance in mice on a high-fat diet (329). Moreover, in humans high circulating RBP4 is associated with insulin resistance in cross-sectional studies (331–336). In addition, a strong relationship between changes in circulating RBP4 and insulin

sensitivity is shown in longitudinal studies (331, 333). Recent data suggest that the elevated circulating RBP4 in insulin-resistant states is a result of increased production from the increased visceral fat mass (332), as well as fatty liver (333).

Altogether, there is strong support to show that fatty liver produces humoral factors affecting insulin signaling in insulin-responsive tissues. Thus, further efforts are warranted to identify these hepatokines.

D. Dissociation of fatty liver and insulin resistance

Although hepatic fat accumulation, both in animals and in humans, is strongly associated with a decrease in insulin sensitivity, a large variability in this relationship exists that cannot be explained by other parameters regulating insulin sensitivity such as overall obesity, body fat distribution, or circulating adipokines. In other words, for the same amount of hepatic steatosis, subjects can be identified who have very high and very low insulin resistance (Fig. 4), suggesting that a dissociation of fatty liver and insulin resistance exists. The paradox of this finding may be due to lipotoxicity. This term was mainly devised by Roger Unger to describe the deleterious effects of lipid accumulation in various tissues (75, 337). According to this concept, triglycerides are probably the least toxic form in which the lipid excess can be stored in ectopic tissues, at least in the short term. The incorporation of fatty acids into triglycerides, as well as their oxidative degradation, thus represents protection from lipotoxicity. However, when these compensatory mechanisms are overwhelmed, fatty acids induce damage to cells resulting in impaired metabolism (75, 249, 337, 338) (Fig. 5).

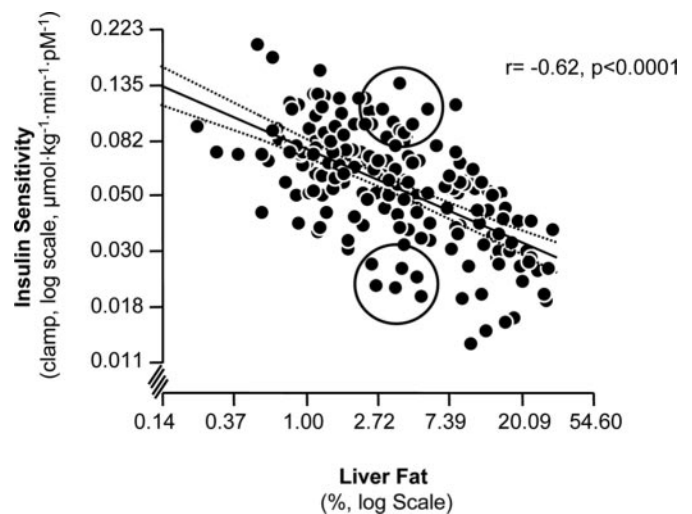


FIG. 4. Variability in the relationship between liver fat and insulin sensitivity in humans. This image depicts the strong, negative relationship between liver fat measured by ^1H -MRS and insulin sensitivity measured by the euglycemic-hyperinsulinemic clamp in 200 individuals without type 2 diabetes (regression line and 95% confidence interval). For a very similar amount of liver fat, individuals can be identified who are relatively insulin sensitive (upper circle) and insulin resistant (lower circle). Major determinants of insulin sensitivity such as age, gender, total and visceral body fat mass measured by MRT, and intramyocellular fat in the tibialis anterior muscle, measured by ^1H -MRS, cannot explain this difference in insulin sensitivity.

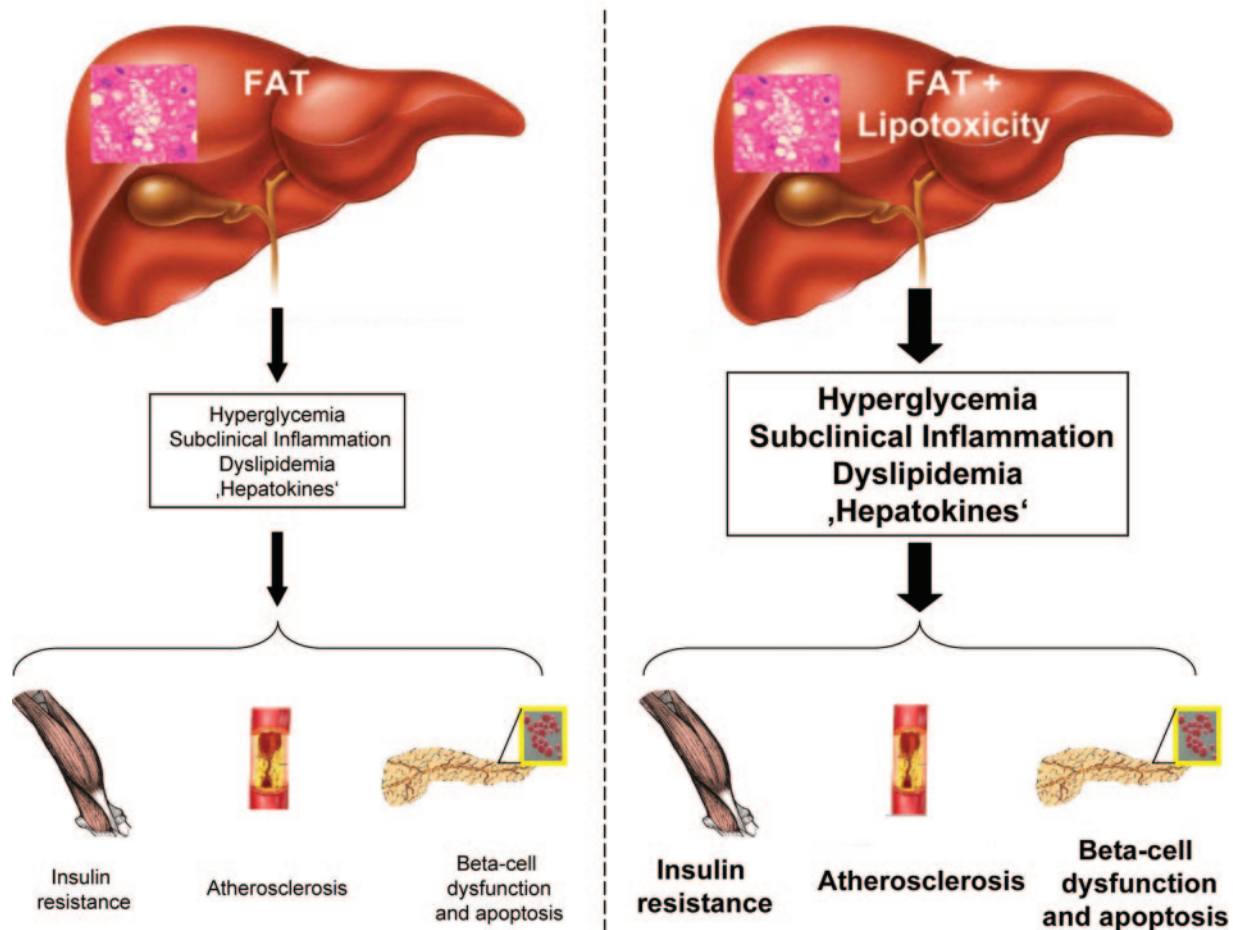


FIG. 5. Metabolic consequences of fatty liver. Fat accumulation in the liver induces hyperglycemia, subclinical inflammation, dyslipidemia, and the secretion of parameters that can be referred to as “hepatokines” (e.g., fetuin-A), thereby inducing insulin resistance, atherosclerosis, and possibly β -cell dysfunction and apoptosis. The degree of these conditions may be moderate [benign fatty liver (*left panel*)]. However, the same amount of hepatic fat accumulation may, by mechanisms that are yet not fully understood, be strongly associated with hepatic lipotoxicity, resulting in aggravation of hyperglycemia, subclinical inflammation, dyslipidemia, and an imbalance in hepatokine production as well as in their metabolic consequences. This state may be referred to as malignant fatty liver (*right panel*).

Several pathways are thought to be operative in this process. Among them, activation of NF- κ B and JNK pathways, as well as the Janus kinase-signal transducer and activator of transcription-3-SOCS-3 pathway, which are involved in insulin resistance (47, 223, 339), is critical. Cai *et al.* (59) elegantly showed that NF- κ B transcriptional targets are activated in liver by obesity and a high-fat diet. This is associated with a chronic state of subacute inflammation and insulin resistance. Inhibition of NF- κ B activation under a high-fat diet still results in hepatic steatosis; however, this intervention is not accompanied by insulin resistance (59). These findings indicate that fat accumulation in the liver leads to subacute hepatic inflammation through NF- κ B activation. In addition, under conditions of inhibited NF- κ B stimulation, fatty liver does not result in insulin resistance. In support of this hypothesis, liver-specific inactivation of the NF- κ B essential modulator gene in mice under a high-fat diet results in hepatic steatosis, but not in insulin resistance (340). The susceptibility to inflammatory responses may modulate the dissociation of fatty liver and insulin resistance. In this aspect, carriers of the $-1031C$ and $-863A$ variants of the SNPs

in the promoter region of the TNF- α gene (*TNF*) have high serum levels of the soluble TNF receptor 2, indicating elevated TNF- α production. Furthermore, they are insulin resistant and have steatohepatitis more frequently than simple steatosis (341). Similar results for other SNPs in *TNF* are reported elsewhere (342).

Another interesting animal model for the dissociation of fatty liver and insulin resistance is the liver-specific acyl:CoA:diacylglycerol acyltransferase 2 (DGAT2) transgene mouse (343). DGAT enzymes, among them particularly DGAT2, catalyze the final step of triacylglycerol biosynthesis (344). Liver-specific DGAT2 overexpressing mice develop hepatic steatosis with a 5-fold increase in liver triglyceride content compared with controls. However, this condition is not accompanied by whole-body or hepatic insulin resistance. In agreement with these novel findings, antisense oligonucleotide treatment targeting the DGAT2 gene reduces liver triglycerides in mice fed a high-fat diet, without improving insulin sensitivity or glucose tolerance (345). In another study, DGAT2 silencing also reduced hepatic steatosis, while insulin sensitivity improved as well. This finding,

however, may be attributable to an effect of DGAT2 silencing on decreasing body weight and epididymal fat pad mass (346). The mechanism for the dissociation of fatty liver and insulin resistance in this animal model is not fully understood. It may be that an increase in triglyceride synthesis protects from fatty acid-induced lipotoxicity. This hypothesis is supported by the finding that on a high-fat diet, activation of JNK and NF- κ B in DGAT2 transgenic mice is not increased compared with controls. Alternatively, the increase in unsaturated fatty acids, which are found in the tissue of these animals and are considered to be less lipotoxic compared with saturated fatty acids, may generate the phenotype.

Support for the involvement of the fatty acid pattern in the dissociation of fatty liver and insulin resistance is provided by another recently described animal model. Mice deficient for the elongation of long-chain fatty acids (*ELOVL*) gene (*Elovl6*) develop obesity and hepatic steatosis, but not insulin resistance, hyperinsulinemia, or hyperglycemia under a high-fat diet (339). *Elovl6* encodes for the enzyme ELOVL, catalyzing the conversion of palmitate (C 16:0) to stearate (C 18:0) as well as palmitoleate (C 16:1n-7) to vaccinate (C 18:1n-7), thus regulating the tissue fatty acid composition (347, 348). Interestingly, amelioration of hepatic insulin resistance in these animals cannot be explained by changes in energy balance or proinflammatory signals. However, a suppression of elongation and degradation of fatty acids, resulting in moderately increased hepatic triglyceride content, as well as a decrease in the diacylglycerol-protein kinase C ϵ pathway occurs (339). This observation is important because hepatic protein kinase C ϵ is involved in the development of hepatic insulin resistance (349). Although these animal data provide novel and mechanistic evidence for the existence of a dissociation of fatty liver and insulin resistance, human studies have not specifically addressed this interesting point. Based on the aforementioned findings in animals, we studied the relationship of a SNP in *DGAT2*, which is associated with obesity (350), with liver fat and insulin resistance in humans. In 200 subjects, the SNP in *DGAT2* is associated with changes in liver fat, but not insulin sensitivity during a lifestyle intervention (our 184), supporting the hypothesis that *DGAT2* may differentially affect liver fat and insulin sensitivity in humans, too.

V. Concluding Remarks

Although the roles of adipose tissue, and particularly VAT, in the pathophysiology of metabolic diseases such as type 2 diabetes, the metabolic syndrome, and atherosclerosis have been carefully studied, the impact of fatty liver in the natural history of these diseases has long been underestimated. With increasing evidence from transgenic and knockout animal models that hepatic steatosis is involved in several major pathways regulating glucose and lipid metabolism, fatty liver gained recognition in the metabolic field of research. This effect was accompanied by the identification of exciting novel targets to prevent and treat hepatic fat accumulation. Moreover, there is strong support indicating that different aspects of fatty liver exist and are associated with severe or merely moderate metabolic disturbances. Fi-

nally, similar to adipose tissue, liver under conditions of an increased lipid load may have important secretory functions, and in analogy to adipokines, hepatokines may become an interesting target for future research.

From a clinical aspect, prevention of ectopic fat deposition in liver, as well as in other insulin-sensitive tissues under conditions of a sedentary lifestyle, overnutrition, and disproportionate adipose tissue distribution, is the primary goal in the protection from obesity-induced insulin resistance. When such efforts are not very effective, targeting lipotoxicity, which appears to be the predominant mediator of metabolic consequences of fatty liver, seems to be an effective strategy to accomplish this mission.

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Address all correspondence and requests for reprints to: Hans-Ulrich Häring, M.D., Department of Internal Medicine, Otfried-Müller-Strasse 10, D-72076 Tübingen, Germany. E-mail: Hans-Ulrich.Haering@med.uni-tuebingen.de

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