Review

Peroxisome proliferator-activated receptor α **target genes**

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Abstract. Peroxisome proliferator-activated receptors (PPARs) are nuclear proteins that belong to the superfamily of nuclear hormone receptors. They mediate the effects of small lipophilic compounds such as long-chain fatty acids and their derivatives on transcription of genes commonly called PPAR target genes. Here we review the involvement of PPAR α in peroxisomal and mitochondrial

fatty acid oxidation, microsomal fatty acid hydroxylation, lipoprotein, bile and amino acid metabolism, glucose homeostasis, biotransformation, inflammation control, hepato-carcinogenesis and other pathways, through a detailed analysis of the different known or putative PPAR α target genes.

Key words. PPARa; transcriptional regulation; target genes; lipid metabolism; PPAR response element.

Introduction

Since they were discovered in the early 1990s, peroxisome proliferator-activated receptors (PPARs) have evolved from another member of the nuclear hormone receptor family to an extremely important set of targets for drug discovery. PPARs are ligand-induced transcription factors that regulate the transcription of target genes in response to specific ligands, both synthetic and endogenous. They recognize a well-defined sequence within the promoter region of target genes and bind to this sequence as a heterodimer with the retinoid X receptor. Three different PPAR genes have been identified in many species, including mouse, rat, guinea pig, human, chicken, fish and amphibian [1–10]. The *PPAR*^a (NR1C1), $PPAR\beta/\delta$ (NR1C2) and $PPAR\gamma$ (NR1C3) genes encode proteins that share a highly conserved structure and molecular mode of action. Nevertheless, the array of genes regulated by each PPAR isotype are divergent and may also differ from one species to another, leading to regulation of distinct biological processes

[11]. The mechanism behind the specificity of regulation by each PPAR isotype is not exactly clear but reflects spatiotemporal expression levels between the different PPARs, as well as differential affinity for promoter elements [4, 12]. Of the three PPAR isotypes known to date, PPAR α has been the best characterized. Inasmuch as most of our knowledge about the biological function of PPAR α is directly coupled to the function of its target genes, the present review will disentangle the various biological effects of PPAR α through a detailed analysis of its target genes (fig. 1).

Similar to other PPARs, transcriptional regulation by PPAR α is achieved by its direct binding to specific nucleotidic sequences known as peroxisome proliferator response elements (PPREs), present in the promoter region of target genes, or sometimes in an intronic sequence of a gene [13–15]. PPREs share a common core sequence consisting of a direct repeat of the consensus sequence AGGTCA spaced by a single nucleotide, which allows the proper binding of $PPAR\alpha$ and its obligate partner the retinoid X receptor α RXR α (NR2B1). The presence of a functional PPRE within a promoter, which means that the PPRE is able to mediate $PPAR\alpha$ -induced

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Figure 1. Schematic representation of a hepatocyte with the diverse functions of PPAR α illustrated. Known target genes of PPAR α are shown within brackets.

transactivation, appears to be the best criterion to classify a gene as a PPAR α target gene (table 1). In addition to upregulating gene expression, $PPAR\alpha$ is also capable of negatively modulating gene expression. We will discuss the diverse molecular mechanisms responsible for this trans-repression.

PPAR^a **expression profile**

To regulate a target gene, an obligatory coexpression pattern of PPAR α and its target gene is required. In rodents, PPAR α is highly expressed in liver, where it is present mainly in parenchymal cells, while endothelial, Kupffer and stellate cells do not seem to express any $PPAR\alpha$ messenger RNA (mRNA) [16–18]. In addition, PPAR α is relatively well expressed in heart, kidney, intestinal mucosa, skeletal muscle and brown fat, which are all tissues characterized by a relatively high rate of fatty acid catabolism [4, 12, 19–21]. Moreover, different groups have reported the presence of $PPAR\alpha$ mRNA in immune cells such as monocytes/macrophages, as well as T and B cells [22–30]. Finally, PPAR α expression was detected in human vascular wall cells such as smooth muscle and endothelial cells as well as in atherosclerotic lesions [23, $31 - 34$].

Regulation of PPAR^a **activity by natural and synthetic agonists**

PPAR α can be activated by both endogenous and synthetic ligands. Briefly, long-chain polyunsaturated fatty acids and eicosanoids such as the inflammatory mediator leukotriene B4, the hydroxyeicosatetraenoic acids and the prostaglandins D1 and D2 are among the best natural PPAR α ligands [35–38]. Endogenous ligand-activation of PPAR α is believed to occur primarily during fasting as large amounts of free fatty acids enter the blood plasma [39, 40]. However, dietary intake of specific fatty acids can also lead to a potent activation of PPAR α [41]. In addition to a host of endogenous ligands, $PPAR\alpha$ is also the molecular target for fibrates, which are synthetic PPAR α agonists that include gemfibrozil, bezafibrate, clofibrate and fenofibrate. These molecules are used to treat dyslipidemia and cardiovascular disease and are becoming increasingly popular as a combination treatment with statins [13, 14, 42].

PPAR^a **and cellular proliferation**

As indicated by their name, peroxisome proliferators, which are synthetic PPAR α agonists, cause peroxisome as well as hepatocyte proliferation in rodent but not human liver. Rather than reflecting the physiological funcTable 1. List of PPAR α regulated genes with at least one functional PPRE identified within the promoter sequence.

Cytosolic fatty acid [57] mouse fatty acid binding/ $>$? > > [193] binding protein transport

(L-FABP)

PPRE, peroxisome proliferator response element; WT, wild-type mouse; KO, PPAR α null mice; \approx , similar gene expression between the two genotypes; $>$, higher gene expression in wild-type mice; \lt , lower gene expression in wild-type mice; ?, no information available; (ϑ) , a mutant-inactive form of PPAR α mRNA remains detectable in the mutant PPAR α null mice [46]; \clubsuit , our unpublished data or Zandbergen et al., unpublished; (Φ), Kersten et al. and Aoyama et al. reported different results [39, 63]; \notin , several groups reported on different conclusions [133, our own unpublished data].

tion of PPAR α , induction of hepatocyte proliferation may be a toxicological and/or a pharmacological effect of $PPAR\alpha$ activation. Hepatocellular proliferation induced by a partial hepatectomy is an effective alternative way to study the role of PPAR α in liver cell proliferation. Anderson et al. reported that following partial hepatectomy, $PPAR\alpha$ null mice display an impairment in liver regeneration, together with a delay of maximal expression of *cyclin-D1* and *c-myc* genes [43]. Feeding wild-type mice a $PPAR\alpha$ agonist increased cyclin-D1, cyclin-dependentkinase 1 (CDK-1), CDK-4 and *c-myc* expression, suggesting their direct regulation by $PPAR\alpha$. In contrast, Rao et al. found no difference in hepatic levels of mRNAs encoding CDK1, CDK2, CDK4, PCNA, cyclin D1 and B1 between the two genotypes as well as no significant dif-

(apo-CIII) bolism

ference in replicative DNA synthesis [44]. Thus, the precise role of PPAR α in liver cell proliferation following hepatectomy remains ambiguous.

Whereas rodents show dramatic peroxisome proliferation and develop liver tumors upon exposure to $PPAR\alpha$ agonists, the same is not true in humans and monkeys, and is less pronounced in hamsters [45, 46]. By using PPAR α null mice, it was shown that peroxisome proliferation and the appearance of tumors were PPAR α dependent [46]. The differential response to peroxisome proliferators between primates and rodents may be due to a difference in basal expression of PPAR α between the two species [47]. Hepatic PPAR α expression is much lower in humans than in rodents. However, using human hepatoma HepG2 cells that were engineered to express human PPAR α at con-

centrations similar to mouse liver, known mouse hepatic PPAR α targets did not change expression [48, 49]. Thus, the difference in hepatic $PPAR\alpha$ level between humans and rodents may not explain per se why humans are refractory to peroxisome and hepatocyte proliferation. The mechanism behind the hepatoproliferative effect of PPAR α agonists may involve Kupffer cells, possibly via mechanisms involving an increase in superoxide, activation of nuclear factor-kappa B ($NF - \kappa B$) and production of tumor necrosis factor-alpha (TNF α). However, Kupffer cells do not express $PPAR\alpha$, whereas hepatocytes do, consistent with the hypothesis that hepatocytes respond to Kupffer cell-derived TNF α via mechanisms dependent on hepatocyte PPAR α [16–18]. Besides stimulating cellular proliferation, hepatic $PPAR\alpha$ also mediates the peroxisome proliferator-induced suppression of apoptosis. Hepatocytes that were transfected with a dominant-negative form of PPAR α , as well as hepatocytes from PPAR α null mice, did not display any decrease in apoptosis by peroxisome proliferators, in contrast to wild-type hepatocytes. Thus, PPAR α combines positive regulation of cellular hepatocyte proliferation with suppression of apoptosis.

PPAR^a **and fatty acid oxidation**

A functional link between fatty acid oxidation and PPAR α was first established in 1992, when it was shown that the peroxisomal acyl-coenzyme A (CoA) oxidase gene, which is involved in peroxisomal fatty acid β -oxidation, is regulated by PPAR α [2]. Since then, numerous genes involved in hepatic fatty acid catabolism were shown to be induced by peroxisome proliferators and PPAR α .

Hepatic fatty acid catabolism consists of several distinct pathways. First, free fatty acids that are generated by adipose tissue lipolysis are taken up from the blood plasma by the liver, where they are activated into their fatty acyl-CoA derivatives. The activated fatty acyl-CoAs are subsequently taken up into the mitochondria or peroxisomes for degradation to acetyl-CoA via β -oxidation. Major differences exist between peroxisomal and mitochondrial fatty acid β -oxidation. Whereas mitochondria oxidize short-, medium- and mostly long-chain fatty acids, peroxisomes oxidize some long-chain but mostly very long chain fatty acids. Both pathways are regulated by PPAR α .

PPAR^a **and cellular fatty acid uptake**

The first step required for oxidation of fatty acids is their transport across the cell membrane. The fatty-acid transport protein-1 gene, which is involved in uptake of longchain fatty acids and oxidized low-density lipoproteins,

was identified as a direct $PPAR\alpha$ target gene with a functional PPRE in its promoter [50, 51]. A functional PPRE was also initially identified in the proximal promoter of the fatty acid translocase (FAT/CD36) gene [52]. Nevertheless, further studies performed by the same group failed to confirm the direct induction of FAT via this PPRE [53]. It was argued that induction by PPAR α ligands probably goes through the distal promoter region of the gene even though no PPRE could be identified. Thus, the mechanism by which PPAR α regulates FAT transcription remains unclear.

Fatty acids per se are inactive molecules that cannot be further metabolized without an obligatory activation step into their fatty acyl-CoA derivatives. The activation step, which is carried out at several intracellular localizations, is under the control of the long-chain fatty acyl-CoA synthetases, whose transcriptional rate is controlled by PPAR α in the liver and by PPAR γ in fat tissue, through a functional PPRE [50, 54]. Thus, PPAR α promotes both fatty acid transport across the cell membrane as well as their activation into a metabolic active form that serves as the substrate for further metabolism.

PPAR^a **and intracellular fatty acid transport**

Different lipid-binding proteins involved in the process of intracellular lipid trafficking have been identified, including keratinocyte (FABP-5), cardiac (FABP-3), hepatic (FABP-1), muscular (FABP-3), brain (FABP-7) and adipocyte fatty acid binding protein (also known as A-FABP, aP2 or FABP-4). One of the functions proposed for these proteins is to serve as a shuttle for fatty acids between the plasma membrane and the nucleus, and selectively enhance the activities of specific PPARs [55, 56]. Interestingly, liver fatty acid binding protein was shown to be upregulated by bezafibrate and fatty acids in a PPAR α -dependent fashion, through a functional PPRE located in the proximal promoter [57]. In contrast, in the small intestine the PPAR β isotype seems to be the relevant PPAR involved in the transcriptional regulation of liver fatty acid binding protein (FABP-2) [57]. This differential regulation might be due to a different relative abundance of PPAR α between the two tissues [4, 12].

A functional intronic PPRE was also localized in both mouse and human versions of the gene for acyl-CoA binding protein, while another PPRE present in the promoter of acyl-CoA binding protein appears to be nonfunctional [58, 59]. Acyl-CoA binding protein specifically binds acyl-CoA esters with high affinity and is believed to efficiently prevent acyl-CoA esters hydrolysis by thioesterases. Therefore, by lowering the concentration of free acyl-CoA ester, upregulation of acyl-CoA binding protein by $PPAR\alpha$ may relieve acyl-CoA inhibition of long-chain fatty acid synthetases.

PPAR^a **and mitochondrial fatty acid uptake**

The mitochondrial oxidation of fatty acids starts with the translocation of activated long-chain fatty acids into the matrix of mitochondria. The transport across the outer mitochondrial membrane is performed by two isotypes of the carnitine palmitoyltransferase (CPT) enzyme I, CPT-I α and CPT-I β . CPTI- α and - β are encoded by two different genes and are considered to catalyze the rate-limiting step in mitochondrial fatty acid β -oxidation [60–62]. The highest expression level of CPT-I α is found in heart, liver and pancreatic β cells, whereas CPT-I β (also called muscle CPT-I) is predominantly expressed in adipose tissue, testis, heart and skeletal muscle. Both were identified as direct positive PPAR α -regulated genes through a functional PPRE present in their respective promoters [60–64]. Whereas long-chain fatty acids but not longchain fatty acyl-CoA esters induce CPT-I α expression in a PPAR α -independent manner via elements localized in the first intron of the gene, induction of CPT-1 α by clofibrate is highly PPAR α dependent [65]. This finding suggests that dietary fatty acids and hypolipidemic drugs modulate CPT-I α expression via different pathways.

Malonyl-CoA is considered as the major physiological allosteric inhibitor of CPT-I. Interestingly, cardiac and likely skeletal malonyl-CoA decarboxylase, which degrade malonyl-CoA to acetyl-CoA, are also PPAR α regulated [66, 67]. In contrast, in the same study expression of acetyl-CoA carboxylase, which synthesizes malonyl-CoA from acetyl-CoA, was not changed between wildtype and PPAR α mutant mice [67]. Thus, aside from upregulating transcription of CPT-I, PPAR α may increase CPT-1 activity by inducing the degradation of natural inhibitors of CPT-1 via regulation of malonyl-CoA decarboxylase.

While CPT-I is localized in the outer mitochondrial membrane, CPT-II, which catalyzes the conversion of acylcarnitine to acyl-CoA, is restricted to the inner mitochondria membrane. Expression of CPT-II was found to be upregulated significantly in response to the PPAR α agonist WY14643 in a PPARa-dependent manner in heart, liver and kidney. In accordance with these observations, a partially conserved PPRE was found within the CPT-II promoter that confers responsiveness to PPAR α ligands [68].

PPAR α and mitochondrial fatty acid β -oxidation

Besides regulating the translocation of fatty acids into the mitochondria, PPAR α also regulates the expression of genes involved in mitochondrial β -oxidation. The short-, medium-, long- and very long chain acyl-CoA dehydrogenase genes encode four different chain-length-specific enzymes that catalyze the first step in mitochondrial fatty acid β -oxidation. A basal PPAR α -dependent regulation was found for all of these genes. Nevertheless, so far a functional PPRE has only been identified for the medium-chain acyl-CoA dehydrogenase gene, yet such a PPRE is most likely present in the promoter region of the other dehydrogenase genes as well [69, table 2]. Using microarray, expression of dodecenoly-CoA δ -isomerase (also known as 3-*cis*-2-*trans*-enoyl-CoA isomerase) and 3-hydroxyacyl-CoA dehydrogenase, which are also involved in the mitochondrial β -oxidation of unsaturated and saturated fatty acids, was found to be decreased in fasted PPAR α null mice, but no PPRE has yet been identified [F. Zandbergen et al., unpublished].

PPAR^a **and peroxisomal fatty acid uptake**

The adrenoleukodystrophy-related genes ABCD2 (ALDR) and ABCD3 (PMP70) encode for ATP-binding cassette half-transporters located in the peroxisomal membrane, whose precise functions are unknown [70, 71]. Expression of both genes was found to be $PPAR\alpha$ dependent and highly sensitive to PPAR α agonists [70]. However, no functional PPRE that may trigger this induction has been identified in 2 kb of the rat ABCD2 proximal promoter, suggesting the possible existence of such a sequence far upstream from the initiation start site of the gene or a more complex mechanism for $PPAR\alpha$ dependent ABCD2 gene regulation. No promoter study for the ABCD3 gene has been reported yet.

PPAR α and peroxisomal fatty acid β -oxidation

Peroxisomes carry out the oxidation of very long chain polyunsaturated fatty acids. The enzyme that catalyzes the first and rate-limiting step in this process is a marker of peroxisome proliferator action, e.g. acyl-CoA oxidase, which was the first direct PPAR α target identified [72]. Acyl-CoA oxidase is a flavoenzyme that introduces a double bond between the α and β carbons of acyl-CoA, generating enoyl-CoA. Acyl-CoA oxidase also transfers electrons to oxygen-producing hydrogen peroxide, H_2O_2 , a product that will be further converted to water and oxygen by catalase. Next, enoyl-CoA hydratase adds water to the double bond of enoyl-CoA, producing hydroxyacyl-CoA. Hydroxyacyl-CoA dehydrogenase subsequently oxidizes the hydroxyacyl-CoA to ketoacyl-CoA and passes the hydrogen to NAD+. These two enzymatic activities exist on a single protein, known as the bifunctional enzyme (BIEN) or enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase. Three different PPREs have been identified in the promoter sequence of the BIEN gene, yet only one allows for efficient transactivation of the BIEN gene by PPAR α [73–78]. In the next step, thiolase cleaves the ketoacyl-CoA to form acetyl-CoA and

Table 2. List of PPAR α -dependent gene regulation (no functional PPRE reported yet).

Table 2 (continued)

Table 2 (continued)

>, higher gene expression in wild-type mice; <, lower expression in wild-type mice; \approx , similar gene expression between the two genotypes; WT, wild-type mouse; KO, knockout PPAR α mouse; †, expressed only in males; \ddagger , expressed only in females; (Σ) , Aoyama et al., and Kersten et al. reported conflicting results [39, 63].

an acyl-CoA shortened by two carbons. The gene encoding 3-ketoacyl-CoA thiolase (thiolase B) was found to be directly regulated by PPAR α [79]. However, it is unclear whether the DR-1 sequence identified within the thiolase B promoter mediates PPAR α transactivation [79]. Other putative targets of PPAR α are the long-chain acyl-CoA thioesterases, which catalyze the hydrolysis of acyl-CoAs into free fatty acids and CoA [80, 81]. Cytosolic, mitochondrial and to a lesser extend peroxisomal acyl-CoA thioestereases were upregulated during fasting in a PPAR α -dependent manner. In addition, PPAR α ligands strongly increased cytosolic and mitochondrial acyl-CoA thioesterase expression, suggesting the direct involvement of PPAR α . Finally, Lopez et al. reported that the sterol carrier protein X gene encoding a thiolase involved in the peroxisomal β -oxidation of branched-chain fatty acids was also directly regulated by $PPAR\alpha$ through two functional PPREs in rat, but whether the same is true in mice remains questionable [64, 82].

Hydrogen peroxide, a compound highly toxic for the cell, is generated by the reaction catalyzed by acyl-CoA oxidase. The enzyme catalase neutralizes hydrogen peroxide by causing its degradation into H_2O and O_2 . Interestingly, in vascular endothelial cells, expression of catalase was shown to be upregulated directly by the PPAR $\gamma/RXR\alpha$ heterodimer through a functional PPRE [83]. As a followup to these data, the possible regulation of catalase gene expression by PPAR α was also investigated. Neither primary mouse hepatocytes nor livers from rats treated with PPAR α activators displayed significant changes in the hepatic levels of catalase mRNA, whereas both catalase protein level and activity were increased [84–86]. In addition, no change in liver catalase mRNA was found between fed or fasted wild-type and $PPAR\alpha$ mutant mice, and ciprofibrate failed to induce a significant upregulation in catalase gene expression [64, 77]. This discrepancy between mRNA and protein is indicative of a posttranscriptional event. Besides, catalase, rat Cu/Zn superoxide dismutase, which protects the cell against oxidative stress by neutralizing superoxide radicals, was also identified as a direct PPAR α target [87]. Based on these data, a protective role of PPAR α against oxidative stress can be envisioned.

PPAR α **and microsomal** ω **-hydroxylation of fatty acids**

 ω -Hydroxylation is a process that occurs almost exclusively in smooth endoplasmic reticulum and represents a minor pathway of hepatic fatty acid catabolism under basal conditions. However, in pathophysiological conditions such as diabetes mellitus or fasting, ω -hydroxylation is enhanced. Fatty acid ω -hydroxylation is governed by a subfamily of cytochrome P450 4A (CYP4A) enzymes (CYP4A, 4B and 4F) expressed constitutively in liver and kidney [88]. PPAR α was shown to upregulate the expression of hepatic cytochrome P450 4A1 in rodents through a functional PPRE [40, 46, 77, 89, 90]. CYP4A3 was also found to be induced by $PPAR\alpha$, but no PPRE has yet been identified [77, 90]. Furthermore, three functional PPRE were localized in the rabbit promoter of the cytochrome P450 4A6-Z gene [91, 92]. Using microarray, we observed a dramatic fasting-induced $PPAR\alpha$ -dependent increase in liver Cyp4A10 expression [F. Zandbergen et al., unpublished].

In conclusion, from the above discussion it is clear that by regulating peroxisomal, mitochondrial and microsomal fatty acid oxidation in a coordinated manner, PPAR α serves as a master regulator of fatty acid catabolism.

PPAR^a **and ketogenesis**

During prolonged fasting, synthesis of ketone bodies in liver is enhanced, in concert with an increase in hepatic fatty acid oxidation. These include beta-hydroxybutyrate, acetoacetate and acetone. The first and rate-limiting step in ketogenesis is catalyzed by mitochondrial 3-hydroxy-3-methylglutaryl-CoA synthase (mHMG-Co AS), which causes condensation of acetyl-CoA and acetoacetyl-CoA in the mitochondria to generate HMG-CoA and free CoA. In accordance with an important role of PPAR α in ketogenesis, a functional PPRE was identified within the promoter of the rat and pig mitochondrial 3-hydroxy-3-methylglutaryl-CoA synthase gene [93–96]. Interestingly, another novel and unexpected mechanism of PPAR α -mHMG-CoA synthase gene regulation was discovered [97]. In addition to regulating transcriptional activity, PPAR α also interacts physically with mHMG-CoA synthase protein, potentiating the PPAR α -dependent transcription of mHMG-CoA synthase. Thus, mHMG-CoA synthase, which is believed to be mainly localized within the mitochondria, specifically stimulates its own transcription rate by behaving as a coactivator of $PPAR\alpha$. The second and final step in ketone body synthesis is catalyzed by HMG-CoA lyase, which according to microarray is upregulated during fasting in a PPAR α -dependent manner [F. Zandbergen et al., unpublished]. No PPRE has yet been identified in the promoter of this gene.

PPAR^a **and hepatic lipogenesis**

Whereas most of the PPAR α target genes are involved in fatty acid catabolism, some genes involved in lipogenesis were identified as $PPAR\alpha$ targets too. Malic enzyme, also known as malate NADP oxidoreductase, catalyzes the oxidative decarboxylation of malate into pyruvate, generating NADPH required for fatty acid biosynthesis. Expression of malic enzyme gene is decreased in livers of PPAR α mutant null mice, and a functional PPRE that confers fibrate responsiveness was found in the promoter of the gene [98]. Other then malic enzyme, stearoyl-CoA desaturase 1, also known as Δ9-desaturase, which catalyzes the rate-limiting step in the biosynthesis of n-9 unsaturated fatty acids from saturated fatty acids, was identified as a direct $PPAR\alpha$ target gene with a functional PPRE in its promoter [99]. Moreover, expression of the related genes Δ 5 desaturase and Δ 6 desaturase was found to be upregulated by PPAR α ligands, and in a PPAR α -dependent fashion for Δ 5 desaturase [100, 101]. Although no PPRE has yet been identified in the $-\Delta$ 5 desaturase promoter, it is likely a direct target of PPAR α , similar to what was found for the $\Delta 6$ desaturase promoter [101]. Thus, several genes involved in fatty acid biosynthesis appear to be regulated by $PPAR\alpha$. The question arises why the same transcription factor would enhance both fatty acid oxidation and fatty acid biosynthesis? Guillou et al. proposed that positive Δ 5, Δ 6 and Δ 9 gene regulation by $PPAR\alpha$ may serve to counteract the excessive fatty acid breakdown caused by the induction of peroxisomal- β -oxidation. Alternatively, as unsaturated fatty acids seem to be the better $PPAR\alpha$ ligand, it is possible that induction of desaturases serves to guarantee an ample supply of endogenous ligands for PPARs. Matsuzaka et al. reported on the dual regulation of $\Delta 5$, $\Delta 6$ by both SREBP1, which is induced during feeding, and PPAR α , which is induced during fasting, placing $\Delta 5$ and $\Delta 6$ in a distinct situation from regular lipogenic enzymes [102]. A similar regulation was also observed for $\Delta 9$ [100, 103]. It was argued that this dual regulation of both desaturases contributes to a stable production of polyunsaturated fatty acids (PUFA) that are essential for cellular function regardless of energy state. However, it is hard to imagine why such a complex mechanism would be necessary to maintain stable expression levels.

PPAR^a **and lipoprotein metabolism**

Fibrates are hypolipidemic drugs that are used clinically for their ability to efficiently decrease plasma triglyceride and increase plasma high-density lipoprotein (HDL) levels in humans. Epidemiological studies have shown an inverse correlation between high plasma HDL levels and cardiovascular diseases, thereby generating interest in the study of the mechanism behind the fibrate-induced increase in plasma HDL. The plasma HDL level is determined by numerous factors including production of apolipoproteins, plasma abundance of phospholipid and cholesteryl-ester transfer proteins, and cellular expression of cell surface receptors, lipases and plasma membrane lipid transporters. Several of these factors have been shown to be under the control of fibrates and PPAR α . At the level of production of apolipoproteins, fibrates upregulate the expression level of the human apolipoprotein A-I (ApoA-1) gene. Indeed, a functional PPRE has been identified in the human apo A-I promoter [104–106]. Intriguingly, in rodents fibrates decrease ApoA-I mRNA [107–109]. While the apparent lack of induction of rat ApoA-I expression by fibrates is due to a slight difference of three nucleotides between the rat and human apo A-I promoter, the PPAR α agonist-induced decrease in rat ApoA-I expression is believed to be mediated through the repressor Rev-erb α , a reported but unconfirmed positive target gene of $PPAR\alpha$ [110]. Expression of the other apoA protein, ApoA-II, is also upregulated by fibrates in a PPAR α -dependent manner [111]. Thus, production of the two major apolipoproteins that are part of HDL is under the influence of PPAR α .

In the circulation, HDL undergoes significant remodeling carried out by two important transfer proteins: cholesteryl-ester transfer protein and phospholipid transfer protein. Phospholipid transfer protein gene expression was found to be stimulated by $PPAR\alpha$, and a functional PPRE has been identified in the mouse promoter [112–114]. Via this mechanism, PPAR α would favor the surface transfer of phospholipids between lipoproteins and promote the remodeling of HDL particles in blood plasma.

HDL is removed from the circulation via the scavenger receptor-class B type I (SR-BI) in liver, perhaps assisted by a putative SR-BI-stabilizing protein called CLAMP (also called PDZK1, Diphor-1, CAP70 or NaPi-Cap1). Interestingly, hepatic protein expression of SR-BI and CLAMP has been reported to be suppressed by fibrates without any change in their respective steady state mRNA, suggesting a posttranscriptional event [115]. The observed effect was absent in PPAR α null mice, indicating the involvement of PPAR α . The PPAR α -induced breakdown of SR-BI protein may represent another mechanism by which PPAR α modulates HDL metabolism.

Besides elevating plasma HDL levels, fibrates are known

for their ability to diminish plasma triglyceride levels. Several mechanisms have been proposed to contribute to this effect, including a reduction of VLDL synthesis and increased catabolism of triglyceride-containing lipoproteins. At the level of lipoprotein catabolism, fibrates inhibit hepatic apolipoprotein C-III gene expression in humans and rats [116–118]. Apolipoprotein C-III is a potent inhibitor of lipoprotein lipase and thereby raises plasma triglyceride levels. Transcriptional suppression of the apolipoprotein C-III gene by fibrates involves the hepatic nuclear factor- 4α . Displacement of hepatic nuclear factor- 4α from the apolipoprotein C-III promoter by activated PPAR^a leads to the suppression of hepatic nuclear factor- 4α -enhanced apolipoprotein C-III gene transactivation. Accordingly, fibrates may exert their hypolipidemic effect by modulating apolipoprotein C-III gene expression.

Although it has been argued that fibrates may lower plasma triglycerides by increasing lipoprotein lipase expression, there is no evidence that $PPAR\alpha$ agonists upregulate lipoprotein lipase mRNA in the tissues where it is mostly expressed, that is muscle and adipose tissue [119]. In fact, it has been reported that $PPAR\alpha$ ligands inhibit lipoprotein lipase activity in cardiomyocytes, which would be expected to raise plasma triglyceride levels [120]. Recently, a novel mechanism for the triglyceride lowering effect of fibrates was proposed. It was observed that the apolipoprotein A5 gene, which is critical for maintaining normal plasma triglyceride levels, is regulated by $PPAR\alpha$ with two functional PPREs located in its promoter [121, 122]. Finally, fibrates and PPAR α may lower plasma triglyceride levels by stimulating hepatic fatty acid oxidation and thereby diminishing their incorporation into triglycerides and their secretion as VLDL.

In addition to the genes mentioned above, several other genes involved in lipoprotein metabolism have been reported to be regulated by $PPAR\alpha$, yet the impact of their regulation is not completely clear. Lipoprotein (a) is a highly atherogenic particle whose main protein constituent is apolipoprotein (a). Puckey et al. purported to have identified a direct DR-1 sequence in the core enhancer of apolipoprotein (a) $[apo(a)]$ gene that binds PPAR α and triggers upregulation of apo(a) mRNA [123]. Using microarray, our group discovered differential expression of the apolipoprotein C-I and LDL receptor-related protein between wild-type and $PPAR\alpha$ null mice, yet the details of this regulation remain to be investigated [F. Zandbergen et al., unpublished]. Regulation of these genes by PPAR α may contribute to the effect of fibrates on plasma HDL and triglyceride concentrations.

PPAR^a **and uncoupling proteins**

Uncoupling describes the movement of protons into the mitochondrial matrix without the concomitant production of ATP. Several channel proteins (called uncoupling proteins, UCPs) that can mediate this proton transport have been identified, i.e. UCP-1, UCP-2 , UCP-3 and UCP-4. UCP-1 is exclusively expressed in brown adipose tissue and is responsible for the generation of heat by this tissue. It was recently identified as a direct PPAR α target gene in brown adipose tissue, suggesting that PPAR α is involved in thermogenesis [124]. However, expression of UCP-1 was unchanged in $PPAR\alpha$ null mice, either in fed or fasted state, casting doubt on the physiological relevance of this regulation [39]. In contrast to UCP-1, UCP-2 is expressed in a wide range of tissues and may have a role in the production of reactive oxygen species, the production of insulin by pancreatic β cells and in the control of the ratio of [adenosine triphosphate]/[adenosine diphosphate]. UCP-3 is expressed primarily in skeletal muscle and may influence whole-body energy metabolism. Interestingly, it was found that cardiac and skeletal muscle *Ucp-3* expression was modulated by PPAR α agonists in a PPAR α dependent manner, whereas the same was not true for UCP-2 [125, 126]. However, in neonatal cardiomyocytes, in primary cultures of hepatocytes, and in an insulinoma cell line $PPAR\alpha$ agonists were able to induce UCP-2 gene expression [127–130]. Taken together, these observations point to a role of $PPAR\alpha$ in UCP-2 and UCP-3 gene regulation. Inasmuch as the functions of UCP-2 and UCP-3 are presently not very clear, the importance and consequences of this regulation remain to be determined.

PPAR α and hepatic bile acid metabolism

Over the past few years, different studies have established a functional role for $PPAR\alpha$ in bile acid homeostasis. De novo hepatic biosynthesis of bile acids is regulated by the key enzyme cholesterol 7α -hydroxylase (Cyp7A1), a microsomal cytochrome P450 isoenzyme. Although several studies have reported on regulation of Cyp7A1 gene expression by PPAR α , conflicting observations were made [131]. It was observed that in human hepatoma HepG2 cells, cotransfection of expression vectors for both PPAR α and RXR α in the presence of PPAR α agonist caused a decrease in human and rat Cyp7A1 promoter activities [132, 133]. Despite the presence of a DR-1 in the Cyp7A1 promoters of both species, no direct binding of PPAR α was detected. It was concluded that PPAR α and its agonists decrease Cyp7A1 expression and activity by reducing the availability of hepatic nuclear factor 4α for binding to this DR-1. The physiological consequences of such regulation were studied in vivo in rats and mice. As in humans, $PPAR\alpha$ dependent downregulation of Cyp7A1 by PPAR α agonists was found in both species [134]. In agreement with these observations, fibrate treatment led to a decrease in bile acid synthesis.

In contrast to the above data, Cheema et al. showed that both human Cyp7A1 and murine Cyp7A1 genes are upregulated by PPAR α /RXR α [135]. A conserved and functional PPRE was identified in the promoter of both species, plus an additional PPRE in the mouse version. This latter element may possibly explain the better responsiveness to fibrates of the mouse Cyp7A1 gene compared with the human gene. Furthermore, Hunt et al. observed that hepatic expression of Cyp7A1 was diminished in PPAR α null mice, particularly under fasting conditions, providing compelling evidence that $PPAR\alpha$ upregulates Cyp7A1 expression [136]. The reasons for the discrepancy with the other study reporting negative regulation of Cyp7A1 by PPAR α are unclear. Other genes implicated in bile acid synthesis that are regulated by PPAR α include sterol-27-hydroxylase (Cyp27), whose activity was downregulated by $PPAR\alpha$ agonists in a PPAR α -dependent manner, and sterol-12 α -hydroxylase (rat Cyp8B1), which was found to be directly upregulated by PPAR α through a functional PPRE [134, 136]. Overall, regulation of Cyp7A1 by PPAR α may help to explain the fibrate-induced increase and decrease in the relative biliary concentration of cholic acid and chenodeoxycholic acid, respectively.

Liver X receptor α is a nuclear receptor that plays an important role in the regulation of Cyp7A1 transcription. Expression of $LXR\alpha$ was found to be stimulated by $PPAR\alpha$ agonist in macrophages, and decreased in livers of fasted PPAR α null mice compared with fasted wildtype mice [137]. Five potential PPRE-like sequences were identified throughout the $LXR\alpha-5'$ flanking region. Some of these PPREs, if not all, may support $PPAR\alpha$ transactivation. By stimulating $LXR\alpha$ expression, PPAR α was suggested to upregulate ABCA1 expression, which is a direct $LXR\alpha$ target gene. ABCA1 promotes efflux of cholesterol from macrophages and other peripheral tissues to HDL, yet its role in the liver is not very clear. Although these data point towards interesting crosstalk between the PPAR α and LXR α signaling pathways, the importance and consequences of this regulation remain to be demonstrated.

Finally, Kok et al. found a fasting- and $PPAR\alpha$ -dependent induction of the canalicular phospholipid translocator (Mdr2/Abcb4) and a complementary increase in phospholipid secretion [138, 139]. Taken together, numerous genes involved in bile metabolism appear to be regulated by PPAR α . Despite this regulation, basal bile formation is unaffected by $PPAR\alpha$ deletion, suggesting that the role of PPAR α in bile metabolism may be more subtle and probably only important under conditions of increased free fatty acids levels, as is the case during fasting [138, 139].

PPAR^a **and intestinal absorption**

Following their synthesis and excretion by the liver into the bile, bile salts end up in the intestine where they will undergo intestinal reabsorption via the transporter ASBT/SLC10A2, which is mainly responsible for the efficient enterohepatic circulation of bile salts [140]. Interestingly, human ASBT was shown to be directly regulated by PPAR α , through a functional DR-1 motif located in its promoter [140]. Thus, PPAR α may be implicated in regulation of the reabsorption of bile salts in the intestine. Bile salts are necessary for efficient biliary phospholipid secretion by Mdr2, which, as mentioned above, is upregulated during fasting in a PPAR α dependent manner, pointing to a possible relationship between both regulatory processes. Recent evidence also suggests that $PPAR\alpha$ may regulate expression of the cellular retinol-binding protein type-II gene, indicating a role of PPAR α in intestinal metabolism of retinoids [141, 142].

PPAR^a **and glucose metabolism**

Maintenance of plasma glucose levels is essential, as very low blood glucose concentrations can lead to brain dysfunction, coma and death. A role of $PPAR\alpha$ in glucose metabolism emerged from several studies showing that PPAR α null mice suffer from pronounced hypoglycemia after fasting [39, 40, 143–145]. Inasmuch as plasma glucose is maintained during fasting by a combination of de novo glucose synthesis (gluconeogenesis) and glycogen breakdown (glycogenolysis), fasting-induced hypoglycemia could be caused by inhibition of either of these two pathways. Alternatively, it is possible that glucose utilization is increased in $PPAR\alpha$ null mice.

PPAR α and β -cell function

By influencing secretion of pancreatic hormones, $PPAR\alpha$ deletion could have a major effect on plasma glucose levels. Whereas Xu et al. failed to find a significant difference in plasma insulin levels between fed or fasted wildtype compared with PPAR α mutant mice, unpublished data from Burcelin indicate that insulin is modestly but significantly elevated in fasted PPAR α null mice [143]. However, plasma glucagon levels were increased as well, and consequently fasting-induced hypoglycemia cannot be ascribed to an altered insulin/glucagon ratio. The mechanism by which PPAR α may alter insulin and glucagon production and/or release remains ambiguous. Pyruvate dehydrogenase kinase 4 was identified as a probable PPAR α target in islets, but the effect of this regulation on glucose-stimulated insulin secretion is not very clear.

PPAR^a **and fatty acid oxidation**

Hepatic fatty acid β -oxidation is associated with the production of certain cofactors (ATP, NADH, acetyl CoA) that have a stimulatory effect on gluconeogenesis. As PPAR α is critical for fatty acid oxidation, it is conceivable that the hypoglycemia in fasted $PPAR\alpha$ mutant mice may be secondary to a defect in fatty acid oxidation [39]. At the level of peripheral tissues, defective fatty acid oxidation as a result of PPAR α deficiency may cause a corresponding increase in the rate of utilization of glucose.

PPAR^a **and glycogenolysis**

Early during the course of fasting, blood glucose is mainly maintained by hepatic glycogen breakdown (glycogenolysis). It was reported by some groups that under basal conditions, hepatic glycogen stores are strongly decreased in PPAR α mutant compared with wild-type mice, providing a potential explanation for fasting hypoglycemia [39, 143]. Decreased hepatic glycogen content is suggestive of a defect in glycogen synthesis or storage, or increased utilization. So far, no specific gene targets of PPAR α in any of these pathways have yet been identified. In contrast, other studies failed to find a difference in basal liver glycogen content between the two sets of mice [77, 145]. The reason for this discrepancy is presently unclear.

PPAR^a **and gluconeogenesis**

Another pathway that may be impaired in PPAR α mutant mice is gluconeogenesis. The major substrates for gluconeogenesis are alanine, lactate and glycerol. Two ratelimiting enzymes are believed to regulate the whole process of gluconeogenesis, phosphoenol-pyruvate carboxykinase and pyruvate carboxylase. Hepatic expression of phosphoenol-pyruvate carboxykinase does not appear to be different between wild-type and PPAR α mutant mice, regardless of the nutritional status [39, 143]. This is surprising considering that the PEPCK promoter contains a functional PPRE, which was shown to be functional in adipocytes [146]. Interestingly, DNA microarrays revealed that fasted PPAR α mutant mice display a reduced hepatic expression of pyruvate carboxylase, as well as lactate dehydrogenase A4 [S. Kersten, unpublished]. This suggests that the hypoglycemia might be due to impaired gluconeogenesis caused by decreased expression of these genes. In line with this, hepatic glucose production from lactate was decreased in both fed and fasted PPAR α mutant mice [143]. However, despite decreased expression of these genes, overall hepatic glucose production was increased in the PPAR α null mice after a 17-h fast. These data are hard to reconcile with the notion that the hypoglycemia in fasted $PPAR\alpha$ null mice may (partially) be attributed to defective gluconeogenesis. No

PPRE has yet been identified in the promoter of either pyruvate carboxylase or lactate dehydrogenase A4.

PPAR^a **and glycolysis**

As mentioned above, hypoglycemia in fasted PPARa null mice may also be caused by increased glucose utilization. The only gene involved in glucose utilization that has been identified as a PPAR α target is pyruvate dehydrogenase kinase isoform 4 (PDK4). PDK4 phosphorylates and inactivates pyruvate dehydrogenase, thereby limiting the flux through glycolysis. It was found that the fastinginduced increase of PDK4 in heart, kidney and skeletal muscle is $PPAR\alpha$ dependent and, furthermore, that direct $PPAR\alpha$ activation upregulates PDK4 expression [147–151]. In PPAR α null mice, the lack of PPAR α -induced PDK4 expression during fasting may lead to a dephosphorylated active form of the pyruvate dehydrogenase complex that, via increased glycolysis, could give rise to increased glucose utilization. So far, no PPRE has yet been identified in the promoter of the PDK4 gene.

PPAR^a **and urea cycle**

Not only does $PPAR\alpha$ govern lipid and glucose metabolism, recent studies have also associated PPAR α with regulation of hepatic amino acid metabolism [152, 153]. By comparing wild-type and PPAR α null mice using oligonucleotide microarray and subtractive hybridization, PPAR α -dependent downregulation of genes involved in major pathways of amino acid metabolism was found, i.e. transamination, deamination, urea cycle, oxidation of alpha keto acids and synthesis of amino acidderived-products, leading to increased plasma urea levels in PPAR α null mice. The precise molecular mechanism behind this regulation is still unknown and requires further investigation. While $PPAR\alpha$ downregulates expression of genes involved in the urea cycle, HNF-4 α and $C/EBP\alpha$ have the opposite effect. It was shown that $C/EBP\alpha$ null mice display lower levels of plasma urea, a consequence of the lack of induction of urea cycle enzymes by $C/EBP\alpha$. The same was true for liver-specific HNF4- α null mice, which display a higher plasma ammonia concentration together with a lower plasma urea concentration [154]. This phenotype may be explained by the lack of HNF-4 α -dependent induction of ornithine transcarbamoylase gene expression. Indeed, two different functional binding sites for HNF-4 α , one being more important than the other, were found. As HNF-4 α and PPAR α both recognize DR-1 sequences, it is possible that PPAR α may interfere negatively with regulation of ornithine transcarbamoylase by HNF-4 α , leading to downregulation of ornithine transcarbamoylase gene expression.

PPAR^a **and biotransformation**

Toxins, drugs, carcinogens and other xenobiotics are eliminated from the body via a series of reactions described as biotransformation. Biotransformation usually consists of three separate steps: First, in phase I, a polar group is introduced into the xenobiotic molecule, making it more reactive. Subsequently, in phase II, the modified xenobiotic is conjugated to a polar molecule such as glucuronic acid or glutathione. Finally, conjugated xenobiotics are excreted into the bile or urine via specific transporters (phase III), mainly by members of the superfamily of ATP-binding cassette transporter proteins [71]. Studies with synthetic PPAR α agonists and PPAR α null mice have indicated that $PPAR\alpha$ is able to both up- and downregulate expression of xenobiotic metabolizing enzymes. Genes that were found to be upregulated by $PPAR\alpha$ agonists in liver include phase I cytosolic epoxide hydrolase and aldehyde dehydrogenase type 3. Comparison of gene expression between wild-type and PPAR α null mice using microarray revealed that the effect of peroxisome proliferators on the expression of these enzymes is clearly mediated by $PPAR\alpha$ [unpublished data]. So far no PPRE has been identified in the promoter of either of these genes.

Numerous genes involved in phase I biotransformation appear to be downregulated by $PPAR\alpha$. This includes several phase I enzymes involved in the hydroxylation (Cyp2A4, Cyp2A1, Cyp3A11,Cyp17) as well as the dehydrogenation (3 α , 11 β and 17 β hydroxysteroid dehydrogenase) of steroids [155–158]. Furthermore, downregulation of hepatic Cyp2A5, Cyp2C29 and Cyp3A11 by lipopolysaccharide is attenuated or blocked in PPAR α null mice [159]. In contrast, expression of 17- β -hydroxysteroid-dehydrogenase type IV is upregulated by PPAR α ligands. Thus, PPAR α seems to govern diverse aspects of steroid metabolism. Interestingly, at the functional level, it was shown that rats fed peroxisome proliferators suffered from alterations in reproductive organs together with impaired estrogen metabolism. Female rats displayed a decrease in serum estradiol levels together with suppression of ovulation, a possible consequence of modulation of the fatty acyl-CoA:estradiol acetyl-transferase protein level by PPAR α [160]. Males suffered from a decrease in testicle size and Sertoli cell vacuolation, but whether this phenotype is connected with the PPAR α mediated induction of fatty acyl-CoA:testosterone acetyltransferase remains to be investigated. Furthermore, peroxisome proliferators were found to markedly influence the profile of site- and stereospecific microsomal metabolites of testosterone. This is likely caused by altered expression of steroid-metabolizing enzyme. Indeed, fibrates decreased CYP2A4 levels both at the protein and mRNA levels [161]. In addition, expression of the malespecific genes α 2 urinary-globulin (α pheromone carrier) and Cyp2C11, (a steroid 2 and 16α hydroxylase) are repressed by peroxisome proliferators, as well as the female-specific Cyp2C12 gene [157]. Overall, it is clear that PPAR α potently downregulates expression of genes involved in steroid metabolism, yet the mechanisms involved still need to be elucidated.

The ability of peroxisome proliferators to influence phase II biotransformation has been extensively documented. However, unlike phase I biotransformation, direct involvement of PPAR α in phase II biotransformation has yet to be demonstrated. A wide array of different peroxisome proliferators are able to decrease the activity of various glutathione-*S*-transferases via changes at both protein and mRNA level [162]. This can result in decreased biliary excretion of glutathione conjugates such as sulphobromophthalein [163]. It also may increase exposure to carcinogenic xenobiotics by retarding their conjugation to glutathione and thereby their detoxification [164]. Fibrates have been shown to decrease glutathione-*S*transferase alpha and mu protein concentrations in rat liver, an effect which is probably mediated by $PPAR\alpha$ [our unpublished results; 165]. In addition to glutathione conjugation, peroxisome proliferators also affect phase II glucuronidation. Whereas bilirubin UDP-glucuronosyltransferase mRNA levels are stimulated by peroxisome proliferators, resulting in increased bilirubin glucuronidation, testosterone glucuronidation is diminished by peroxisome proliferators [166, 167]. Recently, the UDP-glucuronosyltransferase 1A9 gene was identified as a direct positive PPAR α target gene with a functional PPRE in its promoter [168]. In conclusion, exposure to peroxisome proliferators may profoundly influence steroid biotransformation, which is probably mediated by PPAR α , possibly leading to altered metabolism of oral contraceptive and other steroids.

PPAR^a **and white adipose tissue**

It is well established that $PPAR\gamma$ is the major PPAR isotype expressed in white adipose tissue and that $PPAR\alpha$ is barely detectable [4]. Nevertheless, different lines of evidence suggest a functional role of $PPAR\alpha$ in this tissue. The basal expression of resistin in epididymal fat was significantly higher in wild-type than in PPAR α null mice, yet PPAR α agonist had no effect on resistin expression [169]. Furthermore, expression of the fasting-induced adipose factor in white adipose tissue was higher in PPAR α null mice, regardless of the nutritional state [170]. While PPAR α activation may modulate expression of the fasting-induced adipose factor and resistin in fat, it is also possible that the altered expression of these genes in PPAR α null mice are an indirect consequence of metabolic perturbations in the PPAR α null mice. Thus, in spite of its weak expression it is not inconceivable that $PPAR\alpha$ may play a regulatory role in the biology of white adipose tissue.

Trans-repression by PPARa**: implications in acute phase response and inflammation**

A critical role of $PPAR\alpha$ in inflammation was first illustrated by Devchand et al., who provided evidence of a prolonged duration of inflammation in PPAR α null mice [38]. Many studies aimed at defining the molecular pathways behind this phenotype have since been performed and have shown interference of $PPAR\alpha$ with several other transcription factors pathways. PPAR α commonly operates as a positive regulator of gene expression, but effects of PPAR α on inflammatory pathways are mostly carried out by trans-repression. In T lymphocytes $PPAR\alpha$ is expressed at a relatively high level in resting T cells, and diminishes upon activation with a corresponding upregulation of PPAR_Y [27, 28]. Interestingly, treatment of activated T cells with different PPAR α agonists results in decreased interleukin-2 and interferon- γ gene expression [29]. $PPAR\alpha$ was found to mediate trans-repression on gene expression, a process by which $PPAR\alpha$ antagonizes several signal transduction pathways through various DNA-dependent and independent mechanisms. In line with this, gene transactivation by different transcription factors such as NF- κ B, NFAT (nuclear factor of activated T cells), C/EBP (CAAT/box enhancer binding protein), STAT (signal transducer and activator of transcription) and c-Jun/c-Fos, were repressed by $PPAR\alpha$ via DNA binding-independent events such as protein-protein interactions and cofactor competition [31, 32]. Moreover, interference between PPAR α and C/EBP β signaling pathways through depletion of the coactivator glucocorticoid receptor-interacting protein/transcriptional intermediary factor 2 (GRIP1/ TIF2) was identified, leading to reduced $C/EBP\beta$ transactivation of the fibrinogen promoter [171].

Other examples of trans-repression on gene expression by PPAR α are (i) inhibition of cytokine-induced vascular cell adhesion molecule-1 expression by $PPAR\alpha$ activators in human endothelial cells, through interference with $NF-\kappa B$ signaling [32]; (ii) repression of thrombin-induced expression of endothelin-1 by $PPAR\alpha$ agonists by modulating c-Jun/c-Fos DNA binding activities on the endothelin-1 promoter [33]; (iii) Interference with the smad4 transcription factor signaling that results in an inhibition of the transforming growth factor-beta (TGF- β) induced β 5 integrin gene expression [172] and (iv) Inhibition of interleukin (IL)-6 gene expression by PPAR α dependent repression of p65 as well as c-Jun transactivation of the IL-6 promoter [173]. This can be seen as a consequence of protein-protein interactions between different parts of PPAR α , c-Jun and p65, one of the five members of the NF- κ B/Rel family.

Expression of $I \kappa B \alpha$ (for inducer of nuclear factor- κB) was also found to be upregulated by $PPAR\alpha$ [174, 175]. This is important because $I \kappa B \alpha$ is an inhibitory protein of $NF - \kappa B$ that maintains $NF - \kappa B$ in a cytoplasmic inactive form, leading to strongly reduced NF-kB DNA binding and thus preventing the $NF - \kappa B$ -dependent inflammatory response. Surprisingly, PPAR α -mediated I κ B α upregulation did not require any functional PPRE in the $I \kappa B \alpha$ promoter, but rather Sp1 and NF- κ B1 sites. Activated PPAR α , rather than directly binding on the DNA promoter of $I \kappa B \alpha$, enhanced the occupancy of the NF- κB response element located in the $I \kappa B \alpha$ promoter. The ligand binding domain of PPAR α was identified as the part that potentiates p65 (a subunit of $NF- κ B$)-stimulated $I \kappa B \alpha$ transcription in a DRIP205 (VDR interacting protein)/TRAPP220(TR-associated protein)-dependent manner. Thus, these results provide a new molecular basis for PPAR α -induced gene transcription and open new routes of investigations.

Last, cyclooxygenase 2 (COX2) was identified as a direct PPAR α target that was strongly upregulated in mammary epithelial cells to a large diversity of fatty acids and PPAR α agonists [176]. COX2 is believed to be responsible for much of the prostaglandin production in inflamed tissues and was found to be overexpressed in several human cancers.

PPAR α and the acute phase response

Hepatic acute phase response, which describes the early and immediate set of homeostatic control reactions that are induced during inflammatory processes associated with endotoxemia or liver regeneration, is known to be associated with a decrease in the hepatic expression of genes involved in lipid metabolism. PPAR α gene expression is downregulated during the hepatic acute phase response [177, 178]. Treatment of hamsters with endotoxin results in a rapid downregulation of $PPAR\alpha$ mRNA levels as well as of other nuclear receptors, such as RXR, PXR, LXR and FXR. This downregulation is associated with reduced RXR:PPAR binding activities in nuclear extracts as well as a decrease of both basal and WY14643-induced expression of a target gene, acyl-CoA synthetase [178]. The tightly regulated signaling associ-ated with the acute phase response plays also an important role during liver regeneration, which occurs when major parts of the liver tissue are destroyed or removed, e.g. after 70% partial hepatectomy. The very early phase of liver regeneration $(< 4 \text{ h})$ is called the priming phase. Using microarray analysis, it was observed that $PPAR\alpha$ mRNA levels were rapidly downregulated during this priming phase of liver regeneration [177]. No mechanisms, however, were presented and a role of proinflammatory cytokines is unlikely, as cytokines such as IL-6,

IL-2, IL-3, IL-4, IL-5, TNFs and interferon gamma (IFN- γ) were upregulated in the first 4 h after partial hepatectomy [177]. A possible explanation could be that other liver-enriched transcription factors that are upstream of PPAR α are also rapidly downregulated in part by phosphorylation via mitogen-activated protein kinase.

PPAR α can be considered a negative acute phase protein, and it represents a key player in the regulation of the acute phase response. One of the acute phase proteins that is regulated by PPAR α is transferrin. Transferrin was identified as a negative PPAR α target via a mechanism that involves disruption of the HNF4-enhanced expression of transferrin gene, probably by interfering with the ability of HNF4 to transactivate via a PPRE-like element located in the transferrin promoter [157, 179]. Furthermore, the gene expression of two other acute phase proteins, fibrinogen and α -1 acid glycoprotein, was shown to be repressed by PPAR α agonists [157, 171, 180]. Thus, by a novel molecular mechanism involving negative gene regulation, hepatic PPAR α is able to modulate the acute phase response. The cross-talk between proinflammatory signaling and $PPAR\alpha$ -dependent signaling is discussed in more detail elsewhere [181, 182].

Alternative PPAR response elements?

While a DR-1-like sequence is still believed to be the favorite DNA-binding site for PPAR α , different groups have reported on the characterization of new regulatory sequences onto which $PPAR\alpha$ can bind and regulate transcriptional activity. For example, a new kind of PPRE was identified in the promoter of the nuclear orphan receptor Rev-erb α [110]. This PPRE is not a DR-1 but rather a DR-2 motif. An alternative DR-1 sequence was also identified in the human promoter of PPAR α , suggesting a possible autoregulation of its own transcription rate [183]. Whether the same is also true in rodents remains to be investigated and will require further characterization of the mouse PPAR α promoter [184]. Finally, an alternative PPRE was also identified in the proximal promoter of the human CPT-II gene [68]. This PPRE only contains one half-site which is a perfect consensus sequence for $RXR\alpha$, whereas the second half-site normally occupied by $PPAR\alpha$ is not well conserved. Chromatin immunoprecipitation verified the binding of $PPAR\alpha$, and transient transfections experiments confirmed its functionality.

Some PPAR^a **target genes are also PPAR**b**and/or PPAR**g**-regulated genes**

Genes regulated by PPAR α may also be targets of PPAR β and PPARg. This concept has been illustrated by the work

of Yu et al. who overexpressed PPAR $y1$ in the liver of PPAR α null mice [185]. They noticed a strong PPAR γ 1induced expression of genes such as Δ 9 desaturase, malic enzyme and fasting-induced adipose factor, genes that were previously identified as PPAR α targets [98, 99, 170]. In addition, overlapping functions of PPAR α and PPAR β in skeletal muscle and cardiac cells were identified [144, 186]. Last, an interesting parallel in PPAR α and PPAR β function was recently proposed. Whereas hepatic fatty acid β -oxidation is controlled by PPAR α , PPAR β was postulated as a master regulator of fatty acid β -oxidation in brown adipose tissue [187]. Whether this is also true for PPAR α in this tissue remains to be investigated. Thus, it is possible that PPAR α and PPAR β may share partial functional redundancy that renders the analysis of their respective functions difficult. The generation of transgenic mice (double PPAR α/β mutant mice, tissue selective overexpression and ablation of each isotype) may help to bypass this problem.

Conclusions and future perspectives

Starting out as a transcription factor involved in the regulation of peroxisomal fatty acid metabolism, in the past decade PPAR α has taken on the identity of a global regulator of metabolism, governing such diverse processes as inflammation and nutrient metabolism, particularly under conditions of fasting (fig. 2). Indeed, it is mostly during fasting that the effects of PPAR α become manifest. Experiments with PPAR α null mice have clearly demonstrated that deletion of $PPAR\alpha$ has minor effects on fed mice, but dramatically disrupts homeostasis in fasted mice [39, 40, 64].

The advent of modern-day technologies such as transcriptomics and proteomics, which permit the monitoring of thousands of genes or proteins, is expected to lead to further breakthroughs in our understanding of PPAR α function. Examples of such a genomics approach towards PPAR α have recently emerged. Utilizing microarray, our group managed to identify novel pathways governed by PPAR α (hepatic amino acid metabolism) as well as novel specific PPAR α target genes such as the G0/G1 switchgene 2 (GOS-2) [153; Zandbergen et al., unpublished]. DNA arrays also revealed their efficacity in the characterization of new PPAR γ targets in fat, liver and skeletal muscle [188]. A comprehensive metabolomic assessment of lipid metabolites was successfully used to study the impact of the PPAR γ agonist rosiglitazone on lipid metabolism [189]. Finally, proteomics was employed to better characterize the effect of PPAR α ligands on rat liver [87]. A more comprehensive analysis of these studies will

Figure 2. Schematic view of the role of PPAR α in the hepatic reponse to fasting. During fasting, fatty acids are released from adipose tissue and travel to the liver, where they bind and activate PPAR α . Activation of PPAR α results in stimulation of a number of pathways, including fatty acid oxidation, ketogenesis and gluconeogenesis, and in suppression of amino acid catabolism and the acute phase response. This is associated with an increase or decrease of specific components in the blood.

be published elsewehere. Large-scale screening of functional PPRE may also be started using chromatin immunoprecipitation. Using a suitable antibody against PPAR α , it is possible to pull down and purify genomic DNA fragments to which PPAR α is bound. After a cloning step, nucleotide sequencing is performed to determine the identity of each fragment. Chromatin immunoprecipitation appears to be a suitable method for the characterization of a large set of direct PPAR α target genes.

In conclusion, while much is already known about the function and targets of PPAR α , the use of modern genomics tools will further advance our understanding of PPAR α in the next few years. However, although the power of a genomics approach should not be underestimated, the true value of genomics is only uncovered when used in combination with other experimental techniques and approaches.

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