

PPARs: transcriptional effectors of fatty acids and their derivatives

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Abstract. Peroxisome proliferator-activated receptors (PPARs) are nuclear hormone receptors that mediate the effects of fatty acids and their derivatives at the transcriptional level. These receptors stimulate transcription after activation by their cognate ligand and binding to the promoter of target genes. In this review, we discuss how fatty acids affect PPAR functions in the cell. We first describe the structural features of the ligand binding domains of PPARs, as defined by crystallographic analyses. We then present the ligand-binding characteristics of each of the

three PPARs (α , β/δ , γ) and relate ligand activation to various cellular processes: (i) fatty acid catabolism and modulation of the inflammatory response for PPAR α , (ii) embryo implantation, cell proliferation and apoptosis for PPAR β , and (iii) adipocytic differentiation, monocytic differentiation and cell cycle withdrawal for PPAR γ . Finally, we present possible cross-talk between the PPAR pathway and different endocrine routes within the cell, including the thyroid hormone and retinoid pathways.

Key words. Peroxisome proliferator-activated receptor; nuclear receptors; transcription; ligand; eicosanoids; thiazolidinediones; fatty acid catabolism; differentiation.

Introduction

The understanding of tissue-specific effects of fatty acids relies on our knowledge of how these substances and their derivatives flux and signal in the organism. This includes how they are taken up, assimilated, transported in the blood, distributed to the cells and then either utilized as membrane constituents or metabolized to downstream products, some of them being very potent biological mediators. The activity of fatty acids and their metabolites is presently in the limelight. Alterations in their homeostasis are considered as key causes of some of the major pathologies of modern times, such as diabetes, obesity, cardiovascular diseases and cancer. Initially, the effects of fatty acids were thought to be mediated via changes in cellular membrane composition or via effects on signaling cascades [1]. The latter have been extensively studied recently, opening the new field of transcriptional regula-

tion of gene activity via fatty acids [2]. It is through the discovery of soluble nuclear receptors for fatty acids that a direct link between fatty acids and gene regulation has been demonstrated. Indeed, it is now well established that as members of the steroid/thyroid hormone receptors family, the peroxisome proliferator-activated receptors (PPARs) [3] mediate the effects of fatty acids on gene expression and cell fate.

In this review, we summarize newly acquired knowledge regarding fatty acids as ‘hormones’ related to PPARs. First, we will discuss the structural properties of these receptors with respect to ligand binding. We will then describe the functional characteristics of each of the three PPAR isotypes in relation to ligand diversity and the effect on cellular processes. Possible cross-talk between PPARs and other lipid signaling routes will then be discussed, and finally we will conclude by presenting likely scenarios for the evolution of the field.

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Structural organization of PPARs

The PPARs belong to the superfamily of the steroid/thyroid nuclear hormone receptors [4, 5]. They have been identified in many species, such as *Xenopus* [6], mouse [7], rat [8] and human [9]. There are three isotypes (α , β/δ , γ ; NR1C1, NR1C2 and NR1C3, respectively, according to the unified nomenclature of nuclear receptors [10]) discovered so far, which share the typical domain organization of nuclear receptors [11] (fig. 1 A). The N-terminal A/B domain contains a ligand-independent transactivation function. In the α and γ isotypes, the activity of this domain can be regulated by mitogen-activated protein kinase (MAPK) phosphorylation [12, 13]. The C domain is the DNA binding domain with its typical two zinc-finger-like motifs, as previously described for the steroid receptors [14]. The E/F domain is the ligand binding domain. It contains a ligand-dependent transactivation function, AF-2 [6–8], and is able to interact with transcriptional coactivators such as SRC-1 [15–17] and CBP [18–20], in a ligand-dependent manner. PPAR acts on promoters of target genes as a heterodimer with its obligate partner RXR (NR2B) [10, 21–23], the nuclear receptor for 9-*cis* retinoic acid [24].

We herein focus on the characteristics of the ligand binding domain, for which interesting findings have emerged. For a comparative analysis of the three PPAR isotypes we can refer the readers to a comprehensive review on PPARs [25].

The ligand binding domain

The ligand binding domain (LBD) of PPARs contains a transactivation function that was first characterized in transfection assays, by using the PPAR LBD fused to the estrogen receptor DNA binding domain [6, 7]. These studies determined that compounds inducing peroxisome proliferation were able to activate PPARs. Further studies showed that PPARs could also be activated by a variety of polyunsaturated fatty acids, at concentrations in the micromolar range [8, 22], as well as by small synthetic molecules such as thiazolidinediones and L-tyrosine analogs in the nanomolar range [26]. The observed diversity of putative PPAR ligands led to the speculation that it was reflecting some unusual structural properties of the ligand binding domain. Nevertheless, the PPAR LBD presents an overall tridimensional fold, very similar to that of other receptors [27]. The PPAR α [28], PPAR β/δ [29] and PPAR γ LBD [30] (fig. 1 B) consist of 13 α helices and a small four-stranded β sheet forming a large Y-shaped hy-

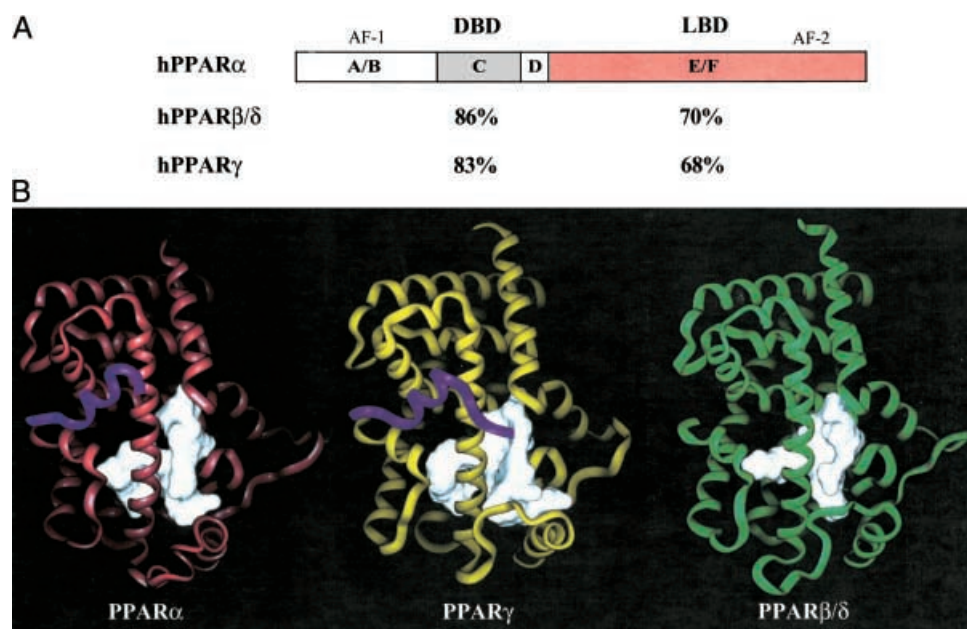


Figure 1. Structure of PPARs. (A) Schematic view of the domain organization of PPARs. Structural and functional domains are depicted. The A/B domain contains the activation function 1 (AF-1), which has a ligand-independent transcriptional activity. The C domain corresponds to the DNA binding domain (DBD). The E/F domain contains the ligand binding domain (LBD) and carries the activation function 2 (AF-2), which has a ligand-dependent transcriptional activity. The percentage of amino acid identity of the DBDs and LBDs of human PPAR β and PPAR γ compared with PPAR α is indicated. (B) Three-dimensional structure of ligand binding domains of PPARs. A comparison of the X-ray crystal structures of PPAR α (red worm), PPAR γ (yellow worm) and PPAR β/δ (green worm) is shown. Each PPAR is complexed to a high-affinity ligand (not pictured). PPAR α and PPAR γ are shown associated to LXXXLL peptides (purple worms), the signature motif of the receptor coactivators. For each PPAR, the solvent-accessible ligand binding pocket is displayed as an off-white surface. (Reproduced from [28]).

drophobic pocket. This pocket represents the ligand binding cavity and has a volume of approximately 1300 Å³, which is about twice that of the other nuclear receptors. For example, the ligand binding cavity of the thyroid hormone receptor has a volume of around 600 Å³ [31]. In the case of PPAR β and γ , the ligands occupy ~30–40% of the pocket, in contrast to the thyroid hormone receptor, where the ligand fills around 90% of the pocket [31]. Besides its large size, another characteristic feature of the PPAR ligand binding pocket is that its bottom portion is sealed by helix 2', which is absent in other nuclear receptors. This particular helix may increase the size of the pocket, and possibly participates in an entry channel for the ligand. The position of the ligand in the PPAR β LBD was determined for eicosapentaenoic acid (EPA). The carboxylic acid of EPA interacts directly with the C-terminal helix containing the activation function 2 core, and its hydrophobic tail can adopt two conformations within the cavity, each of which is stabilized by hydrophobic interactions with the LBD. However, the pocket of PPAR β LBD is somewhat narrow at the vicinity of the AF-2 helix, which makes it hard to accommodate some ligands such as tyrosine-based molecules and contributes to the particular ligand binding profile of the β isotype [28]. Interestingly, the structural alignment of the ligand binding cavities of PPAR α and PPAR γ , combined with mutant analysis, showed that the ligand selectivity depends on the identity of a single amino acid in helix 5 (tyrosine in PPAR α and histidine in PPAR γ). This selectivity seems to be conserved between different ligand classes and corresponds to an intrinsic property of the receptors [28]. The characteristics of the PPAR LBDs give insight into the propensity of PPARs to interact with a variety of natural and synthetic compounds [29, 30].

PPAR activation and biological consequences

PPAR α

Peroxisome proliferators (PPs) were known to affect peroxisomal β -oxidation of fatty acids, besides their effects on increasing peroxisome numbers in rodents. Since they were shown to be PPAR α activators, the effects of PPAR α on fatty acid catabolism were investigated. These analyses revealed that PPAR α controls the transcriptional rate of genes encoding key enzymes of the fatty acid catabolism pathway (see fig. 2). Fatty acid oxidation takes place in specialized organelles: peroxisomes and mitochondria for β -oxidation, and microsomes for ω -oxidation. Importantly, PPAR α transcriptionally regulates the production of enzymes such as acyl-coenzyme A (CoA) oxidase [6], the key enzyme in the peroxisomal β -oxidation pathway, carnitine palmitoyl transferase I [32], implicated in the translocation of fatty acids across the inner mitochon-

drial membrane, as well as CYP4A6, which is an important microsomal ω -hydroxylase [33].

Interestingly, fatty acids directly affect transcription by activating PPAR α [8, 22, 34]. Moreover, it is possible to establish a hierarchy within the list of activators. The best natural PPAR α agonists are long-chain polyunsaturated fatty acids such as arachidonic acid and linoleic acid, while the weakest ones are the short saturated fatty acids. These observations suggested that fatty acids might act as hormones that directly bind to the nuclear receptor PPAR α . The rationale behind this diversity of PPAR α activators, however, was not clear. To establish that some of these activators are true ligands, some indirect means were used. A first approach, called the CARLA method [16], was developed to exploit the interaction of nuclear receptors with transcriptional coactivator proteins such as SRC-1 upon ligand binding. This interaction between the receptor and the coactivator is mediated through a ligand-dependent rearrangement of the LBD of the receptor, involving particularly helix 12 [15, 16]. The analysis of the interaction profile between PPAR α and SRC1 in the presence of a putative ligand provided results consistent with the transactivation profile observed earlier. In general, the polyunsaturated fatty acids were found to be better ligands than the saturated ones. The ligand-induced LBD conformational change was used in various other *in vitro* approaches. One of these methods allows the detection of ligands based on their ability to increase PPAR/RXR DNA binding in gel shift assays. This ligand-induced complex formation assay (LIC) provided results similar to CARLA [35, 36], as did an assay called differential protease sensitivity assay (DPSA), based on ligand-induced protease resistance of the LBD [37]. In addition, consistent results with respect to polyunsaturated fatty acid binding to PPAR α were also obtained using a fluorescence-based method of ligand displacement [38]. Using this assay, polyunsaturated fatty acids such as arachidonic acid and linoleic acid showed apparent K_d values in the nanomolar range (17.3 nM for arachidonic acid, 4.8 nM for linoleic acid). Further investigations identified some eicosanoids as PPAR α ligands. In particular, leukotriene B₄ (LTB₄) produced from arachidonic acid via the lipoxygenase pathway, binds to PPAR α with a K_d of 60–90 nM [38, 39]. The discovery that this molecule, which is well characterized for its implication in chemotaxis [40], is a PPAR α ligand provided a link between this nuclear receptor and inflammation. Confirming this observation, the duration of a LTB₄ or arachidonic acid-induced inflammatory response is enhanced in the PPAR α knockout mouse compared to the wild-type mouse. This result suggests that by binding to PPAR α , LTB₄ might induce its own degradation via the ω - and β -oxidation pathways through PPAR α activation. In PPAR α knockout mice, these catabolic pathways would not be stimulated, hence the increased duration of the inflamma-

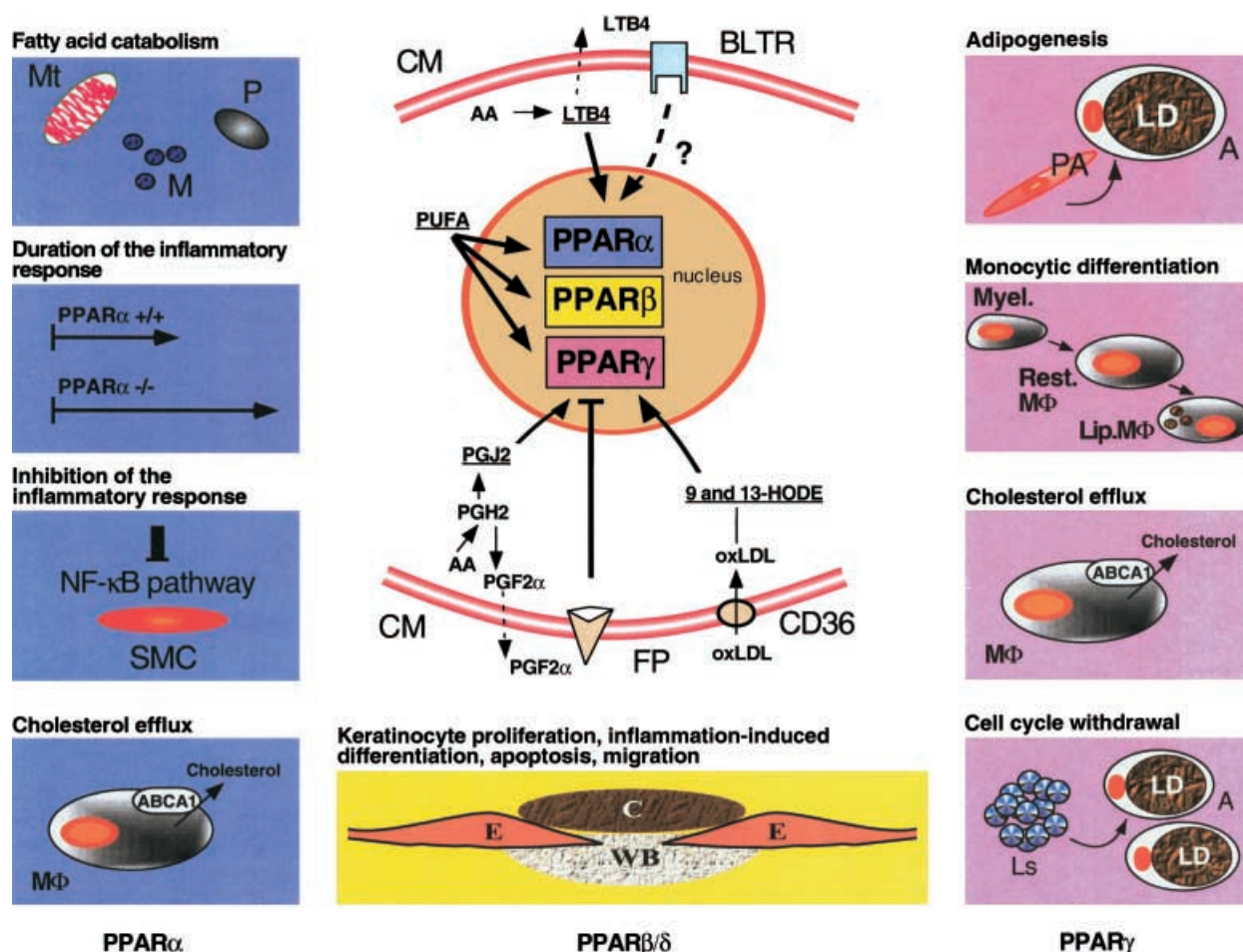


Figure 2. Schematic representation of PPAR functions. PPARs are located in the cell nucleus, where they modulate gene expression, mostly in a ligand-dependent manner. PPAR α (blue boxes) is activated by polyunsaturated fatty acids (PUFA) and by an arachidonic acid (AA) derivative, the LTB $_4$. This latter also binds a membrane receptor (BLTR) with a very high affinity. The cross-talk between the membrane and the nuclear receptor for LTB $_4$ is not yet elucidated. PPAR α is able to enhance expression of genes involved in fatty acid catabolism in mitochondria (Mt), peroxisomes (P) and microsomes (M). In parallel, PPAR α is capable of reducing the duration of an inflammatory reaction in wild-type mice as compared to PPAR α -/- mice, of inhibiting the inflammatory response in smooth muscle cells (SMC) and can stimulate cholesterol efflux from human macrophages (M Φ). PPAR β (yellow boxes) is activated by PUFA. In an in vivo model of skin wound healing (E, epidermis; C, clot; WB, wound bed), PPAR β was recently shown to be involved in the control of keratinocyte proliferation, in inflammation-induced keratinocyte differentiation and in the increase of keratinocyte resistance to TNF- α -induced apoptosis. In addition, PPAR β is also implicated in embryo implantation, myelinization, lipid metabolism and adiposity. PPAR γ (purple boxes) is activated by PUFA, by a PGJ $_2$ metabolite, which derives from AA and by oxidized LDL components, 9- and 13-HODE, which are internalized in the cell via the CD36 scavenger receptor. PPAR γ is a key regulator of adipogenesis and is implicated in the differentiation of pre-adipocytes (PA) to adipocytes (A), characterized phenotypically by their lipid droplets (LD). Monocytic differentiation is also influenced by PPAR γ . In the presence of PPAR γ and RXR ligands, myeloid cell precursors (Myel.) become resting macrophages (Rest. M Φ). These resting M Φ can be turned to lipid-containing M Φ (lip. M Φ) when the PPAR γ and RXR ligands are maintained. In human macrophages (M Φ), and in association with PPAR α , PPAR γ can stimulate cholesterol efflux. PPAR γ is also capable of withdrawing liposarcoma-derived cells (Ls) from cell division to trigger their differentiation to adipocytes (A). Besides transcriptional activation, PPAR γ function can be inhibited by PGF-2 α , which binds to a membrane receptor (FP) located at the cell membrane (CM). This triggers MAPK activation, which phosphorylates PPAR γ , and inhibits its function.

tory response (see fig. 2). Consistent with PPAR α being involved in the control of inflammatory responses, cutaneous wound healing was shown to be impaired in PPAR α null mice during the inflammatory phase of the process [41]. Along the same lines, PPAR α ligands were shown to inhibit the inflammatory response in aortic smooth muscle cells [42], an effect that is lost in the PPAR α null mice [43]. This occurs through the inhibition

of interleukin-1-mediated expression of interleukin-6 and cyclooxygenase-2. The transcriptional inhibition of this key enzyme of the inflammation process occurs as a result of a PPAR α -dependent repression of the nuclear factor kappa B (NF- κ B) pathway (see fig. 2). In addition to LTB $_4$, another lipoxygenase metabolite, the 8(*S*)-hydroxy-eicosatetraenoic acid (HETE), was also revealed as a PPAR α ligand [16, 35]. This eicosanoid is associated

with phorbol ester-induced inflammation, but so far no study has addressed the question of a role of PPAR α in this particular mechanism. In addition to its regulatory role in inflammation processes, and in association with PPAR γ , PPAR α was shown to mediate cholesterol efflux from human macrophages. This is likely due to the induction of the nuclear receptor LXR (NR1H3, [10]) expression, which in turn upregulates the expression of the reverse cholesterol transporter ABCA1. It will be interesting in the future to assess the clinical effects of PPAR α agonists on acute inflammatory situations and atherosclerosis.

PPAR β

PPAR β is so far the most elusive among the three PPAR isotypes. Due to its broad tissue distribution, it is difficult, a priori, to foresee a specific function for this receptor. A mouse knockout model, although difficult to generate due to a highly penetrant lethality [41, 44], indicates a role for PPAR β in embryo implantation, as well as in myelination, lipid metabolism and adiposity [44, 45]. In an in vivo skin wound healing model, PPAR β was recently shown to be involved in the control of keratinocyte proliferation, to be necessary for inflammation-induced keratinocyte differentiation and to increase keratinocyte resistance to tumor necrosis factor- α (TNF- α)-induced apoptosis [41, 46]. PPAR β can also be activated by peroxisome proliferators and fatty acids to induce gene expression [16, 22], although transcriptional activation by these compounds appears weaker than for PPAR α . Interestingly, the activator profile is also biased towards the polyunsaturated fatty acids, which has to do with structural constraints in the LBD and the flexibility provided by the double bonds in the hydrocarbon chain of polyunsaturated fatty acids. In an attempt to identify naturally occurring ligands for PPAR β , acetone extracts of rat tissues were shown to contain an activity that enhances PPAR β -mediated transcription [47]. High-pressure liquid chromatography (HPLC) purification of this activity identified methylpalmitate as a potent activator. This compound, however, also activates the PPAR α isotype. Therefore, the hunt for natural selective ligands of PPAR β is still open. There are, however, synthetic molecules able to selectively activate PPAR β . Using a focused combinatorial library, biased towards PPAR binding, it was possible to identify a fibrate derivative, the GW 2433 compound, capable of selectively activating the PPAR β isotype [48]. Two other synthetic compounds, the L165041 (a phenoxycetic acid derivative) and GW501516 are PPAR β -selective agonists [49, 50]. However, PPAR β shows species-dependent binding characteristics [51]. For instance, bezafibrate is a *Xenopus* PPAR β specific ligand, but its activity is much weaker on the mammalian β isotype than it is on the mammalian α isotype [16].

Knowledge concerning PPAR β functions and identification of PPAR β selective synthetic ligands are still recent. There-

fore, the therapeutic potential of this receptor is still unknown. The development of an adequate knockout system for PPAR β and the discovery of the physiological ligands will certainly be of very high interest in the near future.

PPAR γ

A more restricted profile of activators distinguishes PPAR γ from the two other PPAR isotypes. Indeed, PPAR γ is more selective for polyunsaturated fatty acids versus other fatty acids [16, 52]. Another interesting feature is its limited tissue distribution: abundant in adipose tissue, and at much lower levels elsewhere [53, 54]. Using retrovirally transduced cells, it was possible to demonstrate that PPAR γ is a major player in the adipocyte differentiation program [55, 56]. Uncommitted fibroblasts can be driven by PPAR γ to become adipocytes in a ligand-dependent way (see fig. 2). A ligand-dependent role of PPAR γ was also established in the transdifferentiation program of myoblasts to adipocytes [57]. Together, these observations reveal the primordial role of PPAR γ in the definition of the adipocytic fate, and its study contributes to a better understanding of the adipocyte lineage within the organism. Furthermore, the finding that synthetic compounds with antidiabetic properties are true PPAR γ ligands [58] attracted much attention on this isotype. The thiazolidinediones (TZD) group of molecules (troglitazone, pioglitazone and rosiglitazone/BRL 49653) act positively on insulin action and negatively on glucose levels in the blood. They are able first to bind PPAR γ , and then trigger adipogenesis. Moreover, they provide a very plausible link between the regulation of glucose status and PPAR γ activity [59]. A possible mechanism by which TZDs reduce insulin resistance is that they direct fatty acids away from skeletal muscle by stimulating their uptake by the adipose tissue. As a result, there would be increased glucose utilization by skeletal muscles. However, it has been observed that mice lacking adipose tissue still benefit from reduction of insulin resistance in response to TZD treatment [60], suggesting that an additional mechanism is at work. Interestingly, L-tyrosine-based insulin sensitizers are also PPAR γ ligands, which reinforces the role of PPAR γ in insulin resistance [26]. In addition to polyunsaturated fatty acids, the prostanoid 15 Δ -prostaglandin J₂ (PG J₂) was identified as a PPAR γ ligand [16, 61, 62]. This molecule derives from arachidonic acid, via the cyclooxygenase-2 pathway that produces prostaglandins. It is not clear, however, whether this molecule is the physiological ligand of PPAR γ . In terms of natural PPAR γ ligands, an interesting model is the one provided by the monocytic lineage [63]. Indeed, PPAR γ is well expressed in activated macrophages [64]. In these cells, PPAR γ expression is induced by oxidized LDL (oxLDL). Analysis of oxLDL lipid content revealed the presence of two oxygenated derivatives of linoleic

acid, which are 9-HODE and 13-HODE (hydroxyoctadecadienoic acid), two PPAR γ ligands. Their affinity for PPAR γ is comparable to their precursor, linoleic acid. However, a concerted series of events could favor the action of 9- and 13-HODE as ligands. Indeed, the cell surface scavenger receptor CD36, whose gene is a target of PPAR γ [64], is involved in the uptake of oxLDL by the cell, hence providing a source of ligands for PPAR γ . Interestingly, the activation of PPAR γ seems to be antiatherogenic in macrophages [65–67]. In fact, the internalization of lipids by CD36 is counterbalanced by a PPAR γ -mediated upregulation of the reverse cholesterol transporter ABCA1 expression, probably through the enhanced expression of the nuclear receptor LXR. The whole cascade results in a net lipid efflux. It is interesting to note that CD36 is also upregulated during the adipogenic program and that a dynamic lipid flux could occur in these differentiated cells, as it is the case in macrophages.

Finally, an indirect consequence of PPAR γ association with the adipocyte differentiation pathway is its potential ability to drive dividing cells towards a differentiated adipocytic state [68]. This can occur in liposarcomas, where PPAR γ is expressed. Under the effect of TZD, PPAR γ action withdraws these malignant cells from the cell cycle [69]. The overall effect in cell culture is the growth arrest of the sarcoma (see fig. 2). In clinical trials, the administration of TZD to patients suffering from liposarcoma induced a terminal adipocytic differentiation of tumor cells, with the downregulation of cell proliferation markers [70]. Interestingly, the treatment of liposarcoma cells with retinoids enhances the TZD effect, since PPAR γ functions as a heterodimer with RXR (retinoid X receptor). A similar situation is observed in breast adenocarcinoma cells, with respect to the ability of PPAR γ to reduce cell growth [71]. It will be interesting, in the future, to test whether natural PPAR γ ligands are also able to trigger growth arrest in carcinogenic situations. In contrast to these observations, PPAR γ agonists were shown to increase the frequency and size of colon tumors in mice bearing a mutation in the adenomatous polyposis colon tumor suppressor gene (APC) [72, 73]. It is possible that depending on the context, PPAR γ action could be either beneficial or deleterious. The debate is still open and deserves further study.

Cross-talk with endocrine signaling pathways

The transcriptional activity of PPARs is influenced by the endocrine status of the cell. Clearly, retinoids positively affect PPAR-RXR heterodimer activity by binding to RXR [22, 74]. Inversely, thyroid hormone, which controls some fatty acid metabolism genes via its nuclear receptor (TR), seems to act negatively on PPAR action. An exam-

ple of this negative effect is the inhibition of ciprofibrate-induced expression of the rat peroxisomal enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase gene by thyroid hormone [75]. Ciprofibrate, which is a fibrate derivative, acts through PPAR to activate transcription. The inhibitory effect of thyroid hormone might involve the titration of RXR, which becomes limiting for PPAR [76]. This functional inhibition could also involve non-RXR interacting molecules which remain to be identified. Another important cellular status for PPAR activity is the fatty acid content of the cell. Indeed, fatty acids and their derivatives participate in transcriptional signaling cascades [77], having more than their traditional structural and energy-providing roles. As mentioned earlier, PPAR γ is the nuclear receptor for 15 Δ -prostaglandin J₂, which derives from PGH₂, a cyclooxygenase 2-dependent metabolite of arachidonic acid. PGH₂ is also catabolized to PGF₂ α . This prostanoid is targeted to the outer cell membrane and binds to a G-protein-coupled receptor [78]. Interestingly, PGF₂ α is able to inhibit PPAR γ functions in adipogenesis [79] (see fig. 2). This occurs through PGF₂ α activation of the MAPK pathway, and subsequent PPAR γ phosphorylation and inhibition of its transcriptional activity. A similar cell membrane-nuclear receptor cross-talk occurs with PPAR α . Indeed, a membrane receptor for LTB₄ has been cloned [80], and it can share ligands with PPAR α [36]. It will be interesting to evaluate whether LTB₄ signaling at the cell membrane is linked to PPAR α activity. Finally, the nuclear receptor LXR, which binds cholesterol derivatives, such as the 24(S)-hydroxycholesterol [81], is implicated in the regulation of cholesterol homeostasis. LXR α knockout mice show impaired bile acid metabolism under high-cholesterol diet. This defect in LXR eventually leads to a serious alteration in liver function [82]. Since both PPAR and LXR are regulated by diet and interact with RXR to activate transcription, it is not surprising that LXR and PPAR functions are interconnected [83, 84].

Concluding remarks

The exploration of PPAR biology was one of the most fruitful in the world of nuclear hormone receptors. PPARs are implicated in many cellular processes, from cell cycle to cell differentiation, from inflammation to apoptosis, and are crucial for energy homeostasis [25]. The design of selective ligands for each isotype, agonists and antagonists, has been and will be interesting for both fundamental and therapeutic applications. Academic and pharmaceutical research have been complementary in the discovery of new ligands in a sort of ‘pharma cycle’: (i) identification of novel natural ligands by classical means, (ii) design of combinatorial libraries, (iii) in vitro testing, based on induced structural conformational changes, or

other characteristics and (iv) *in vivo* analyses, using cell-based approaches and animal models. Understanding how eicosanoids can influence PPAR-mediated gene expression will require better understanding of the intracellular and intranuclear concentration and trafficking of these substances. Most fatty acid derivatives are subject to oxidation processes as well as to interaction with transport molecules, which has to be taken into account in receptor-ligand interaction studies. This could also apply for RXR, the heterodimer partner of PPAR. Not least, ligand diversity coupled to subtle differences in the induced modifications of the LBD three-dimensional structure may determine the composition of interacting proteins in the machinery responsible for transcriptional initiation. This diversity would participate in the numerous PPAR functions within the organism.

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