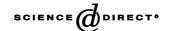


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### Nuclear receptor signaling in macrophages

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#### **Abstract**

Macrophages play diverse roles in host defense and in maintenance of homeostasis. Based on their ability to promote inflammatory responses, inappropriate macrophage function also contributes to numerous pathological processes, including atherosclerosis, rheumatoid arthritis and inflammatory bowel disease. Members of the nuclear receptor superfamily of ligand-dependent transcriptions factors have emerged as key regulators of inflammation and lipid homeostasis in macrophages. These include the glucocorticoid receptor (GR), which inhibits inflammatory programs of gene expression in response to natural corticosteroids and synthetic anti-inflammatory ligands such as dexamethasone. Also, in response to endogenous eicosanoids and oxysterols, respectively, peroxisome proliferator-activated receptors (PPARs) and liver X receptors (LXRs) regulate transcriptional programs involved in inflammatory responses and lipid homeostasis. Identification of their mechanisms of action should help guide the development of new therapeutic agents useful in the treatment of diseases in which macrophages play critical pathogenic roles.

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#### 1. Introduction

Nuclear receptors (NR) are members of a superfamily of ligand-dependent transcription factors that regulate diverse aspects of reproduction, development, homeostasis and immune function [1–6]. The NR superfamily includes receptors for steroid hormones, such as the estrogen (ER) and glucocorticoid (GR) receptors, receptors for nonsteroidal ligands, such as the thyroid hormone (TR) and retinoic acid (RAR) receptors, as well as receptors that bind diverse products of lipid metabolism, such as peroxisome proliferator-activated (PPAR) and liver X receptors (LXR). The NR superfamily also includes a large number of orphan receptors for which ligands have not been identified [5,6]. Several members of the NR superfamily have been shown to play important physiologic roles in macrophages (Table 1). In this review, we will focus on these receptors and their role in macrophage biology.

Members of the NR superfamily share a common structure. There is a variable N-terminal region that contains a ligand-independent transactivation domain (AF1) and a highly conserved DNA binding domain (DBD), containing two zinc finger motifs that target the receptor to specific

DNA sequences known as hormone response elements (HREs). NRs also contain a C-terminal region with the ligand binding domain (LBD), the dimerization interface, and a ligand-dependent activation function (AF-2). Most NRs activate transcription as dimers, either homodimers or heterodimers with the retinoid X receptor (RXR), although a subset can bind and stimulate transcription as monomers. Upon ligand binding, nuclear receptors undergo a conformational change that coordinately dissociates corepressors and facilitates recruitment of coactivator proteins, thereby promoting transcriptional activation [7–11].

Members of the NR family regulate transcription by several mechanisms and they can both activate and inhibit gene expression [12]. The prototypic activity of NRs is ligand-dependent activation of transcription by binding to specific HREs in target genes [11,12]. Several mechanisms of transcriptional inhibition have also been established. In the absence of ligand, a subset of NRs that heterodimerize with RXR, including TR, LXR and RAR, are capable of actively repressing target genes by binding to HREs [13–16]. In addition, several other NRs, including GR, LXR and PPAR are capable of inhibiting the activities of other transcription factors, such as the activator protein-1 (AP-1) and the nuclear factor (NF)-kB, in a ligand-dependent manner. This effect does not require DNA binding by the NR and is referred to as transrepression.

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Table 1 NR expression in macrophage populations

NR	Expression in macrophage populations	Ligands
ERα (NR3A1) ERβ (NR3A2)	PM, BMDM, blood monocytes, osteoclasts, microglia, Kupffer cells, dendritic cells <sup>a</sup> [30,153,153–157] Osteoclasts [155]	17β-Estradiol, androstenedione, 3β,17β-androstenediol [37,158]
GRα (NR3C1) GRβ (NR3C2)	PM, dendritic cells, microglia, osteoclasts, blood monocytes <sup>a</sup> [57,159–162] Osteoclasts, alveolar macrophages [160,162]	Glucocorticoids [163]
LXRα (NR1H3), LXRβ (NR1H2)	PM, BMDM, Kupffer cells [15,115,164]	22( <i>R</i> )-Hydroxycholesterol, 24( <i>S</i> )-hydroxycholesterol, 24( <i>S</i> ),25-epoxycholesterol, 27-hydroxycholesterol [47,165]
PPARα (NR1C1) PPARγ (NR1C3) PPARδ (NR1C2)	Human blood monocytes, low levels in Kupffer cells [72,164] PM, Kupffer cells, dendritic cells, microglia [19,153,164,167–169] PM, BMDM, Kupffer cells, osteoclasts <sup>a</sup> [19,164,170]	LTB4, 8-HETE, Fas [166] PUFAs, FAs, 15d-PGJ2, TZDs, 13-HODE, 9-HODE, 5-HETE [166] FAs, carbaprostacyclin [166]
RARα (NR1B1) RARβ (NR1B2) RARγ (NR1B3)	Kupffer cells, dendritic cells, osteoclasts, blood monocytes [171–173] Kupffer cells, blood monocytes, dendritic cells [171,172] Microglia, Kupffer cells [171,176]	ATRA, 9-cis-RA [174,175]
RXRα (NR2B1)  RXRβ (NR2B2)  RXRγ (NR2B3)	PM, BMDM, blood monocytes, microglia, Kupffer cells, dendritic cells <sup>a</sup> [171,172,176] Kupffer cells, osteoclasts [171,173] Kupffer cells [171]	9-cis-RA, FAs, methoprene acid, DHA [177,178]
TRα (NR1A1), TRβ (NR1A2)	Osteoclasts [179]	Thyroid hormones [180]
VDR (NR1I1)	BMDM [181]	1,25(OH) <sub>2</sub> D <sub>3</sub> [182]

The data represent documented expression of each nuclear receptor in macrophage populations. Most of the studies mentioned here are based on rodent models. However, we have to take into consideration that differences between species might exist. 1,25(OH)<sub>2</sub>D<sub>3</sub>, 1α,25-dihydroxyvitamin D3; 9-cis-RA, 9-cis-retinoic acid; ATRA, all-trans retinoic acid; DHA, docosahexaenoic acid; HODE, hydroxyoctadecadienoic acid; HETE, hydroxyeicosatetraenoic acid; LTB-4, leukotriene-4; PUFAs, polyunsaturated fatty acids; TZDs, thiazolidinediones; BMDM, bone marrow-derived macrophages; PM, peritoneal macrophages.

Transrepression is thought to be the primary mechanism by which nuclear receptors inhibit pro-inflammatory genes in macrophages [17–20].

# 2. Roles of nuclear receptors in macrophage differentiation

The expression of a number of NRs has been documented in macrophages (Table 1). While GR $\alpha$ , VDR, RARs, and LXRs are constitutively expressed in macrophages, ER $\alpha$  and PPAR $\gamma$  expression increases during macrophage differentiation [19,21,22]. In addition, PPAR $\gamma$  expression is upregulated during the inflammatory response, and can be induced *in vitro* by interleukin (IL)-4 and other immunoregulatory molecules [21,23]. In contrast, interferon (IFN)- $\gamma$  and lipopolysaccharide (LPS) repress the expression of PPAR $\gamma$  [24].

In macrophages, NRs have three general physiologic roles. First, they negatively regulate inflammatory responses mediated by AP-1 and NF- $\kappa$ B transcription factors. Emerging evidence suggests that these actions represent important functions of GR $\alpha$ , ER $\alpha$ , PPARs and

LXRs in the macrophage. NRs namely PPARs and LXRs also regulate lipid homeostasis. These two roles will be extensively discussed later in this review. The third role, mediated by a smaller subset of nuclear receptors, influences specialized programs of macrophage differentiation.

The macrophage lineage has the capability to give rise to a family of related cells that execute specialized roles, such as microglia, osteoclasts, Kupffer and dendritic cells [25]. Ligands for a number of NRs have been shown to affect the differentiation of these specialized macrophages. For example, precursors of the monocyte hematopoietic lineage stimulated with macrophage colony-stimulating factor (M-CSF) and receptor activator of NF- $\kappa$ B ligand (RANKL) can differentiate into mature bone-resorbing osteoclasts [26]. Interestingly, this differentiation program can be inhibited by the addition of either estrogenic [27] or PPAR $\gamma$  ligands [28]. In contrast, glucocorticoids also decrease bone resorption, but appear to do so by increasing osteoclast apoptosis [29].

In the presence of granulocyte-colony macrophage stimulating factor (GM-CSF) and IL-4, dendritic cells can be generated by *in vitro* differentiation of macrophage precursors. Corticosteroids, anti-estrogens or vitamin D analogs

<sup>&</sup>lt;sup>a</sup>A. Valledor, M. Ricote, G. Pascual, Unpublished results.

inhibit this differentiation program [30–33]. VDR ligands can also affect the tolerogenic properties of mature dendritic cells, favoring the induction of regulatory rather than effector T cell responses [34]. In addition, vitamin D analogs enhance the differentiation of monocytes into macrophages, suggesting that VDR plays a role balancing monocytic lineage developmental choices [35]. However the *in vivo* significance of these findings remains to be established. In a similar manner the thyroid hormone promotes the growth and morphologic differentiation of microglia [36].

### 3. Endogenous ligands (systemic vs. local)

Ligand availability represents one of the most important determinants of nuclear receptor activity. Classical steroid hormone receptors such as GR regulate macrophage gene expression in response to circulating hormones that are produced under the control of the hypothalamic–pituitary–adrenal axis. In contrast, PPARs and LXRs regulate gene

expression by responding to locally produced metabolites of fatty acid and cholesterol (Fig. 1).

Estrogen is an endocrine hormone regulated by the hypothalamic-gonadal axis. In addition differentiated macrophages express and regulate the enzyme aromatase, which converts serum dehydroepiandrosterone (DHEA) into the immunomodulatory estrogens 3β,17β-androstenediol and androstenedione [37]. Also, macrophages serve as an extra-renal source of 1\alpha,25-dihydroxyvitamin D<sub>3</sub>  $(1,25(OH)_2D_3)$ . 25-Hydroxyvitamin D3-1 $\alpha$ -hydroxylase (25(OH)D<sub>3</sub>-1α-hydroxylase), the key enzyme in 1,25-(OH)<sub>2</sub>D<sub>3</sub> production, is expressed in monocyte-derived macrophages. In addition, following LPS stimulation microglia and dendritic cells are able to produce 1,25(OH)<sub>2</sub>D<sub>3</sub> [32,38]. These studies suggest that the high localized production of 1,25(OH)<sub>2</sub>D<sub>3</sub> may serve as a paracrine signal during bacterial infection, favoring macrophage differentiation [32].

During inflammatory responses, PPARs can be activated by eicosanoids, which are produced by metabolism of

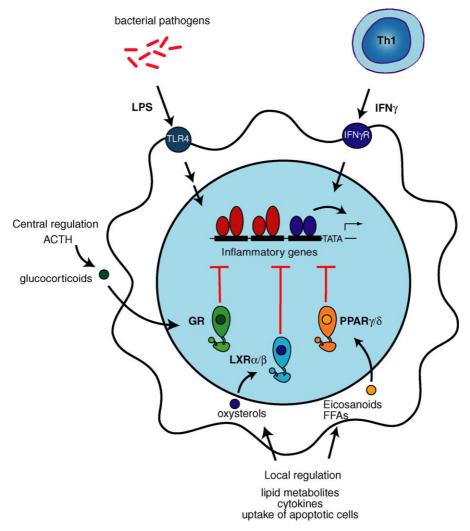


Fig. 1. PPARs, LXRs and GR inhibit inflammatory response genes in macrophages. GR regulates macrophage gene expression in response to circulating hormones that are produced under the control of the hypothalamic–pituitary–adrenal axis. PPARs and LXRs regulate gene expression by responding to locally produced ligands. ACTH, adrenocorticotrope hormone; FFAs, free-fatty acids; IFN-γ, interferon-γ; LPS, lipopolysaccharide; Th1, T helper cells.

arachidonic acid and other long chain polyunsaturated fatty acids (PUFAs) [39]. For example, ligands for PPAR $\alpha$  are leukotriene (LT)B4 and 8(S)-hydroxyecosatetraenoic acid (HETE), whereas 15-deoxy- $\Delta^{12,14}$ -prostaglandin J $_2$  (15d-PGJ2), 15-HETE and 13-hydroxyoctadecadienoic acid (HODE) act as ligands for PPAR $\gamma$ . 13-HODE and 15-HETE can be enzymatically generated by the IL-4 inducible 12/15-lipoxygenase, suggesting that IL-4 can coordinately regulate the expression and activity of PPAR $\gamma$  [23,40]. PPAR $\gamma$  is also activated by the thiazolidinedione class of drugs (TZDs) that act as insulin sensitizers and are used in the treatment of type 2 diabetes mellitus [41].

LXRs are activated by specific oxidized forms of cholesterol (oxysterols) [42–44], such as 24(*S*)-hydroxycholesterol and 22(*R*)-hydroxycholesterol, or by certain intermediates of the cholesterol biosynthetic pathway such as 24(*S*),25-epoxycholesterol [44,45]. In macrophages, sterol 27-hydrolase (CYP27) is able to modify cholesterol into a naturally occurring ligand for LXRs [46,47]. NRs can regulate macrophage gene expression in response to changes in cellular lipids and arachidonic acid metabolites that occur during inflammatory responses.

## 4. Nuclear receptors in macrophage-mediated inflammation

Glucocorticoids are widely used to control a variety of inflammatory diseases including asthma, inflammatory bowel disease, systemic lupus erythematosus, dermatitis and arthritis [48-50]. Endogenous glucocorticoids are released in response to a variety of stressors (starvation, pain, trauma, infection, etc.) and are essential for maintenance of homeostatic functions (Fig. 1; [51]). The mechanistic basis of the anti-inflammatory actions of glucocorticoids remains poorly understood [48,49]. Accumulating evidence suggests that these effects largely result from inhibition of signal-dependent transcription factors that mediate inflammatory programs of gene activation such as NF-κB, AP-1 and STATs [49,52]. Genes that are strongly repressed by GR agonists include GM-CSF [53], cytokines (tumor necrosis factor (TNF)-α, IL-4, IL-5, IL-1, IL-6, IL-8, IL-12) [54,55], and inflammatory mediators (inducible nitric oxide synthase (iNOS) [56,57] and cyclooxygenase (COX)-2) [58]. Despite the requirement for the GR LBD and DBD for transrepression activity, the majority of the promoters and enhancers for these genes do not contain functional glucocorticoid response elements (GREs) [49,59,60]. These observations suggest that GRmediated transrepression involves mechanisms distinct from classical GR transactivation of target genes [61]. One established mechanism involves direct interaction between GR and negatively regulated transcription factors such as AP-1 and NF-κB [59,60]. Glucocorticoids also inhibit signaling of mitogen-activated protein kinase pathways that mediate the expression of inflammatory genes

[62,63]. A third proposed mechanism for transrepression involves competition for coactivator complexes [64,65]. Modification of the degree of phosphorylation of the C-terminal repeat of RNA polymerase at NF-κB target genes has also been suggested as the basis for the GR-mediated transrepression [66]. Recent work has shown that GR directly inhibits NF-κB-induced histone acetyltransferase (HAT) activity and recruits histone deacetylases [67]. These observations demonstrate that GR has multiple modes of action and shows the complexity of the crosstalk between signaling pathways.

Similar to GR, other NRs including ER, VDR, PPARs and LXRs antagonize the expression of an overlapping set of NF-κB and AP-1 regulated genes in macrophages (Fig. 1 and [18–20,68–73]). This transrepression function requires both the LBD and DBD, but there is no direct binding to HREs in the enhancer or promoter regions of these genes [20,70,73–75]. Mechanisms similar to GR-mediated transrepression have been suggested for other nuclear receptors. However to date, the mechanism of transrepression is not yet clear. VDR also inhibits inflammatory gene expression by downregulating NF-κB activation or by inducing the expression of both transforming growth factor (TGF)-β and IL-4 [76]. Likewise 1,25-(OH)<sub>2</sub>D<sub>3</sub> has been shown to ameliorate experimental autoimmune encephalomyelitis, rheumatoid arthritis, systemic lupus erythematosus, and inflammatory bowel disease [76].

In the last few years, PPARs and LXRs have emerged as key regulators of inflammatory and immune responses in macrophages [77-91]. Natural and synthetic PPARγ ligands have been shown to exert anti-inflammatory effects in murine models of atherosclerosis, inflammatory bowel disease, allergic encephalomyelitis and psoriasis [77–81,86–91]. In those studies, PPARγ agonists were shown to inhibit the induction of inflammatory genes by LPS, IL-1 $\beta$  and IFN- $\gamma$ . However, the mechanism and the validity of the anti-inflammatory role for PPARs is very controversial. 15d-PGJ2 was found to inhibit NF-κBdependent transcription through a PPARy-independent mechanism [92,93] and the doses of TZDs that exert maximal inhibitory effects on LPS-inducible genes are significantly higher than the concentration at which these compounds bind efficiently to PPARy [19,94]. Furthermore, two reports have shown that deletion of the PPAR $\gamma$ gene in stem cell-derived macrophages does not alter basal or stimulated cytokine production [94,95]. In addition, these studies showed that high concentrations of PPARy ligands still inhibit cytokine responses to LPS stimulation in PPARγ-null cells. These findings suggest that PPARγ ligands exert some of their anti-inflammatory effects independently of the expression of PPAR $\gamma$ .

More recent studies using mRNA expression profiling and PPAR $\gamma$  knockout macrophages demonstrated that the inhibitory effects of rosiglitazone on LPS and IFN- $\gamma$  responses are PPAR $\gamma$ -dependent when the drug is used at concentrations close to their binding affinity. However,

at higher concentrations the inhibitory effects are PPAR $\gamma$ -independent [24]. Several lines of evidence suggest that PPAR $\gamma$ -independent effects of rosiglitazone are due to activation of PPAR $\delta$  [24]. These studies establish overlapping transrepression functions of PPAR $\gamma$  and PPAR $\delta$  in macrophages. A recent manuscript has suggested that PPAR $\delta$  represses inflammatory genes including the chemokine monocyte-chemoattractant protein-1 (MCP-1), IL-1 $\beta$  and the metalloproteinase MMP-9 by an unconventional ligand-dependent transcriptional mechanism involving the binding of PPAR $\delta$  to transcriptional repressors [96].

Interestingly, rosiglitazone has recently been shown to reduce circulating concentrations of inflammatory markers of cardiovascular disease in type 2 diabetic patients such as C-reactive protein, MMP-9 and TNF- $\alpha$  [97]. These findings suggest that negative regulation of gene expression may also be the basis for some of the insulin-sensitizing effects of rosiglitazone observed in diabetic patients.

Recently, LXR agonists have been shown to inhibit the macrophage response to bacterial pathogens and to antagonize a number of pro-inflammatory genes in macrophages. These include IL-1 $\beta$ , IL-6, MMP-9, iNOS, COX-2, MCP-1 and MCP-3, macrophage inflammatory protein (MIP)-1 $\beta$  and IP-10 [20,73]. LXR-deficient mice

exhibited enhanced responses to inflammatory stimuli and LXR ligands reduced inflammation in murine models of contact dermatitis [20] and atherosclerosis [84,85]. These observations suggest that LXR and PPAR agonists may exert their anti-atherogenic effect at least in part by limiting the production of inflammatory mediators in the arterial wall [98].

## 5. Nuclear receptors in macrophage-mediated lipid homeostasis

Tight regulation of cellular lipid levels is necessary for the maintenance of normal cellular functions. LXRs and PPARs are critical orchestrators of macrophage lipid homeostasis (Fig. 2). Like most cells, macrophages take up circulating lipoproteins via the low-density lipoprotein (LDL) receptor [99]. Excess cholesterol inhibits proteolytic activation of sterol regulatory element binding proteins (SREBPs), which are transcription factors that promote cholesterol and triglyceride biosynthesis and LDL receptor expression [100]. Resident macrophages also secrete molecules that modify extracellular LDL, e.g. by oxidation (oxLDL), converting it into a form that is efficiently recognized by macrophage scavenger receptors, such as

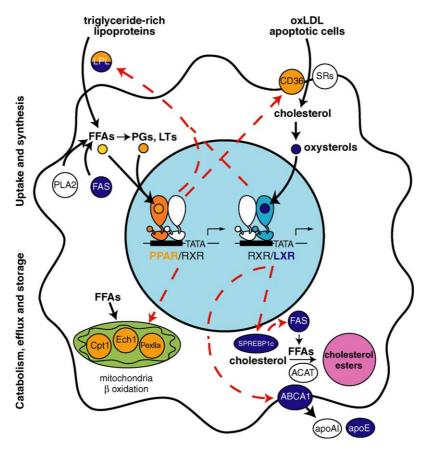


Fig. 2. LXRs and PPARs regulate the expression of genes involved in macrophage lipid homeostasis. LXR target genes are indicated in blue, while PPAR target genes are shown in orange. ACAT, acetyl-coenzyme A acyltransferase; FFAs, free fatty acids; LTs, leukotriens; PGs, prostaglandins; PLA2, phospholipase A2; SRs, scavenger receptors.

CD36 [101]. Unlike native LDL, oxLDL fails to downregulate scavenger receptors resulting in massive cholesterol accumulation and conversion of macrophages into foam cells, a major hallmark of early atherosclerotic lesions [102-105]. The lipid content in macrophages is also influenced by phagocytosis of apoptotic bodies and necrotic cells, a process mediated by CD36 and other scavenger receptors [106]. Several studies have shown that the CD36 gene is a direct target of PPAR $\gamma$  [94,95,107,108]. The observation that oxidized lipids present in oxLDL, including 9-HODE and 13-HODE, have the capability to activate PPAR $\gamma$  [107,108] suggests that this NR is involved in a positive feedback loop that drives foam cell formation. However, despite enhancing CD36 expression, TZDs do not significantly induce cellular cholesterol accumulation in mouse or human primary macrophages [95,109]. Indeed, an anti-atherogenic role has been recently established for PPARy based on the use of different murine models of atherosclerosis [77–81].

Lipid efflux is critical for maintaining macrophage lipid homeostasis. Members of the ATP-binding cassette (ABC) family of transporters have been recently implicated in mediating lipid efflux from a variety of cells, including macrophages. In particular, ABCA1 transports intracellular phospholipids and cholesterol to exogenous nascent HDL particles, which contain lipid-poor apolipoprotein (apo) acceptors, such as apoAI [110]. This mechanism plays an important role in reverse cholesterol transport, the process by which cholesterol is mobilized from peripheral cells to the liver for its conversion to bile acids [111]. Mutations in ABCA1 result in Tangier disease, a condition in which patients have extremely low levels of circulating HDL, massive accumulation of cholesterol in tissue macrophages, and an increased risk for developing atherosclerosis [112,113]. Therefore, upregulation of ABCA1 potentially exerts protective effects by clearing excess cholesterol from macrophages in the arterial wall. Studies have established the connection between nuclear receptor action and reverse cholesterol transport by demonstrating that LXRs directly regulate ABCA1 expression and cholesterol efflux in human and murine cells, including macrophages [114-117]. In line with these observations LXR ligands have been recently shown to inhibit the development of atherosclerosis in mice [82,84,85].

Crosstalk between the PPAR and the LXR pathways has been shown to be important in the regulation of lipid efflux. Two independent studies demonstrated that PPAR $\alpha$  and PPAR $\gamma$  upregulate the expression of ABCA1 and promote cholesterol efflux in human macrophages through a transcriptional cascade mediated by LXR $\alpha$  [81,109]. The ability of TZDs to stimulate cholesterol efflux was completely abolished in PPAR $\gamma$ -null embryonic stem cells [81,118]. However, discrepancies exist between different macrophage models, as other groups have observed little or no effect of PPAR $\gamma$  agonists on ABCA1 or LXR $\alpha$  expression in murine primary macrophages [24,80].

LXRs and PPARs affect lipid efflux in macrophages by additional mechanisms. First, PPARa agonists reduced cholesterol esterification resulting in increased availability of free cholesterol for efflux via the ABCA1 pathway [119]. Second, PPARa stimulates cholesterol efflux from macrophage-derived foam cells via upregulation of the CLA-1/SR-BI system [120]. However, in conflict with these studies, PPAR $\alpha$  and PPAR $\gamma$  have been also shown to down-regulate the expression of macrophage cholesteryl ester hydrolase (CEH) [119,121], an enzyme required for hydrolysis and release of cholesterol from foam cells. Finally, both LXRs and PPARγ are able to directly induce the expression of another member of the ATP binding cassette family, ABCG1 [24,118,122], although the exact relevance of this regulation in lipid homeostasis needs to be determined.

Surprisingly, recent studies using microarray technology revealed that, in contrast to adipose tissue, only a limited subset of genes in macrophages is subject to positive regulation by PPARγ [24]. In addition to CD36 and ABCG1, PPARγ targets in macrophages include adipose differentiation-related protein (ADRP), α-mannosidase II, carnitine palmitoyl transferase (Cpt1) and the peroxisomal enzymes Ech1 and Pex11a. Interestingly, these experiments also revealed the considerable overlap between PPAR $\delta$  and PPAR $\gamma$  in the positive regulation of macrophage gene expression. However, the net effect of PPARδ activation in macrophage lipid homeostasis is controversial. Hydrolysis and uptake of triglycerides present in very low-density lipoproteins (VLDL) can activate PPAR $\delta$  in macrophages [123,124]. Treatment of macrophages with VLDL results in triglyceride accumulation and upregulation of ADRP in a PPARδ-dependent manner [123]. Furthermore, by upregulating genes involved in cholesterol uptake, including CD36 and SR-A, and downregulating genes implicated in lipid metabolism and efflux, such as cholesterol 27-hydroxylase (Cyp27) and apoE, PPARδ is thought to play a role in macrophage cholesterol accumulation [125]. This contrasts with the capability of PPAR $\delta$  to upregulate ABCA1 expression and cholesterol efflux [126]. However, recent studies using PPARδ-deficient mice confirmed a pro-atherogenic role for this nuclear receptor. Lesion reduction in PPARδ-/- mice was not related to changes in lipid uptake or efflux, but to the decreased expression of genes involved in inflammation and macrophage recruitment [96].

Macrophages participate in lipoprotein metabolism by secreting apolipoproteins (apo) and enzymes involved in lipoprotein modification. Treatment of human and murine macrophages with LXR agonists results in the induction of several apolipoproteins, including apoE, apoCI, apoCIV and apoCII [127,128]. PPARγ ligands also induce the expression of apoE [118]. Each of these apolipoproteins plays specific roles in lipid homeostasis. In particular, ApoE, a component of VLDL, intermediate-density lipoproteins (IDL) and chylomicron remnants, plays an

important anti-atherogenic role [129]. In the artery wall, secreted apoE promotes cholesterol efflux thereby reducing macrophage cholesterol ester accumulation [130–133], yet the relative importance of apoE-dependent cholesterol efflux, as compared with the ABCA1/apoAIdependent system has not been established. LXR, PPARa and  $\gamma$  ligands, have been also shown to positively modulate macrophage expression of lipoprotein modifying enzymes, including phospholipid transfer protein (PLTP) [134–136] and lipoprotein lipase (LPL) [118,137,138]. Intriguingly, despite the positive effect on mRNA expression, PPARa and  $\gamma$  activation was reported to result in a net reduction in LPL secretion and activity [138]. The effect of changes on LPL is not clear since this enzyme has been attributed both pro and anti-atherogenic properties [139–143]. The combined action of PLTP and LPL may result in enhanced generation of pre-β-HDL particles; LPL hydrolyzes VLDL and generates phospholipids and apolipoproteins that are subsequently transferred to pre-β-HDL particles by the action of PLTP [144–147]. The coordinated effects of LXR on LPL synthesis and cholesterol efflux probably enhance the clearance of cholesterol-rich lipoproteins from the arterial wall.

Despite their role in reverse cholesterol transport, LXR agonists promote fatty acid and triglyceride biosynthesis. In many cellular types, including macrophages, the expression of the transcription factor SREBP-1c is induced by LXR activation [148,149]. SREBP1c positively regulates the expression of a number of enzymes involved in fatty acid synthesis and triglyceride formation, including fatty acid synthase and stearoyl coenzyme A desaturase. LXRs can also directly bind and activate fatty acid synthase [150]. The positive regulation of lipogenesis by LXRs may be a mechanism to facilitate cholesterol esterification. In addition, fatty acid synthesis and its subsequent desaturation may provide ligands for other nuclear receptors, including PPARs [151].

The fact that synthetic LXR agonists are potent triggers of lipogenesis limits their potential use in the treatment of atherosclerosis. Recent studies show that unliganded LXR/RXR heterodimers actively repress target genes by recruiting corepressors (NCoR and SMRT) [15]. In LXR-deficient macrophages, corepressors fail to be associated to LXR target genes, which results in increased ABCA1 expression, but not SREBP1c. These findings suggest that the development of selective LXR modulators that disrupt the binding of LXR to corepressors without promoting coactivator recruitment may enhance cholesterol efflux without triggering lipogenesis.

#### 6. Conclusions and future directions

Macrophages express several members of the NR superfamily and are able to produce endogenous ligands for these receptors. Natural and synthetic ligands for these receptors influence inflammatory responses, specialized macrophage functions and lipid homeostasis. Recent progress in defining the physiological roles of these receptors suggests that they may be important targets for the development of new classes of ligands useful in the prevention and treatment of hyperlipidemia, diabetes and chronic inflammatory diseases, including atherosclerosis. While these findings have important biological and pharmacological implications, regulation of macrophage gene expression by members of the nuclear receptor family remains relatively unexplored. Future studies using engineered mouse models and functional genomic approaches are needed to clearly establish the mechanisms by which nuclear receptors exert their anti-atherogenic and antiinflammatory actions. These findings should allow the development of nuclear receptor-selective modulators that retain therapeutic actions with reduced side effects. For example, it may be possible to develop ligands for GR that retain the ability to inhibit NF-κB, without inducing gluconeogenesis [152]. Such ligands could exert antiinflammatory effects without many of the undesirable side effects of currently available steroid hormone analogs.

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