

Peroxisome proliferator-activated receptor γ (PPAR γ) and sepsis

Andreas von Knethen, Mathias Soller and Bernhard Brüne

Department of Biochemistry I-Pathobiochemistry, Johann Wolfgang Goethe-University Frankfurt, Faculty of Medicine, 60590 Frankfurt am Main, Germany

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Abstract

This review describes the role of the nuclear hormone receptor PPAR γ as a double-edged sword in sepsis. On the one hand, PPAR γ inhibits pro-inflammatory gene expression, predominantly by scavenging transcription factors and their cofactors, thus preventing them from binding to their cognate binding sites in the promoters of target genes. The expressions of the affected genes, such as those for inducible nitric oxide synthase, TNF- α , or IL-1 β , are repressed. Therefore, PPAR γ is suggested to be beneficial in hyper-inflammatory diseases, such as sepsis. In animal models of sepsis, PPAR γ agonist pretreatment auspiciously attenuated inflammation compared with control animals, accompanied by their improved survival rate. On the other hand, PPAR γ provokes apoptosis, which in the hyper-inflammatory phase of sepsis might be helpful because the number of immune cells, such as monocytes, macrophages, and neutrophils, involved in secreting high amounts of pro-inflammatory mediators will be reduced. In contrast, during the anti-inflammatory phase, cell death of immune cells, especially of T lymphocytes, is supposed to be deleterious. Under these circumstances, a second infection cannot be adequately answered, thus causing septic shock and multi-organ dysfunction syndrome. Therefore the role of PPAR γ is still ambiguous. Particularly its role in initiating apoptosis awaits further clarification to finally elucidate its impact on sepsis development.

Key words: inflammation, T cells, sepsis, apoptosis.

Corresponding author: Andreas von Knethen, Department of Biochemistry I-Pathobiochemistry, Johann Wolfgang Goethe-University, Faculty of Medicine, Theodor-Stern-Kai 7, 60590 Frankfurt/Main, Germany, tel.: +49 69 6301-6989, fax: +49 69 6301-4203, e-mail: v_knethen@zbc.kgu.de

SEPSIS

Sepsis is the most common cause of death in intensive care units. Although medical care has improved over the last decades, the incidence of sepsis and septic shock have increased significantly over the last 20 years [20, 35, 36]. It has been estimated that in the USA, 751,000 patients develop sepsis and septic shock every year, with an overall mortality rate of 28.6% [28]. In Europe, severe sepsis and septic shock affect three people in every 1000 and kill at least 135,000 patients each year [22].

A refined definition of sepsis was provided by Bone et al. in 1989 [6]. This definition was approved by the consensus conference of the American College of Chest Physicians and Society of Critical Care Medicine in 1991. As agreed, sepsis is characterized by a severe inflammatory response syndrome (SIRS) evoked by an infection. SIRS is defined as a general hyper-inflamma-

tory reaction of various causes, such as infection, trauma, or burn [7]. If organ dysfunction occurs, it is designated as severe sepsis, which often results in septic shock. Because this definition was established more than 10 years ago, many new insights in sepsis pathophysiology were not considered in this sepsis criterion. However, sepsis basically is characterized by high or very low blood temperature, palpitations, cool blue extremities, and low blood pressure. An extreme fall in blood pressure, which starves the major organs, results in septic shock [2, 15].

During sepsis, the interaction of infection and immunity is very important. The origin of infection is unimportant for sepsis development. All pathogens can thus possibly induce sepsis. Immune cell-pathogen contact induces an inflammatory response by the activation of monocytes, macrophages, and neutrophils [4, 17]. These cells release tumor necrosis factor (TNF)- α and interleukin (IL)-1 β , the primary pro-inflammatory

cytokines (Fig. 1), provoking local immune responses such as vascular dilatation, causing a lower blood pressure [15]. This immune response is boosted by a panel of secondary pro-inflammatory mediators, such as reactive oxygen or nitrogen species and degradation products from fatty acids. Additionally, the coagulation cascade is triggered, decreasing fibrinolysis, which causes the formation of micro-thrombi in capillaries and finally evokes multi-organ dysfunction syndrome (MODS) [39]. Following this hyper-inflammatory phase, or sometimes occurring simultaneously, soluble TNF- α receptors, IL-1-receptor antagonists, IL-4, or IL-10 are produced as anti-inflammatory molecules switching the cellular phenotype from pro- to anti-inflammatory (Fig. 1). This is often accompanied by cell death of immune-competent cells, which finally amplifies the anti-inflammatory response [24, 46].

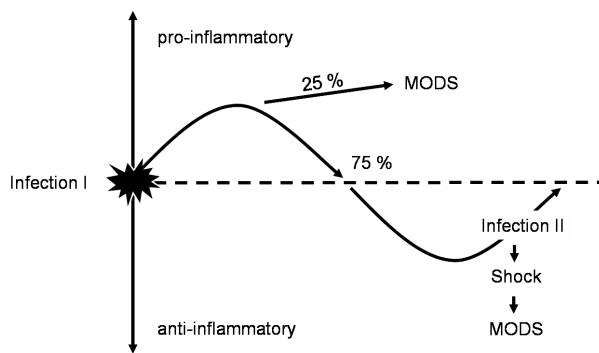


Fig. 1. Sepsis is immunologically divided into two phases. The first is characterized by a hyper-inflammatory state of the immune system, accompanied by the synthesis of large amounts of pro-inflammatory cytokines (TNF- α , IL-1 β) and other mediators (ROS, NO). In 25% of all cases this may finally result in the development of MODS, often followed by the death of the patient. Often (75%) the first phase is followed by a second period, where anti-inflammatory mechanisms prevail, confining the hyper-inflammatory phase. However, a secondary infection in this phase may provoke a second formation of MODS, with its harmful consequences.

In general, an immune response should be confined after the infection has terminated. However, under certain circumstances the immune response is shut off, which provokes a shift to an anti-inflammatory and desensitized phenotype, although the infection has not been completely eliminated. Therefore, the pathogen might provoke a second infection, which now cannot be appropriately answered by an immune response. During sepsis, this stage is referred to as compensatory anti-inflammatory response syndrome (CARS) and is often accompanied by septic shock and MODS [16, 30].

Therefore, improvement of therapy strategies to treat this pathological setting is mandatory. Because it is well established that sepsis is a systemic inflammatory response, attended by an excessive synthesis of pro-inflammatory cytokines and the release of other mediators, such as nitric oxide or basic degradation products

from fatty acids, finally causing septic shock and MODS, approaches which inhibit the immoderate production of pro-inflammatory messenger molecules are gaining increased interest.

PPAR γ – A MODULATOR OF INFLAMMATORY GENE EXPRESSION

One more recently identified factor which is of potential interest for the therapy and, most likely, the prevention of sepsis is PPAR γ . PPAR γ belongs to the nuclear hormone receptor family. It was originally identified as most essential in glucose metabolism [14]. Thus, synthetic PPAR γ agonists, the so-called “thiazolidinediones” (TDZs), are used in diabetes type 2 therapy as insulin sensitizers [49]. However, not only this function of PPAR γ is interesting for its use in sepsis treatment, but also its anti-inflammatory properties, which have been characterized in immune cells such as B and T lymphocytes, monocytes, macrophages, dendritic cells, and granulocytes [3, 27, 34, 42, 45, 48]. PPAR γ is a transcription factor which, upon ligand binding, forms a heterodimer with the retinoic acid X receptor α and then binds to peroxisome proliferator-activated receptor response elements in the promoter region of its target gene, provoking its expression or repression. Interestingly, PPAR γ cannot only act via DNA binding, but also in a DNA-independent manner. This attribute is important for its anti-inflammatory role because this feature is mainly responsible for blocking pro-inflammatory gene expression.

So far, five different PPAR γ -dependent mechanisms have been identified. First, PPAR γ can scavenge transcriptional co-factors, such as steroid receptor co-activator-1 (SRC-1) or CREB binding protein (CBP/p300). Bound to PPAR γ , these co-factors are not available for initiating gene expression (Fig. 2A). Because transcriptional co-factors are indispensable for nuclear factor (NF)- κ B-dependent gene induction, NF- κ B-mediated pro-inflammatory cytokine expression is retained [26, 27]. Second, PPAR γ can also directly associate with transcription factors such as NF- κ B, NF-AT, AP-1, or STAT. These are important transcription factors involved in pro-inflammatory gene expression. Blocking them causes a significant attenuation of pro-inflammatory gene expression (Fig. 2B) [9, 18, 37, 41, 45, 48]. Third, PPAR γ can inhibit mitogen-activated protein kinase (MAPK) by a so far unknown mechanism [13]. This inhibition prevents MAPK from phosphorylating and thereby activating downstream transcription factors, which are necessary for MAPK-dependent pro-inflammatory gene expression (Fig. 2C). Additionally, PPAR γ can block protein kinase C (PKC) α translocation and thereby PKC α signaling, which normally provokes activation of the NADPH oxidase system and production of reactive oxygen species, known as the respiratory burst of macrophages [23]. The underlying principle in this case is not completely clear, but due to

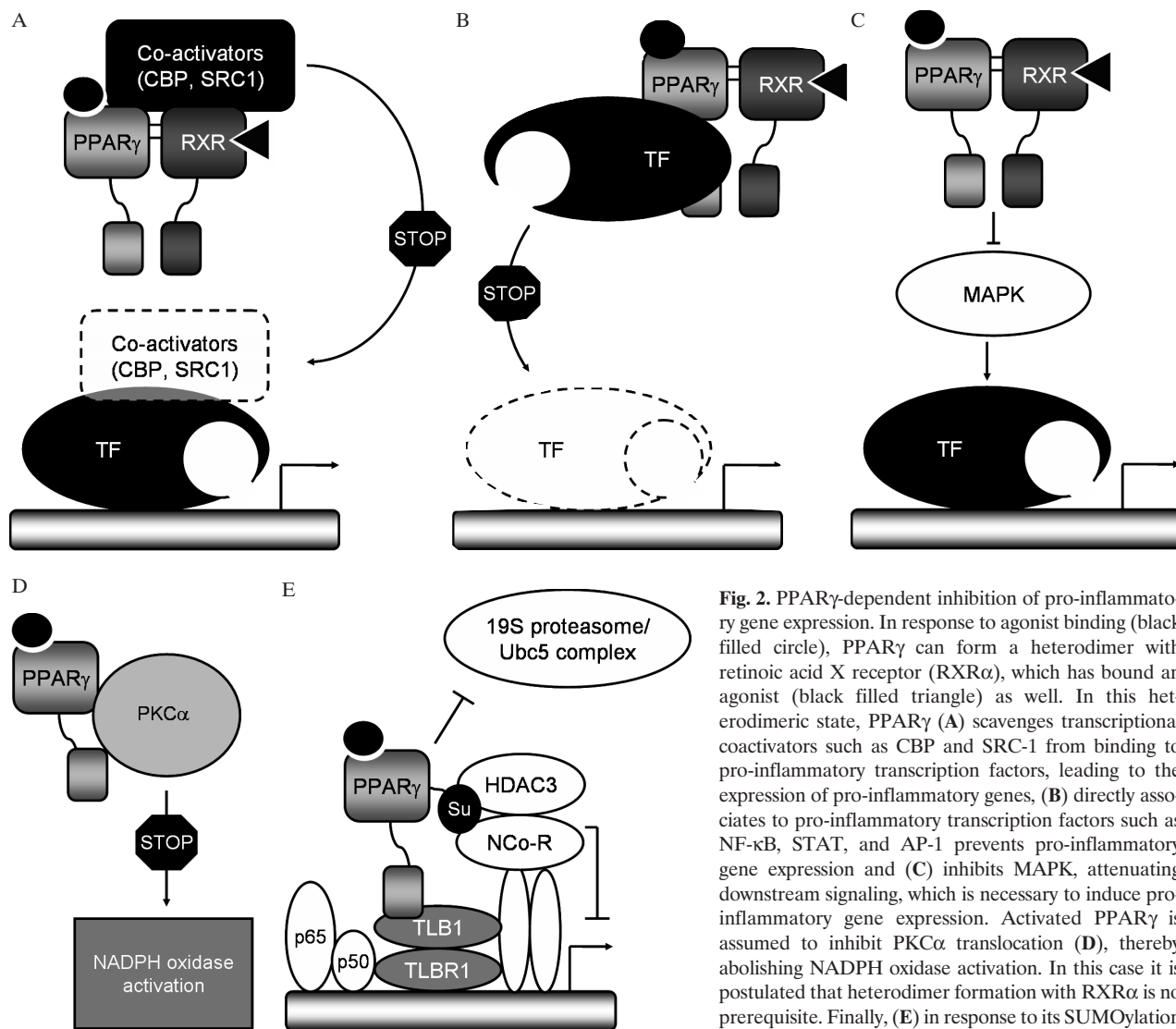


Fig. 2. PPAR γ -dependent inhibition of pro-inflammatory gene expression. In response to agonist binding (black filled circle), PPAR γ can form a heterodimer with retinoic acid X receptor (RXR α), which has bound an agonist (black filled triangle) as well. In this heterodimeric state, PPAR γ (A) scavenges transcriptional coactivators such as CBP and SRC-1 from binding to pro-inflammatory transcription factors, leading to the expression of pro-inflammatory genes, (B) directly associates to pro-inflammatory transcription factors such as NF- κ B, STAT, and AP-1 prevents pro-inflammatory gene expression and (C) inhibits MAPK, attenuating downstream signaling, which is necessary to induce pro-inflammatory gene expression. Activated PPAR γ is assumed to inhibit PKC α translocation (D), thereby abolishing NADPH oxidase activation. In this case it is postulated that heterodimer formation with RXR α is no prerequisite. Finally, (E) in response to its SUMOylation (Su), PPAR γ inhibits proteasomal degradation of the NCo-R-HDAC3-TLB1-TLBR1 complex, which in turn would allow NF- κ B-(p50/p65 heterodimer)-dependent pro-inflammatory gene expression.

the short time necessary for its occurrence, gene regulatory mechanisms can be excluded. Thus direct PPAR γ -PKC α binding might be hypothesized (Fig. 2D). Further experiments have to finally identify the basis of this observed phenomenon. However, blocking the oxidative burst further impairs immune function. Very recent data suggest a fifth possibility of how PPAR γ may affect pro-inflammatory gene expression (Fig. 2E). Pascual et al. [33] provided evidence that PPAR γ can trans-repress NF- κ B-dependent genes by inhibiting the removal of the nuclear receptor co-repressor (NCo-R)-histone deacetylase-3 (HDAC3)-transducin beta-like protein 1 (TLB1)-TLBR1 complex by the ubiquitination machinery from the promoter. Pretreatment with the TZD rosiglitazone causes recruitment of PPAR γ to the repressive complex, which prevents subsequent recruitment of the ubiquitination machinery required to clear the repressive complex from the promoter. NF- κ B-

-dependent pro-inflammatory gene expression is thus abolished.

These possibilities of PPAR γ to modulate and/or block pro-inflammatory gene expression and the synthesis of other pro-inflammatory mediators obviously support a potential role in sepsis treatment and contingent prevention.

PPAR γ – AN INHIBITOR OF SEPSIS

Taking the anti-inflammatory properties of PPAR γ into consideration, Collin and Thiemermann in 2003 [11] demonstrated in a rat sepsis model for the first time that the endogenous PPAR γ agonist 15-deoxy- $\Delta^{12,14}$ -PGJ $_2$ (15-dPGJ $_2$) reduced liver injury, as documented by the fall in serum transaminases. In 2004 the same group provided evidence that during hemorrhagic shock,

endogenously synthesized PPAR γ agonists restricted the degree of liver injury because in the experimental rat model the PPAR γ antagonist GW9662 attenuated this restriction [1, 12]. Interestingly, in contrast to the data obtained during hemorrhagic shock, no endogenous PPAR γ agonist was generated during endotoxic shock. Thus, at least in the rat sepsis model, no endogenous PPAR γ agonists are synthesized. From these results one may conclude that exogenously administered PPAR γ agonists may compensate for this deficiency and even might be more effective in down-modulating or inhibiting the systemic inflammatory response observed during sepsis. Concerning these reports, no mechanistic aspects of PPAR γ -dependent signaling pathways have been identified. Therefore, to elucidate the molecular mechanisms used by PPAR γ to protect animals from sepsis, Kaplan et al. [25] demonstrated in 2005 that in the mouse sepsis model induced by subjecting the animals to peritoneal injection of lipopolysaccharide (LPS; 25 mg/kg), treatment of the mice with 1 mg/kg 15-dPGJ₂ three hours after LPS injection improved the survival rate of animals to 55% compared with 9% in vehicle-treated mice. Survival was monitored for 72 h. Analysis of the lungs of animals which did not receive 15-dPGJ₂ showed marked lung injury, as characterized by hemorrhage, infiltration of inflammatory cells, and reduction of alveolar space. Increased expressions of intercellular adhesion molecule-1, vascular cellular adhesion molecule-1, and E-selectin were observed in the lung and small intestine. These inflammatory events were associated with reduced expression of PPAR γ and with activation of the pro-inflammatory transcription factor NF- κ B in the lung. 15-dPGJ₂ treatment of animals reduced adhesion molecule expression and neutrophil infiltration. These beneficial effects were associated with reduced activation of NF- κ B, whereas expression and DNA binding of PPAR γ were increased in the lung.

The above study supports the hypothesis that PPAR γ might improve the clinical picture of sepsis by inhibiting NF- κ B-dependent pro-inflammatory gene expression. However, one may speculate that the endotoxin model used is not an appropriate system to mimic septic conditions [8]. Thus, Siddiqui et al. [38] very recently provided further evidence for a PPAR γ -dependent improvement of sepsis outcome. In their study they also used a rat model, but in contrast to the work of Collin and Thiemeermann [11], they employed a different sepsis model. Rats were subjected to sepsis by cecal ligation and puncture. They provided evidence that persisting PPAR γ expression in the liver attenuated tissue injury, reduced mortality, and decreased TNF- α expression in septic animals. To achieve this protective effect they applied the phytochemical curcumin. With this substance the protective effect was independent of the time point of administration, i.e. before or after the onset of sepsis. Pretreatment of the animals with the PPAR γ antagonist GW9662 restored the septic characteristics and substantiated a PPAR γ -dependent effect. In addition to the animal model, they stated that stimulation of RAW 264.7

mouse macrophages with curcumin inhibits endotoxin-induced increases in TNF- α expression. In RAW 264.7 cells, PPAR γ was markedly up-regulated, further supporting its role during macrophage desensitization.

In line with this report, we found that LPS/interferon (IFN)- γ treatment of RAW 264.7 macrophages provoked DNA binding and transcriptional activation of PPAR γ starting from 2 h onwards with a maximum at 15 h after LPS/IFN- γ stimulation [44]. Based on this finding, we proposed that a pro-inflammatory activation regimen provokes the endogenous production of a PPAR γ agonist or activator which in turn signals in an autocrine and/or paracrine manner to activate PPAR γ . The activated transcription factor is then able to switch the cellular phenotype from pro- to anti-inflammatory. This can be achieved by scavenging cofactors and transcription factors or inhibiting signaling pathways that release pro-inflammatory mediators in a DNA-unbound state or by blocking transcription of relevant genes encoding proteins such as NADPH oxidase components by direct DNA binding. As shown in the rat model of sepsis, endogenous PPAR γ ligands are not produced during endotoxic shock. Thus compensatory therapy with PPAR γ agonists such as TZDs might be beneficial in the hyper-inflammatory phase of sepsis. However, besides these anti-inflammatory properties of PPAR γ , PPAR γ can also induce cell death.

PPAR γ -DEPENDENT APOPTOSIS – A TRIGGER OF SEPSIS?

Activation of PPAR γ in response to its agonists, e.g. TZDs or arachidonic acid metabolites, may initiate apoptosis. Different pathways for this pro-apoptotic role of PPAR γ have been identified. In pre-monocytic THP-1 cells, the TZD pioglitazone induces apoptosis via caspase-3 and -9 activation, which was prevented by the PPAR γ antagonist GW9662, supporting PPAR γ -dependent apoptosis [5]. In line with this report, Chen et al. [10] observed PPAR γ -mediated apoptosis in response to the TZDs rosiglitazone, troglitazone, and ciglitazone in HL-60 cells. In their experiments, apoptosis was caspase-3 dependent. A role of PPAR γ was verified using its antagonists GW9662 and BADGE, blocking caspase-3 and PARP cleavage. These data corroborated the work of Yamakawa-Karakida et al. [47], showing apoptosis in HL-60 cells in response to the PPAR γ agonists 15-dPGJ₂ and troglitazone via caspase-3 activation. In addition, they found that PPAR γ -dependent apoptosis in HL-60 cells is mediated by downregulating c-myc expression via blocking Tcf-4 activity, a transcription factor known to induce c-myc. PPAR γ -mediated apoptosis in lymphocytes has been observed as well. Padilla et al. [32] provided evidence that PPAR γ is expressed in primary B cells and B cell lymphomas. Stimulation of these cells with PPAR γ agonists provoke apoptosis [31]. However, no PPAR γ antagonist or PPAR γ dominant negative mutants were used in this

study to prove the involvement of PPAR γ . Therefore a PPAR γ -independent mechanism cannot be completely excluded. This is different in T cells. There, PPAR γ expression has been described by several groups. PPAR γ is marginally expressed in resting T cells, but significantly induced in response to T cell activation. In T cells derived from peripheral blood of sepsis patients, PPAR γ is significantly upregulated as well. These data support the assumption that PPAR γ activation in T cells may cause cell death and concomitant T cell depletion in sepsis. Based on these PPAR γ expression results, it is not surprising that T cells from sepsis patients were highly sensitive to PPAR γ -dependent apoptosis. In these experiments, specificity of a PPAR γ -dependent mechanism was confirmed using the PPAR α agonist WY14643, which did not alter cell viability. In addition, the PPAR γ antagonist SR-202 inhibited TZD-induced cell death in T cells, further supporting a PPAR γ -dependent mechanism [40, 42]. These data suggested one pathway how T cells might be depleted during sepsis, which has been observed by several groups [19, 21, 29, 43]. T cell depletion might be one reason for the development of CARS and a concomitant possible second infection with its deleterious consequences.

CONCLUSION

Based on recent findings, the assumption that activation of PPAR γ might be helpful in treating sepsis is strongly supported. Its anti-inflammatory property can terminate the first pro-inflammatory phase of sepsis (Fig. 3), thus not allowing a systemic inflammatory reaction to occur. However, in the second phase of sepsis, with its anti-inflammatory and probably desensitized characteristics, any loss of immune cells might be deleterious if a second infection develops or the first infection recurs (Fig. 3). Therefore, a possible impact of activated PPAR γ should be considered as a contingent side effect of PPAR γ agonist treatment. Further studies are required to finally elucidate the role of PPAR γ -dependent apoptosis in the development of sepsis.

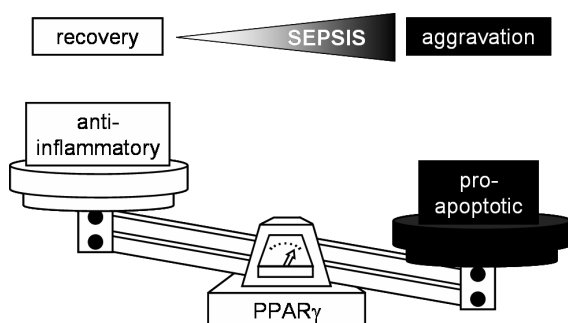


Fig. 3. The role of PPAR γ in sepsis is ambiguous. Its anti-inflammatory impact seems to be beneficial in sepsis treatment, aiding at least in part in the patients recovery. In contrast, its possible pro-apoptotic role appears to be more deleterious, aggravating the patient's state of health.

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