Mutual repression between steroid and xenobiotic receptor and NF-κB signaling pathways links xenobiotic metabolism and inflammation

Changcheng Zhou,1 Michelle M. Tabb,1 Edward L. Nelson,2 Felix Grün,1 Suman Verma,1 Asal Sadatrafiei,1 Min Lin,3 Shyamali Mallick,3 Barry M. Forman,3 Kenneth E. Thummel,4 and Bruce Blumberg1

1Department of Developmental and Cell Biology, 2Department of Medicine, and Department of Molecular Biology and Biochemistry, University of California, Irvine, Irvine, California, USA. 3Department of Gene Regulation and Drug Discovery, City of Hope National Medical Center, Beckman Research Institute, Gonda Diabetes Research Center, Duarte, California, USA. 4Department of Pharmaceutics, University of Washington, Seattle, Washington, USA.

While it has long been known that inflammation and infection reduce expression of hepatic cytochrome P450 (CYP) genes involved in xenobiotic metabolism and that exposure to xenobiotic chemicals can impair immune function, the molecular mechanisms underlying both of these phenomena have remained largely unknown. Here we show that activation of the nuclear steroid and xenobiotic receptor (SXR) by commonly used drugs in humans inhibits the activity of NF-κB, a key regulator of inflammation and the immune response. NF-κB target genes are upregulated and small bowel inflammation is significantly increased in mice lacking the SXR ortholog pregnane X receptor (PXR), thereby demonstrating a direct link between SXR and drug-mediated antagonism of NF-κB. Interestingly, NF-κB activation reciprocally inhibits SXR and its target genes whereas inhibition of NF-κB enhances SXR activity. This SXR/PXR–NF-κB axis provides a molecular explanation for the suppression of hepatic CYP mRNAs by inflammatory stimuli as well as the immunosuppressant effects of xenobiotics and SXR-responsive drugs. This mechanistic relationship has clinical consequences for individuals undergoing therapeutic exposure to the wide variety of drugs that are also SXR agonists.

Introduction
Rifampicin (RIF) is a macrolide antibiotic first used as an antitubercular agent and now used as a component in the multidrug treatment of a wide variety of bacterial and fungal diseases (1–3). RIF therapy is complicated by its propensity to cause drug interactions by inducing hepatic drug-metabolizing enzymes such as cytochrome P450 3A4 (CYP3A4) (4). RIF also acts as an immunosuppressant to suppress humoral and cellular immunological responses in liver cells, and its immunosuppressive role has been well described in humans (5–9). Calleja et al. suggested that the immunosuppressive effects of RIF were mediated by RIF acting as a ligand for the glucocorticoid receptor (GR) (10), but this result was not replicated by other groups that showed that RIF is not a biologically significant ligand for GR (11, 12).

We and others have shown that RIF is a potent ligand of the orphan nuclear receptor, steroid and xenobiotic receptor (SXR) (13), also known as pregnane X receptor (PXR) (14), PAR (15), and NR1I2. SXR plays a central role in the transcriptional regulation of CYP3A4 (16), which is among the most important enzymes of the CYP family since it is responsible for the metabolism of more than 50% of clinically used drugs and a corresponding number of xenobiotic chemicals (17). SXR is activated by a diverse array of pharmaceutical agents, including RIF, Taxol, phenytoin, SR12813, clotrimazole, mifepristone (RU486), phenobarbital, the herbal antidepressant St. John’s wort, and peptide mimetic HIV protease inhibitors such as ritonavir (16, 18, 19). These studies indicate that SXR functions as a xenobiotic sensor (13) to coordinately regulate drug clearance in the liver and intestine via induction of genes involved in drug and xenobiotic metabolism, including oxidation (phase I), conjugation (phase II), and transport (phase III) (20). Gene knockout studies have confirmed a role for SXR in regulating the metabolism of endogenous steroids and dietary and xenobiotic compounds (21).

Although RIF activation of SXR explains its ability to induce drug-metabolizing enzymes such as CYP3A4, the mechanism through which RIF exerts immunosuppressive effects remains unclear. Interestingly, several other pharmaceutical agents such as phenytoin and RU486 also activate SXR and exert immunosuppressive side effects (22–26). On the other hand, it has also long been known that inflammation and infection reduce hepatic CYP expression (27–29), and studies have shown that proinflammatory cytokines such as IL-1 and TNF-α can downregulate CYP gene expression (29, 30). However, the mechanisms through which inflammatory signals downregulate hepatic CYP genes are also unclear. CYP suppression has been proposed to be important for the response of organisms to physiological and pathophysiological signals (29). Although SXR is a major regulator of CYP gene expres-
translocate to the nucleus and directly regulate the expression of its target genes (36). Functional crosstalk between NF-κB and several other steroid receptors (e.g., estrogen receptor, progesterone receptor, and androgen receptor) has been demonstrated and suggested to have physiological significance (34).

Here we report that activation of SXR by RIF and other agonists antagonizes the activity of NF-κB in vitro and in vivo. SXR inhibits NF-κB–mediated reporter activity as well as the expression of NF-κB target genes. Mice deficient in the SXR ortholog PXR show increased expression of NF-κB target genes in multiple tissues associated with increased intestinal inflammation. Not only does SXR inhibit NF-κB activity, but activation of NF-κB inhibits SXR activity and the expression of SXR target genes. Inhibition of NF-κB also enhances the activity of SXR and the expression of its target genes. Thus, the negative crosstalk between SXR and NF-κB not only reveals the possible mechanism underlying the immunosuppressive effects of RIF but also explains the well-recognized decreased expression of hepatic CYP genes during inflammation or infection. These observations reveal SXR’s novel function as a negative mediator of inflammation and immunity and suggest an important relationship between drug and xenobiotic metabolism and the immune system or immunologic responses. Therefore, our results provide critical mechanistic insights for effectively treating an increasing number of infectious diseases and understanding physiologic effects of select “alternative medicines.” They may also have direct clinical consequence for treatment of immunocompromised patients and help us to understand homeostatic mechanisms involving inflammation and metabolism.

Results

**SXR agonists inhibit NF-κB–regulated proinflammatory genes.** Several commonly used clinical drugs including RIF are able to activate SXR and induce CYP3A4 expression. For example, phenytoin, a widely used anticonvulsant drug, exhibits efficacious induction of liver CYP3A4 enzyme by activation of SXR (19). Interestingly, phenytoin therapy has common immunosuppressive side effects, and phenytoin has also been used to treat a variety of inflammatory diseases such as rheumatoid arthritis (22–24, 37). To test whether activation of SXR has effects on inflammation, liver samples collected from 10 donors who had undergone phenytoin therapy of varying duration were analyzed for expression of mRNA encoding the major proinflammatory cytokine TNF-α. In accord with the reported antiinflammatory effects of phenytoin, TNF-α mRNA expression was significantly lower in the livers of donors taking phenytoin (Figure 1A). Phenytoin also significantly induced the expression of hepatic CYP genes during inflammation or infection. These observations reveal SXR’s novel function as a negative mediator of inflammation and immunity and suggest an important relationship between drug and xenobiotic metabolism and the immune system or immunologic responses. Therefore, our results provide critical mechanistic insights for effectively treating an increasing number of infectious diseases and understanding physiologic effects of select “alternative medicines.” They may also have direct clinical consequence for treatment of immunocompromised patients and help us to understand homeostatic mechanisms involving inflammation and metabolism.
constitutive androstan receptor (CAR) (38), it’s unlikely that CAR is involved in phenytoin-mediated CYP3A4 induction since CAR only exhibits very weak binding and functional activation of the CYP3A4 promoter and has pronounced selectivity for CYP2B6 over CYP3A4 (39). Nevertheless, these experiments cannot exclude the possible involvement of CAR in TNF-α inhibition.

The GR and several other nuclear receptors have been shown to interact with the NF-κB pathway and exhibit antiinflammatory effects (34). Considering that RIF is a strong activator of SXR, but not other nuclear receptors, and that another SXR agonist, phenytoin, can inhibit the NF-κB target gene TNF-α, we hypothesized that the immunosuppressive effects of RIF and other SXR agonists are mediated by interference with NF-κB. We tested the ability of SXR to antagonize NF-κB signaling by analyzing the expression of NF-κB target genes in response to SXR activators in 2 cell types where SXR is abundant: human primary hepatocytes and intestinal LS180 cells. Cells were pretreated with 10 μM of the SXR agonists, clotrimazole, RIF, or RU486 for 18 hours before stimulation for 3 hours with either 100 nm 12-0-tetradecanoyl-phorbol-13-acetate (TPA) or 10 ng/ml TNF-α. Quantitative real-time PCR (QRT-PCR) analysis showed that TPA and TNF-α-induced expression of the NF-κB target genes IL-2, COX-2, 1κBz, and TNF-α in primary hepatocytes (Figure 1, B–E) and LS180 cells (Figure 1, F and G). All 3 of the SXR agonists tested blunted the stimulation of NF-κB target gene expression by NF-κB activators in both cell lines (Figure 1, B–G), confirming and extending the phenytoin result (Figure 1A). In accord with these results, activation of mouse PXR by pregnenolone-16α-carbonitrile (PCN) in primary mouse hepatocytes also significantly inhibited TNF-α-induced NF-κB target gene expression (Supplemental Figure 1; supplemental material available online with this article; doi:10.1172/JCI26283DS1).

Pharmacokinetic studies have shown that the plasma levels of RIF can reach micromolar concentration, and it has been well documented that administration of RIF significantly induces CYP3A4 expression in the liver and intestine (4, 40). Therefore, the concentration used to treat cells is physiologically relevant. Four different human– or mouse SXR/PXR ligands all lead to substantial and significant decreases in NF-κB target gene activity in the presence of NF-κB activators. This indicates that activation of SXR indeed can inhibit NF-κB-mediated gene expression.
RIF inhibits NF-κB activity in an SXR-dependent manner. Since SXR agonists such as RIF inhibit NF-κB target gene expression, we next tested whether RIF inhibited NF-κB activity in an SXR-dependent manner. The effects of RIF on regulation of NF-κB reporter activity were determined in HepG2 liver cells transfected with an NF-κB reporter in the presence or absence of SXR expression plasmid. Treatment with known NF-κB pathway activators such as TPA or TNF-α resulted in a marked increase in NF-κB reporter activity (Figure 2A). NF-κB activity was inhibited by RIF in the presence of SXR, but RIF treatment had no significant effect on NF-κB activity in the absence of the SXR expression vector. Consistent with previous reports, dexamethasone (DEX) inhibited NF-κB activity when GR was overexpressed whereas RIF treatment only inhibited NF-κB activity when SXR was overexpressed (Figure 2B). This suggests that RIF is not acting as a ligand for GR, but rather as an SXR-specific ligand. We confirmed this point in separate GR cotransfection experiments (Supplemental Figure 2). RIF inhibition of NF-κB activity was dose dependent in the presence of SXR (Figure 2C). The constitutively active VP16-SXR was also able to inhibit NF-κB reporter activity while the VP16 activation domain alone had no effect on NF-κB activity (Supplemental Figure 3). Taken together, these data indicate that repression of NF-κB by RIF is mediated by SXR and not by GR.

The COX-2 promoter contains an NF-κB–binding site that is required for maximal response to TNF-α. We used a reporter construct containing this promoter to analyze the effect of RIF on NF-κB activity and to confirm the above findings from a synthetic NF-κB reporter in a naturally occurring promoter. Consistent with the results using the NF-κB reporter, HepG2 cells transfected with the COX-2 reporter and treated with RIF showed inhibition of COX-2 reporter activity in an SXR-dependent manner (Figure 2D). We infer that activation of SXR is able to antagonize NF-κB signaling and inhibit expression of its target genes.

To eliminate the possibility that the compounds were affecting other pathways, we activated the NF-κB reporter by overexpressing p65 (RelA) protein, which is primarily responsible for NF-κB transactivation. As expected, p65 activated the NF-κB reporter and RIF inhibited this activation in a concentration-dependent manner (Figure 2E). Interestingly, SXR inhibited p65 activity in the absence of added ligand, and RIF further enhanced this repression mediated by SXR. The observed inhibition was also proportional to the ratio of SXR to p65 expression vectors. When cells were transfected with SXR and p65 expression vector in a 2:1 molar ratio, the ability of SXR to repress NF-κB activity was comparable to that of the NF-κB inhibitor dominant-negative mutant IκBα (IκBαM) (Figure 2F).
Activation of NF-κB antagonizes SXR signaling in human and mouse cells. It has long been known that expression of hepatic CYP genes is decreased during infections or by inflammatory stimuli (27). Compared with our knowledge of CYP induction, the mechanisms for CYP suppression are poorly understood (29). Since SXR is a major regulator for several CYP genes and NF-κB is the central transcriptional regulator of the immune and inflammatory responses, we hypothesized that activation of NF-κB could inhibit SXR activity. SXR reporter activity was induced by RIF, and this induction was reduced by addition of the NF-κB inducer TPA (Figure 3A). Similarly, expression of p65 strongly repressed RIF-induced SXR reporter activity (Figure 3B). On the other hand, overexpression of IκBαM, which can inhibit endogenous NF-κB activity (41), not only rescued p65-mediated repression of SXR but also enhanced both basal and activated SXR activity (Figure 3B). This suggests that SXR activity is normally inhibited by NF-κB in vivo and that IκBαM releases this transrepression by directly binding to NF-κB subunits and inhibiting NF-κB activities. Since NF-κB is ubiquitously expressed, repression of SXR by NF-κB may be relevant in tissues other than liver and intestine where SXR is abundant. Such tissues include kidney, lung, bone, and normal and neoplastic breast tissues where SXR is expressed at lower but detectable levels and where SXR function remains to be elucidated (42, 43).

We next tested whether NF-κB activation affected the expression of the SXR target gene CYP3A4 in human primary hepatocytes and intestinal LS180 cells. Treatment with either TPA or TNF-α almost completely blocked the induction of CYP3A4 mRNA by SXR (Figure 3, C and D). SXR expression was not significantly changed by TNF-α treatment, suggesting that the inhibition of CYP3A4 expression is not related to changes in SXR levels (Figure 3E). Furthermore, mouse primary hepatocytes were also isolated and treated with the mouse PXR ligand PCN in the presence or absence of 10 ng/ml of mouse TNF-α. As expected, PCN significantly induced CYP3A11 expression. Similar to the results obtained in human cell lines, this induction was abolished when the cells were treated with 10 ng/ml mouse TNF-α (Figure 3F). Last, inhibition of endogenous NF-κB activity by cotransfection of IκBαM enhanced the ability of VP16-SXR to induce expression of CYP3A4 in LS180 cells (Supplemental Figure 4). This is consistent with our transfection results showing that IκBαM enhanced SXR-mediated reporter activity (Figure 3B). We infer that NF-κB can antagonize SXR signaling, establishing that the crosstalk between SXR and NF-κB can be bidirectional.

Activation of PXR inhibits NF-κB signaling in vivo, and NF-κB target gene expression is upregulated in PXR knockout mice. If there is a biologically relevant, mutually inhibitory interaction between SXR and NF-κB, one would expect this to be reflected in tissues from knockout animals. To test this, we first prepared primary hepatocytes from WT and PXR knockout mice and evaluated the expression of NF-κB target genes, particularly some proinflammatory cytokines, by QRT-PCR. The expression levels of those cytokines were low compared with that of CYP3A11 (cycle threshold \(Ct = ~20\)), but they were all readily detectable by QRT-PCR (IL-6, \(Ct = ~29\); IL-2, \(Ct = ~27\); TNF-α, \(Ct = ~27\); COX, \(Ct = ~26\)). Interestingly, the proinflammatory cytokines, including IL-6, IL-2, TNF-α, and COX-2, were elevated in primary hepatocytes of PXR−/− compared with WT mice (Figure 4A). These results would be expected if endogenous PXR normally restricts the activity of NF-κB in WT mice. Furthermore, consistent with the results obtained in human primary hepatocytes and LS180 cells, induction of the NF-κB target genes, IκBα and TNF-α, by PCN treatment in hepatocytes isolated from WT mice. However, in hepatocytes isolated from PXR−/− mice, PCN had no effect on mouse TNF-α-induced expression of IκBα and TNF-α (Figure 4B and C). This further suggests that repression of NF-κB target gene by PCN is mediated by the PXR signaling pathway.

We next tested the ability of the PXR signaling pathway to inhibit NF-κB–dependent gene expression in vivo. WT and PXR−/− mice were injected intraperitoneally with the PXR ligand PCN for 3 consecutive days, and total RNAs were isolated from PXR-abundant tissues — liver and intestine. PXR and NF-κB target genes were analyzed by QRT-PCR. As expected, PCN treatment significantly induced PXR target gene CYP3A11 in both liver and intestine of WT mice but not PXR−/− mice (Figure 5A). Consistent with the results obtained in primary hepatocytes, loss of PXR resulted in elevated expression of NF-κB target genes in the liver and intestine (Figure 5B). The elevated levels of NF-κB target genes...
are statistically significant but not as high as those in primary hepatocytes, which may reflect cell type specificity of differences in the whole animal compared with isolated hepatocytes. Some of those proinflammatory genes, such as IL-6, IL-1β, and IL-1α, were elevated in both liver and intestine of PXR–/– mice whereas others, such as IL-2, IL-15, and ICAM-1, were only upregulated in liver, which may be due to the tissue-type specific effects. Furthermore, PCN treatment can inhibit the expression of most NF-κB target genes tested in WT mice but had no significant effect on those genes in PXR–/– mice. These results suggest that PXR/SXR is able to negatively regulate NF-κB activity in vivo and loss of PXR resulted in increased expression of NF-κB target genes. Our data are also consistent with a recent report showing that production of the proinflammatory cytokines TNF-α and IL-1β is significantly inhibited in RIF-treated human mononuclear cells (44).

Small bowel inflammation in PXR knockout mice. The gene expression profiles from PXR–/– and WT mice suggested that PXR–/– animals would have a more proinflammatory stance that would be directly reflected in the tissues with normal high-level PXR expression. Histological examination of the various tissues of WT and PXR–/– animals demonstrated a marked difference in the small intestine (Figure 6, A and B, and Supplemental Figure 5) and confirmed the previously reported absence of histological differences in other major tissues (45). Multiple tissues from PXR-deficient and WT mice, ranging from 12 to 16 weeks of age, were evaluated. The jejunal tissues in all 5 PXR–/– mice demonstrated an increase in the depth of the intervillous crypts and a marked mononuclear cell inflammatory infiltrate restricted to the mucosa (Figure 6B). Notably, we did not identify crypt abscesses, granulomata, definitive villous blunting, or evidence of vasculopathy. The bowel inflammation in PXR knockout mice cannot be explained by infection with Helicobacter, a common bacterial contaminant found in many animal facilities. We tested intestines isolated from both WT and PXR–/– mice and found that both were infected with Helicobacter as measured by PCR (data not shown). Moreover, no alteration was observed in the expression of multidrug resistance gene 1a (MDR1a) in intestine or liver of the PXR–/– animals (46, 47) (data not shown), suggesting that the inflammation probably does not result from loss of MDR1a expression as has been reported in the MDR1a knockout model (48). The inflammatory infiltrate is associated with more prominent epithelial nuclear atypia and an increased fragility to the villous epithelium. In contrast to the small bowel, there were no histological changes evident in the colon of PXR–/– mice. It was recently reported that genetic variation in the SXR gene, associated with altered activity of SXR, is also strongly correlated with susceptibility to inflammatory bowel diseases (IBDs), including Crohn disease and ulcerative colitis (49). SXR expression is downregulated in the gut of IBD patients (50). These reports suggest that dysregulation of SXR expression or activity may contribute to the pathophysiology of these diseases. Taken together with the results from human cells above (Figure 4), our observations suggest that SXR/PXR may normally function
Patients are being treated with RIF (51). Therefore, our studies
the emergence of highly resistant bacteria, a growing number of
tuberculosis infections in the susceptible HIV-infected population and
SXR-mediated interference with NF-

is clearly documented, our studies suggest that equally effective
the treatment of all diseases caused by

and immunosuppressive effects of RU486. RIF is widely used in

activates the GR, potentially leading to glucocorticoid-like immu

we hypoth

and pathophysiological signals.

It has recently been reported that SXR can also negatively regu

and SRC-2, thus limiting transactivation mediated by the proges

Another report showed that TNF-α was able to sig

The mammalian xenobiotic response is mediated primarily

CYP3A4, the most abundant human CYP isofrom, is the most

important since it is responsible for the metabolism of more than

50% of clinically used drugs and a corresponding number of xeno

biotic chemicals (17). It has long been known that expression of

hepatic CYP genes can be profoundly decreased by various infec

ious and inflammatory stimuli, with concomitant clinical and
toxicological consequences (27). Since SXR is a major regulator of

CYP3A4 (16) and NF-κB is the central transcriptional regula

tor of the immune and inflammatory responses (36), we hypoth

thesized that these pathways each inhibit the activity of the other. As

shown above, NF-κB activation inhibits SXR activity and CYP3A4
gene expression whereas inhibition of NF-κB activity by IκBαM is

able to rescue repressed SXR activity and enhance SXR-mediated

CYP3A4 expression. Similarly, SXR activation inhibits the activity of

NF-κB and the expression of its target genes. The expression of

NF-κB target genes is substantially upregulated in multiple tis

ues, and small bowel inflammation is significantly increased in

PXR knockout mice.

Although it has previously been reported that RIF binds to and

activates the GR, potentially leading to glucocorticoid-like immu

nosuppressive effects (10), we confirmed that RIF had no effect on

GR activity, which is consistent with the results from other groups

(11, 12). Instead, both RIF and the GR antagonist RU486 activated

SXR and inhibited NF-κB activity. This reveals the likely mecha

nism underlying the immunosuppressive effects of RIF and also

provides an alternative explanation for the dual antgliucocorticoid

and immunosuppressive effects of RU486. RIF is widely used in

the treatment of all diseases caused by Mycobacterium tuberculosis

and its relatives (1). Although the clinical benefit in this setting is

clearly documented, our studies suggest that equally effective antimi

crobial compounds that do not engage SXR may have greater effec

Such compounds would not be expected to induce SXR-mediated interference with NF-κB action or SXR-regulated
drug metabolic enzymes. With the increasing incidence of tuber

culosis infections in the susceptible HIV-infected population and

the emergence of highly resistant bacteria, a growing number of

patients are being treated with RIF (51). Therefore, our studies

may have direct clinical consequences for treatment of tuberculo

sis and other infections in immunocompromised patients, includ

ing those with AIDS.

In addition to the liver and intestine, SXR is also expressed at low

levels in other tissues, including kidney and lung (42), bone (43),
normal and neoplastic breast tissue (52, 53), and peripheral blood
mononuclear cells (54, 55). It is currently unclear what role SXR is

playing in those tissues. NF-κB, on the other hand, is ubiquitously

expressed and may also repress SXR activity in those tissues. Since

the NF-κB inhibitor IκBαM can enhance both basal and activated

SXR activity and SXR-mediated CYP3A4 gene expression (Figure 3B

and Supplemental Figure 4), release of NF-κB repression by IκBαM

may provide a way to reveal SXR’s novel functions in those tissues.

Crosstalk between NF-κB and the aryl hydrocarbon receptor

(AhR) that prevented AhR from activating the CYP1A1 genes was

previously demonstrated (56). Other studies showed that injec

tion of LPS into mouse liver led to a reduction in CYP3A and

CYP2B expression that was associated with a marked reduction of

PXR and CAR mRNA levels (57). In contrast, we showed that

downregulation of CYP3A4 mRNA expression in human primary

hepatocytes or intestinal cells was not associated with changes in

SXR mRNA expression. This is consistent with a recent report that

shows that SXR gene expression is unaffected by TNF-α in intesti

nal cells (50). Another report showed that TNF-α was able to sig

ificantly reduce mRNA for nuclear receptor coactivators SRC-1

and SRC-2, thus limiting transactivation mediated by the prog

esterone receptor (58). These results show that there is unlikely to

be a single common mechanism for the downregulation of CYP

genes by inflammatory mediators. The mutually inhibitory inter

action between SXR and NF-κB provides an important new mecha

nism for downregulation of CYP3A4 by inflammatory mediators

that is important for the response of organisms to physiological and

pathophysiological signals.

It has recently been reported that SXR can also negatively regu

late other signaling pathways. For example, SXR normally repress

car-mediated expression of genes involved in bilirubin clear

ance. These genes are upregulated in PXR knockout mice (59). Our

study has revealed that SXR can also repress NF-κB-mediated gene

activation. This repression is SXR dependent, and its ligands fur

ther enhance the repression. Similarly to some CAR target genes,

NF-κB target genes, particularly proinflammatory cytokines, are

also upregulated in PXR knockout mice. Although transrepression

by nuclear receptors and crosstalk between nuclear receptors and

other signaling pathways have been extensively studied, the molec

ular mechanisms are still far from being completely understood

(32). For instance, many plausible models have been proposed for

the crosstalk between NF-κB and GR, and each of them is support

ed by experimental evidence. However, the models are mutually

inconsistent in many ways, and the topic remains highly controver

sial (33, 34). Moreover, it was found recently that transrepression of

NF-κB target genes by another nuclear receptor – PPARγ – is

mediated by SUMOylation of PPARγ (60). Interestingly, the SXR

ligand–binding domain also contains a consensus SUMOylation

site. Further investigation will reveal whether SUMOylation of

SXR mediates transrepression of NF-κB signaling pathway.

As a key regulator of inflammation, activated NF-κB is fre

quently detected in various inflammatory diseases and tumors.

We observed increased proinflammatory gene expression in PXR

knockout mice, which is likely due to the loss of repression of

NF-κB by PXR in vivo. Furthermore, the small bowel of PXR

Figure 6

Histological evidence of increased small bowel inflammation. H&E-

stained, formalin-fixed, paraffin-embedded, transverse sections of

proximal jejunum obtained 1 cm from the gastroduodenal junction. (A)

Representative sections from WT mice. (B) Representative sections

from PXR-deficient mice. Magnification, ×100.
knockout mice exhibits a prominent, increased chronic inflammatory infiltrate. This histological pattern of a mucosal mononuclear inflammatory infiltrate is reminiscent of that seen in humans with IBDs such as colonic disease (61, 62). Although the hallmark villous atrophy was not seen in these specimens, variants of colonic disease with villous hypertrophy or modest atrophy have been described (Marsh I, Marsh II, and Marsh IIIa subtypes) (62).

Interestingly, current thinking on the pathophysiology of colonic disease relies heavily on dysregulation of the enteric immune activity (62, 63). Elements reflective of other specific allergic or IBD diagnoses were also absent. It remains to be seen if specific dietary, toxic, or infectious challenges will manifest additional histological changes in the small bowel and other tissues. Recent work has shown that NF-κB plays key roles in linking inflammation to various kinds of tumor development, including colon and liver cancer (64–66). Therefore, this prominent inflammatory infiltrate that is present without specific challenge suggests that these animals may develop inflammation-associated neoplasms, either lymphoreticular or epithelial, with increasing age (67, 68). The anatomically limited inflammation argues for a localized mucosal effect of the loss of PXR expression in a tissue that normally expresses significant levels of PXR. The increased small bowel inflammation in PXR knockout mice is consistent with 2 recent studies that correlated loss of SXR/PXR expression or activity in the gut with the pathophysiology of IBDs (49, 50). The presence of increased chronic inflammation in the small bowel of PXR knockout mice also supports the involvement of SXR/PXR in regulating proinflammatory gene expression through repression of NF-κB activity. On the other hand, inhibition or disruption of the NF-κB pathway can effectively attenuate inflammatory response and formation of inflammation-associated tumors (64, 66). This makes NF-κB inhibition a proposed therapeutic strategy in the treatment of inflammation and cancer. Therefore, the crossstalk between NF-κB and SXR may provide a connection between xenobiotic metabolism and inflammatory disease and could lead to new insights into treatment strategies for inflammation and inflammation-associated cancer. The mutually inhibitory crossstalk between SXR and NF-κB widens the pharmacological implications of SXR action beyond drug interactions and the xenobiotic response and establishes an important relationship between xenobiotic metabolism and inflammation or immune response.

**Methods**

Reagents and plasmids. RIF, DEX, RU486, clotrimazole, recombinant human TNF-α, and TPA were purchased from Sigma-Aldrich. Anti-SXR antibody and anti-NF-κB p65 antibodies were purchased from Santa Cruz Biotechnology Inc. SXR, GR, and CMXβgal expression vectors have been previously described. 1κBαM, which contains a serine to alanine mutation in amino acids 32 and 36 of p65 expression vectors, was kindly provided by X. Lin (University of Texas M.D. Anderson Cancer Center, Houston, Texas, USA). SXR-dependent reporter (XREM-LUC) has been described (69), and NF-κB-dependent reporter (NF-κBx3-LUC) and COX-2 promoter (COX-2-LUC) were kindly provided by C. Glass (UCSD, La Jolla, California, USA) and P. Tontonoz (UCLA, Los Angeles, California, USA) (70).

Cell culture and transfections. The human hepatic cell line HepG2, intestinal epithelial cell line LS180, and mouse macrophage cell line RAW264.7 were obtained from ATCC and cultured in DMEM containing 10% FBS at 37°C in 5% CO₂. The cells were seeded into 6-well plates and grown in DMEM-10% FBS until 70–80% confluence. Twenty-four hours before treatment, the medium was replaced with DMEM containing 10% resin-charcoal-stripped FBS. Immediately before treatment, the medium was removed; the cells were washed once with PBS and then treated with compounds or DMSO vehicle for various times as indicated in Results. Human primary hepatocytes were obtained from the Liver Tissue Procurement and Distribution System (LTPADS) as attached cells in 6-well plates. Mouse primary hepatocytes were isolated from WT and PXR knockout mice as described (71). The hepatocytes were maintained in hepatocyte medium (Sigma-Aldrich) for at least 24 hours before treatment.

Transfection assays and LUC and β-gal were performed as described (69). Cells were seeded into 12-well plates overnight and transiently transfected by FuGene 6 (Roche Diagnostics). Twenty-four hours after transfection, the cells were treated as indicated in Figures 1 and 2. The cells were lysed 24 hours after treatment, and β-gal and luciferase assays were performed as described. Reporter gene activity was normalized to the β-gal transfection controls and the results expressed as normalized RLU per OD β-gal per minute to facilitate comparisons between plates. Each data point represents the average of triplicate experiments ± SEM and was replicated in independent experiments.

**RNA isolation and QRT-PCR analysis.** Total RNA was isolated from LS180 cells, primary hepatocytes, and mouse and human tissues using TRIzol Reagent (Invitrogen) according to the manufacturer-supplied protocol. The collection and use of human tissue for research was approved by the University of Washington Human Subjects Review Board. Samples of human livers from white donors were selected from the University of Washington School of Pharmacy Human Tissue Bank. QRT-PCR was performed using gene specific primers and the SYBR Green RT-PCR Kit (Applied Biosystems) in a DNA Engine Opticon Fluorescence Detection System (MJ Research). All samples were quantified using the comparative Ct method for relative quantification of gene expression, normalized to GAPDH (69). The following primer sets were used in this study: IL-2 (5′-CAACTCTCTGTTGCTGTTG-3′ and 5′-GTCCT-GAATTGAGTGT-3′), TF-α (5′-AACCTCTCCTGGCATCCA-3′ and 5′-GGAAGACCCCTCAGAGTAG-3′); IkBα (5′-GGCT-GAAAAAGAGCGGCTTA-3′ and 5′-CCATCTGCTGCTACTCTCC-3′); COX-2 (5′-TGAGACCTGAGTATTGCCC-3′ and 5′-TGTCGTGATGGAAGCA-3′); CYP3A4 (5′-GGCTCTTATCAAGGACTTAAAT-3′ and 5′-GTCCTAATATACACTCTACAGA-3′); RXR (5′-GATGGAAGGCCTGAGGA-3′ and 5′-TGGTTGAAGAACGACAGCAG-3′); GAPDH (5′-GGTCTTCAAGGAGTAGAACC-3′ and 5′-AGGGGAGATTGTCGTAGG-3′); mouse CYP3A11 (5′-CAGCTTGGTGCTCCTCCTACC-3′ and 5′-TCAAAACACCCCCCATGTTC-3′); mouse IkBα (5′-TGAAGGAGCAGGAGTACAGC-3′ and 5′-TTTGGTTAGATGGTACAG-3′); mouse IL-1 (5′-CCCTGCACTGATACCATCTTC-3′ and 5′-GTCACAGTGTTGGCTACAG-3′); mouse COX-2 (5′-TGAGACACTATTCCACCAAC-3′ and 5′-GCACTGATGTTGCAGGCACG-3′); mouse COX-2 (5′-TGCAGTCAGTGTGGTGTGGT-3′); mouse COX-2 (5′-TGAGACACTATTCCACCAAC-3′ and 5′-GCACTGATGTTGCAGGCACG-3′); mouse COX-2 (5′-TGAGACACTATTCCACCAAC-3′ and 5′-GCACTGATGTTGCAGGCACG-3′); mouse GAPDH (5′-GTCCTTCAAGGAGTAGAACC-3′ and 5′-AGGGGAGATTGTCGTAGG-3′); mouse TF-α (5′-CCCTGCACTGATACCATCTTC-3′ and 5′-GTCACAGTGTTGGCTACAG-3′); mouse COX-2 (5′-TGAGACACTATTCCACCAAC-3′ and 5′-GCACTGATGTTGCAGGCACG-3′); mouse GAPDH (5′-GTCCTTCAAGGAGTAGAACC-3′ and 5′-AGGGGAGATTGTCGTAGG-3′); mouse IL-1 (5′-GCACTCCTTTTCTTAACATTTCC-3′ and 5′-GATGGAAGGCCTGAGGA-3′); mouse GAPDH (5′-GTCCTTCAAGGAGTAGAACC-3′ and 5′-AGGGGAGATTGTCGTAGG-3′); mouse GAPDH (5′-GTCCTTCAAGGAGTAGAACC-3′ and 5′-AGGGGAGATTGTCGTAGG-3′);

**Animals and histological evaluation.** PXR−/− and C57BL/6J (WT) mice were maintained on standard chow. Ten-week-old male C57BL/6J and PXR−/− mice received intraperitoneal injections of either the PXR ligand PCN (50 mg/kg) or DMSO control solution for 3 consecutive days. On the third day, mice were euthanized and tissues were harvested for further analysis.
For histological evaluation, multiple tissues from PXR−/− and WT mice were fixed in formalin, embedded in paraffin, sectioned, and stained with H&E. Animal care and use was in accordance with applicable standards and approved by the Institutional Animal Care and Use Committees at the University of California, Irvine, and the City of Hope National Medical Center.

Statistics. Differences between 2 groups were analyzed using 2-sample, 2-tailed Student’s t test. A P value of less than 0.05 was considered to be significant. All data are presented in the text and figures as the mean ± SEM.

Acknowledgments

We thank R. Kaigh and members of the Blumberg laboratory for critically reading the manuscript; A. Garcia for technical support; T. Moore for assistance with mouse dissection; Y. Xu for human tissue sample preparation; and X. Lin, D. Chakravarti, L.P. Freedman, and C. Glass for plasmids. This work was supported by grants from the NIH (GM-60572), US Environmental Protection Agency (STAR R830686), and the Department of Defense (DAMD17-02-1-0323) to B. Blumberg, and the NIH (AT00886) to B.M. Forman and (GM063666) to K.E. Thummel. Normal human hepatocytes were obtained through the Liver Tissue Procurement and Distribution System (LTPADS), funded by NIH contract N01-DK-9-2310. A. Sadatrafiei was the recipient of a University of California, Irvine, Undergraduate Research Opportunity grant.

Received for publication July 14, 2006, and accepted in revised form May 23, 2006.

Address correspondence to: Bruce Blumberg, 5205 McAlaugh Hall, Department of Developmental and Cell Biology, University of California, Irvine, Irvine, California 92697-2300, USA. Phone: (949) 824-8573; Fax: (949) 824-4709; E-mail: blumberg@uci.edu.

Changcheng Zhou’s present address is: Department of Pharmaceutics, University of Washington, Seattle, Washington, USA.


