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Systemic Analysis of PPARγ in Mouse Macrophage Populations Reveals Marked Diversity in Expression with Critical Roles in Resolution of Inflammation and Airway Immunity

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Although peroxisome proliferator-activated receptor γ (PPARγ) has anti-inflammatory actions in macrophages, which macrophage populations express PPARγ in vivo and how it regulates tissue homeostasis in the steady state and during inflammation remains unclear. We now show that lung and spleen macrophages selectively expressed PPARγ among resting tissue macrophages. In addition, Ly-6C\textsuperscript{hi} monocytes recruited to an inflammatory site induced PPARγ activation, which macrophages derived from Ly-6C\textsuperscript{hi} monocytes were unresponsive to PPARγ agonists, whereas PPARγ deficiency in red pulp macrophages did not influence inflammatory cytokine production.

Overall, we uncovered critical roles for macrophage PPARγ in promoting resolution of inflammation and maintaining functionality in lung macrophages where it plays a pivotal role in supporting pulmonary host defense. In addition, this work identifies specific macrophage populations as potential targets for the anti-inflammatory actions of PPARγ agonists.


Peroxisome proliferator-activated receptor γ (PPARγ) is a ligand-controlled transcription factor of the nuclear receptor family capable of regulating gene expression by transactivation or transrepression (1). First discovered as the master regulator of the genetic program supporting adipocyte differentiation, PPARγ is involved in the regulation of a number of physiological processes such as the response to insulin, cell proliferation, cellular lipid metabolism, and inflammation (2). Thus, PPARγ activation is an attractive therapeutic target in a variety of diseases such as type 2 diabetes, cancer, atherosclerosis, and immune disorders. Activation of PPARγ can be achieved by natural fatty acid derivatives as well as synthetic ligands from the thiazolidinedione family, the latter being used clinically to improve insulin sensitivity in type 2 diabetic patients (3).

The anti-inflammatory role of PPARγ came to the forefront in the late 1990s when 15-deoxy-\(\Delta^{12,14}\)-PGJ\(_2\) (15d-PGJ\(_2\)) and thiazolidinediones were shown to dampen macrophage activation in vitro by activating PPARγ (4–5). Since then, the anti-inflammatory role of PPARγ agonists has been extensively documented in vitro and in vivo (1, 6). Indeed, PPARγ agonists suppress dextran sodium sulfate-induced colitis (7), obesity-induced insulin resistance (8), and the progression of atherosclerosis (9). By contrast, deletion of PPARγ in macrophages exacerbates the development of atherosclerosis (10, 11), colitis (12), and obesity-induced insulin resistance in type 2 diabetic patients (3).

The datasets presented in this article have been submitted to the National Center for Biotechnology Information/Gene Expression Omnibus (http://www.ncbi.nlm.nih.gov/geo/) under accession numbers GSE15907 and GSE32034.

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resistance (13). On the basis of these studies, a model emerges wherein macrophages are universally central targets of PPARγ modulation. However, it is not known whether all monocyte/macrophage populations express PPARγ or rely on its activation to maintain homeostasis or to carry out their functions in different organs during inflammation. Ultimately, the design and development of therapeutic strategies based on the use of PPARγ agonists to combat inflammatory diseases would benefit from the identification of the specific macrophage populations potentially responsive to these agonists.

In this context, we decided to profile the expression of PPARγ in a range of macrophage populations extracted from different organs, delineate its preferential site of expression, and examine the impact of its deficiency during the steady state and after inflammatory challenge in relevant tissues. We show in vivo that PPARγ is induced in monocytes recruited to sites of inflammation as they differentiate into macrophages, and its function is required to fully turn off inflammatory cell recruitment during resolution. In resting tissue macrophages, PPARγ expression was found to be restricted to specific populations, which are lung and splenic red pulp macrophages. In the lung but not the spleen, deficiency of PPARγ in macrophages was associated with low-level spontaneous inflammation in the steady state and profound alterations in macrophage gene expression. Challenge with Streptococcus pneumoniae revealed that deletion of PPARγ in lung macrophages impaired host defense, delaying bacterial clearance and thereby accelerating infection-induced mortality. Overall, these findings uncovered a key role of macrophage PPARγ in supporting resolution of inflammation while pointing specifically to the lung as an inflamed peritoneal macrophages were CD115+F4/80intLy6-C expression. In the spleen, red pulp macrophages were CD45+CD11cloMHC II+CD103−

**Materials and Methods**

**Animals and Methods**

LysM-cre mice (C57BL/6J) and PPARγ floxed mice (C57BL/6J) were obtained from The Jackson Laboratory and crossed in house to generate mice with PPARγ deficiency in myeloid cells (hereafter named LysM-Cre × PPARγ<sup>flox/flox</sup>). LysM-cre × Rosa26-stop<sup>lox</sup>-EGFP reporter mice were bred in-house. Csf2rb<sup>−/−</sup> mice (C57BL/6J) were bred in-house. All other microarrays on mononuclear phagocytes were carried out as part of a specific pathogen-free environment and used in accordance with protocols approved by the Institutional Animal Care and Utilization Committee at Mount Sinai School of Medicine.

**Microarray analysis**

Monocytes were identified as CD115<sup>+</sup> low side-scatter cells and sorted into two subsets based on Ly6-C expression as described previously (14, 15). All other microarrays on mononuclear phagocytes were carried out as part of the Immunological Genome Project (http://www.immgen.org) (16). The isolation procedures and corresponding flow plots for all cells can be found on the ImmGen Web site. Steady-state macrophages from the peritoneum were sorted into two populations (17), including CD11b<sup>+</sup>F4/80<sup>+</sup>MHC II<sup>+</sup>Ly6-C<sup>+</sup>B220<sup>−</sup> and CD115<sup>+</sup>F4/80<sup>+</sup>MHC II<sup>−</sup>Ly6-C<sup>−</sup>B220<sup>+</sup> populations; inflamed peritoneal macrophages were CD11b<sup>+</sup>F4/80<sup>+</sup>Ly6-C<sup>−</sup>B220<sup>+</sup>, whereas neutrophils were sorted as Ly6-G<sup>+</sup>Ly6-C<sup>−</sup>CD11b<sup>+</sup>B220<sup>−</sup> cells. In the lung, macrophages were sorted as CD11c<sup>+</sup>MHC II<sup>−</sup>SiglecF<sup>+</sup>CD11b<sup>+</sup> cells (18), and lung dendritic cells (DCs) as CD11c<sup>+</sup>MHC II<sup>−</sup> cells that were either CD11b<sup>+</sup> (CD11b<sup>+</sup> DCs) or CD103<sup>−</sup>CD11c<sup>+</sup>DCs (19). Gut macrophages were CD45<sup>+</sup>CD11c<sup>+</sup>MHC II<sup>−</sup>CD103<sup>−</sup>CD11b<sup>−</sup> cells (20). In the spleen, red pulp macrophages were F4/80<sup>+</sup>MHC II<sup>+</sup> cells, and DC subsets were CD11c<sup>+</sup>MHC II<sup>−</sup> cells that differentially expressed CD4<sup>+</sup>CD11b<sup>+</sup>CD4<sup>+</sup>CD8<sup>+</sup> (21). RNA was prepared from sorted populations from C57BL/6J mice after sorting directly into TRIzol reagent, amplified, and hybridized on the Affymetrix Mouse Gene 1.0 ST. For data analysis using ImmGen datasets, raw data for all populations were normalized using the robust multiarray averaging algorithm. Extensive quality control documents are available on the ImmGen Web site. All datasets have been deposited at the National Center for Biotechnology Information/Gene Expression Omnibus under accession number GSE15907 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE15907). Microarrays on blood monocytes treated with a PPARγ agonist were performed as previously described (15) using Affymetrix GeneChip 430 2.0 arrays. Corresponding datasets have been deposited at National Center for Biotechnology Information/Gene Expression Omnibus under accession number GSE32034 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32034).

**Blood and tissue sample preparation for flow cytometry**

Mouse blood was collected by nonterminal submandibular or terminal cardiac puncture, and RBCs were lysed in hypotonic buffer (PharmLyse; BD Biosciences). Total leukocytes were quantitated by fresh blood dilution in Turk’s solution (Ricca Chemical). Lungs were harvested, minced, incubated in HBSS containing 3% FBS and collagenase D for 1 h, passed through an 18-gauge needle to obtain homogeneous cell suspensions, and filtered using a 100-μm cell strainer. Bronchoalveolar lavage was obtained by flushing the airways four times with HBSS. Spleens were minced, placed into the cup portion of a cell strainer, and then gently mashed and pushed through the cell strainer. RBCs were then lysed in hypotonic buffer. Peritoneal exudates were collected using cold HBSS. Cell suspensions were then stained with appropriate Abs for 30 min on ice, and data were acquired on a BD FACS Canto II Flow Cytometer (BD Biosciences) and analyzed with FlowJo software (Tree Star).

Fluorescent conjugates of anti-mouse CD115 (AF598), F4/80 (BM8), CD45 (30-F11), CD11c (N418), IA-IE (M5/114,15,2), CD4 (GK1.5), CD8 (53,6,7), CD45.2 (104), and CD45.1 (A20) were purchased from eBioscience. Anti-mouse Gr-1 (Ly-6-C/R6C) and CD11b-PE (G01) were purchased from BioLegend. Anti-mouse F4/80 (CI-A3-1) was purchased from eBioscience. Anti-I-Ab FITC was purchased from Immunotech. Anti-mouse fatty acid binding protein 4 (FABP4) (Bafi1443) was from R&D Systems.

**Immunoblot analysis**

FACS sorted cells were homogenized in lysis buffer containing protease inhibitors. Protein extracts were run on Criterion gels (Bio-Rad) and blotted onto nitrocellulose membranes. After blocking, immunoblots were incubated with primary Abs against PPARγ and β-actin (Cell signaling). Blots were then incubated with fluorescent secondary Abs and proteins were detected using the fluorescence-based Odyssey Infrared Imaging System (LI-COR Biosciences).

**Macrophage transfection**

Peritoneal macrophages were retrieved by lavage from C57BL/6 Ly5-Cre × PPARγ<sup>flox</sup> and wild-type controls 5 d after thioglycollate instillation. Then, 5 × 10<sup>6</sup> macrophages were injected into the peritoneum of naive CD45.1<sup>−</sup> mice, and the number of recruited CD45.1<sup>+</sup> neutrophils was assessed 24 h later.

**Monocyte labeling in vivo**

Ly-6C<sup>hi</sup> monocytes were labeled in vivo by i.v. injection of 1 μm Fluoresbrite green fluorescent (YG) pink microspheres (Polysciences) diluted 1:4 in sterile PBS (22). Ly-6C<sup>hi</sup> monocytes were labeled with beads using the same protocol, except that beads were administered 3 d after i.v. injection of clodronate-loaded liposomes (250 μl/mouse) (22). Labeling efficiency was verified by flow cytometry 1 and/or 2 d after labeling by analysis of blood collected i.v. through the submandibular vein. Clodronate was a gift from Roche and was incorporated into liposomes as described previously (24).

**Analysis of gene expression by quantitative real-time PCR**

RNA samples were prepared using TRIzol reagent (Invitrogen) from thioglycollate-elicited macrophages isolated from mice at sacrifice. Each RNA preparation was hybridized with oligo dT<sub>12</sub>–<sub>18</sub> (Invitrogen) and reverse transcribed using Superscript III reverse transcriptase (Invitrogen). Quantitative real-time PCR was performed using a LightCycler PCR System (Roche) as described previously (25). Expression data were analyzed by...
crossing points calculated from the LightCycler data analysis software and corrected for PCR efficiencies of both the target and the reference gene.

Analysis of bacterial burden

Bacterial burden was quantified by plating 10 µl of lung homogenates serially diluted in trypticase soy broth (BD) on blood agar plates (trypticase soy broth plus 1.875% agar plus 5% sheep blood). After incubating plates at 37°C for 18–24 h, colonies were counted.

Statistical analysis

Data are expressed as mean ± SEM. Statistical differences were assessed using a two-tailed t test or ANOVA (with Tukey’s posttest analysis) with GraphPad Prism software. A p value < 0.05 was considered statistically significant.

Results

Differential expression of PPARγ and regulation of canonical PPARγ target genes among different tissue macrophage populations

To better understand the role of PPARγ in mononuclear phagocytes, we first assessed PPARγ mRNA expression in blood monocytes, resident macrophages from different tissues, including the lung, splenic red pulp, brain (microglia), gut, and peritoneum, as well as in inflammatory peritoneal macrophages. For monocytes, we independently assessed the two major circulating subsets that in mice differentially express Ly6-C and which have counterparts in other species, including humans (14, 26). We compared these populations to spleen and lung conventional DC subsets as counterparts in other species, including humans (14, 26). We compared these populations to spleen and lung conventional DC subsets as well as neutrophils. The populations were sorted (see http://www.imgen.org for detailed sorting strategies) and further analyzed by gene array. PPARγ mRNA was differentially expressed over several orders of magnitude in different mononuclear phagocytes (Fig. 1A). Macrophages from the steady-state peritoneum, brain, and gut expressed only low levels of PPARγ, equivalent to the signal intensity in Ly-6Ch monocytes and neutrophils. By contrast, high levels of PPARγ mRNA were observed in Ly-6Clo monocytes, splenic red pulp macrophages, and pulmonary macrophages (Fig. 1A). Consistent with this, treatment of wild-type mice with the PPARγ agonist rosiglitazone induced further expression of the PPARγ-inducible CD36 protein at the cell surface of Ly-6Clo but not Ly-6Ch monocytes in wild-type animals, suggesting that only the Ly-6Ch but not Ly-6Clo monocytes were responsive to PPARγ activation (Fig. 1B). Indeed, PPARγ activation profoundly impacted the transcriptome of Ly-6Clo monocytes (602 genes downregulated and 1222 genes upregulated, 2-fold cutoff) (Fig. 1C, Supplemental Table I) and especially affected gene signatures such as “DC maturation,” “p53 signaling,” and “NFAT and immune response” (E.L. Gautier and G.J. Randolph, unpublished observations). By contrast, Ly-6Ch monocytes were largely unresponsive to the agonist (66 genes downregulated and 77 genes upregulated) (Fig. 1C, Supplemental Table II), suggesting that the levels of PPARγ in Ly-6Ch monocytes, and by extension in neutrophils, DCs, steady-state peritoneum, brain, and gut macrophages, are too low to confer significant responsiveness to PPARγ ligands under homeostatic conditions. This was further confirmed as neutrophils, DCs, and peritoneal macrophages did not upregulate the expression of the two prototypic PPARγ target genes CD36 and FABP4 following PPARγ agonist treatment (pioglitazone), whereas other populations that express PPARγ upregulated CD36 and/or FABP4 (Fig. 1D). Populations that upregulated CD36 and FABP4 in response to PPARγ agonists typically did so in a PPARγ-dependent manner (Fig. 1E), but diversity in expression of these canonical PPARγ targets was substantial. Lung macrophages did not express surface levels of CD36, even after PPARγ agonist treatment (Fig. 1E), but blood Ly6-Clo monocytes increased CD36 expression in response to pioglitazone in a PPARγ-dependent manner (Fig. 1E). FABP4 was differentially expressed among lung macrophages, raising the possibility of heterogeneity in this population, and its expression was completely dependent on PPARγ, whether at baseline or after pioglitazone treatment. By contrast, basal FABP4 was not dependent on PPARγ in spleen macrophages, although it was responsive to induction by pioglitazone in a PPARγ-dependent manner (Fig. 1E). Overall, these data point to a great diversity in PPARγ expression among resting differentiated macrophages, indicating that PPARγ upregulation is not necessarily an inevitable consequence of macrophage development (27) and revealing that the expression of putative PPARγ target genes is regulated somewhat differently in different tissue macrophage populations.

Acquisition of PPARγ expression by Ly-6Ch monocyte-derived inflammatory macrophages is necessary for full resolution of acute inflammation

PPARγ activity has been associated with anti-inflammatory responses. In the inflammatory milieu of the thioglycollate-treated peritoneum, elicited macrophages from the peritoneal cavity expressed 3-fold higher PPARγ mRNA than blood Ly-6Ch monocytes (Fig. 2A) from which they derive (14, 28). PPARγ was functional in these cells because PPARγ activation using a synthetic ligand increased cell surface expression of the PPARγ-inducible protein CD36 (data not shown), and PPARγ was efficiently deleted in these cells in LysM-Cre × PPARγfl/flfox mice (Fig. 2B). In wild-type mice, leukocytes accumulate for several days after thioglycollate injection, with a marked resolution phase between days 5 and 8 when inflammatory macrophage numbers decline to baseline levels (29). To examine whether PPARγ deficiency in Ly-6Ch monocyte-derived inflammatory peritoneal macrophages would alter the initiation and/or the resolution of thioglycollate-induced inflammation, we used LysM-Cre × PPARγfl/flfox mice that in this study lack PPARγ expression specifically in macrophages, because neutrophils do not express PPARγ. First, using LysM-Cre × Rosa26-stoploxEGFP reporter mice to identify cells with use of the LysM promoter using GFP expression, we confirmed that >90% of inflammatory macrophages in the inflamed peritoneum would be targeted in LysM-Cre × PPARγfl/flfox mice in addition to macrophages in resting peritoneum and neutrophils (data not shown). In the steady state, the total numbers of the two peritoneal resident macrophage populations (17) (CD11b+F4/80MHIC-II− or CD11b+F4/80MHIC-II+) were unchanged in LysM-Cre × PPARγfl/flfox mice as compared with controls, and the numbers of infiltrated neutrophils and Ly-6Ch monocytes were similarly very low in the presence or absence of PPARγ (data not shown).

During the course of peritonitis, early accumulation of CD11b+ inflammatory macrophages (Fig. 2C) in the peritoneum was unaltered by PPARγ deficiency 1 d after instillation of thioglycollate but was slightly decreased after 5 and 8 d in LysM-Cre × PPARγfl/flfox mice (Fig. 2D). However, we noted a 3-5-fold increase in the number of infiltrated Ly-6Ch monocytes at both days 5 and 8 compared with control mice (Fig. 2C, 2E), whereas circulating monocyte subset numbers remained similar over time in both LysM-Cre × PPARγfl/flfox mice and controls (data not shown). Because Ly-6Ch is retained only transiently after monocyte recruitment into tissues (26, 30, 31), these data revealed that monocyte recruitment to the peritoneal cavity did not fully shut down in LysM-Cre × PPARγfl/flfox mice. Furthermore, although early accumulation of neutrophils (6 and 24 h) was comparable between LysM-Cre × PPARγfl/flfox mice and control animals, peritoneal neutrophil numbers were likewise elevated 3- to 4-fold.
FIGURE 1. PPARγ gene expression profiling and regulation of canonical PPARγ target genes in mononuclear phagocytes. (A) PPARγ mRNA expression was analyzed by gene array and depicted to show signal intensity in sorted myeloid cell populations. Data are derived from three separate analyses that are each derived from n = 5 mice. (B) Cell surface expression of CD36 analyzed by flow cytometry on monocyte subsets from mice fed a regular chow diet (−) or a diet supplemented with the PPARγ agonist rosiglitazone (agonist) for a week (n = 5 mice/group). (C) The number of genes regulated in monocyte subsets following PPARγ activation by rosiglitazone assessed through whole-genome array analysis. (D) Protein levels of CD36 and FABP4 in myeloid populations at the steady state and following PPARγ agonist treatment (agonist, pioglitazone) were monitored by flow cytometry. (E) Expression of CD36 and FABP4 in myeloid populations of LysM-Cre × PPARγlox/lox mice (PPARγΔMac/PMN) and controls (CTRL) at the steady state and following PPARγ agonist treatment (agonist, pioglitazone). Mean fluorescence intensity (MFI) is plotted (n = 3–4 mice/group). Mϕ, Macrophage.
in LysM-Cre × PPARγfloxflox mice during the usual resolution phase occurring between days 5 and 8 (Fig. 2F). Concomitantly, blood neutrophil counts were elevated at these later time points in LysM-Cre × PPARγfloxflox mice compared with controls (data not shown), marking systemic inflammation. Interestingly, the increase in peritoneal neutrophils and Ly-6Chi monocytes, as well as the decrease in inflammatory macrophages, were still evident at day 14 postthioglycollate treatment, the latest time point examined (data not shown). Transfer of 5 × 10⁶ thioglycollate-elicited macrophages, retrieved from donors during the early resolution phase occurring between days 5 and 8, to the peritoneum of resting mice led to recruitment of neutrophils (Fig. 2G) and monocytes (Fig. 2H), and these numbers were doubled when transferred macrophages lacked PPARγ. PPARγ-deficient thioglycollate-elicited macrophages, retrieved at day 5, had increased mRNA expression of Il1b, Il6, and Ccr2 and decreased levels of Cd36, Cd51, and Tgfb1 compared with controls (Fig. 2I). Collectively, these data show that PPARγ deficiency in myeloid cells has little impact on the early phases of an inflammatory response. However, macrophage PPARγ expression in thioglycollate-elicited inflammatory macrophages is necessary to bring about resolution. Indeed, its deficiency leads to a state of chronic low-grade inflammation, at least in part because macrophages retain a more proinflammatory phenotype.

PPARγ activation promotes macrophage-dependent cessation of neutrophil recruitment and favors resolution of acute inflammation

Given the data above indicating that the cessation of leukocyte recruitment that characterizes resolution of inflammation is impaired in LysM-Cre × PPARγfloxflox mice, we sought to determine whether treatment with PPARγ agonists would conversely favor the shutdown of leukocyte recruitment in wild-type animals. Indeed, PPARγ agonist treatment reduced neutrophil counts in the peritoneum following thioglycollate administration at each time point studied, especially in the later phases of inflammation (Fig. 3A). This effect required PPARγ expression in macrophages because treatment with the PPARγ agonist failed to reduce neutrophil counts in the cavity of LysM-Cre × PPARγfloxflox mice (Fig. 3B). These data support the concept that PPARγ activation suppresses the recruitment of leukocytes in later phases of tissue injury in a macrophage PPARγ-dependent manner, promoting resolution of inflammation.

PPARγ deletion in macrophages leads to low-grade constitutive inflammation in the lung but not in the spleen

Considering our findings that PPARγ expression in inflammatory macrophages as well as its activation by pharmacological agonists...
favors resolution of acute inflammation, we wondered whether deletion of PPARγ in resting macrophage populations that normally express high levels of PPARγ (lung and splenic red pulp macrophages) would promote inflammation. LysM-Cre X PPARγ^lox/lox^ mice (PPARγ^Mac/PMN^) fed a regular diet or a diet containing the PPARγ agonist pioglitazone (agonist) (n = 8–10 mice/group).

FIGURE 3. PPARγ activation favors the resolution of acute inflammation. (A) Neutrophil counts in the peritoneum at 1, 5, and 8 d after peritonitis induction in wild-type mice fed a regular diet or a diet containing the PPARγ agonist pioglitazone (agonist) (n = 8–10 mice/group). (B) Peritoneal neutrophil counts 5 d after peritonitis induction in LysM-Cre X PPARγ^lox/lox^ mice (PPARγ^Mac/PMN^) fed a regular diet or a diet containing the PPARγ agonist pioglitazone (agonist) (n = 4–5 mice/group).

Total splenocyte numbers were similar in LysM-Cre X PPARγ^lox/lox^ mice and controls (data not shown), but red pulp macrophages (F4/80^hi^ CD11b^lo^) were approximately one-third less numerous in LysM-Cre X PPARγ^lox/lox^ spleens (Fig. 4A), possibly arguing for a role of PPARγ in the maintenance of this population. There were no signs of inflammation in the resting spleen of LysM-Cre X PPARγ^lox/lox^ mice because splenic Ly-6C^hi^ monocyte and neutrophil numbers were comparable to controls (Fig. 4B). Consistent with peritoneal inflammation, macrophage PPARγ deficiency did not have an impact on the induction of inflammation in the spleen at an early time point after i.v. administration of LPS (day 1; Fig. 4C), whereas it led to increased neutrophils and Ly-6C^hi^ monocytes recruitment to the spleen at a later time point (day 5; Fig. 4D), again arguing for a key role of PPARγ in resolution of inflammation.

When we examined the lung, we observed that PPARγ deletion in macrophages led to a low-grade inflammatory response without supplying an overt exogenous stimulus. Indeed, we observed increased leukocyte infiltration with elevated numbers of neutrophils (Fig. 4E) and CD4^+^ and CD8^+^ T lymphocytes (Fig. 4F), whereas macrophage numbers were comparable to controls (Fig. 4E).

Overall, whereas PPARγ is expressed by both splenic red pulp and pulmonary macrophages, its deficiency only obviously had an impact on lung tissue homeostasis in the steady state, arguing for an interaction between tissue environment and the outcome of altered macrophage PPARγ signaling.
Altered gene expression and lipid homeostasis in lung macrophages deficient in PPARγ

The low-grade inflammation observed only in the lung but not in the spleen suggested that the impact of PPARγ might be environment dependent. The alveolar space is permanently filled with a surfactant made of lipids (90%) and proteins (10%) (32), and we noted increased cellular lipid content in lung macrophages lacking PPARγ, as indicated by increased sterol staining using Bodipy FL (Fig. 5A), in line with previous work reporting the development of pulmonary alveolar proteinosis in these mice (33, 34). Then, to better understand the role of PPARγ in lung macrophages, microarray analysis was performed on sorted lung macrophages from LysM-Cre × PPARγ<sup>flox/flox</sup> mice and controls. This whole-genome array analysis uncovered 721 genes that were downregulated, and 2088 genes whose expression was increased in lung macrophages, suggesting a profound alteration of their transcriptome (Supplemental Tables III, IV). In line with their increased intracellular sterol content, we found that PPARγ-deficient lung macrophages induced a number of mRNA transcripts associated with cellular lipid metabolism and in particular those associated with an increase in activity of the LXR transcription factor. Expression levels of Nrlh2 (also known as LXRβ), a sensor of intracellular sterol levels, and its partner Rrxx were increased in lung macrophages obtained from LysM-Cre × PPARγ<sup>flox/flox</sup> mice as compared with controls (Fig. 5B). Consequently, the expression levels of several target genes of the LXR/RXR heterodimer (Abca1, Srebfl1, Apoe, Mylpc, Abcg1, Scd2, and Scd1) were equally increased (Fig. 5B). Finally, the mRNA level of the scavenger receptor Msr1 and of the triacylglycerol synthesis enzyme Dgat1 were also enhanced (Fig. 5B). This expression profile was mirrored by decreased expression of genes involved in the cholesterol biosynthetic pathway (Hmgcs1, Srebfl2, Hmgcr, Fdft1, Dhc24, Sfle, and Idil) and in the uptake of extracellular cholesterol (Ldlr) (Fig. 5B). Because the vast majority of these genes are not known to be under the direct control of PPARγ, these data suggest that many of the genes regulated in this study are regulated indirectly. Because we observed an increase in the percentage of MHC-II<sup>+</sup> lung macrophages in LysM-Cre × PPARγ<sup>flox/flox</sup> mice (Fig. 5C), we sought to determine whether this was correlated with an increased expression of genes associated with macrophage activation. We found increased mRNA levels of genes encoding costimulatory molecules (Cd86, H2-Dbh2, H2-Ab1, and H2-Aa), members of the IFN regulatory factor family of transcription factors (Ifr3, Ifr5, and Ifr8), innate immune receptors (Tlr7, Tlr8, and Trem2), and the proinflammatory mediator Mif (Fig. 5D). Moreover, mRNA expression levels of members of the S100 protein family (S100a13, S100a4, and S100a6), known to mediate inflammatory signals, were upregulated in lung macrophages from LysM-Cre × PPARγ<sup>flox/flox</sup> mice (Fig. 5D). However, other genes involved in inflammation such as transcription factors (Fos, Nrk4a1, Jun, Jund, and Junb), the TLR Tlr2, the scavenger receptor Marco, and the surfactant opsonin Sftp4 were downregulated (Fig. 5D). Consistent with the increased intracellular lipid content observed in lung macrophages from LysM-Cre × PPARγ<sup>flox/flox</sup> mice, we noted that the mRNA expression of several phospholipases (Pla2g6, Plcb1, Pnpla6, Plid3, and Plid4) was increased in these cells as well as the expression of genes involved in PG and thromboxane synthesis (Pgs1, Ptgr2, Ptgs1, and Tbxas1) (Fig. 5E). We also noted that numerous genes regulated by the transcription factor Nrf2, a master regulator of the anti-inflammatory transcription factor Nrf2, a master regulator of the anti-inflammatory response, were upregulated (Fig. 5E). The low-grade inflammation observed only in the lung but not in the spleen suggested that the impact of PPARγ might be environment dependent. The alveolar space is permanently filled with a surfactant made of lipids (90%) and proteins (10%) (32), and we noted increased cellular lipid content in lung macrophages lacking PPARγ, as indicated by increased sterol staining using Bodipy FL (Fig. 5A), in line with previous work reporting the development of pulmonary alveolar proteinosis in these mice (33, 34). Then, to better understand the role of PPARγ in lung macrophages, microarray analysis was performed on sorted lung macrophages from LysM-Cre × PPARγ<sup>flox/flox</sup> mice and controls. This whole-genome array analysis uncovered 721 genes that were downregulated, and 2088 genes whose expression was increased in lung macrophages, suggesting a profound alteration of their transcriptome (Supplemental Tables III, IV). In line with their increased intracellular sterol content, we found that PPARγ-deficient lung macrophages induced a number of mRNA transcripts associated with cellular lipid metabolism and in particular those associated with an increase in activity of the LXR transcription factor. Expression levels of Nrlh2 (also known as LXRβ), a sensor of intracellular sterol levels, and its partner Rrxx were increased in lung macrophages obtained from LysM-Cre × PPARγ<sup>flox/flox</sup> mice as compared with controls (Fig. 5B). Consequently, the expression levels of several target genes of the LXR/RXR heterodimer (Abca1, Srebfl1, Apoe, Mylpc, Abcg1, Scd2, and Scd1) were equally increased (Fig. 5B). Finally, the mRNA level of the scavenger receptor Msr1 and of the triacylglycerol synthesis enzyme Dgat1 were also enhanced (Fig. 5B). This expression profile was mirrored by decreased expression of genes involved in the cholesterol biosynthetic pathway (Hmgcs1, Srebfl2, Hmgcr, Fdft1, Dhc24, Sfle, and Idil) and in the uptake of extracellular cholesterol (Ldlr) (Fig. 5B). Because the vast majority of these genes are not known to be under the direct control of PPARγ, these data suggest that many of the genes regulated in this study are regulated indirectly. Because we observed an increase in the percentage of MHC-II<sup>+</sup> lung macrophages in LysM-Cre × PPARγ<sup>flox/flox</sup> mice (Fig. 5C), we sought to determine whether this was correlated with an increased expression of genes associated with macrophage activation. We found increased mRNA levels of genes encoding costimulatory molecules (Cd86, H2-Dbh2, H2-Ab1, and H2-Aa), members of the IFN regulatory factor family of transcription factors (Ifr3, Ifr5, and Ifr8), innate immune receptors (Tlr7, Tlr8, and Trem2), and the proinflammatory mediator Mif (Fig. 5D). Moreover, mRNA expression levels of members of the S100 protein family (S100a13, S100a4, and S100a6), known to mediate inflammatory signals, were upregulated in lung macrophages from LysM-Cre × PPARγ<sup>flox/flox</sup> mice (Fig. 5D). However, other genes involved in inflammation such as transcription factors (Fos, Nrk4a1, Jun, Jund, and Junb), the TLR Tlr2, the scavenger receptor Marco, and the surfactant opsonin Sftp4 were downregulated (Fig. 5D). Consistent with the increased intracellular lipid content observed in lung macrophages from LysM-Cre × PPARγ<sup>flox/flox</sup> mice, we noted that the mRNA expression of several phospholipases (Pla2g6, Plcb1, Pnpla6, Plid3, and Plid4) was increased in these cells as well as the expression of genes involved in PG and thromboxane synthesis (Pgs1, Ptgr2, Ptgs1, and Tbxas1) (Fig. 5E). We also noted that numerous genes regulated by the transcription factor Nrf2, a master regulator of the anti-inflammatory response, were upregulated (Fig. 5E).
oxidant response, were upregulated in PPARγ-deficient pulmonary macrophages compared with controls, indicating increased oxidative stress in LysM-Cre × PPARγ<sup>lox/fox</sup> mice (Fig. 5F). Finally, mRNA levels of mediators of autophagy (Atg5, Dram1, Beclin1, and Atg7) and apoptosis (Casp2, Casp9, Bax, and Aifm2) were increased in lung macrophages lacking PPARγ compared with controls (Fig. 5G). Taken together, these findings reveal that PPARγ-deficient pulmonary macrophages present a markedly altered transcriptome, most likely secondary to the lipid loading, affecting several key pathways related to classical macrophage functions.

Impaired bacterial clearance in the lungs and accelerated mortality in mice lacking PPARγ in macrophages following S. pneumoniae infection

Given that the gene expression profile of lung macrophages deficient in PPARγ is profoundly altered, we next investigated whether infectious challenge of LysM-Cre × PPARγ<sup>lox/fox</sup> mice would lead to a perturbed innate immune response to pathogens. In this study, we found that LysM-Cre × PPARγ<sup>lox/fox</sup> mice were more susceptible to infection with S. pneumoniae. Weight loss associated with infection was more pronounced in LysM-Cre × PPARγ<sup>lox/fox</sup> compared with controls over a period of 4 d before death occurred (Fig. 6A). This increased susceptibility to S. pneumoniae infection was due to impaired bacterial clearance because bacterial burden was increased by ∼1 log in the lung of LysM-Cre × PPARγ<sup>lox/fox</sup> mice compared with controls 48 h postinfection (Fig. 6B). This correlated with faster dissemination of the bacteria into the bloodstream (data not shown) as well as accelerated death in these mice (Fig. 6C). LysM-Cre × PPARγ<sup>lox/fox</sup> mice challenged with a lower dose of the pathogen similarly succumbed faster than controls. Indeed, whereas 100% of control mice were still alive 6 d postinfection, only 40% of LysM-Cre × PPARγ<sup>lox/fox</sup> mice survived to this time point (Fig. 6D). Surprisingly, we observed similar neutrophil and Ly-6Ch<sup>+</sup> monocyte recruitment to the bronchoalveolar space and the lung 24 h postinfection in LysM-Cre × PPARγ<sup>lox/fox</sup> mice and controls (Fig. 6E). Increased bacterial burden in LysM-Cre × PPARγ<sup>lox/fox</sup> mice was not due to impaired phagocytosis because labeled S. pneumoniae were taken up by PPARγ-deficient alveolar macrophages as efficiently as controls in vivo (Fig. 6F). However, resident alveolar and interstitial pulmonary macrophage counts were significantly decreased by ∼50 and 35%, respectively, 24 h after instillation of S. pneumoniae (Fig. 6G). Finally, the disease pulmonary alveolar proteinosis (PAP) is due to alterations in GM-CSF signaling, and it was recently shown that PPARγ expression in GM-CSF-deficient lung macrophages was low (35). Furthermore, viral vectors to restore PPARγ in GM-CSF knockout mice led to reduced lipid accumulation and increased cholesterol efflux in lung macrophages (36). Because PAP is associated with increased susceptibility to infection, we sought to determine whether PPARγ activation could improve bacterial clearance in Csf2rb<sup>−/−</sup>-Csf2rb2<sup>−/−</sup> mice (37). Indeed, Csf2rb<sup>−/−</sup>-Csf2rb2<sup>−/−</sup> mice, which also display alveolar proteinosis, have significantly higher bacterial burden (∼2 logs) than wild-type control mice and PPARγ activation by

**FIGURE 6.** PPARγ expression in lung macrophage is necessary to combat infection. (A) Body weight loss was determined following infection in LysM-Cre × PPARγ<sup>lox/fox</sup> mice (PPARγ<sup>ΔMac/PMN</sup>) and controls (CTRL) (n = 9 mice/group). (B) Lung bacterial load was measured 48 h postinfection in LysM-Cre × PPARγ<sup>lox/fox</sup> mice (PPARγ<sup>ΔMac/PMN</sup>) and controls (CTRL) (n = 9 mice/group). Survival from infection was assessed over a period of 12 d following high-dose (2 × 10<sup>6</sup> CFU) (C) and low-dose (5 × 10<sup>5</sup> CFU) (D) S. pneumoniae inoculation in the lung of LysM-Cre × PPARγ<sup>lox/fox</sup> mice (PPARγ<sup>ΔMac/PMN</sup>) and controls (CTRL) (n = 5–8 mice/group). (E) Neutrophil and Ly-6Ch<sup>+</sup> monocyte counts in the bronchoalveolar lavage (BAL) and the lung of LysM-Cre × PPARγ<sup>lox/fox</sup> mice (PPARγ<sup>ΔMac/PMN</sup>) and controls (CTRL) were determined 24 h postinfection (n = 7–8 mice/group). (F) PKH26-labeled S. pneumoniae phagocytosis by resident alveolar macrophages was assessed by flow cytometry 30 min after inoculation (n = 6 mice/group). (G) Alveolar and pulmonary-resident macrophages counts in LysM-Cre × PPARγ<sup>lox/fox</sup> mice (PPARγ<sup>ΔMac/PMN</sup>) and controls (CTRL) 24 h postinfection (n = 7–8 mice/group). (H) Lung bacterial burden was determined 48 h after S. pneumoniae inoculation in the lungs of wild-type mice, Csf2rb<sup>−/−</sup>-Csf2rb2<sup>−/−</sup> mice, and Csf2rb<sup>−/−</sup>-Csf2rb2<sup>−/−</sup> mice with prior treatment with the PPARγ agonist pioglitazone for 2 wk (n = 3–4 mice/group).
pioglitazone partially decreased this enhanced burden (Fig. 6H). Therefore, these data now connect PPARγ to host defense and control of bacterial burden in the lung through maintenance of local macrophage functions.

**Discussion**

The anti-inflammatory role of PPARγ in macrophages is well established. However, little is known regarding its impact on specific resting macrophage populations as well as on the dynamic of inflammation in vivo. It was recently recognized that establishing the expression profile of PPARγ in tissue macrophages in vivo would be helpful in clarifying its role in the regulation of inflammatory processes (38). In this study, we unexpectedly revealed that many resident macrophages do not express substantial levels of PPARγ, including those in the brain, peritoneum, and gut. The level of PPARγ in these cells was as low as in Ly-6C<sup>hi</sup> monocytes, which show no PPARγ activity after synthetic PPARγ agonist administration in vivo. By contrast to these tissues and cells, Ly-6C<sup>lo</sup> blood monocytes and resting red pulp splenic and pulmonary macrophages expressed high levels of mRNA for PPARγ. In addition, PPARγ was induced in inflammatory macrophages differentiating from circulating Ly-6C<sup>hi</sup> monocytes entering an inflammatory site, albeit to a lower level than observed in the resting macrophages that were positive. In different tissues, the expression of canonical PPARγ target genes such as CD36 and FABP4 was distinct even among those macrophages that were PPARγ<sup>+</sup>, highlighting the importance of context in regulation of PPARγ-related pathways and underscoring the diversity observed among macrophages from different organs.

Because the ability of PPARγ to transrepress inflammatory genes has been thoroughly documented (1), we expected that macrophage loss of PPARγ during thioglycollate-mediated peritonitis would lead to a more proinflammatory phenotype. However, the absence of PPARγ in LysM-Cre × PPARγ<sup>lox/fox</sup> mice did not impact the accumulation of leukocytes during the initial phase of the inflammatory response. This could be explained by the fact that immature and differentiating Ly-6C<sup>hi</sup> monocytes, which express negligible or low levels of PPARγ, were dominant at this time point. By contrast, persistent neutrophil and Ly-6C<sup>lo</sup> monocyte influx occurs in LysM-Cre × PPARγ<sup>lox/fox</sup> mice during the later period when more differentiated inflammatory macrophages, which now express PPARγ, begin to dominate and when resolution is observed in control mice. These data suggest, therefore, that PPARγ plays especially important roles in the late stages and resolution of inflammation. These roles very likely include repression of proinflammatory genes, and indeed, we observed that proinflammatory genes were elevated in PPARγ-deficient thioglycollate-elicited macrophages but may also include impaired induction of genes associated with repair and healing. Previous studies have linked PPARγ with the development of alternatively activated macrophages (39) and with tissue repair in injured muscle (30), and IL-4 is known to promote the production of PPARγ ligands (40). An elegant in-depth study recently revealed that although PPARγ is not required for development of alternatively activated macrophages in C57BL/6j mice, there is synergy with IL-4 such that the transcription factor Stat6 that is critical for IL-4 signaling binds to the enhancer elements in PPARγ target genes and markedly augments the PPARγ response (41). Our findings that PPARγ appears to play a bigger role in determining the rate/magnitude of contraction of the inflammatory response rather than the magnitude of earlier phases fits well with concepts of PPARγ playing a key role in tissue repair, healing, and overall resolution.

Future studies on the possible interface between PPARγ and lipids previously associated with resolution (42) seem in order. At present, resolvins are known not to serve as PPARγ ligands (42), but an intersection between PPARγ and the pathways that regulate such proresolution mediators may exist. Ligands for PPARγ during resolution may be limiting, because we observed that provision of synthetic ligands to mice hastened the shutdown of neutrophil recruitment in a macrophage PPARγ-dependent manner during the terminal phases of thioglycollate-induced inflammation. This finding is in line with recent published data in a model of granulomatous disease (43) and supports the logic of therapeutically enhancing PPARγ activity to promote resolution of ongoing inflammation.

Highest expression of PPARγ mRNA among macrophages in the mouse, resting or inflamed, was observed in the lung. Analysis of FABP4 expression in lung macrophages suggests that there may be heterogeneity among lung macrophages with regard to expression or activity of PPARγ. We show that the absence of PPARγ in LysM-Cre × PPARγ<sup>lox/fox</sup> mice induced mild lung inflammation in the absence of experimental challenge. This underlying inflammation may stem from a key role for PPARγ expression by macrophages to maintain cellular as well as tissue lipid homeostasis in the presence of pulmonary surfactant lipids. Indeed, previous work indicates that lipid surfactant accumulates in the alveoli of LysM-Cre × PPARγ<sup>lox/fox</sup> mice (33, 34). Consistent with this observation, we found that expressions of genes that regulate intracellular lipid homeostasis are markedly altered in pulmonary macrophages lacking PPARγ. Genes involved in sterol uptake and synthesis were downregulated, whereas genes linked to cholesterol sensing and efflux were upregulated, and in particular, mRNA transcripts controlled by LXR were induced. Likely, the enhanced sterol loading drives induction of the LXR pathway as a mechanism to deal with the high lipid loading. In addition, we found that numerous pathways associated with a range of macrophage functions were altered in the absence of PPARγ in lung macrophages, and genes associated with cell death were upregulated, leading to the conclusion that disruption of PPARγ signaling profoundly altered their transcriptome. However, the changes in gene expression are complex and most likely do not reflect changes associated only with direct PPARγ targets. Indirect changes likely reflect a sequence of events that occur in response to the loss of PPARγ in macrophages, which usually express PPARγ in the lung.

With the expectation that the absence of PPARγ in lung macrophages would exacerbate inflammation in the context of infection and subsequently favor bacterial clearance, we infected control and LysM-Cre × PPARγ<sup>lox/fox</sup> mice with *S. pneumoniae*. Bolstering our expectations that the inflammatory infiltrate may be increased in response to this infection were data in the literature indicating that mice lacking the cholesterol efflux gene Abcg1, and thus a gene expected to intersect functionally with PPARγ, manifest enhanced inflammation and increased bacterial clearance in response to infection in the lung (44). Following infection, weight loss and mortality were surprisingly accelerated in LysM-Cre × PPARγ<sup>lox/fox</sup> mice with *S. pneumoniae*. These data suggest, therefore, that PPARγ plays especially important roles in the late stages and resolution of inflammation. These roles very likely include repression of proinflammatory genes, and indeed, we observed that proinflammatory genes were elevated in PPARγ-deficient thioglycollate-elicited macrophages but may also include impaired induction of genes associated with repair and healing. Previous studies have linked PPARγ with the development of alternatively activated macrophages (39) and with tissue repair in injured muscle (30), and IL-4 is known to promote the production of PPARγ ligands (40). An elegant in-depth study recently revealed that although PPARγ is not required for development of alternatively activated macrophages in C57BL/6j mice, there is synergy with IL-4 such that the transcription factor Stat6 that is critical for IL-4 signaling binds to the enhancer elements in PPARγ target genes and markedly augments the PPARγ response (41). Our findings that PPARγ appears to play a bigger role in determining the rate/magnitude of contraction of the inflammatory response rather than the magnitude of earlier phases fits well with concepts of PPARγ playing a key role in tissue repair, healing, and overall resolution.

Future studies on the possible interface between PPARγ and lipids previously associated with resolution (42) seem in order.
tions such as impaired phagocytosis of bacteria were eliminated. Although future work will be required to be sure that macrophage death accounts for why LysM-Cre × PPARγ−/− mice succumb to *S. pneumoniae* infection more than control mice, we believe that the observation that macrophage PPARγ deficiency impacts the outcome of infection is quite significant on its own. Patients with PAP, a disease linked to impaired GM-CSF signaling, have an increased risk of superinfection (32), and it is known that suppressed GM-CSF signaling leads to lower PPARγ levels in the lung (35). Moreover, *Csf2rb−/− Csf2rb−/−* mice, a model mouse of PAP, are more susceptible to *S. pneumoniae* infection (37). Although it was already recognized that increasing PPARγ in models of PAP might reverse aspects of the disease such as lipid accumulation in macrophages, our data substantiate a link between the loss of PPARγ per se and increased susceptibility to infection in PAP. Importantly, downregulation of PPARγ and/or impairment in PPARγ signaling is also observed in cystic fibrosis (45–47), and PPARγ agonist treatment has been recently shown to ameliorate the severity of the cystic fibrosis phenotype in mice (47). Because cystic fibrosis is also tightly associated with an increased susceptibility to lung infection (48), PPARγ in *S. pneumoniae* is a negative regulator of macrophage Csf2rb function and hence critical for normal skeletal muscle and hepatic insulin sensitivity and full anti-diabetic effects of thiazolidinediones. *J. Clin. Invest.* 117: 2557–2569.


