CCR4 Is a Key Modulator of Innate Immune Responses

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CCR4 Is a Key Modulator of Innate Immune Responses

Traci L. Ness, Jillian L. Ewing, Cory M. Hogaboam, and Steven L. Kunkel

CONSISTENT WITH ALTERNATIVE ACTIVATION, INCLUDING ELEVATED SECRETION OF TYPE 2 CYTOKINES/CHEMOKINES AND THE FOUND IN INFLAMMATORY ZONE

Inflammation, including pulmonary fibrosis (2, 3), eosinophilic pneumonia (4), CCR4 receptor ligands is associated with the pathogenesis of several diseases on dendritic cells, macrophages, NK cells, platelets, and basophils, receptors have been repeatedly implicated in the pathogenesis of defenses against infection and trauma, chemokines and their re-
tion, inflammatory mediator release, changes in cell shape, and cellular migration. Although required for innate and acquired host defenses against infection and trauma, chemokines and their rece-
ceptors have been repeatedly implicated in the pathogenesis of chronic inflammatory diseases including allergy and autoimmune disease.

CCR4 is a high affinity receptor for CCL17 and CCL22 found on dendritic cells, macrophages, NK cells, platelets, and basophils, but it is predominantly known for its expression on T cells, especially of the Th2 phenotype (1). Increased expression of CCR4 and its ligands is associated with the pathogenesis of several diseases including pulmonary fibrosis (2, 3), eosinophilic pneumonia (4), hepatic inflammation (5), granuloma development (6), and diabe-
tes (7). Each of these is characterized by the infiltration of CCR4+ T cells into affected sites. Neutralization of CCR4 ligands prevents T cell-mediated airway inflammation, liver injury, granuloma for-
mation, and development of insulitis and diabetes in appropriate disease models (5–9). The role of CCR4 is less certain, as specific neutralizing Abs or antagonists have not been described in the literature.

CCR4−/− mice were derived in an effort to define the role of CCR4 in the development of Th2-mediated disease (10). Although CCR4 deletion has no apparent effect on Th2 differentiation in acute allergic models (10), it does affect differentiation in chronic disease (11). In the context of type 1 responses, CCR4−/− mice have diminished inflammatory responses. For example, cardiac allograft survival is significantly improved in CCR4−/− mice. A skewed population of infiltrating cells is comprised of increased numbers of CD8+ T cells and decreased CD4+ T and NK1.1+ CD3− cells (12). CCR4−/− mice are also more resistant to the effects of LPS challenge, exhibiting reduced proinflammatory cytokines and peritoneal macrophage recruitment (10).

The purpose of this study was to further define the mechanism of increased LPS resistance, as well as resistance to other TLR agonists. Peritoneal macrophages from CCR4−/− mice exhibited many features characteristic of alternatively activated macrophages (aaMφ), including skewed type 2 cytokine/chemokine and found in inflammatory zone 1 (FIZZ1) synthesis. MyD88-dependent NF-κB signaling was significantly down-regulated in CCR4−/− macrophages, whereas p38 MAPK and JNK pathways were in-
creased. These studies provide further evidence that despite its well-recognized role as a director of adaptive T cell driven re-
sponses, CCR4 is also an essential player in innate immunity.

Materials and Methods

In vivo studies

Male wild-type (WT) C57BL/6 mice (6–8 wk) were purchased from Tac-
onic Farms. CCR4−/− mice were provided by Tularik and were generated as previously described (10). Mice were bred and housed under specific pathogen-free conditions, and all animal experiments were approved by the Animal Use Committee at the University of Michigan (Ann Arbor, MI).

Mice received a single dose of LPS (Esherichia coli O55:B5; Sigma-Aldrich) i.p. and survived was monitored. In other studies, mice were given 10 mg/kg LPS, 50 μg of Pam3Cys-Ser-(Lys)4 (Pam3Cys; EMC Microcollections), or 4 × 108 E. coli (O86a:K6; American Type Culture Collection) i.p. and later bled and subjected to 2 ml of peritoneal lavage. Serum
Table I. Custom primer and probe sequences used for real-time RT-PCR analysis

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<thead>
<tr>
<th>Target</th>
<th>Primers (5’-3’)</th>
<th>Probes (5’-FAM and 3’-TAMRA)</th>
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<td>TLR2</td>
<td>Fwd - GCCACATTTCCACGACTT Rev - GCTGCCTCTTGCCCTGG</td>
<td>TGGTACCTGAGAATGATGGGCCGTG</td>
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<td>TLR4</td>
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<td>SYBR Green</td>
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<tr>
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<td>Fwd - GAAAGTCGACCCTACGACCA CAT Rev - AGTGGTTACCGACCCCTGACCTGG</td>
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</tr>
<tr>
<td>TLR9</td>
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<tr>
<td>FIZZ1</td>
<td>Fwd - TCCAGCTAATCTACCTCTCACCAGTT Rev - GACCCACCTTGCTACTGGACAGTG</td>
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<tr>
<td>T1/ST2</td>
<td>Fwd - GCAAGTCTGACATGCTCCAATGTTAT Rev - CCGAACCCAGGAGGAATTTA</td>
<td>SYBR Green</td>
</tr>
</tbody>
</table>

*Fwd, Forward; Rev, reverse.

Values of $\rho < 0.05$ (*), $\rho < 0.005$ (**), and $\rho < 0.0005$ (***)) are indicated for significant differences between WT and CCR4$^{-/-}$ treatment groups.

Results

**CCR4$^{-/-}$ mice are more resistant to TLR agonist and bacterial challenge**

As our laboratory has demonstrated phenotypic differences for CCR4$^{-/-}$ mice in other murine models of disease, we were interested in the mechanism of LPS resistance previously reported for these mice (10). WT and CCR4$^{-/-}$ mice were challenged i.p. with 1–100 mg/kg LPS (Fig. 1A). High-dose challenge was lethal to WT and CCR4$^{-/-}$ mice; however, mortality was significantly delayed in CCR4$^{-/-}$ mice. An intermediate dose (10 mg/kg LPS) killed all WT mice by 72 h, whereas only 20% of CCR4$^{-/-}$ mice were affected at this time. After 6 days, 60% of CCR4$^{-/-}$ mice survived, indicating that the protection was long-lasting. A 1 mg/kg LPS dose was not lethal for either strain. The intermediate dose (10 mg/kg) was used for further studies involving in vivo LPS administration. In an extension of these studies, challenge with PamCys, a synthetic TLR2 agonist, induced tissue pathology in WT mice. Serum levels of AST and ALT were significantly elevated in WT but not CCR4$^{-/-}$ mice 24 h after i.p. injection (Fig. 1B).
indicating that knockout mice have unique resistance to multiple bacterial Ags.

LPS administration initiates a “cytokine storm” characterized by high levels of inflammatory cytokines, especially TNF-α (15). rTNF-α alone can recapitulate many of the physiologic changes induced by LPS or sepsis, including fever, alterations in blood pressure, and weight loss (16). Thus, it was of interest to determine whether resistance to TLR agonist challenge in CCR4−/− mice was related to hyporesponsiveness to TNF-α. A 50-μg TNF-α i.v. challenge was equally lethal to WT and CCR4−/− mice (data not shown), suggesting that the protection against TLR agonists was not due to a defect in TNF-α responsiveness.

The next question we addressed was whether immune responses protecting CCR4−/− mice against the effects of Ag challenge also protected these mice against a live infection. Accordingly, WT and CCR4−/− mice were given 4 × 10⁸ CFU of a pathogenic strain of E. coli i.p., and bacterial loads were measured 24 h after infection (Fig. 2A). CCR4−/− mice had significantly less bacteria at the site of infection and more than a log reduction in systemic levels as compared with WT mice. Similarly, bacterial levels in the liver and lung were lower in CCR4−/− vs WT mice (data not shown).

Infection altered the local and systemic concentrations of several cytokines and chemokines. Fig. 2B illustrates the cytokines/chemokines that had differential WT and CCR4−/− expression. Compared with WT mice, CCR4−/− mice produced significantly more peritoneal IL-10 early after infection and less proinflammatory CCL3 at later times. Serum CCL2 was higher in CCR4−/− mice at 4 h but significantly less than WT levels at 24 h. Reductions in CCL2 and CCL3 secretion from CCR4−/− mice were likely due to both decreased bacterial load and the anti-inflammatory effects of enhanced IL-10 production.

Early recruitment of TLR-expressing cells is enhanced in LPS-treated CCR4−/− mice

TLRs are a pivotal group of pattern recognition receptors responsible for sensing the presence of pathogens and initiating immune responses. Therefore, TLR expression was evaluated on cells recruited to the peritoneal cavity in response to 10 mg/kg LPS (Fig. 3A). Basal levels of TLR transcripts were similar between strains, with reduced TLR4 expression in CCR4−/− cells. TLR2 was significantly up-regulated on WT peritoneal cells at 1–2 h after LPS treatment, whereas no changes were seen for other TLRs assayed.
Conversely, significant increases in TLR2, 4, 6, and 9 expression were noted in CCR4−/− cells as early as 30 min post-LPS treatment, with peak expression at 1 h. Peak expression in CCR4−/− cells was significantly higher than that observed for cells from WT mice. These data suggest that TLRs are immediately induced in CCR4−/− cells, contributing to a rapid response to pathogen challenge.

To characterize the cellular response, we assessed the kinetics of leukocyte recruitment into the peritoneum after LPS challenge. Equal numbers of resident cells were detected in untreated WT and CCR4−/− mice (Fig. 3B). Significantly higher numbers of leukocytes were seen in CCR4−/− mice as compared with WT mice early after treatment (4 h), but no differences were observed at later times (24–48 h; data not shown). The CD11b+ F4-80+ cell population was higher in CCR4−/− than WT mice at 4 h, and CCR4−/− mice had significantly more infiltrating CD11b+ TLR2+ and CD11b+ TLR4+ cells (Fig. 3C). Our findings demonstrate that CCR4−/− mice mobilize LPS-responsive leukocytes to the site of challenge more rapidly and aggressively than WT mice. Increases in TLR expression and leukocyte recruitment typically lead to a robust inflammatory response, yet CCR4−/− mice are LPS resistant, prompting further investigation of the phenotype of CCR4−/− peritoneal cells.

ST2, the receptor for IL-33 (17) and a negative regulator of TLR4 (18), has been mainly studied in association with its specific function in TH2 cells. However, ST2 may also play a role in the innate immune response, as suggested by our findings.

**FIGURE 3.** CCR4−/− mice have increased numbers of TLR-expressing cells after LPS challenge in vivo. WT and CCR4−/− mice (n = 3–5) were given 10 mg/kg LPS i.p. Peritoneal cells were collected at 0–120 min or 0–4 h post-LPS challenge for RNA (A) and flow cytometry (B–D) analyses, respectively. A, Real-time quantitative PCR was used to analyze TLR expression after LPS challenge. TLR expression was normalized to individual GAPDH levels and converted to fold difference relative to basal WT expression. B–D, Peritoneal cell totals were determined for each mouse. Cells (5 × 10^5) were double stained with Abs to murine CD11b and one of the following: F4–80 (B), TLR2 or TLR4 (C), or ST2 (D). Macrophage-like cells were gated and isotype Abs were used as controls. The results shown represent data from one of at least three independent experiments. *, p < 0.05; **, p < 0.005.
expression on Th2 cells; however, it is also found on fibroblasts, mast cells, and macrophages. Interestingly, significantly more CD11b+/ST2+ cells were recruited to the peritoneal cavities of CCR4−/− vs WT mice 24 h post-LPS (Fig. 3D). ST2 is critical to Th2-mediated responses, as neutralization increases IFN-γ and suppresses IL-4 and IL-5 production (19). Because aaMφ secretes several Th2-related cytokines/chemokines, ST2 may also be a specific marker for these cells (20).

CCR4−/− macrophages exhibit features of an alternatively activated phenotype

TLR expression was significantly higher on peritoneal cells from LPS-treated CCR4−/− mice as compared with similarly treated WT mice. Elevated expression was partially due to increased cellular recruitment, but TLR transcript levels were also increased in total peritoneal cells. Because resident macrophages are key to initiating an immediate innate response, peritoneal macrophages were isolated from naive mice and analyzed in vitro. CCR4−/− macrophages expressed higher basal levels of TLR2 and TLR4 than in WT cells (Fig. 4A). Furthermore, these cells secreted significantly more CCL2 (Fig. 4B) and CCL6 (data not shown) than WT cells. Following in vitro LPS challenge, macrophages up-regulated several cytokines and chemokines. No differences were noted in CCL3 production, but CCR4−/− macrophages produced significantly more CCL2 than WT cells. Higher CCL17 concentrations were also detected, which may have been due to the absence of CCR4-mediated feedback regulation. FIZZ1 secretion was significantly higher in CCR4−/− cells than in WT cells but was not affected by LPS treatment.

CCL2, CCL17, and FIZZ1 expression is characteristic of aaMφ (21, 22). Increased secretion of these factors from CCR4−/− macrophages prompted investigation of IL-4- and/or IL-13-driven alternative activation of these cells. Basal IL-10, CCL2, CCL17, and FIZZ1 transcript levels were higher in CCR4−/− macrophages than in WT cells (Fig. 5). With the exception of CCL17, higher protein levels were also detected. IL-4/IL-13-induced increases in CCL2, CCL17, and FIZZ1 expression confirmed alternative activation of WT macrophages, although concentrations of these factors were significantly higher from CCR4−/− macrophages. Although its expression was not induced by cytokine treatment, IL-10 concentrations remained significantly higher from CCR4−/− vs WT macrophages. These data support the concept that CCR4−/− mice have a resident population of peritoneal macrophages with many features of aaMφ.

NF-κB signaling is inhibited, but p38 MAPK and JNK pathways are increased in CCR4−/− macrophages

Most TLR-dependent inflammatory cytokine/chemokine synthesis is dependent on NF-κB. Phosphorylation of the inhibitor protein, IκBα, releases NF-κB into the nucleus where it initiates the transcription of inflammatory mediators. NF-κB p65 was measured in WT and CCR4−/− nuclear extracts in an effort to evaluate the overall activation of this pathway. Thioglycolate was used to augment macrophage recruitment to the peritoneal cavity to obtain sufficient numbers of cells for treatment and nuclear extract preparation. Pretreatment levels of nuclear p65 were 31% lower in CCR4−/− peritoneal macrophages as compared with WT (Fig. 6A). In vitro Pam3,Cys or LPS treatment significantly induced WT activation/translocation of NF-κB p65, but minimal NF-κB activation was measured in CCR4−/− peritoneal macrophages.

Because activation of the NF-κB pathway was suppressed in CCR4−/− macrophages, other pathways of transcription factor activation were also analyzed. Although resident peritoneal macrophages had similar levels of p38 MAPK, activated JNK was significantly higher in untreated cells from CCR4−/− mice than from WT mice (83% elevation; Fig. 6B). Pam3,Cys and LPS induced phosphorylation of p38 MAPK and JNK; however, all CCR4−/− treatment groups displayed significantly more activation than their WT counterparts. These data indicate that enhanced p38 MAPK and JNK signaling may compensate for NF-κB deficiency, allowing altered cytokine/chemokine expression from CCR4−/− macrophages in response to TLR agonists.

In an effort to identify the TLR/NF-κB defect, naive WT and CCR4−/− macrophages were treated with LPS and intermediate signaling mediators were measured using Western blotting. Basal expression of TRAF6 and IκBα was similar for both strains, but CCR4−/− macrophages had ~2-fold less MyD88 and phosphorylated-IκBα than WT cells. LPS immediately increased MyD88, IRAK1, TRAF6, and IκBα expression and IκBα phosphorylation in WT peritoneal macrophages with peak expression between 5 and 30 min (Fig. 7, left column). With the exception of IRAK1, almost no induction was seen in CCR4−/− cells. Basal IRAK1 levels were 2-fold higher in naive CCR4−/− vs WT macrophages. LPS triggered rapid IRAK1 expression in CCR4−/− cells (5 min), whereas similar levels were not produced in WT cells until 30 min after LPS challenge.

IL-4 and IL-13 are well known for their ability to polarize T cells into a Th2 phenotype and have recently been shown to have a similar effect on macrophage development. CCR4−/− macrophages have defective NF-κB signaling, and we have demonstrated that these cells share many features with aaMφ. Therefore, we sought to determine whether alternative activation would alter NF-κB signaling in WT macrophages. Differentiated macrophages were stimulated with LPS, and signaling
mediators were measured (Fig. 7, right column). Overall, LPS was unable to up-regulate expression of MyD88, IRAK1, TRAF6, or IκBα in IL-4-/IL-13-pretreated WT macrophages, and no changes were seen in the phosphorylation of IκBα. A similar profile was observed for pretreated CCR4−/− macrophages, indicating that the phenotype of naive CCR4−/− macrophages is similar to that of aaMφ.

**Discussion**

Coordinated interaction between both innate and acquired immune responses is crucial to the development of an effective response to foreign stimuli. In addition to regulating both arms of the immune system, chemokines and their receptors have also been recognized as key mediators of the cross-talk integrating nonspecific and specific defenses. Although CCR4 has been extensively studied in the context of acquired immunity, this investigation attempted to assess the contribution of CCR4 in models triggering innate immunity. Because previous studies have shown that CCR4−/− mice provide a protective phenotype to LPS challenge (23), we were interested in understanding the mechanisms of this resistance.

Our initial investigation confirmed that CCR4−/− mice were resistant to the in vivo effects of LPS, albeit at a reduced level than that previously reported (10). Contrary to these early studies using CCR4−/− mice backcrossed with C57BL/6 mice for four generations, our 10th generation mice were susceptible to a 100 mg/kg dose of LPS but were significantly resistant to a lower 10 mg/kg dose as compared with WT controls. Continued backcrossing may explain some of the phenotypic differences between these studies, as C57BL/6 mice are known to produce a more vigorous type 1 (IFN-γ-mediated) cytokine response (24) that can result in acute septic shock. In addition to LPS, we also demonstrated that CCR4−/− mice are more resistant to challenge with Pam3Cys.

The innate immune system is responsible for the nonspecific recognition of foreign invaders. Pattern recognition receptors, including TLRs, interact with conserved structures found on invading microbes. Several TLRs are involved in the recognition of bacterial Ags such as LPS (TLR4), diacyl lipopeptides (TLR2/TLR6), flagellin (TLR5), and CpG DNA (TLR9). TLR binding elicits the production of inflammatory chemokines, as well as a multitude of other immune molecules, that attract and coordinate the activities of both innate and specific immune cells.

We demonstrated that CCR4−/− mice were protected against in vivo challenge with two different TLR agonists, LPS and Pam3Cys, as well as a live bacterial infection. Alterations in TLR
expression and ultimately the recognition of bacterial Ags could be responsible for some of the different in vivo responses observed between WT and CCR4−/− mice. In fact, CCR4−/− mice exhibited increased transcript levels of all TLRs assayed after LPS treatment. A profile of the different leukocyte populations demonstrated that CCR4−/− mice had significantly higher numbers of CD11b^+F4/80^−, CD11b^+TLR2^−, and CD11b^+TLR4^+ leukocytes than WT animals at 4 h after LPS challenge. Thus, one potential mechanism for increased resistance in CCR4−/− mice may be enhanced pathogen recognition and leukocyte recruitment directed at the expeditious elimination of the bacteria and its Ags. Although increasing TLR expression facilitates a more rapid response to pathogens, we would expect the overall inflammatory response to be increased as well. Bacterial Ags such as LPS are well known for their ability to incite an overwhelming storm of inflammatory cytokines such as that observed during sepsis. Despite increases in TLR expression of CCR4−/− mice, few changes were seen in the overall chemokine profiles of infected WT and CCR4−/− mice. Therefore, other factors or mechanisms must be present that protect CCR4−/− mice from the tissue injury and mortality observed in WT mice after PamCys or LPS challenge, respectively.

The peritoneal cavity is normally a sterile environment, and macrophages are the principal resident leukocytes responsible for surveying this environment for pathogens and initiating the appropriate immune responses. The basal level of TLR expression in these cells provides a measure of their general ability to respond to bacterial stimuli. Analyses of naive resident peritoneal macrophages from WT and CCR4−/− mice revealed higher TLR2 and TLR4 expression in CCR4−/− macrophages, indicating an enhanced potential for pathogen recognition by knockout mice. Further analyses indicated different cytokine/chemokine profiles for WT vs CCR4−/− macrophages. Interestingly, no differences were seen in the expression of the inflammatory mediator CCL3, but naive and LPS-treated CCR4−/− macrophages produced significantly more anti-inflammatory/immunomodulatory mediators (IL-10, CCL2, CCL6, and CCL17) than similarly treated WT macrophages. This skewed response supports the decreased susceptibility of CCR4−/− mice to LPS/PamCys challenge in vivo. Although IL-10 has been shown to alter TLR4 expression, little information exists with regard to the ability of chemokines to alter the expression pattern of various TLRs. In preliminary investigations we did not observe significant alterations in TLR expression in WT mice treated with chemokines known to be associated with a polarized M2 response, including CCL2, CCL6, or CCL17.

Similarly as in T cell polarization, macrophages differentiate into classically activated macrophages (M1) or aaM (M2) (20, 22). Recently, IL-10, CCL2, and CCL17 expression has been associated with the development of aaM and the inhibition of classical activation (21, 25, 26). Our data suggested that CCR4−/− mice had a resident population of macrophages displaying a cytokine/chemokine phenotype characteristic of aaM. FIZZ1 is an antagonistically regulated by IL-4 and IFN-γ and, therefore, is often used as a marker of aaM (25, 27). CCR4−/− macrophages expressed significantly higher levels of FIZZ1 than WT macrophages. Although alternative activation of WT macrophages using IL-4 and IL-13 treatment resulted in production of CCL2, CCL17, and FIZZ1, expression of these factors and IL-10 was always higher in CCR4−/− macrophages. These data provide further evidence illustrating that CCR4−/− mice have resident macrophages possessing an alternatively activated phenotype.

Although the focus of this investigation was on the peritoneal cells and leukocytes elicited into the peritoneum, we were interested in determining whether macrophages from other tissues have an altered phenotype in the CCR4−/− mice. In preliminary studies, arginase 1, a mediator associated with macrophage polarization to an M2 phenotype, was found to be overexpressed in bone marrow-derived macrophages recovered from CCR4−/− animals challenged in vivo and subsequently treated in vitro with either LPS or CpG. This finding suggests that the peritoneal macrophages are not unique in possessing the ability to express a polarized phenotype upon challenge.

Our final set of studies focused on analyzing the signaling cascades initiated by TLR binding in WT and CCR4−/− macrophages. Considering our data illustrating the expression profiles of these two different strains of cells, we predicted that we would also discover differences in the signaling pathways activated by TLR challenge. NF-κB is the primary transcription factor responsible for initiating transcription of most inflammatory cytokines/chemokines. When inactive, it is held in the cytoplasm by the inhibitor protein IκBα. Activation of this pathway results in phosphorylation of IκBα, releasing NF-κB into the nucleus where it is active. Therefore, nuclear NF-κB was measured to indirectly assess the overall activity of this pathway. Untreated CCR4−/− cells had reduced levels of nuclear p65 compared with basal WT levels. LPS and PamCys were potent triggers of this pathway in WT cells; however, neither had an effect on CCR4−/− macrophages. This finding is extremely important, as suppression of this pathway would provide a mechanism explaining the reduced storm of cytokines initiated during an in vivo LPS challenge, improving tissue and host survival.

Despite the absence of NF-κB activation, macrophages from CCR4−/− mice produce high levels of anti-inflammatory/regulatory cytokines and chemokines, suggesting that other transcriptional pathways are up-regulated. In fact, we observed significantly higher induction of both p38 MAPK and JNK pathways in CCR4−/− macrophages in comparison to WT cells. Both p38

FIGURE 6. CCR4 modulates transcription factor activation. A, Macrophages from thioglycollate-recruited peritoneal cells (10^6/dish) were rested overnight and treated with medium, 2.5 μg/ml PamCys, or 1 μg/ml LPS. Nuclear extracts were prepared at 4 h after treatment (peak expression), and 20 μg of the extracts were analyzed using an NF-κB p65 ELISA. B, Naive resident peritoneal cells were plated (10^6 macrophages/well), rested overnight, and stimulated with medium, PamCys, or LPS. Phosphorylated p38 MAPK and JNK were measured at 30 min by ELISA. Absorbance was normalized to cells per well. All results shown represent data from two independent assays. *, p < 0.05; **, p < 0.005; ***, p < 0.0005.
MAPK and JNK are members of the serine/threonine MAPK family and are involved in inflammatory and stress responses. p38 MAPK targets several transcription factors including STAT1, Myc/Max, Elk-1, CHOP, MEF2, ATF-2, and CREB, whereas JNK activates c-Jun, ATF-2, Elk-1, JunD, and AP-1. Therefore, altered signaling pathways are able to compensate for NF-κB deficiency in CCR4−/− mice but skew the cytokine/chemokine responses following challenge with TLR agonists. A similar phenomenon was noted for tumor-associated macrophages (TAMs) (28). TAMs were associated with an alternatively activated phenotype, demonstrated high levels of IL-10 and CCL2, exhibited defective NF-κB signaling, and up-regulated IRF-3/STAT1 signaling. These studies with TAMs appear to parallel our studies with CCR4−/− macrophages and accentuate their similarities to aaMφ.

All TLRs, with the exception of TLR3, are able to stimulate the MyD88-dependent signaling pathway, increasing NF-κB translocation (29). Upon ligand binding, the adaptor protein MyD88 interacts with the cytoplasmic tail of the TLR and initiates the activation of a cascade of intracellular signaling mediators, including IRAK1 and TRAF6. In CCR4−/− macrophages, activation of this entire pathway, with the exception of IRAK1, is suppressed. IRAK1 has been shown to initiate STAT3-dependent IL-10 expression (30), potentially contributing to the increased IL-10 production seen in CCR4−/− mice and macrophages. IL-4/IL-13 treatment of WT macrophages shut down activation of the NF-κB pathway, indicating that alternative activation inhibits classical activation of NF-κB while driving the use of other pathways.

In summary, our data provide a novel mechanistic insight into the role of CCR4 in the innate immune response. Using CCR4−/− mice, we have demonstrated that these animals are resistant to the deleterious effects of TLR agonist challenge, as well as bacterial infection. The response of these mice to CpG challenge/TLR9 activation is the subject of ongoing studies in our laboratory. Although CCR4−/− mice have increased early cellular recruitment in response to LPS, CCR4−/− macrophages possess an altered phenotype, more closely resembling aaMφ. These cells rapidly induce TLR expression, allowing the recognition and binding of pathogens. Finally, the signal transduction pathways in these macrophages are altered, diminishing the NF-κB response and thus preventing the classic cytokine storm that is induced in inflammatory diseases such as sepsis.

Disclosures
The authors have no financial conflict of interest.
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