TLR9 regulates Th1 responses and cooperates with TLR2 in mediating optimal resistance to Mycobacterium tuberculosis

Andre Bafica,1,3 Charles A. Scanga,1 Carl G. Feng,1 Cynthia Leifer,2 Allen Cheever,4 and Alan Sher1

1Immunobiology Section, Laboratory of Parasitic Diseases, and 2Experimental Immunology Branch, National Cancer Institute, National Institutes of Health, Bethesda, MD 20892
2Laboratorio de Imunorregulacao e Microbiologia, Centro de Pesquisas Goncalo Moniz, FIOCRUZ, Bahia 40296-710, Brazil
4Biomedical Research Institute, Rockville, MD 20852

To investigate the role of Toll-like receptor (TLR)9 in the immune response to mycobacteria as well as its cooperation with TLR2, a receptor known to be triggered by several major mycobacterial ligands, we analyzed the resistance of TLR9−/− as well as TLR2/9 double knockout mice to aerosol infection with Mycobacterium tuberculosis. Infected TLR9−/− but not TLR2−/− mice displayed defective mycobacteria-induced interleukin (IL)-12p40 and interferon (IFN)-γ responses in vivo, but in common with TLR2−/− animals, the TLR9−/− mice exhibited only minor reductions in acute resistance to low dose pathogen challenge.

When compared with either of the single TLR-deficient animals, TLR2/9−/− mice displayed markedly enhanced susceptibility to infection in association with combined defects in proinflammatory cytokine production in vitro, IFN-γ recall responses ex vivo, and altered pulmonary pathology. Cooperation between TLR9 and TLR2 was also evident at the level of the in vivo response to live M. tuberculosis, where dendritic cells and macrophages from TLR2/9−/− mice exhibited a greater defect in IL-12 response than the equivalent cell populations from single TLR9-deficient animals. These findings reveal a previously unappreciated role for TLR9 in the host response to M. tuberculosis and illustrate TLR collaboration in host resistance to a major human pathogen.

Toll-like receptors (TLRs) are thought to play a critical role in both innate resistance and the initiation of adaptive immunity to infectious agents (1, 2). TLRs are known to recognize distinct molecular structures on microbes, and in several cases (e.g., recognition of viruses by TLR3, TLR7, TLR8, and TLR9), different sets of TLRs have been associated with the response to different classes of microorganisms (1). Although the available evidence suggests that multiple rather than single TLRs are required for innate defense against most pathogens (for review see reference 2), it is not clear how signals from different TLRs are orchestrated in generating a protective response. In particular, there is controversy as to whether at the in vivo level multiple TLR interactions are required to trigger individual effector elements or whether TLR cooperation stems from the interaction of distinct effector mechanisms, each triggered by individual TLRs.

TLR signaling has been postulated to have a major involvement in the regulation of host resistance to Mycobacterium tuberculosis (3, 4), an important human pathogen that infects over one third of the world’s population (5). Immunological control of M. tuberculosis infection has been shown to depend on Th1 CD4+ T cells as well as TNF, IFN-γ, and IL-12 (6–14). The latter cytokine, produced largely by APCs such as DCs and macrophages, is thought to function in mycobacterial immunity by both inducing and maintaining the Th1-mediated IFN-γ response (8, 9, 15). M. tuberculosis as well as other mycobacteria contain well-characterized TLR ligands that are potent in vitro stimuli of a number of proinflammatory cytokines, including TNF and IL-12 (16–19). A role for TLR signaling in host resistance to M. tuberculosis is further supported by the observation that mice deficient in Myd88, a major adaptor molecule

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A. Bafica and C.A. Scanga contributed equally to this work.

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required for signaling events by most TLR/IL-1R family members, show greatly enhanced susceptibility to aerosol infection with the pathogen, equivalent to that observed with IFN-γ-deficient mice (20, 11). Infected MyD88−/− animals, in addition to their loss of resistance, display impaired proinflammatory cytokine synthesis, which was found to correlate with decreased nitric oxide synthase 2 expression and diminished IFN-γ synthesis (20). In addition, MyD88-deficient APCs display a marked reduction in the synthesis of IL-12, TNF, and nitric oxide when exposed to M. tuberculosis in vitro (21, 22).

Although MyD88 appears to play a major role in resistance to M. tuberculosis, it has been difficult to attribute this requirement to the function of a single TLR. Thus, mice deficient in TLR2, TLR4, TLR6, IL-1, or IL-18, although in some cases displaying specific defects in antimycobacterial responses, exhibit only minor increases in susceptibility to low dose aerosenic challenge (23–28). For example, M. tuberculosis–infected TLR2−/− mice, although showing defective granuloma formation, display only a small elevation in pulmonary bacterial loads late in infection and survive for at least 150 d (28). Interestingly, however, when infected with unconventionally high doses of M. tuberculosis, TLR2−/− but not TLR4−/− mice exhibit greatly enhanced susceptibility compared with WT animals (23, 24). This loss in resistance is accompanied by alterations in proinflammatory cytokine and nitric oxide synthase 2 expression as well as the pulmonary granulomatous response (28). TLR2 also has been shown to play an important role in the regulation of antimycobacterial-induced cytokine production by APCs in vitro (23, 28–30). Nevertheless, it is difficult to reconcile this evidence for TLR2 involvement with the minimal loss in resistance consistently observed in TLR2−/− mice challenged with low level physiological doses of M. tuberculosis.

One interpretation of the above findings is that host resistance to M. tuberculosis depends on a previously unevaluated TLR–ligand interaction. TLR9 is one such TLR/IL-1R family member whose involvement in control of M. tuberculosis infection has never been formally addressed. TLR9 was initially described as recognizing unmethylated CpG motifs in bacterial and viral DNA (31, 32) and was shown to be responsible for the immunostimulatory effects of these nucleic acids. In this regard, it is of interest that the original demonstration of the adjuvant properties of DNA emerged from studies on Mycobacterium bovis (bacillus of Calmette and Guerin [BCG]) (33) and that DNA from M. tuberculosis as well as other mycobacteria has subsequently been shown to contain highly immunostimulatory CpG motifs (34–37). TLR9 is known to be localized in endosomes as well as phagolysomes, where it could be triggered by mycobacterial DNA after uptake of the pathogen (38–41). For these reasons we considered TLR9 to be an important candidate pattern-recognition receptor that might account for the MyD88 dependency of host resistance to M. tuberculosis.

In this study, we show that DNA from M. tuberculosis is indeed a potent stimulus of TLR9-dependent proinflammatory cytokine production by both DCs and macrophages and that the in vitro responses of these cells to live mycobacteria are also partially dependent on TLR9. In addition, our data indicate that TLR9 plays an important role in the regulation of the mycobacteria-induced Th1 responses during M. tuberculosis infection in vivo. Finally, we demonstrate that mice doubly deficient in TLR9 and TLR2 show enhanced susceptibility to M. tuberculosis not observed in mice lacking either TLR2 or TLR9 alone. Taken together, these data reveal a role for TLR9 in the immune response to M. tuberculosis and provide an important example of TLR collaboration in host resistance to infection.

RESULTS

DNA from M. tuberculosis induces proinflammatory cytokine responses through a TLR9–dependent pathway

To assess whether TLR9 plays a role in M. tuberculosis infection, we first asked if the stimulation of proinflammatory responses by mycobacterial DNA documented in previous studies (33–37) depends on this TLR as would be predicted. As shown in Fig. S1 A, available at http://www.jem.org/cgi/content/full/jem.20051782/DC1, purified DNA from M. tuberculosis, BCG, or Escherichia coli stimulated IL-12p40 production by splenic CD11c+ DCs from WT mice. Importantly, this response was found to be TLR9–dependent as was M. tuberculosis DNA–induced IL-12p40, TNF, and IFN-α production by BM–derived DCs (BMDCs; Figs. S1, B and C, and S3) and TNF and IL-6 synthesis by BM–derived macrophages (BMM; Fig. S1, D and E). In keeping with previously published data demonstrating a requirement for endosomal acidification in immune stimulation by CpG oligonucleotides (42), the response of splenic DCs to mycobacterial DNA was found to be inhibited by chloroquine treatment (not depicted). Taken together, these results indicate that mycobacterial DNA is a potent stimulus for TLR9–dependent cytokine production by murine APCs.

The in vitro IL-12 response of APCs to M. tuberculosis bacilli is regulated by both TLR9 and TLR2, whereas TNF is controlled primarily by TLR2

Having demonstrated TLR9–dependent proinflammatory responses to mycobacterial DNA, we next asked whether TLR9 regulates cytokine production stimulated by live M. tuberculosis in freshly isolated splenic DCs. In addition, we simultaneously assessed the involvement of TLR2 because this receptor has previously been shown to influence proinflammatory cytokine production by BM–derived APC populations in response to M. tuberculosis infection (23, 28, 43).

As shown in Fig. 1 A, live M. tuberculosis induced IL-12p40 secretion by splenic DCs in a dose–dependent manner, and this response was markedly reduced in the absence of MyD88. Heat-killed mycobacteria also induced IL-12p40 production, indicating that this response is not dependent on DC infection. Nevertheless, in agreement with a previous study (44), M. tuberculosis–induced IL-12 synthesis was...
and IL-12p40 was determined by ELISA. Results are means

spleen cells from WT or MyD88

in the culture supernatants by ELISA. Results are means ± SE of triplicate

lymphocytes from WT or MyD88

A, B, and C. Three performed.

cate measurements. Experiments shown are representative of at least
greatly impaired in the presence of cytochalasin D, suggesting

To test whether TLR9 and TLR2 have additive effects

spleen cells from WT or MyD88

on the IFN-α response of BMDCs to

We generated TLR2/9-deficient mice and tested the response of

TLR2 also appeared to preferentially regulate the low

Th1 responses.

To determine whether TLR2 and TLR9 have additive effects

Given that the role of TLR2 in the IL-12 response by

IFN-α production by DCs from MyD88

eral antigen-presenting cells (APCs) were stimulated with LPS

TLR2/9-deficient mice and tested the response of

and comparable to that seen with DCs from MyD88-deficient

mice (Fig. 1 D). TLR2/TLR9 cooperation was also

Figure 1. Role for both TLR9 and TLR2 in the MyD88-dependent

The role of TLR9 and TLR2 in the MyD88-dependent

www.jem.org/cgi/content/full/jem.20051782/DC1), although in agreement with previously published data in a similar in vitro system (43), levels of the IL-12 heterodimer

Because macrophages play a major role in the response to

mycobacteria, we also investigated TLR2/TLR9 involvement in proinflammatory cytokine production by these cells. BMM from TLR2- or TLR9-deficient mice showed significant reductions in bacteria-stimulated IL-12 synthesis (Fig. 2 A). Moreover, DKO BMM showed reduced cytokine responses comparable to those seen in MyD88−/− APC populations (Fig. 2), suggesting that TLR2 and TLR9 act in concert in signaling IL-12 responses by these cells. In contrast, TNF and IL-6 production by macrophages appeared to be controlled primarily by TLR2 and not TLR9 (Fig. 2, B and C). TLR2 also appeared to preferentially regulate the low level TNF response observed in BMDCs (Fig. S2 C) and splenic DCs (not depicted).
TLR2 and TLR9 cooperate in host resistance to M. tuberculosis infection

To assess and compare the respective roles of TLR2 and TLR9 in resistance to infection in vivo, we measured survival, bacterial loads, and histopathology in TLR2−/−, TLR9−/−, TLR2/9−/−, MyD88−/−, and WT control mice infected by the aerosol route with a low dose (50–100 CFUs) of virulent M. tuberculosis. At this challenge level, all WT animals survived for at least 200 d, whereas all MyD88−/− animals succumbed within 75 d as reported previously (20, 21). Most single TLR2−/− and TLR9−/− mice survived for the full 200-d period of the experiment, with some attrition occurring after day 100 (Fig. 3 A). In contrast, infected TLR2/9−/− mice began to die much earlier, and all succumbed within 120 d (Fig. 3 A).

In several previous studies, a more profound effect of TLR2 deficiency on host resistance to M. tuberculosis was revealed at higher challenge doses (23, 28). In analogous fashion, TLR9-deficient mice were shown to be highly susceptible to challenge with 500 CFUs/mouse, with all of the animals now succumbing by day 70 (Fig. 3 A).

The observed effects of TLR deficiency on host resistance correlated with changes in pulmonary bacterial load measured at days 21 and 42 after infection with a low dose inocula (Fig. 3 B). Thus, as reported previously (20, 21), MyD88−/− mice showed greatly increased bacterial burdens in comparison to WT animals, a difference that approached 2 logs by day 42 after infection. In contrast, the single TLR2−/− and TLR9−/− mice showed only minor increases in mycobacterial loads at both time points (Fig. 3 B), and it was only at day 100 after infection that these differences in CFUs reached statistical significance (not depicted). Importantly, at day 21 after infection, TLR2/9−/− animals displayed increases in pulmonary bacterial counts equivalent to those observed in the MyD88−/− mice, and at day 42, the TLR2/9−/− animals still maintained significantly higher CFUs when compared with WT or each of the single TLR-deficient mice, albeit lower than the bacterial counts in the MyD88−/− animals (Fig. 3 B). Similar alterations in CFUs were observed in the spleens from the same animals (not depicted). Although single TLR9−/− mice challenged with a low dose of M. tuberculosis failed to display significantly higher pathogen loads than WT animals at days 21 and 42, they exhibited statistically significant increases in CFUs when challenged with the higher dose (500 CFUs) inocula (Fig. 4 B), and this loss in resistance correlated with diminished ex vivo IL-12p40 production detected in lung homogenates (not depicted).
Cooperative effects of TLR2 and TLR9 on the pulmonary histopathologic response to *M. tuberculosis*

To determine whether the increased susceptibility of TLR9−/− and TLR2/9−/− mice is reflected in the tissue response to *M. tuberculosis*, we examined the lungs of the animals at day 42 after infection. As reported previously (20), lungs from MyD88−/− animals exhibited widespread necrosis with few distinct granulomas (Fig. 5, B and G) and showed marked increases in acid-fast–stained bacilli (Fig. 5 L) when compared with WT mice (Fig. 5, A, F, and K). Also in agreement with previous studies (28), lungs from infected TLR2−/− mice showed increased inflammation with exuberant polymorphonuclear infiltrates, interstitial pneumonitis, and general disruption of granuloma morphology (Fig. 5, C, H, and M).

In contrast, lungs from TLR9−/− mice showed no major difference in overall histopathology (Fig. 5, D and I) or granuloma numbers (not depicted) when compared with lungs from similar infected WT animals. And like lungs from TLR2−/− mice, lungs from TLR9−/− mice showed only marginal increases in acid-fast–stained bacteria (Fig. 5, K–N). However, a striking difference was seen in the lungs of the day 42 infected TLR2/9−/− animals in comparison with either of the single TLR-deficient or WT mice. Sections from the former animals displayed widespread inflammation (Fig. 5, E and J), even more extreme than that seen in the TLR2−/− mice (Fig. 5, C and H) and closely resembling that observed in the MyD88−/− animals (Fig. 5, B).

**Figure 5.** Lungs from TLR2/9−/− mice display exacerbated pulmonary pathology and increased acid-fast bacilli. Formalin-fixed, paraffin-embedded pulmonary tissue sections from day 42 infected mice were stained with hematoxylin and eosin (A–J). Note the increased inflammation in TLR2−/− and TLR2/9−/− lungs (A and E), with the more extreme pathology in the latter group. Acid-fast bacilli in lung tissue were stained with the Ziehl-Neelsen method (K–O). Representative sections from infected WT (A, F, and K), MyD88−/− (B, G, and L), TLR2−/− (C, H, and M), TLR9−/− (D, I, and N), and TLR2/9−/− (E, J, and O) mice are shown. Original magnification is 5 (A–E), 20 (F–J), and 10 (K–O).

**Figure 6.** Influence of TLR9 on the generation of IFN-γ–producing CD4+ T cells and Th1–associated cytokines in *M. tuberculosis*–infected mice. (A) Lung cells isolated from day 30 infected mice were stimulated with anti-CD3 mAb, and intracellular IFN-γ production was determined by flow cytometry after gating lymphocyte populations by forward and side scatter parameters. The FACS profiles of anti-CD4– and anti-CD8–stained lymphocytes in A are from pooled cells from two mice and are representative of results from four animals per group. The majority (85–95%) of the IFN-γ–positive CD4+ population in the lung preparations from infected MyD88 KO mice is likely to represent dead cells, consistent with their abundance in sections of the same tissue (Fig. 5, B and G). Percentage of CD4+ and CD8+ T cells that stain positively for IFN-γ calculated from the experiments shown in A. Relative expression of anti-CD4– and anti-CD8–stained lymphocytes in A are from pooled cells from two mice and are representative of results from four animals per group. The majority (85–95%) of the IFN-γ–positive CD4+ cells shown in the dot plots in the top panel were determined to be CD8+ T cells (unpublished data). Based on its nonspecific staining with multiple antibodies, the CD4 dim IFN-γ–positive population in the lung preparations from infected MyD88 KO mice is likely to represent dead cells, consistent with their abundance in sections of the same tissue (Fig. 5, B and G). Percentage of CD4+ and CD8+ T cells that stain positively for IFN-γ calculated from the experiments shown in A. Relative expression of anti-CD4– and anti-CD8–stained lymphocytes in A are from pooled cells from two mice and are representative of results from four animals per group. The majority (85–95%) of the IFN-γ–positive CD4+ cells shown in the dot plots in the top panel were determined to be CD8+ T cells (unpublished data). Based on its nonspecific staining with multiple antibodies, the CD4 dim IFN-γ–positive population in the lung preparations from infected MyD88 KO mice is likely to represent dead cells, consistent with their abundance in sections of the same tissue (Fig. 5, B and G). Percentage of CD4+ and CD8+ T cells that stain positively for IFN-γ calculated from the experiments shown in A. Relative expression of anti-CD4– and anti-CD8–stained lymphocytes in A are from pooled cells from two mice and are representative of results from four animals per group. The majority (85–95%) of the IFN-γ–positive CD4+ cells shown in the dot plots in the top panel were determined to be CD8+ T cells (unpublished data). Based on its nonspecific staining with multiple antibodies, the CD4 dim IFN-γ–positive population in the lung preparations from infected MyD88 KO mice is likely to represent dead cells, consistent with their abundance in sections of the same tissue (Fig. 5, B and G).
and G). Moreover, lungs from the TLR2/9−/− animals exhibited focal necrosis, a process rarely seen in WT or single TLR-deficient mice but common in MyD88−/− mice. In addition, numerous acid-fast bacilli were clearly evident in lung tissue from the double TLR-deficient hosts (Fig. 5 O), consistent with the increased pulmonary CFUs observed in these animals (Fig. 3 B).

In contrast to TLR2, TLR9 controls IFN-γ production by CD4+ T cells in M. tuberculosis–infected animals

Because IL-12–dependent IFN-γ is a major mediator of resistance to M. tuberculosis and our data indicated a major influence of TLR9 on bacteria-induced IL-12 production in vitro (Fig. 1 D), we asked whether defects in in vivo IFN-γ responses are also evident in TLR9 as well as in TLR2/9−/− mice. When measured at 30 d after infection by intracellular cytokine staining after ex vivo anti-CD3 stimulation, ~40% of pulmonary CD4+ cells from WT animals were found to secrete IFN-γ, and this response was diminished by 60–70% in the equivalent population from MyD88−/− mice (Fig. 6, A and B). Importantly, TLR9−/− and TLR2/9−/− but not TLR2-deficient mice showed significant reductions in IFN-γ CD4+ cells as well as in lung IFN-γ and IL-12p40 mRNA expression, although the observed decreases were less than those seen in MyD88−/− mice (Fig. 6, B–D). In contrast, none of the KO mice showed deficiencies in IFN-γ CD8+ cells (Fig. 6 B), and it is possible the retention of this cell population in the TLR9−/− and TLR2/9−/− contributes to their partial resistance. Measurement of changes in IL-12p70 production was not possible because the heterodimer is not present in sufficient quantity in sera or lung homogenates to allow detection by ELISA.

To confirm that these differences reflect alterations in M. tuberculosis–specific Th1 priming, we tested the recall responses of splenic CD4+ T cells from day 30 infected mice using BMDCs from WT mice that had been infected in vitro with different doses of live mycobacteria as APCs. As shown in Fig. 6 E, major defects in M. tuberculosis–specific IFN-γ responses were observed in the TLR9−/−, MyD88−/−, and TLR2/9−/− mice but not in the TLR2/−/− animals.

**DISCUSSION**

The greatly enhanced susceptibility of MyD88−/− mice to M. tuberculosis is perhaps the strongest evidence for a role of TLR/IL-1R signaling in host resistance to this pathogen. Nevertheless, in previous studies it has been difficult to assign this defect to the role of any individual TLR/IL-1R family member. Because mice deficient in each of the known TLRs have not yet been systematically screened, the possibility remains that one yet-to-be-investigated TLR accounts for MyD88-dependent resistance. An alternative explanation proposed by others (2, 46) as a general concept for TLR function is that multiple TLRs act in concert in determining pathogen control. In this study, we have identified a previously unrecognized TLR–ligand interaction that contributes to the innate and adaptive immune response to M. tuberculosis and provided clear-cut evidence for its cooperation with a second TLR signal in host resistance to this bacterium.

Although mycobacterial DNA has long been linked to the adjuvant properties of BCG as well as mycobacterial extracts (34–36), it is only with the recent discovery of immunostimulatory CpG motifs (31) and their recognition by TLR9 (47) that the basis of this effect of mycobacteria on the immune system has been properly appreciated. Nevertheless, the role of TLR9/DNA interaction on host resistance to M. tuberculosis or to other medically important mycobacteria has never been systematically examined. The findings presented here confirm that mycobacterial DNA does indeed stimulate proinflammatory cytokine synthesis through TLR9 and further establish a role for this TLR in the IL-12 and Th1 responses to live M. tuberculosis in vitro as well as in vivo. Although these defects were associated with only minor increases in pulmonary bacterial loads and decreases in host survival at low dose challenge, TLR9−/− mice displayed markedly enhanced susceptibility when exposed to higher dose bacterial inocula (Fig. 4) as described previously for TLR2−/− animals (23, 28). However, in direct contrast to TLR2−/− mice, infected TLR9−/− animals did not show major alterations in granulomatous pathology or in vitro TNF production by APCs. Thus, although TLR9−/− and TLR2−/− mice show comparable changes in resistance to M. tuberculosis infection at both low and high dose infection, they exhibit distinct immune response defects to this pathogen in vivo.

It is likely that TLR9 triggering by mycobacteria requires bacterial uptake and phagolysosomal fusion, as drugs that inhibit these two processes dampened the TLR9-dependent IL-12 response of APCs. Therefore, we hypothesize that M. tuberculosis triggers TLR9 by releasing DNA from either bacteria dying within phagolysosomes or through the uptake of dead bacilli. An alternative possibility that cannot be ruled out at present is that mycobacteria possess TLR9 ligands distinct from genomic bacterial DNA. A recently described precedent is the stimulation of TLR9 by hemozoin pigment from malaria (48).

Although TLR9 alone had distinct but partial effects on host resistance to M. tuberculosis, these were clearly enhanced in mice doubly deficient in TLR9 and TLR2 as reflected in both increased bacterial load and reduced mean survival. In addition, DCs from TLR2/9 DKO mice showed greater impairment in their mycobacteria-induced IL-12 responses than did the equivalent populations from each of the single TLR−/− animals. In each of the above parameters, the observed effects of the absence of TLR9 and TLR2 appeared to be additive in the TLR2/9 DKO mice, although the pulmonary pathology and bacterial burden in these animals as measured by both CFU and acid-fast bacilli in situ staining showed evidence of synergy (Figs. 3 and 5, M–O). Nevertheless, in terms of the other parameters analyzed, the phenotype of the TLR2/9 DKO animals is more complex. For example, redundancy was observed in the regulation of IL-12p40 production by TLR2 and TLR9 in BMDCs (Fig. S2...
A). Moreover, as discussed above, in several cases individual immune deficiencies appeared to be linked to single TLRs. For example, *M. tuberculosis*-induced TNF production appears to be controlled by TLR2 and recall IFN-γ responses by TLR9.

It has recently been proposed in several studies (46, 49) that TLR signals synergize in the triggering of IL-12 and other Th1-promoting mediators by DCs. This hypothesis, based largely on experiments examining the interactions of multiple TLR ligands on DC responses, argues that the induction and maintenance of an effective immune response against microbes depends on the recognition of a “pathogen code” by a combination of different TLRs. Our results partially support this concept because some but not all of the *M. tuberculosis*-induced TLR effects were synergistic in vivo. Nevertheless, it is likely that specific combinations of TLRs act in concert by instead stimulating distinct responses that together are required for effective microbial control, a mechanism also requiring a pathogen code. This mechanism also would depend on induction thresholds related to both the dose and kinetics of infection.

Although our in vivo data reveal a major cooperative interaction between TLR9 and TLR2 in host resistance to mycobacteria, this is clearly not the case for other TLR combinations. Thus, TLR2/4−/− and TLR9−/− mice have been found to display unimpaired resistance to *M. tuberculosis* as well as BCG infection (45, 50). Moreover, in a recent experiment, we failed to observe increased susceptibility to *M. tuberculosis* in animals deficient in TIRAP, an adaptor molecule required for MyD88-dependent signaling by both TLR2 and TLR4, relative to mice singly deficient in TLR2 (unpublished data). It is of interest that both TLR2−/− and TLR9−/− mice display clearly enhanced susceptibility to high dose *M. tuberculosis* infection, a property that does not appear to be shared by TLR4−/− animals (23). This observation suggests that screening of different TLR/IL-1R–deficient mice by high dose challenge could be used as a strategy for detecting additional signaling receptors that cooperate with TLR2 and TLR9 in explaining the MyD88-dependent control of *M. tuberculosis* infection. Having shown cooperation between two TLR/IL-1R family members in host resistance to this pathogen, the next obvious step is to determine whether even greater effects on control of *M. tuberculosis* will be evident in mice with the appropriate triple receptor deficiency.

The findings of this study in the murine tuberculosis model have several implications for the investigation of the role of TLR/IL-1R in susceptibility of humans to mycobacterial infection and disease. The involvement of these receptors has been suggested from genetic studies correlating single nucleotide polymorphisms within the TLR2 gene, with disease severity in patients infected with *M. leprae* (51) or susceptibility to infection in populations exposed to *M. tuberculosis* (52, 53). Our observations that TLR9 also contributes to host resistance to mycobacterial infection suggests that polymorphisms in this gene (e.g., TLR9 single nucleotide polymorphisms at −1,237 and −2,428; reference 54) should also be examined in the same type of genetic study and predicts that more extreme disease susceptibility will be seen in patients with simultaneous mutations in both TLR2 and TLR9. At a more general level, the evidence that different TLRs cooperate in determining host resistance to infection in murine experimental models supports the notion that complex polygenic analyses involving the interaction of multiple rather than single TLR gene family alleles might be required to reveal major functions for the TLR/IL-1R system in innate immunity to human infectious diseases.

### MATERIALS AND METHODS

**Experimental animals.** WT control C57BL/6 mice were purchased from Taconic Farms. Breeding pairs of MyD88−/−, TLR2−/−, and TLR9−/− mice were obtained from S. Akira (Osaka University, Osaka, Japan) via D. Golenbock (University of Massachusetts Medical School, Worcester, MA) and R. Seder (National Institutes of Health [NIH], Bethesda, MD). The MyD88−/− and TLR9−/− mice had been backcrossed to C57BL/6 for 10 generations, and the TLR2−/− animals had been backcrossed for five generations. TLR2/9−/− animals were generated by mating TLR2−/− with TLR9−/− deficient animals. These F1 animals were then intercrossed to derive homozygous TLR2/9−/− mice identified by PCR of tail snips (unpublished data). Because of the known influence of 129/SvJ genes in host resistance to intravenous *M. tuberculosis* infection (55) and the finite although remote possibility that the relevant genes may have been retained in the TLR2−/− parents of this cross, we compared the resistance of C57BL/6 and B6/129F2 mice under the conditions of low dose aerosol infection used. In agreement with studies by other investigators (56–59), we observed no significant differences in survival and bacterial loads between the two mouse groups (unpublished data). Animals were bred and maintained at an American Association of Laboratory Animal Care–accredited facility at the National Institute of Allergy and Infectious Diseases [NIAID], NIH. Mice of both sexes between 8- and 14-wk old were used in all experiments.

**TLR agonists and other reagents.** The synthetic lipoprotein Pam3Cys(S-[2,3-bis(palmitoyloxy)-(2-RS)-propyl]-N-lysyl-OH, trihydrochloride) was obtained from EMC Microcollections. Peptide glycans (Staphylococcus aureus), ultra-pure LPS (E. coli 0111:B4), endotoxin-free E. coli DNA (K12), and CpG oligo DNA (1826) were purchased from InvivoGen. Purified genomic DNA from *M. tuberculosis* H37Rv was provided by J. Belisle (Colorado State University, Fort Collins, CO) under the NIH, NIAID contract NO1 AI75320 “Tuberculosis Research Materials and Vaccine Testing.” Purified genomic DNA from *Mycobacterium sp* (BCG) was purchased from American Type Culture Collection (no. 19015D). Chloroquine and cytochalasin D were obtained from Sigma-Aldrich.

**APCs and cell cultures.** Splenic CD11c+ cells were obtained by incubation of splenic cell suspensions with anti-CD11c MicroBeads (Miltenyi Biotec) for 15 min at 4°C followed by a washing step in PBS/bovine serum albumin and then sorted in an AutoMACS (isolation mode POSSEL_S; Miltenyi Biotec). Analysis of the sorted cells showed purity >95%.

**BMDCs were generated as originally described elsewhere (60). In brief, BM cells were removed from the femurs and tibias of mice and cultured in RPMI 1640 (GIBCO BRL) supplemented with 2 mM l-glutamine, heat-inactivated 10% FCS, 100 μg/ml penicillin, 100 μg/ml streptomycin, 5 × 10−3 M 2-mercaptoethanol (complete media; all from Sigma-Aldrich), plus 20 ng/ml GM-CSF (GIBCO BRL). On days 3 and 6, complete media was added containing 10 ng/ml GM-CSF. BMDCs were used at days 6–7 of culture.**
conditioned medium (as a source of M-CSF), and incubated for 7 d at 37°C, 5% CO2.

**M. tuberculosis infections.** For in vitro exposure of APCs to *M. tuberculosis*, the virulent strain H37Rv was prepared from frozen stocks as described previously (62). In some experiments, mycobacteria were killed by heating at 60°C for 1 h. DCs and BMM were exposed to different multiplicities of infection (MOI) of mycobacteria or TLR agonists in complete media for 18–24 h. In one set of experiments, splenic DCs were first preincubated with 5 μg/ml chloroquine or cytochalasin D for 30 min at 37°C. Cells were then exposed to mycobacteria (MOI = 1) or 10 μg/ml LPS as a control. Supernatants were then harvested, and ELISAs for IL-12p40, TNF, and IL-6 (R&D Systems) as well as for IFN-α (PBL Biomedical Laboratories) were performed.

For in vivo mycobacterial infection, mice were infected as described previously (58). In brief, animals were placed in a closed, nose-only aortalization system (CH Technologies) and exposed for 15 min to nebulized *M. tuberculosis* to deliver 50–100 bacteria/mouse (low dose inoculum). In a different set of experiments, mice were infected with ~500 bacteria/mouse (high dose inoculum). To assess mycobacterial load, lungs and spleens were harvested at several times after infection, and tissue homogenates were diluted in PBS/Tween-20 and cultured on 7H11 agar plates as described previously (63). Colony counts were determined 21 d later.

**Flow cytometry.** Single cell suspensions from individual mice were immunostained as described previously (15). In brief, for intracellular detection of IFN-γ, total lung cells were stimulated with 10 μg/ml of plate-bound anti-CD3 at 37°C for 6 h, and brefeldin A was added during the last 2 h. Cells were then surface stained with mAb to CD4 (clone RM4-5) or control. The following primer pairs were used: for IFN-γ, 5′-CGGATCC-CCATG-3′ (forward) and 5′-CAGGAGCTACATG-3′ (reverse). In a different set of experiments, APCs were incubated with anti-CD4 MicroBeads (Miltenyi Biotec) for 15 min at 4°C. Cells were then exposed to 37°C/H11034 stimulation of IFN-γ, fixed, and permeabilized. Intracellular IFN-γ was detected with anti–IFN-γ mAb (clone XMG1.2). Data were collected using a FACS Calibur (BD Immunocytometry Systems) with CellQuest (BD Biosciences) and analyzed with FlowJo software (Tree Star). All mAbs were obtained from BD Biosciences.

**Measurement of cytokine gene expression in lung tissue.** Total RNA was isolated from lungs, and real-time RT-PCR was performed on an ABI Prism 7900 sequence detection system (Applied Biosystems) using TaqMan Gene Expression Assay (Applied Biosystems). In brief, for intracellular detection of IFN-γ, total lung cells were stimulated with 10 μg/ml of plate-bound anti-CD3 at 37°C for 6 h, and brefeldin A was added during the last 2 h. Cells were then surface stained with mAb to CD4 (clone RM4-5) or control. The following primer pairs were used: for IFN-γ, 5′-CGGATCC-CCATG-3′ (forward) and 5′-CAGGAGCTACATG-3′ (reverse). In a different set of experiments, APCs were incubated with anti-CD4 MicroBeads (Miltenyi Biotec) for 15 min at 4°C. Cells were then exposed to 37°C/H11034 stimulation of IFN-γ, fixed, and permeabilized. Intracellular IFN-γ was detected with anti–IFN-γ mAb (clone XMG1.2). Data were collected using a FACS Calibur (BD Immunocytometry Systems) with CellQuest (BD Biosciences) and analyzed with FlowJo software (Tree Star). All mAbs were obtained from BD Biosciences.

**REFERENCES**


