Malaria primes the innate immune response due to interferon-γ induced enhancement of toll-like receptor expression and function

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Malaria-induced sepsis is associated with an intense proinflammatory cytokineemia for which the underlying mechanisms are poorly understood. It has been demonstrated that experimental infection of humans with Plasmodium falciparum primes Toll-like receptor (TLR)-mediated proinflammatory responses. Nevertheless, the relevance of this phenomenon during natural infection and, more importantly, the mechanisms by which malaria mediates TLR hyperresponsiveness are unclear. Here we show that TLR responses are boosted in febrile patients during natural infection with P. falciparum. Microarray analyses demonstrated that an extraordinary percentage of the up-regulated genes, including genes involving TLR signaling, had sites for IFN-inducible transcription factors. To further define the mechanism involved in malaria-mediated “priming,” we infected mice with Plasmodium chabaudi. The human data were remarkably predictive of what we observed in the rodent malaria model. Malaria-induced priming of TLR responses correlated with increased expression of TLR mRNA in a TLR9-, MyD88-, and IFN-γ-dependent manner. Acutely infected WT mice were highly susceptible to LPS-induced lethality while TLR9−/−, IL12−/− and to a greater extent, IFN-γ−/− mice were protected. Our data provide unprecedented evidence that TLR9 and MyD88 are essential to initiate IL12 and IFNγ responses and favor host hyperresponsiveness to TLR agonists resulting in overproduction of proinflammatory cytokines and the sepsis-like symptoms of acute malaria.

Malaria constitutes the most devastating global health problem in human history. The pathogenesis of malaria is multifactorial. Serious sequelae can result from 3 primary pathophysiological events: (i) red blood cell destruction; (ii) adhesion of infected erythrocytes to the capillary veins, especially in the CNS; and (iii) an excessive proinflammatory response. The latter is responsible for symptoms such as rigors, headache, chills, spiking fever, sweating, vasodilatation, and hypoglycemia (1, 2). The initial proinflammatory response during malaria appears to play a critical role in the development of cerebral malaria (3), anemia (4), and thus, death.

Toll-like receptors (TLRs) are receptors of the innate immune system that recognize a variety of microbial products such as LPS from Gram-negative bacteria (5). More recently, it was shown that TLRs also recognize molecules derived from protozoan parasites, including Plasmodium (6–10). Indeed, there is a growing body of literature that TLRs are central mediators of proinflammatory responses during malaria (11). For example, mice deficient in MyD88, an essential adapter molecule for all of the TLRs except TLR3, displayed impaired synthesis of proinflammatory cytokines and commensurate attenuation of symptoms when infected with different Plasmodium strains (12–14).

Despite concerted effort, a consensus on which malarial molecule is responsible for activating cytokine production in immune cells has not been achieved. Two candidates have been proposed: malarial glycosylphosphatidylinositol (GPI) anchors and parasite-derived DNA bound to hemozoin. These putative “malarial toxins” have been shown to activate TLR2 and TLR9, respectively (8, 10). As human polymorphisms that affect the outcome of malaria have been described for TLR2, TLR9 (15, 16), and MAL/TRAP (17), it seems likely that TLRs are involved in innate immune responses to malaria and possible that TLRs 2 and 9 are the main receptors involved.

One approach to define a role for a specific TLR in disease is to examine affected patients for the development of tolerance through a defined signal transduction pathway. LPS-challenged humans, for example, are hyporesponsive to LPS-mediated responses when subsequently re-challenged (18). Cells from patients with Gram-negative bacterial septicemia are similarly hyporesponsive to LPS (19), indicating that the TLR4 pathway has entered into a state of innate immune “tolerance” (20). Tolerance almost certainly exists in malaria, as patients from areas where reinfection occurs almost daily often do not exhibit the signs and symptoms of disease despite the presence of blood parasites (21, 22).

McCall et al. studied TLR function in peripheral blood mononuclear cells (PBMC) from individuals experimentally infected with malaria (23). Their results suggested that as a result of malaria infection, the innate immune response was enhanced to TLR1/TLR2 and TLR4 agonists. This finding was most surprising because it is markedly dissimilar to numerous reports of immune hyperresponsiveness (often referred to as “immune paralysis”) during bacterial sepsis even though this syndrome, in many respects,
mimics malaria. However, due to the nature of human experimental infection, subjects in this study were minimally symptomatic with very low parasitemia. This suggested to us that the effects they described were confined to the very earliest stages of malaria infection and that tolerance had not yet developed at the time that patient blood was collected for study. Furthermore, no obvious mechanism of the priming observed was delineated.

It was for this reason that we attempted to identify TLR usage during acute natural malaria with the idea that naturally infected patients would, in time, develop specific tolerance to the appropriate TLR ligand after experiencing high levels of parasitemia for a period of several days. In fact, we found that acute infection with Plasmodium falciparum in humans resulted in enhanced activation of innate immune cells to TLR agonists. This phenomenon was reproduced in Plasmodium chabaudi AS infected mice and occurred in a TLR9/IL 12/IFNγ-dependent manner. The mechanism by which malaria infection primes the innate immune responses of the host was found to be that TLR9 activation during Plasmodium infection initiates endogenous IL 12 and IFNγ production, which in turn enhances TLR expression and “primed” associated signaling pathways. Our data indicate that this augmented TLR expression leads to a stage of hyperresponsiveness to TLR agonists, and, as confirmed in mice, dramatically enhances the deleterious effect of an endotoxin challenge, as might occur in humans during infection with Gram-negative pathogens such as Salmonella.

Results

Increased TLR Responses During Acute P. falciparum Infection. PBMCs were isolated from P. falciparum naturally infected subjects to investigate TLR responses during acute malaria infection. PBMCs obtained from control subjects living in the same endemic area were analyzed in parallel (Fig. 1). With the sole exception of the TLR3 ligand, pI:C, increases in all TLR responses were observed in PBMCs from individuals acutely infected compared to healthy subjects (Fig. 1). Together, these results suggested that P. falciparum infection primes cells to subsequent TLR stimulation.

Chemotherapy Reverses Hyperresponsiveness of TLR Responses. Plasma samples from subjects with acute P. falciparum infection collected before and 3–4 weeks after curative mefloquine chemotherapy were used for evaluation of cytokines. P. falciparum infection led to a significant enhancement of systemic levels of proinflammatory cytokines. All patients reported greatly improved sense of well being and the absence of symptoms after therapy. The clinical characteristics of these patients are listed in Table S1. Coincident with this clinical improvement, cytokine levels were significantly diminished after chemotherapy (Fig. 2A). After curative chemotherapy, cytokine levels produced in response to TLR stimulation were back to baseline levels (Fig. 2B).

TLR/IFN Pathways Are Boosted During Acute Malaria Infection. To define the mechanism by which malaria mediates up-regulation of proinflammatory cytokines, we profiled mRNA obtained from infected individuals before and after curative chemotherapy. Fig. 2C and Table S2 show a panel of select genes up-regulated as a result of P. falciparum infection. Although neither TLR3 nor TLR9 expression was dramatically altered, TLR7 expression was enhanced approximately 2.6-fold (P < 0.01, data not shown). Statistically significant changes were also observed with TLRs 1, 2, 4, and 8 (P < 0.05). Genes involved in TLR signaling pathways consistently showed changes during P. falciparum infection (Fig. 2C). Expression of CD36, a coreceptor for TLR2 associated with the recognition of malaria parasites and subsequent induction of proinflammatory cytokines (24), was also up-regulated. In addition, we observed enhanced expression of various elements of IFN signaling pathways (Table S2). An analysis of the promoters of the up-regulated genes revealed that a large number of these genes had sites for IFN-inducible transcription factors (Table S3). The transcriptional changes of select genes in TLR or related signal transduction pathways were validated by qPCR (Fig. 2D). To determine if the up-regulation of TLR mRNA results in increased protein expression, we assessed the surface expression of TLR2 and TLR4 by flow cytometry. Expression of TLR2 and TLR4 were significantly augmented in CD11c+CD14+ monocytes (Fig. 3 and S1).

Increased TLR Responses During Acute P. chabaudi Infection. Next, we evaluated the response of mouse spleen cells to TLR ligands during
experimental infection with *P. chabaudi* AS. In this model, mice are injected i.p. with $10^5$ infected red blood cells (iRBCs). Although animals exhibit signs of disease, lethal infection is uncommon. The parasitemia course in WT mice was typical for experimental animals exhibit signs of disease, lethal infection is uncommon. The parasitemia course in WT mice was typical for experimental animals, although during the second week after infection a drop in IFN production (approximately 20-fold) by splenocytes isolated from mice during acute *P. chabaudi* infection (7 days post infection) when compared to control mice (Fig. 4B). During the following weeks, IFNγ levels produced in response to TLR agonists were comparable to those found in control mice, although during the second week after infection a drop in IFNγ responses was observed. Taken together, our results show that rodent malaria recapitulates the innate immune response in human disease, leading to proinflammatory priming of TLR responses.

![Fig. 2. Cytokine response in symptomatic malaria patients is reversed after curative chemotherapy. (A) Levels of 6 cytokines (TNFα, IL1β, IL6, IL8, IL10, and IL12p70) were determined in the plasma of *P. falciparum* infected subjects before treatment (closed triangles) or 30 days after treatment (open boxes) using CBA. (B) PBMC isolated from *P. falciparum* infected individuals before (closed triangles) or after treatment (open boxes) were cultured in the presence of the indicated stimuli for 20 h. Levels of TNF-α, IL1β, and IL12p40 were measured in culture supernatants by ELISA. Significant differences are indicated with *p*-values using paired t test or Wilcoxon matched-pairs signed-ranks test when a normality test failed. (C) Results of the clusterization. Each row represents a gene and each column the Log2 of the ratio of gene expression level. "Before treatment"/"After treatment" for the gene in question. (D) Validation of the results by qPCR is shown for some of the genes in the Fig. 1C. Each row represents a gene tested and each column the log2 of the ratio of the quantity of cDNA. "Before treatment"/"After treatment" standardized by the β2microglobuline cDNA.

![Fig. 3. Increased expression of TLR2 and TLR4 in monocytic cells from symptomatic malaria patients. PBMC were isolated from acute infected individuals before and 30 days after treatment and analyzed ex vivo through flow cytometry. The expression of TLR2 and TLR4 was evaluated in CD14+ and CD11c+ cells. Representative histogram showing fluorescence intensity of TLR2 in CD14+ (Left) and CD11c+ (Right) cells.

![Fig. 4. Hyperresponsiveness of spleen cells from mice undergoing acute malaria. C57BL/6 mice were challenged with $10^5$ iRBCs and followed every 3 days for (A) parasitemia and (B) levels of IFN measured in culture supernatants 48 h post stimulation. The results are averages of 5 animals from a representative out of 2 experiments that yield similar results.]
MyD88 and IFN-γ-Dependent Up-Regulation of TLR mRNA Correlates with P. chabaudi Mediated-Priming of TLR Responses. One explanation for the enhanced response to TLR ligands during infection would be that levels of receptor expression are increased. We therefore evaluated the levels of TLR mRNA in spleens of WT C57BL/6, TLR9−/−, MyD88−/−, and IFNγ−/− mice during P. chabaudi infection. Significant up-regulation of all of the TLRs tested was observed in WT mice at 6 days post infection and was clearly trending back to baseline by day 9. Up-regulation of TLR expression was significantly diminished in TLR9−/−, MyD88−/−, and IFNγ−/− mice (Fig. S4). As expected, 7 days post infection, splenocytes from WT mice produced large amounts of IFNγ while cells from infected TLR9−/− mice produced significantly lower levels of this (Fig. 5B) and other cytokines (Fig. S3) in response to TLR ligands.

TLR9, IL12, IFNγ, and T Cells Mediate Hyperresponsiveness and Susceptibility to Endotoxin Shock During Malaria. We have gained further insights into the role of TLR9 in priming innate immune responses during malaria. We show that in vitro stimulation of bone marrow derived dendritic cells (BMDCs) with P. chabaudi iRBCs induced IL12 production in a manner that depends on TLR9 (Fig. S4A). To assess the mechanism and relevance of TLR hyperresponsiveness during acute infection, we infected WT, TLR9−/−, IL12−/−, IFNγ−/− and RAG−/− mice with P. chabaudi and challenged them with LPS 7 days postinfection. WT mice produce high levels of proinflammatory cytokines (Fig. S4) and became very susceptible to i.v. injection of a sub lethal LPS challenge (i.e., 10 μg) (Table 1). TLR2−/− mice were as susceptible as WT (data not shown) while TLR9−/− mice produce significantly lower levels of proinflammatory cytokines (Fig. S4B) and become more resistant to LPS challenge (Table 1). IL12−/− mice showed impaired production of proinflammatory cytokines (Fig. S4B) and full resistance to low doses of LPS, while IFNγ−/− mice were completely resistant to even higher LPS dose (i.e., 100 μg) despite the fact that these mice faced higher parasitemia (Table 1). RAG−/− mice showed intermediate resistance to low and high doses of LPS. Together, these results show that the IL12/IFNγ axis is crucial for malaria induced-priming of TLR responses and that TLR9 have an impact on this phenomenon.

Discussion
The major findings of this study can be summarized as follows: augmented TLR responses in patients naturally infected with P. falciparum were associated both with cytokinemia and clinical symptoms of malaria. The vast majority of the highly inducible genes involved in the innate immune response, including the TLRs, appear to be IFN inducible. We hypothesize that augmented expression of genes in the TLR pathway favor the recognition of Plasmodium by phagocytes. Finally, the state of being acutely infected with malaria heightens the innate immune response to challenge with unrelated microbial products in an MyD88−/−, TLR9−/−, IL12−/−, and IFNγ-dependent manner.

The manner in which the innate immune system is activated in malaria is difficult to precisely define. We are still not certain what ligand or ligands are responsible for stimulating cytokine production, although it is intriguing that a large number of TLR components are regulated downstream from an IFN response. Overall, the innate immune response to acute malaria results in an immunological state that is notably enhanced. Such a “primed” immune system could be expected to prevent super infection with bacteria or viruses and might be crucial for host survival. On the other hand,

Table 1. TLR9−/−, IL12−/−, IFNγ−/− and RAG−/− mice undergoing acute malaria display increased in vivo resistance to low LPS doses

<table>
<thead>
<tr>
<th>Mouse</th>
<th>Condition</th>
<th>LPS dose (μg/mouse)</th>
<th>Number of dead/tested mice</th>
<th>Mortality, %</th>
<th>Mean parasitemia, %</th>
<th>p value chi-square test</th>
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<tr>
<td>C57BL/6</td>
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<td>0 0 0</td>
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<td>0/6 0/34 0/22 0/23</td>
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<td>9 9 9</td>
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</tr>
<tr>
<td>IL12−/−</td>
<td>Infected</td>
<td>10 100</td>
<td>0/9 0/5</td>
<td>0 0</td>
<td>0 0</td>
<td></td>
</tr>
<tr>
<td>IFNγ−/−</td>
<td>Infected</td>
<td>10 100</td>
<td>0/16 0/6 0/8 0/8</td>
<td>0 33 3 3 3</td>
<td>12 15 19 22</td>
<td></td>
</tr>
<tr>
<td>RAG−/−</td>
<td>Infected</td>
<td>10 100</td>
<td>0/4 0/4</td>
<td>0 0</td>
<td>0 0</td>
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</tr>
</tbody>
</table>

Fig. 5. Over expression of TLRs during acute rodent malaria. (A) Total RNA was isolated from spleens of WT, TLR9−/−, MyD88−/−, and IFNγ−/− mice before and after 6 and 9 days of infection with P. chabaudi. TLRs mRNA levels were measured by quantitative Real time PCR. The relative level of mRNA was determined by the comparative threshold cycle method, whereby data for each sample were normalized to β-actin and expressed as a fold change compared with uninfected controls. Bars are means ± SEM from 4 animals per group performed in duplicate. Arrows indicate where differences were statistically significant (P < 0.05) compared to mRNA levels found in WT mice. (B) Spleen cells were harvested from WT, TLR9−/− and IFNγ−/− mice before and after 7 and 14 days of infection and cultivated in the presence of the indicated stimuli. IFNγ levels were measured in supernatants 48 h later. Results are means ± SEM of twelve animals from 3 independent experiments. Arrows indicate levels of cytokines which differed statistically (P < 0.05) from those observed in WT mice.

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a highly deleterious hypercytokinemia would be expected to ensue should a robust bacterial or viral invasion occur.

McCall and colleagues recently reported that adult individuals experimentally infected with *P. falciparum* were primed for responses to some, but not all, TLR ligands. These authors found an enhanced response to LPS (TLR4) and Pam3CysK4 (TLR2/TLR1) (23). Our results are notably different because the enhanced innate immune response was far more pronounced, and we found an enhanced response to all TLR ligands except pI:C. Although McCall et al. made an effort to correlate TLR2/4 expression with the priming they observed; they did not see enhanced expression in TLR2/4 in monocytes. The most likely reason for the limited degree of priming and the lack of enhanced TLR expression was due to the differences in the total body burden of parasites and the duration of parasitemia. It is useful to recall that the experimental volunteers were treated as soon as they become symptomatic and/or parasitemic, while our patients often did not present at our malaria clinic until they had fevers and rigors for more than a week. As the average experimentally infected subject was parasitemic for approximately 9 days (23), we infer that our patients were infected for a period of no more than 2 weeks before study.

While virtually every cytokine response we tested was enhanced in malaria-infected individuals, this was not the case for the anti-inflammatory cytokine, IL10. IL10 levels were greatly increased in the plasma of malaria patients. However, when PBMCs from infected patients were stimulated with TLR ligands, we often observed either no change in the IL-10 response or a suppression of IL-10 release by PBMCs (data not shown). Therefore, it can be concluded that the priming of cells for enhanced TLR responses is not coordinated throughout the entire transcriptome, but specifically applies to a defined group of important proinflammatory genes.

The in vivo consequences of malaria-induced priming appear to be important and applicable to infection with other *Plasmodium* species. Thus, *P. chabaudi*-infected mice had evidence of priming and developed a lethal hypersensitivity to very small amounts of LPS in a TLR9-, IL12-, and IFNγ-dependent fashion. Indeed, these data are some of the best to date that malarial DNA recognition might be pathophysiological significant by engaging TLR9, as we previously proposed (10). As IFNγ is not produced in abundance by phagocytes, and is expressed in mouse lymphocytes (26), the mechanism appears to involve cross talk between the innate and the acquired arms of the immune system.

IFNγ has been shown not only to increase TLR expression but also to prime cells to LPS responses in a number of experimental infections (27–30) and has also been pointed as crucial to prime macrophages to release high amounts of TNF upon LPS administration and contribute to LPS induced septic shock (31). We (12) and others (14) have shown that TLR9 accounts for a considerable amount of IFNγ produced during malaria. Furthermore, production of IL12, a potent IFNγ inducer, is diminished in BMDCs from TLR9+/− mice upon in vitro stimulation with *P. chabaudi* IRBCs. Thus, it is reasonable to assume that the mechanism by which TLR9 mediates priming of host innate responses during malaria is by mediating parasite recognition and initiating IFNγ production. This assumption is strongly supported by findings in the *Propionibacterium* model in which TLR9-mediated production of IFNγ and IL12 is required to induce priming (32). Thus, we believe that the initial activation of innate immune responses is initiated by activation of TLR9 and induction of IL12 by innate immune cells (e.g., DCs and macrophages) resulting in production of IFNγ by NK and T cells (33, 34). In turn, the produced IFNγ will prime host cells to overexpress TLRs and become hyperresponsive to TLR agonists (Fig. 5C).

One can speculate on the consequences for the human host caused by malarial priming. The enhanced ability to respond to microbial ligands during immune surveillance probably protects the host from bacterial invasion. The areas of the world with the highest incidence and prevalence of malaria also have a high incidence of invasive bacterial infections, including *Salmonella*, *Pneumococcus*, and *Meningococcus* (35). In general, the innate immune response represents the classic “two-edged sword.” Priming means that the innate immune system has an enhanced capacity to be over activated during secondary infection and initiate the septic shock syndrome. Coinfection with bacteria is not only common, but, as we might have predicted from these results, patients with malaria and bacteremia die at 3 times the frequency of individuals with malaria alone (36). In addition to the ability of bacterial products to activate a hyper immune response during coinfection, the likelihood that parasite and/or endogenous TLR agonists act as second stimuli for cells primed during malaria should not be disregarded. To begin, different *P. falciparum* derived TLR agonists, such as GPI anchors (8) and DNA bound to hemozoin (10), might activate an enhanced innate immune response and result in unchecked inflammation. Moreover, host endogenous ligands that are weak TLR agonists have been described (37). Such endogenous molecules might, under the right circumstances (e.g., parasite-induced apoptosis), exacerbate the proinflammatory state of patients with malaria, even though under ordinary circumstances, they lack potency. Thus, it is our hypothesis that proinflammatory priming during malaria favors activation of TLRs by components from host and/or microbial origins and has the capability to induce injurious inflammatory states, including cerebral malaria.

The observation that the innate immune system is primed during febrile malaria could not have been predicted intuitively. In bacterial sepsis, most immune responses appear to be strongly suppressed, thus leading to an immune state that is often described as “immunoparalysis” (38). Although immunosuppressive therapy was once thought to be highly protective during septic shock (39) and the use of high dose steroids was commonplace, it is now recognized that this therapy increases mortality (40). By the time a patient with bacterial sepsis is diagnosed, the innate immune system is globally and profoundly immunosuppressed. Hence, additional anti-inflammatory therapy is unlikely to alter the course of events. Just the opposite appears to occur in acute malaria. Although anti-inflammatory approaches to life-threatening malaria have never been proven to be beneficial, it seems that the potential for targeted immunosuppressive therapy should not be ignored. By defining the innate immune response during the severest forms of malaria, as we have done here in patients with moderate illness, such strategies could be rationally designed and tested. Clearly, a better understanding of the innate immune response is critical if novel therapies are to be rationally designed.

Materials and Methods

Reagents. Unless stated elsewhere, all reagents were from Sigma-Aldrich. CL075 was obtained from Invivogen; ODN 7909 was synthesized by ALPHa DNA as phosphorothioate-linked ODNs; Pam2CysK4 was from EMC Microcollection; CpG ODN 2007 was from the Coley Pharmaceutical Group. LPS was repurified by phenol chloroform extraction as described (41). MAbs to CD11c and TNFα were from BD PharMingen. MAbs to TLR2 and TLR4 were from eBiomics. RPMI and DMEM were from Gibco. Cytokine ELISA kits were from R&D Systems.

Subjects. The study was approved by the Ethic and Research Council of the Rene Rachou Institute and the Brazilian Council of Ethics and Research (approval number 10567). Patients with acute febrile *P. falciparum* malaria (*n* = 57) were seen in the outpatient malaria clinic in the Tropical Medicine Research Center in Porto Velho, Brazil, an endemic malaria region in the Amazon basin. Informed consent was obtained before enrollment. All patients gave a history of recent fever and constitutional signs; none presented with severe anaemia or cerebral malaria (see Table S1). Average ages of patients and a group of controls were 29.4 ± 12.8 and 31.2 ± 7.36 respectively. Up to 100 cc of blood was obtained immediately after confirmation of *P. falciparum* infection by a standard peripheral smear and 3–4 weeks after mefloquine therapy. PCR was used to confirm infection and cure, as well as to confirm coinfection with *P. vivax* (42). Each patient served as his or her own control; additional control individuals (*n* = 16) included noninfected subjects living in Porto Velho and malaria naïve individuals living in Belo Horizonte, Brazil, where malaria is not endemic.
The analyzed using Flowjo software (TreeStar). CD14-FITC, (BD Biosciences), TLR2-PE, TLR4-PE (eBiosciences). Cells were passed by forward or side scatter to separate lymphocytes from monocytes and assessed for fluorescence using CellQuest software (BD Biosciences). Data were analyzed using Flowjo software (TreeStar).

Analysis of Cell Surface Expression of TLRs. Mouse splenocytes during rodent malaria were determined every 2–3 days throughout the infection period. PBMC Stimulation Assays. Mice were infected i.p. with 10⁵ iRBCs. Spleens were isolated using a sterile technique and assayed by qPCR. Total RNA was isolated from mouse spleens over the course of infection, as described. Sequences of primers are listed in Table S4.

Cytokine Measurements. Except where noted, all measurements of cytokines were performed using commercially available ELISA kits (R&D Systems). Serum cytokines from P. falciparum infected-patients were quantified with the CBA inflammation kit (Becton-Dickinson).

Real Time PCR Analysis (qPCR). Total RNA was isolated from mouse spleens over the course of infection, as described. Sequences of primers are listed in Table S4. Relative level of gene expression was determined by the comparative threshold cycle (Ct) method using the formula 2⁻ΔΔCt whereby data for each sample were normalized to β-actin mRNA levels and expressed as a fold change compared with uninfected controls.

Statistical Analysis. All data were analyzed using Graphpad Instat 4.0 Software. Cytokine measurements from stimulated human PBMCs were analyzed using two-tailed student’s t-test. Mann-Whitney testing was used for non-parametric analysis when data did not fit a Gaussian distribution. A P value = 0.05 was considered to be statistically significant.

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**Table S2.** Main cellular pathways triggered during *P. falciparum* malaria

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<th>Database Name</th>
<th>Pathway Name</th>
<th>p-value</th>
<th>Up-regulated genes</th>
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<tr>
<td>KEGG</td>
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<td></td>
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Table S3. IFNγ-inducible genes are largely induced during *P. falciparum* malaria

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<td>100</td>
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<td>CWKKANNY</td>
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Table S4. Sequences of primers used in qPCR reactions

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<th>Primer</th>
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<th>Reverse (5’- 3’)</th>
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<td>TLR3</td>
<td>TTGCGTTGCGAAGTGGAAG</td>
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<td>TLR4</td>
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<td>TLR7</td>
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<td>TLR9</td>
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<td>B-actin</td>
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Supporting Information

Franklin et al. 10.1073/pnas.0809742106

SI Materials and Methods

Microarray Experiments. A total of 23 patients were enrolled for RNA profiling; 2 were ultimately disqualified for study because of treatment failure or PCR-documented coinfection with *Plasmodium vivax*. Total RNA was extracted from PBMCs using an RNeasy kit (Qiagen) following the manufacturer’s recommendations. RNA integrity and purity was analyzed with an Experion Automated Electrophoresis System (Bio-Rad) and a ND-1000 spectrophotometer (NanoDrop Technologies Inc.). The first 7 specimens were amplified using the senseAMP kit from Genisphere and arrayed using an operon custom microarray chip (designed by Drs. B. Seed and M. Freeman, Harvard University, Cambridge, MA) containing approximately 17,000 unique cDNA at the Massachusetts General Hospital microarray facility.

The gene expression profiling of the remaining samples was performed using Illumina HumanWG-6 v2.0 Expression BeadChips (Illumina Inc.), which contains approximately 47,000 transcripts, at the SCIBLU Genomics DNA Microarray Resource Centre at Lund University. Three hundred nanogram of total RNA was reverse transcribed and subsequently in vitro transcribed to cRNA using the Illumina TotalPrep RNA Amplification Kit (Illumina Inc.). The cRNA (1.5 μg) was mixed with hybridization buffer and added to the BeadChips for hybridization at 58 °C for 18 h. BeadChips were then washed, blocked, and stained with streptavidin-Cy3, before they were washed again and dried by centrifugation.

Microarray Data Analysis. For the Operon arrays, simple filtering, normalization and averaging were carried out using BASE (BioArray Software Environment) (https://base.mgh.harvard.edu/). Tiger Multi Experiment Viewer (TMEV) was used for cluster analysis. The *p*-values were based on permutation with a standard Bonferroni correction. Selected genes were analyzed with KMC algorithm (K median).

For the analysis of Illumina arrays, raw signal intensities were normalized using cubic spline normalization method and log transformed (log2). Genes were filtered to include only genes with signal intensity greater than the average from the negative controls in at least one of the samples with a detection *p* value less than 0.01. Differences in gene expression between the 2 conditions were considered significant if *P* < 0.01 with a paired *t* test with Benjamini-Hochberg correction for multiple testing and a fold change greater than 1.7.

The biological function of the genes up-regulated in one or both data sets during disease was analyzed with Onto Express (http://vortex.cs.wayne.edu/projects.htm). The potential utilization of transcription factor binding sites was further analyzed using the web-based online tool from Advanced Biomedical Computer Center ABCC (http://grid.abcc.ncifcrf.gov).
Fig. S1.  Paired (Right) and not paired (Left) scatter plot, respectively, of TLR2 and TLR4 MFI in CD14<sup>+</sup> (A) and CD11c<sup>+</sup> (B) cells from patients before and after treatment. Significant differences are indicated with p-values using paired t test or unpaired t test.
Fig. S2. Severe symptoms associated with peak of cytokine production during *P. chabaudi* infection in mice. (A) Body weight and body temperature and (B) serum levels of cytokines (i.e. IFN, MCP-1, TNF, IL10, and IL6) measured in C57BL/6 mice infected with *P. chabaudi* at various days post infection. The results are averages of 5 animals from a representative out of 2 experiments that yield similar results.
Fig. S3. IL-12 and NO levels in splenocytes supernatants from C57BL/6, TLR9−/− and IFN−/− mice before and after 7 and 14 days post infection cultivated in the presence of the indicated stimuli. Results are means ± SEM of 12 animals from 3 independent experiments. Arrows indicate levels of cytokines which differed statistically (P < 0.05) from those observed in WT. mice.
Fig. S4. (A) BMDCs from TLR9−/− mice have impaired IL12 production upon stimulation with P. chabaudi iRBCs. BMDCs (2 × 10⁵) from WT and TLR9−/− mice were incubated with P. chabaudi iRBCs (10:1) for 12 h when compared to WT mice. Levels of IL12 were measured in culture supernatants by ELISA. The results are averages of 4 animals from a representative out of 2 experiments that yield similar results. (B) Levels of cytokine in sera of C57BL/6, TLR9−/−, IL-12−/−, or IFNγ−/− mice inoculated with P. chabaudi and challenged with LPS. Mice were infected with 10⁵ P. chabaudi-iRBCs. Non-infected red blood cells (nRBCs) were used as control. At day 7 postinfection mice were challenged with 10 µg of E. coli LPS. Cytokine levels were assessed in sera by CBA 9 h after LPS challenge. (C) Theoretical scheme of the role of TLR9/IL12/IFN-γ axis in mediating pro-inflammatory priming during malaria.
Other Supporting Information Files

Table S1
Table S2
Table S3
Table S4