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Prolonged Neutrophil Dysfunction after *Plasmodium falciparum* Malaria Is Related to Hemolysis and Heme Oxygenase-1 Induction

Aubrey J. Cunnington,*† Madi Njie,‡ Simon Correa,† Ebako N. Taken,† Eleanor M. Riley,* and Michael Walther*‡

It is not known why people are more susceptible to bacterial infections such as nontyphoid *Salmonella* during and after a malaria infection, but in mice, malarial hemolysis impairs resistance to nontyphoid *Salmonella* by impairing the neutrophil oxidative burst. This acquired neutrophil dysfunction is a consequence of induction of the cytoprotective, heme-degrading enzyme heme oxygenase-1 (HO-1) in neutrophil progenitors in bone marrow. In this study, we assessed whether neutrophil dysfunction occurs in humans with malaria and how this relates to hemolysis. We evaluated neutrophil function in 58 Gambian children with *Plasmodium falciparum* malaria [55 (95%) with uncomplicated disease] and examined associations with erythrocyte count, haptoglobin, hemopexin, plasma heme, expression of receptors for heme uptake, and HO-1 induction. Malaria caused the appearance of a dominant population of neutrophils with reduced oxidative burst activity, which gradually normalized over 8 wk of follow-up. The degree of neutrophil impairment correlated significantly with markers of hemolysis and HO-1 induction. HO-1 expression was increased in blood during acute malaria, but at a cellular level HO-1 expression was modulated by changes in surface expression of the haptoglobin receptor (CD163). These findings demonstrate that neutrophil dysfunction occurs in *P. falciparum* malaria and support the relevance of the mechanistic studies in mice. Furthermore, they suggest the presence of a regulatory pathway to limit HO-1 induction by hemolysis in the context of infection and indicate new targets for therapeutic intervention to abrogate the susceptibility to bacterial infection in the context of hemolysis in humans. *The Journal of Immunology*, 2012, 189: 5336–5346.

*Plasmodium falciparum* caused an estimated 655,000 deaths and 216 million cases of malaria globally in 2010 (1), but this almost certainly underestimates the indirect health burden (2), which includes increased susceptibility to Gram-negative bacterial infections (3, 4), particularly nontyphoid *Salmonella* (NTS) (3, 5, 6). In areas with high malaria transmission, these indirect effects of malaria infection may explain more than half of the child mortality (2) and community-acquired bacteraemia (4). The incidence of NTS closely reflects that of malaria (4, 6, 7), and there is compelling evidence that *P. falciparum* malaria increases susceptibility to NTS bacteraemia in humans. In The Gambia, the incidence of NTS bacteraemia has declined dramatically over the past 30 y, mirroring the decline in the incidence of malaria (7); this observation has since been confirmed in Kenya (4). In the pre-antibiotic era, malaria therapy for treatment of neurosyphilis was frequently complicated by NTS bacteraemia even when NTS infection was otherwise very rare (8), and quinine alone often cured endemic malaria–NTS coinfection (9). NTS bacteraemia incidence was found to be more closely related to malaria incidence than to stool carriage of NTS (6), and in Kenyan children, sickle cell trait was found to have a protective effect against bacteraemia, which was dependent on the protection it affords against malaria (4). Several studies have shown that susceptibility to NTS is greatest in the context of severe malarial anaemia (5, 6), whereas others have found that the greatest risk occurred in children with recent rather than current malaria infection (10, 11).

Most mechanisms that have been proposed to account for the susceptibility to NTS that occurs in malaria involve monocyte and macrophage dysfunction. Malaria may impair monocyte and macrophage function through direct adhesion of infected RBCs (12), through the accumulation of hemozoin within these cells (13), or by impairment of systemic IL-12 production (14). However, other studies in mice have demonstrated that hemolysis—caused by malaria or in any other way—increases susceptibility to NTS and some other bacterial infections, whereas blood loss alone does not (15–17). We have recently shown in a mouse model of malarial anaemia that resistance to *Salmonella typhimurium* is impaired as a result of neutrophil dysfunction (rather than monocyte/macrophage dysfunction) caused by liberation of heme during hemolysis and by induction of the cytoprotective heme-catabolizing enzyme heme oxygenase-1 (HO-1) (18). In this model system, HO-1 induction in myeloid progenitor cells in the bone marrow leads to production of granulocytes with reduced oxidative burst activity, and their mobilization into the blood is enhanced by both hemolysis-derived heme and the response to bacterial coinfection. This results in the accumulation of func-

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Abbreviations used in this article: CRP, C-reactive protein; HO, heme oxygenase; HO-1, heme oxygenase-1; LB, Larua–Bertani; MFI, median fluorescence intensity; NTS, nontyphoid *Salmonella*; PfHRP-2, *P. falciparum* histidine rich protein-2; qRT-PCR, quantitative RT-PCR.

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tionally impaired granulocytes in the circulation that are able to phagocytose *S. typhimurium* but not able to kill the bacteria effectively, providing a new niche for bacterial replication. We found that normal resistance to *S. typhimurium* was restored by inhibition of heme oxygenase (HO) with the competitive inhibitor tin protoporphyrin, a drug that can be used to treat hyperbilirubinemia in newborns (19), suggesting that HO inhibitors might represent a novel therapeutic intervention to abrogate the susceptibility to NTS induced by malaria.

Humans and mice with genetic deficiency of subunits of the phagocytic NADPH oxidase, a complex enzyme that catalyzes the generation of superoxide radicals in phagocytic cells, are known to be susceptible to NTS infection (20, 21), and the importance of the neutrophil oxidative burst for killing of serum-opsonized *Salmonella* by blood leukocytes from African children has been demonstrated in vitro (22). Impairment of the neutrophil oxidative burst in humans with malaria would thus be a compelling explanation for susceptibility to NTS bacteremia. In the current study, we investigated whether the same mechanism may apply in humans by examining neutrophil function in a cohort of children with predominantly uncomplicated malaria. Despite the fact that this population would not be considered at high risk of NTS coinfection, we found that malaria caused a marked abnormality of function in a large proportion of neutrophils, with impairment of oxidative burst capacity but not degranulation. The severity of the impairment of the neutrophil oxidative burst was strongly associated with hemolysis and prior induction of HO-1, but the duration of impairment was much longer than expected, lasting up to 8 wk postinfection.

Materials and Methods

**Study subjects and procedures**

The study and all procedures were approved by the Gambian government/Medical Research Council Laboratories Joint Ethics Committee and the London School of Hygiene and Tropical Medicine Ethics Committee. All human samples were collected with written informed consent from the participant or from the parent or legal guardian of child participants. Between September and December 2010, 58 Gambian children with *P. falciparum* malaria (defined by compatible clinical symptoms and >5000 asexual parasites/µl blood) were recruited within a longitudinal study investigating clinical, immunological, and parasitological factors in mild and severe malaria, details of which have been published (23). Briefly, subjects were recruited, without selection for disease severity, from three peri-urban health centers: the Medical Research Council Gate Clinic, Brikama Health Center, and the Jammeh Foundation for Peace Hospital, Serrekunda. Primary parasitemia (to determine eligibility for inclusion in the study) was estimated from Field’s stained thick blood films and subsequently accurately counted from 50 fields on Giemsa-stained thin blood smears. All children underwent full clinical examination and were managed in accordance with Gambian government guidelines, treated with artemether–lumefantrine for 3 d. Severe malaria was defined using modified World Health Organization criteria (24): severe anemia, defined as hemoglobin <7 g/dl and 25% decrease in cell count between time 0 and 120 min. Phagocytosis was assessed after 15 min of incubation at 37°C in 1% Triton, and plating onto LB agar, with CFUs counted 16–18 h later. Neutrophils and *Salmonella phagocytosis and killing assays* CD15+ cells were isolated from whole blood, after RBC lysis and labeling with GFP-expressing anti-CD15 (concentration confirmed by serial dilution) were opsonized in 10% pooled healthy Gambian adult serum [derived from 10 donors, as has been described by others (22)] for 20 min in the dark at room temperature. Neutrophils and *Salmonella* were divided into rhodamine- and rhodamine− populations at the midpoint of the nadir between peaks.

**Flow cytometry for cell surface receptors and intracellular HO-1 expression**

Whole blood was subjected to ammonium chloride RBC lysis and, after washing, cell pellets were resuspended in surface marker Ab mixture [FITC anti-CD91 (A2Mr-2; AbD Serotec), PE anti-CD16b (CLB-gran11.5; BD Pharmingen), PerCP anti-CD14 (Meph; BD Pharmingen), allophycocyanin anti-CD11b (125927; R&D Systems)] or a similar mixture instead containing the corresponding manufacturer-matched isotype control Abs for CD91 (mouse IgG1), CD16b (11711; mouse IgG1). Cells were permuted with the Cytofix/Cytoperm (BD Biosciences) before intracellular staining with polyclonal anti–HO-1 (SPA-895; Assay Designs) or an equivalent concentration of polyclonal control rabbit serum (Covance), followed by PE-Cy7− conjugated secondary Ab [F(ab′)2 anti-rabbit IgG; Santa Cruz Biotechnology]. The expression of HO-1, CD163, and CD91 were quantified as the percentage of MFI to the respective isotype control Ab for the same sample.

**Neutrophil isolation and Salmonella phagocytosis and killing assays**

CD15+ cells were isolated from whole blood, after RBC lysis and labeling with allophycocyanin anti-CD15, using anti-CD15 magnetic beads and MS columns (all from Miltenyi Biotech) according to the manufacturer’s instructions. CD15+ cells were resuspended in RPMI 1640 plus 2 mM L-glutamine at a concentration of 10^7/ml. GFP-expressing *S. typhimurium* (concentration confirmed by serial dilution) were opsonized in 10% pooled healthy Gambian adult serum [derived from 10 donors, as has been described by others (22)] for 20 min in the dark at room temperature. Neutrophils and *Salmonella* were mixed continuously at a ratio of 50:1 at 60 rpm at 37°C. Bacterial counts were assessed at time 0 and 120 min by 10-fold dilutions of aliquots of the neutrophil− *S. typhimurium* suspension in 1% Triton, and plated onto LB agar, with CFUs counted 16–18 h later. Bacterial killing was quantified as the percentage reduction in bacterial count between time 0 and 120 min. Phagocytosis was assessed after 15 min of incubation by removing the neutrophil− *S. typhimurium* suspension directly into PBS 4% paraformaldehyde and analyzing by flow cytometry. To control for autofluorescence and surface binding of bacteria without phagocytosis, control samples were prepared in an identical manner except...
that neutrophils and *S. typhimurium* were both fixed with 4% formaldehyde before mixing together. The proportion of cells phagocytosing bacteria was determined by subtraction of the proportion of GFP<sup>+</sup> cells in the fixed-control samples from that in the respective unfixed sample.

**ELISAs**

Plasma levels of *P. falciparum* histidine rich protein-2 (PfHRP-2; Cellabs), hemoglobin, haptoglobin (both Genway), C-reactive protein (CRP; R&D Systems), and HO-1 (Enzo Life Sciences) were measured by ELISA. All ELISA assays were performed according to the manufacturer’s instructions, and samples for each assay were performed in a single batch.

**Heme assay**

Total plasma heme (i.e., plasma hemoglobin plus free- and protein-bound heme) was measured using a colorimetric heme assay kit (QuantChrom heme; BioAssay Systems).

**Quantitative RT-PCR**

Total RNA was extracted from PAX tubes using PAXgene blood RNA kits (Qiagen) according to the manufacturer’s instructions and converted into cDNA using a reverse transcription reagent kit (Invitrogen). HMOX1 (141250) gene expression was determined by quantitative RT-PCR (qRT-PCR) on a DNA Engine Opticon (MJ Research) using a TaqMan Probe kit with primers (all Metabion) as described by Hirai et al. (27). 18S rRNA was used as an endogenous reference gene, as its expression has been shown to be stable in acute and convalescent samples from malaria cases regardless of disease severity (23), and was amplified with a commercial kit (rRNA primers and VIC labeled probe; Applied Biosystems). Data were analyzed using Opticon Monitor 3 analysis software (Bio-Rad). HMOX1 expression was quantified as the ratio of the transcript number of the HMOX1 to 18S rRNA.

**Estimation of total parasite biomass**

Total parasite biomass was calculated from plasma PfHRP-2 concentration using the method of Dondorp et al. (28). This assumes that PfHRP-2 concentration is an integral of all PfHRP-2 released in preceding rounds of schizogony (when infected erythrocytes rupture to release merozoites) and is therefore a reliable indicator of cumulative hemoysis since the start of the infection (28). We modified the calculation to account for the relatively higher blood volume at lower body weight in small children (29). To account for variation in size of children, parasite biomass was expressed as parasites per kilogram body weight.

**Statistics**

The study was designed to detect a 30% difference in neutrophil oxidative burst activity between samples at day 0 and day 28 with 80% power at the 0.05 significance level, allowing for 15% loss to follow-up. Statistical analysis was performed using PASW Statistics 18 (SPSS). Variables were examined for normality of distribution, and most were found to be nonnormal. Two-tailed tests were performed using PASW Statistics 18 (SPSS). Regardless of disease severity (23), and was amplified with a commercial kit (rRNA primers and VIC labeled probe; Applied Biosystems). Data were analyzed using Opticon Monitor 3 analysis software (Bio-Rad). HMOX1 expression was quantified as the ratio of the transcript number of the HMOX1 to 18S rRNA.

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**Results**

**Subjects**

Fifty-eight children with *P. falciparum* malaria were recruited to the study, 55 (94.8%) of whom had uncomplicated malaria (Table I). Four children had recurrent episodes of parasitemia during the course of follow-up and were excluded from longitudinal analyses; another 13 children were lost to follow-up or withdrew consent. Thus, at days 7, 28, and 56, the number (%) of children in follow-up were 52 (89.6%), 46 (79.3%), and 41 (70.1%), respectively.

**Prolonged impairment of the neutrophil oxidative burst**

We assessed the PMA-stimulated oxidative burst of neutrophils using a whole-blood flow cytometric assay based on the oxidation of dihydrorhodamine 123 to its fluorescent derivative rhodamine, where the magnitude of the oxidative burst is quantified by the rhodamine fluorescence intensity (26). The assay was modified to allow simultaneous assessment of degranulation based on upregulation of CD11b (32) and surface staining of CD15 to identify neutrophils. We found that neutrophils (Fig. 1A) from subjects with acute malaria (day 0) showed an abnormal, bimodal distribution of oxidative burst activity (Fig. 1B), with distinct populations of rhodamine<sup>Hi</sup> and rhodamine<sup>Lo</sup> cells, whereas CD11b expression showed a unimodal distribution (Fig. 1C). Overall, neutrophil rhodamine MFI increased significantly over time (Fig. 1D), but in view of the bimodal distribution of neutrophil rhodamine fluorescence, we also compared the proportion of cells that were rhodamine<sup>Hi</sup> and the rhodamine MFI of the rhodamine<sup>Lo</sup> cells over time. The proportion of rhodamine<sup>Lo</sup> cells decreased significantly during the convalescent period (Fig. 1E) but remained above that of healthy controls for at least 56 d; the rhodamine MFI of the rhodamine<sup>Lo</sup> cells also significantly increased over time (Fig. 1F). In contrast, there was no evidence of abnormalities in neutrophil degranulation as assessed by CD11b expression (Fig. 1G). Of interest, the rhodamine MFI of the rhodamine<sup>Hi</sup> cells was higher on days 0 and 7 after presentation (p = 0.04 and p < 0.001 respectively, Wilcoxon matched pairs test) than on day 56 (Fig. 1H), suggesting that the oxidative burst is primed in these neutrophils (33). These findings are consistent with our observations in mice that hemolysis and infection can prime the oxidative burst of mature, circulating neutrophils while simultaneously mobilizing immature neutrophils with impaired oxidative burst activity from the bone marrow (18). However the duration of these neutrophil abnormalities after *P. falciparum* infection was longer than we expected. We assessed whether a similar abnormality was present in monocytes in peripheral blood (Supplemental Fig. 1A) but found that the oxidative burst appeared to be slightly enhanced on day 0 compared with other time points (Supplemental Fig. 1B, 1C).

**Hemolysis and neutrophil dysfunction**

We have previously shown that hemolysis-derived heme impairs neutrophil function during malaria infection in mice through two related mechanisms: mobilization of functionally immature neutrophils from bone marrow, and impairment of the oxidative burst capacity of developing neutrophils due to HO-1 induction in bone marrow progenitors (18). RBC destruction in malaria is multifactorial, but the severity of intravascular hemolysis can be inferred from levels of the plasma proteins haptoglobin and hemopexin (34), which provide sequential lines of defense against heme-mediated toxicity by binding cell-free hemoglobin and cell-free heme, respectively (35). Only once haptoglobin is depleted do levels of hemopexin begin to fall, indicating that heme is being released from cell-free hemoglobin (36).

To assess the extent of hemolysis in study participants, we measured erythrocyte count and total parasite biomass (Table I), total plasma heme (Fig. 2A), haptoglobin (Fig. 2B), and hemopexin (Fig. 2C) and examined their correlation with the proportion and function of rhodamine<sup>Lo</sup> neutrophils (Table II). Although only 13 (22.4%) children were actually anemic by Gambian reference standards (Hb <9.5 g/dl) (30), total plasma heme levels were significantly greater on day 0 than on day 28 (Fig. 2A). Levels of haptoglobin showed a bimodal distribution (Fig. 2B), consistent with the expected depletion of haptoglobin by hemolysis in some
subjects (36), but also increased production of haptoglobin as part of the acute-phase response in other subjects (37, 38). Hemopexin levels, however, were relatively normally distributed and very similar to healthy controls (Fig. 2C), suggesting that in these subjects with predominantly uncomplicated malaria, hemolysis does not liberate sufficient cell-free heme to deplete plasma hemopexin (35, 36).

Because rhodamine<sub>L0</sub> cells may be similar to the functionally immature granulocytes released into the circulation during malaria and NTS infection in mice (18), we assessed whether their frequency would be consistent with their mobilization as part of an inflammatory response (39), but did not correlate directly with measures of frequent hemolysis being the major determinant of the impairment of the oxidative burst among rhodamine<sub>L0</sub> neutrophils (rhodamine<sub>L0</sub> but functionally abnormal neutrophils. By contrast, the magnitude of release of rhodamine<sub>L0</sub> neutrophils into the circulation in children with uncomplicated malaria, but parasite burden and consequent hemolysis being the major determinant of the impairment of the oxidative burst in rhodamine<sub>L0</sub> neutrophils. Neither variable was significantly associated with the proportion of pigment containing neutrophils.

**Table I.** Demographic, clinical, and laboratory characteristics at recruitment

<table>
<thead>
<tr>
<th>Variable</th>
<th>Category</th>
<th>n&lt;sup&gt;a&lt;/sup&gt; (%)</th>
<th>Median (IQR)</th>
<th>Normal Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex</td>
<td>Male</td>
<td>36 (62)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Female</td>
<td>22 (38)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ethnicity</td>
<td>Mandingo</td>
<td>25 (43)</td>
<td></td>
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<tr>
<td></td>
<td>Fula</td>
<td>10 (17)</td>
<td></td>
<td></td>
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<tr>
<td></td>
<td>Wolof</td>
<td>7 (12)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Manjago</td>
<td>5 (9)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Jola</td>
<td>5 (9)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Serere</td>
<td>4 (7)</td>
<td></td>
<td></td>
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<tr>
<td></td>
<td>Aku</td>
<td>1 (2)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Fanti</td>
<td>1 (2)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age (y)</td>
<td>Uncomplicated</td>
<td>55 (95)</td>
<td>8 (4–12)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Severe</td>
<td>3 (5)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Prostration</td>
<td>2</td>
<td></td>
<td></td>
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<tr>
<td></td>
<td>Lactic acidosis</td>
<td>1</td>
<td></td>
<td></td>
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<tr>
<td>Plasmodium species</td>
<td>P. falciparum</td>
<td>55 (95)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>P. falciparum and P. malariae</td>
<td>3 (5)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sickle cell screen</td>
<td>Negative</td>
<td>53 (91)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>AS</td>
<td>1 (2)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Not done</td>
<td>4 (7)</td>
<td></td>
<td></td>
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<tr>
<td>Hemoglobin, g/dl</td>
<td></td>
<td>58</td>
<td>11.5 (9.98–12.5)</td>
<td>9.5–14.4&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>Erythrocyte count, ×10&lt;sup&gt;12&lt;/sup&gt;/l</td>
<td></td>
<td>58</td>
<td>4.26 (3.83–4.66)</td>
<td></td>
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<tr>
<td>Mean corpuscular volume, fL</td>
<td></td>
<td>56</td>
<td>76.9 (73.5–80.7)</td>
<td>67.8–90.0&lt;sup&gt;d&lt;/sup&gt;</td>
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<tr>
<td>Leukocyte count, ×10&lt;sup&gt;3&lt;/sup&gt;/l</td>
<td></td>
<td>57</td>
<td>8.50 (6.74–10.3)</td>
<td>4.1–11.1&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>Percent neutrophils</td>
<td></td>
<td>58</td>
<td>74.8 (66.3–83.0)</td>
<td>35–75&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>Percent bands&lt;sup&gt;d&lt;/sup&gt;</td>
<td></td>
<td>58</td>
<td>1.39 (0.57–2.75)</td>
<td>0–10&lt;sup&gt;c&lt;/sup&gt;</td>
</tr>
<tr>
<td>Percent immature&lt;sup&gt;d,e&lt;/sup&gt;</td>
<td></td>
<td>58</td>
<td>5.32 (2.71–10.8)</td>
<td>0&lt;sup&gt;c&lt;/sup&gt;</td>
</tr>
<tr>
<td>Percent pigmented&lt;sup&gt;d&lt;/sup&gt;</td>
<td></td>
<td>58</td>
<td>1.22 (0.42–4.08)</td>
<td></td>
</tr>
<tr>
<td>Percent of monocytes with pigment</td>
<td></td>
<td>58</td>
<td>20 (0–50)</td>
<td></td>
</tr>
<tr>
<td>Parasite density, parasites/μl</td>
<td></td>
<td>57</td>
<td>92,800 (28,200–219,000)</td>
<td></td>
</tr>
<tr>
<td>Parasite biomass, parasites/kg</td>
<td></td>
<td>55</td>
<td>1.23 × 10&lt;sup&gt;10&lt;/sup&gt; (5.21 × 10&lt;sup&gt;9&lt;/sup&gt; to 2.14 × 10&lt;sup&gt;10&lt;/sup&gt;)</td>
<td></td>
</tr>
<tr>
<td>CRP, mg/l</td>
<td></td>
<td>46</td>
<td>106.4 (64.5–234.3)</td>
<td></td>
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<tr>
<td>Lactate, mmol/l</td>
<td></td>
<td>42</td>
<td>2.0 (1.6–2.45)</td>
<td></td>
</tr>
</tbody>
</table>

<sup>a</sup>Data were not available for every variable for every subject.

<sup>b</sup>90% reference interval for Gambian children aged 6–12 y (30), where available, for laboratory parameters.

<sup>c</sup>General pediatric reference interval (31), where available, for laboratory parameters.

<sup>d</sup>Percentage of all neutrophils.

<sup>e</sup>Neutrophil precursors less mature than band forms.

AS, Hemoglobin AS heterozygote; IQR, interquartile range.

other, we analyzed their effects on rhodamine<sub>L0</sub> neutrophil MFI using a general linear model. After stepwise elimination of the least significant variables in the model, only parasite biomass remained significantly associated with rhodamine<sub>L0</sub> neutrophil MFI (F = 16.036, p < 0.001). Overall, these results are consistent with the acute-phase inflammatory response being the primary determinant of release of rhodamine<sub>L0</sub> neutrophils into the circulation in children with uncomplicated malaria, but parasite burden and consequent hemolysis being the major determinant of the impairment of the oxidative burst in rhodamine<sub>L0</sub> neutrophils. Neither variable was associated with the proportion of pigment containing neutrophils.

**Factors associated with HO-1 induction**

In malaria-infected mice, we found that heme-mediated HO-1 induction in neutrophil progenitors in bone marrow was necessary to impair the oxidative burst of developing neutrophils (18). Because there were no clinical indications for bone marrow aspiration in any of the study subjects, our analysis of the HO-1 pathway was restricted to parameters measurable in peripheral blood, namely plasma HO-1, whole-blood HMOX1 gene expression, and HO-1 protein expression in peripheral blood cells. Also, because the induction of cellular HO-1 by haptoglobin–hemoglobin or heme–hemopexin complexes depends on the presence of surface receptors for their uptake (CD163 and CD91, respectively) (37, 40, 41), we examined CD163 and CD91 expression on monocytes and neutrophils.
As previously reported in mice (18) and humans (42), HO-1 expression (assessed by fluorescence intensity) in circulating neutrophils was not increased in acute malaria infection compared with convalescence (data not shown). In contrast, monocyte HO-1 expression was higher on day 0 than on days 7 or 28 (Fig. 3A). Plasma HO-1 was higher in subjects on day 0 than in healthy control children (Fig. 3B), and as we have previously reported (42), whole-blood \textit{HMOX1} expression was significantly higher on day 0 than after recovery on day 28 (Fig. 3C).

In control subjects, CD163 and CD91 were expressed on the surface of monocytes but were not detectable on neutrophils (Fig. 3D). In children with malaria, monocyte CD163 expression was significantly lower at day 0 than on days 7 and 28 (Fig. 3E), whereas CD163 remained undetectable on neutrophils from most subjects (Fig. 3F). CD91 expression did not change significantly over time on monocytes (Fig. 3G) or neutrophils (Fig. 3H), although when all subjects were considered together, there did appear to be very low level CD91 expression on neutrophils at all time points.

To explore further the likely pathways of HO-1 induction during malaria infection, we constructed a simple conceptual model (Fig. 4), beginning with the malaria parasite as the cause of hemolysis, inflammation, and tissue hypoxia/ischemia (43)—all of which may induce HO-1 expression (44)—and analyzed univariate correlations between the various measures of HO-1 induction. As expected, parasite biomass was strongly correlated with total plasma heme and CRP. Plasma HO-1 correlated much more strongly with CRP and lactate than with plasma heme, supporting the idea that it
Levels in six healthy control children are also shown. Distribution of plasma hemopexin levels at day 0, comparison, levels in six healthy control children are also shown. (A) Total plasma heme on day 0 and day 28 compared using Wilcoxon matched pairs test for those with data at both time points ($n = 32$). (B) Distribution of plasma haptoglobin levels at day 0, $n = 57$. For comparison, levels in six healthy control children are also shown. (C) Distribution of plasma hemopexin levels at day 0, $n = 49$. For comparison, levels in six healthy control children are also shown.

May be released in response to harmful and inflammatory stimuli. Surprisingly, however, neither whole-blood $HMOX1$ expression nor monocyte-specific HO-1 correlated significantly with total plasma heme, CRP, or lactate. As the haptoglobin receptor CD163 has been reported to be downregulated during inflammation (45) and to be shed from the cell surface during acute, uncomplicated malaria infections (46), we explored whether monocyte-specific HO-1 expression might be confounded by changes in expression of CD163 using a general linear model controlling for the effect of CD163 expression. This revealed a significant interaction between total plasma heme and CD163 expression, but strong independent associations between monocyte HO-1 and total plasma heme ($F = 15.1, p < 0.001$) and monocyte HO-1 and CD163 expression ($F = 9.378, p = 0.003$). In other words, monocyte HO-1 induction would closely correlate with total plasma heme, but downregulation of surface CD163 prevents the uptake of hemoglobin–haptoglobin complexes and hence limits HO-1 induction. This explains in part the discordance between different measures of the HO-1 induction pathway in blood. In summary, this analysis demonstrates that HO-1 protein expression in myeloid cells can be increased by hemoglobin and heme liberated during malarial hemolysis, although this effect is limited by reductions in surface CD163 expression.

Neutrophil oxidative burst and prior HO-1 induction

In mice, we had observed that suppression of the oxidative burst of circulating neutrophils by hemolysis required the release of immature neutrophils from bone marrow, requiring either a lag time or an additional stimulus (such as NTS infection) to cause these cells rapidly to enter the circulation (18). Having observed that an abnormal population of neutrophils was present for a prolonged period of time after $P. falciparum$, we looked for evidence of an association between HO-1 induction on day 0 and neutrophil oxidative burst on day 7. We used the ratio of day 0 to day 28 whole-blood $HMOX1$ expression as an indicator of induction in acute malaria. We found a significant negative correlation between $HMOX1$ expression and the rhodamine MFI of rhodamine$^{lo}$ neutrophils on day 7 (Spearman’s correlation coefficient $= -0.352, p = 0.028, n = 39$). There was no significant correlation with the proportion of rhodamine$^{lo}$ cells on day 7 (Spearman’s correlation coefficient $= -0.101, p = 0.542, n = 39$).

Although the kinetics of the process of HO-1 induction, suppression of oxidative burst capacity in developing neutrophils, and subsequent release of the functionally immature neutrophils into the circulation are unknown, the observed association between HO-1 induction during acute disease and neutrophil dysfunction during early convalescence is consistent with this sequence of events.

Salmonella phagocytosis and killing

As we have observed that neutrophil killing (but not phagocytosis) of $S. typhimurium$ is defective in malaria-infected mice (18), we assessed the ex vivo killing and phagocytosis of serum-opsonized $S. typhimurium$ by neutrophils isolated from whole blood of subjects and controls from whom sufficient blood remained after the preceding assays (Fig. 5A–C). Bacterial killing, calculated as the reduction in the viable bacterial count 2 h after coculture, was slightly higher on day 0 than at subsequent time points (Fig. 5A). There was no significant correlation between bacterial killing on day 0 and either the proportion of rhodamine$^{lo}$ neutrophils, the rhodamine MFI of the rhodamine$^{lo}$ neutrophils, total plasma

![Image](http://www.jimmunol.org/)

**FIGURE 2.** Indicators of hemolysis in subjects with $P. falciparum$ malaria. (A) Total plasma heme on day 0 and day 28 compared using Wilcoxon matched pairs test for those with data at both time points ($n = 32$). (B) Distribution of plasma haptoglobin levels at day 0, $n = 57$. For comparison, levels in six healthy control children are also shown. (C) Distribution of plasma hemopexin levels at day 0, $n = 49$. For comparison, levels in six healthy control children are also shown.

Table II. Association of neutrophil dysfunction with hemolysis on day 0

<table>
<thead>
<tr>
<th>Variable</th>
<th>Percent Rhodamine$^{lo}$ Neutrophils</th>
<th>Rhodamine MFI of Rhodamine$^{lo}$ Neutrophils</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$n$</td>
<td>Correlation Coefficient</td>
</tr>
<tr>
<td>Parasite biomass/kg</td>
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</tr>
<tr>
<td>Erythrocyte count</td>
<td>56</td>
<td>$-0.001$</td>
</tr>
<tr>
<td>Haptoglobin</td>
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<td>0.004</td>
</tr>
<tr>
<td>Total plasma heme</td>
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<td>0.222</td>
</tr>
<tr>
<td>CRP</td>
<td>44</td>
<td>0.350</td>
</tr>
<tr>
<td>Immature neutrophil percent</td>
<td>56</td>
<td>0.232</td>
</tr>
<tr>
<td>Pigmented neutrophil percent</td>
<td>56</td>
<td>$-0.017$</td>
</tr>
</tbody>
</table>

Indicators of hemolysis, inflammation, and neutrophil characteristics were assessed for correlation with the proportion of rhodamine$^{lo}$ neutrophils and with the rhodamine MFI of rhodamine$^{lo}$ neutrophils on day 0 using Spearman’s correlation. *Data were not available for every variable for every subject.*
heme, or parasite biomass (data not shown). Bacterial phagocytosis, determined by flow cytometric analysis of the proportion of GFP+ neutrophils after 15-min coculture (Fig. 5B), did not vary significantly over time after infection (Fig. 5C). However, phagocytosis at day 0 was inversely correlated with parasite biomass (n = 26, Spearman’s correlation coefficient = -0.512, p = 0.008), and with total plasma heme (n = 28, Spearman’s correlation coefficient = -0.441, p = 0.019) (Fig. 5D). Taken together with the neutrophil oxidative burst assay data (Fig. 1F, 1H), these data indicate that although there may be some degree of (heme-mediated) priming of neutrophil function in children with acute malaria (day 0), which enhances bacterial killing during acute illness (47), phagocytosis of S. typhimurium by circulating neutrophils becomes increasingly impaired with increasing parasite burden and increasingly severe hemolysis, and the ability of neutrophils to kill S. typhimurium once they are phagocytosed might also become impaired.

Discussion

Although the association between malaria infection and susceptibility to NTS bacteremia has been recognized for almost a century (9), the mechanism has been elusive. The strongest association is with severe malarial anemia (5, 6), and at least two other conditions associated with hemolytic anemia—sickle cell disease (48) and acute bartonellosis (49)—also predispose to NTS bacteremia. This is likely a result of both the nature of the defect in host defense induced by malaria and the prevailing epidemiology of invasive bacterial infection: NTS is one of the most common causes of bacteremia in Sub-Saharan Africa (50, 51). In a mouse model, we recently showed that hemolysis due to malaria or phenylhydrazine treatment impaired resistance to S. typhimurium, which could be recapitulated by treatment with hemin and abrogated by treatment with the HO inhibitor tin protoporphyrin (18). We found that bacteria accumulated in circulating neutrophils and that these neutrophils were defective in killing S. typhimurium, associated with impairment of their oxidative burst response, which is an essential mechanism for killing S. typhimurium (21). This was due to heme-mediated induction of HO-1 in granulocyte precursors in bone marrow, causing neutrophils leaving the bone marrow to have a reduced capacity to mount an effective oxidative burst. It is not known whether bacteria accumulate preferentially in neutrophils in humans with malaria and NTS coinfections, but in the pre-antibiotic era, neutrophils and NTS were often found colocalized in abscesses that formed at the site of i.m. quinine injection in coinfect ed individuals (9). Although neutrophil function has not been extensively studied in malaria, there are several case reports...
of patients with severe malarial hemolysis spontaneously developing fungal sepsis (52–54), which is typically associated with neutropenia and neutrophil dysfunction.

The current study was designed to determine whether Gambian children with *P. falciparum* malaria have evidence of neutrophil dysfunction similar to that observed in mice infected with *Plasmodium yoelii* 17XNL. We hypothesized that the neutrophil oxidative burst would be impaired in children with malaria, and the severity of this impairment would be related to hemolysis and HO-1 induction. However, we also predicted that the impairment of neutrophil function would be relatively mild because declining malaria transmission in The Gambia has led to a decrease in the incidence of severe malarial anemia and malaria–NTS coinfection (7). Overall, our results are consistent with our hypothesis: the oxidative burst activity of circulating neutrophils was profoundly abnormal in subjects with acute *P. falciparum* malaria and most severely impaired in children with the highest parasite burdens and greatest hemolysis, albeit the magnitude of this impairment did not translate into a clinically significant defect in neutrophil killing of *S. typhimurium* in vitro. We also found that these abnormalities persisted for at least 56 d and that bacterial phagocytosis and killing appeared to deteriorate during the early convalescent period (up to 28 d), findings that may be consistent with descriptions of increased susceptibility to NTS bacteremia in children who have recently had malaria (6, 10) and the gradual emergence of dysfunctional neutrophils from bone marrow after HO-1 induction during the acute infection (18). To facilitate comparison with our studies in mice (18), we assessed neutrophil function using PMA as the stimulus for the oxidative burst. Although this is not a physiological stimulus, the advantages of this method are i) that it produces a strong oxidative burst (55, 56), which is clearly distinguished from any low-level activation caused by malaria infection per se; ii) it is not dependent on phagocytosis (which might also be impaired by malaria) (55, 56); and iii) variations in the magnitude of the PMA-induced oxidative burst are directly related to the ability of humans to survive infections (57).

Consistent with data from mice and humans (18, 42, 58), we observed induction of HO-1 during acute malaria. Although dissecting the causal and consequential pathways of HO-1 induction is difficult in an observational study, we constructed a conceptual model of likely pathways leading to HO-1 induction based on existing literature (Fig. 4) (44) and used this model to guide our statistical analysis. Plasma HO-1 levels correlated more strongly with plasma lactate and CRP concentrations than with plasma heme concentrations, suggesting that plasma HO-1 may be predominantly a response to inflammation and hypoxia and a marker of cell damage. As noted previously, intracellular HO-1 protein expression was not significantly upregulated in acute malaria in circulating neutrophils (42), presumably because they lack CD163 expression, whereas monocytes did show evidence of increased HO-1 protein expression in acute malaria. However, there was not a significant univariate association between total plasma heme concentration and HO-1 expression in monocytes, which could be explained statistically by the reduced levels of monocyte surface CD163 expression in acute malaria. This explanation is fully consistent with the subjects in this study having only mild hemolysis [most had hemoglobin values within the normal range for their age (30), none had severe malarial anemia, and only half had low haptoglobin levels] and with the assumption (as hemopexin levels were not depleted) that very little of the total circulating heme represents cell-free heme. In this case, HO-1 induction due to hemolysis would be expected to proceed predominantly through CD163-mediated uptake of haptoglobin–hemoglobin complexes, and reduction in surface CD163 would be expected to limit HO-1 induction (45). In contrast, severe hemolysis would be expected to generate cell-free heme and lead to HO-1 induction and heme catabolism in cells expressing the surface receptor (CD91) for heme–hemopexin complexes, which appears to be invariantly expressed during infection. Indeed, we previously found elevated carboxyhemoglobin levels, an indirect measure of HO activity, only in children with severe malarial anemia suggesting that heme catabolism is constrained in acute malaria and only detectably increased in cases with the most severe hemolysis (59). It is conceivable that by reducing CD163 expression in the context of infection, monocytes are rendered relatively resistant to HO-1 induction by hemolysis, perhaps preventing HO-1–mediated impairment of their normal inflammatory responses (45, 60). However, it is currently unknown whether either CD163 or CD91 expression is required for HO-1 induction in immature myeloid cells and their progenitors in human bone marrow. If HO-1 induction in bone marrow is responsible for the observed neutrophil dysfunction [as it is in mice (18)], either it may be independent of CD163 or CD163 may not be downregulated in the bone marrow to the same extent as in blood monocytes. We did not examine the effect of *HMOX1* promoter (GT)n length polymorphisms in this study because the majority of subjects had uncomplicated malaria with mild hemolysis, and we expected that under these circum-

![Figure 4](http://www.jimmunol.org/)
Phagocytosis expressed as the percentage of GFP+ neutrophils after 15-min incubation. The percentage of GFP+ cells was calculated by subtracting the proportion of GFP+CD15+ cells was determined in samples where both neutrophils and S. typhimurium were mixed with S. typhimurium at a ratio of 50:1 and killing was expressed as the percentage reduction in bacterial numbers after 2-h incubation. Statistical comparison using Friedman’s two-way ANOVA for all subjects with valid data at all time points, n = 18. Data from control subjects shown for comparison. (B) Representative flow cytometry plots showing phagocytosis of GFP+ S. typhimurium by neutrophils isolated on day 0. RBCs and debris were excluded based on forward scatter and side scatter characteristics, then single cells were selected based on pulse width and forward scatter characteristics (upper row). The proportion of GFP+CD15+ cells was determined in samples where both neutrophils and S. typhimurium were fixed in 4% formaldehyde prior to incubation (to control for surface binding without phagocytosis) and in unfixed samples (lower row). (C) Phagocytosis of S. typhimurium. Neutrophils isolated on days 0, 7, 28, and 56 after presentation with P. falciparum malaria were mixed with S. typhimurium at a ratio of 50:1 and phagocytosis expressed as the percentage of GFP+ neutrophils after 15-min incubation. The percentage of GFP+ cells was calculated by subtracting the proportion of GFP+ cells in formaldehyde fixed samples from that in unfixed samples. Statistical comparison using Friedman’s two-way ANOVA for all subjects with valid data at all time points, n = 7. Data from control subjects shown for comparison. (D) Correlation of phagocytosis (on day 0) with parasite biomass on day 0 (left-hand panel, n = 26) and total plasma heme on day 0 (right-hand panel, n = 28).
neutrophils above a threshold required to induce susceptibility to NTS.

The prolonged duration of abnormal neutrophil oxidative burst activity, extending up to 8 wk after acute infection in some subjects, was unexpected. This is unlikely to be due to antimalarial treatment, because artemisinin-based treatments cause mild enhancement of the oxidative burst and suppression of phagocytosis, the opposite of what we observed (63). Two possible explanations are the effect of persisting hemozoin and fundamental alteration in myelopoiesis. Hemozoin is an insoluble heme polymer, the end product of hemoglobin digestion inside the parasitized red cell, and is able to induce HO-1 (and impair the oxidative burst in phagocytes) but is not catabolized (13, 64). Prolonged persistence of hemozoin in phagocytic cells in the bone marrow (65) could cause prolonged HO-1 induction and abnormal development of neutrophils (18). Associated with this or through separate mechanisms, a novel myeloid progenitor phenotype may be generated in P. falciparum malaria, as has been observed in rodent malaria infection (66), and may lead to sustained abnormal granulopoiesis.

The major limitations of our study are that most subjects had relatively mild hemolysis and that we did not have bone marrow samples to confirm HO-1 induction in neutrophil progenitors. To recruit a significant number of subjects with severe malarial hemolysis would require a much larger study, probably conducted in a higher-transmission setting. To study prospectively whether the severity of neutrophil dysfunction at recruitment correlated with susceptibility to NTS bacteremia during convalescence would require an even larger and more logistically complex study. To obtain bone marrow aspirates from children with malaria would be difficult to justify ethically unless appropriate sedation and analgesia could be provided without additional risk of complications.

Nevertheless, our findings have a number of important implications. First, we show that the oxidative burst capacity of a large proportion of neutrophils is markedly abnormal in children with P. falciparum malaria, supporting the translation of findings in a mouse model (18). Second, neutrophil function recovers only very slowly over the 2 mo after treatment, providing an explanation for the association of susceptibility to NTS with recent malaria (10, 11). In the mouse model, hemolysis-induced neutrophil dysfunction could be abrogated by competitive inhibition of HO with tin protoporphyrin (18), but using this treatment in acute malaria would be challenging because HO-1 is also important for tolerance to cytotoxic effects of cell-free heme in mouse models (58, 67). Alternative therapeutic strategies would be administration of tin protoporphyrin upon completion of antimalarial treatment, with the aim of restoring neutrophil function during convalescence and preventing the susceptibility to NTS caused by recent malaria, or prioritization of children at greatest risk of persistent neutrophil dysfunction for prophylactic antibiotic treatment. Third, we propose the downregulation of the haptoglobin receptor CD163 on neutrophils (18) as a novel host-protective homeostatic response to hemolysis and inflammation, which may prevent HO-1 induction from impairing monocyte function. Further experimental studies are needed to confirm the effects of manipulating CD163 expression during infections, but manipulation of this axis would hold promise for both the modulation of inflammation and optimization of iron reutilization during chronic infections.

Acknowledgments

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Disclosures

The authors have no financial conflicts of interest.

References


SUPPLEMENTARY FIGURE 1. *P. falciparum* malaria enhances monocyte oxidative burst. (A) Representative FACS plots showing the gating of the monocyte population based on forward scatter and side scatter characteristics followed by selection of single cells based on pulse width and forward scatter. (B) Rhodamine fluorescence of unstimulated (filled histogram) and PMA-stimulated monocytes (unfilled histogram) on days 0, 7, 28 and 56 after presentation with *P. falciparum* malaria. Representative plots from a healthy control child are also shown for comparison. (C) Longitudinal analysis of monocyte oxidative burst, compared using Friedman’s two way ANOVA for all subjects with valid data at all time points, n=33. Healthy controls are also shown for comparison, but not included in the statistical analysis. Horizontal lines represent medians.