Apoptosis and dysfunction of blood dendritic cells in patients with falciparum and vivax malaria

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Malaria causes significant morbidity worldwide and a vaccine is urgently required. Plasmodium infection causes considerable immune dysregulation, and elicitation of vaccine immunity remains challenging. Given the central role of dendritic cells (DCs) in initiating immunity, understanding their biology during malaria will improve vaccination outcomes. Circulating DCs are particularly important, as they shape immune responses in vivo and reflect the functional status of other subpopulations. We performed cross-sectional and longitudinal assessments of the frequency, phenotype, and function of circulating DC in 67 Papuan adults during acute uncomplicated *P. falciparum*, *P. vivax*, and convalescent *P. falciparum* infections. We demonstrate that malaria patients display a significant reduction in circulating DC numbers and the concurrent accumulation of immature cells. Such alteration is associated with marked levels of spontaneous apoptosis and impairment in the ability of DC to mature, capture, and present antigens to T cells. Interestingly, sustained levels of plasma IL-10 were observed in patients with acute infection and were implicated in the induction of DC apoptosis. DC apoptosis was reversed upon IL-10 blockade, and DC function recovered when IL-10 levels returned to baseline by convalescence. Our data provide key information on the mechanisms behind DC suppression during malaria and will assist in developing strategies to better harness DC’s immunotherapeutic potential.

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of DC biology during acute malaria is paramount to improve vaccination outcomes.

Circulating DCs are particularly important as they replenish tissue-residing DCs and shape immune responses in vivo (Banchereau et al., 2000). These cells can be identified as mononuclear cells expressing MHC-II molecules (HLA-DR) but lacking common lineage markers (Savary et al., 1998). This blood DC compartment includes two different subsets discernible into myeloid DC (mDC) or plasmacytoid DC (pDC) based on their reciprocal expression of CD11c or CD123 antigens (Robinson et al., 1999). Moreover, mDC can be further subdivided into three subtypes based on the respective expression of CD141, CD16, and CD1c antigens (Piccioli et al., 2007; Jongbloed et al., 2010). Despite their importance, most studies have only assessed blood DC’s numerical phenotype and few functional studies have been reported to date. Numerical characterizations indicate that children with Pf display less activated mDC during acute uncomplicated infection (Urban et al., 2001a) yet increased numbers of mDC during severe infection (Urban et al., 2006). Adults with Pf exhibit reduced pDC during acute uncomplicated, severe (Pichyangkul et al., 2004), or pregnancy malaria (Diallo et al., 2008). Similarly, adults infected with Pv display reduced mDC and pDC numbers (Jangpatarapongsa et al., 2008). We have also demonstrated numerical blood DC reductions and increased apoptosis before patent parasitemia in healthy donors undergoing an experimental low-dose P. falciparum challenge (Woodberry et al., 2012).

Further functional characterization, in contrast, has mainly been undertaken using in vitro or murine DC models (Urban et al., 2001b; Perry et al., 2005; Elliott et al., 2007; Bettiol et al., 2010). However, rodent DCs or DCs generated in vitro after prolonged culture with cytokines are unlikely to reflect the functional status of human DC populations circulating in vivo.

To address these questions, evaluate the role of different Plasmodium species on circulating DC, and determine the type and duration of DC impairment after antimalarial treatment, we performed cross-sectional and longitudinal assessments of all circulating DC subsets during uncomplicated Pf and Pv including convalescent Pf infection in 67 Papuan adults. Results were compared with a cohort of 17 malaria-exposed uninfected and asymptomatic Papuan adults. Given the low frequency of blood DC and restricted volumes that could be taken from patients, subcohorts were used for the various analyses. Our results demonstrate that the marked loss of functional DC in the peripheral circulation of patients with Pf or Pv malaria is associated with significant levels of spontaneous...
DC apoptosis. Impaired viability and numerical changes also correlate with functional impairment in the ability of DCs to up-regulate costimulatory and MHC-class II molecules as well as antigen uptake and presentation to CD4 T cells. Interestingly, elevated and sustained levels of plasma IL-10, as observed in patients with \textit{Pf} or \textit{Pv}, were implicated in the induction of DC apoptosis. As such, DC apoptosis was reversed upon IL-10 blockade and DC function recovered completely after completion of antimalarial treatment and normalization of IL-10 levels by convalescence. Our data provide key information on the mechanisms behind blood DC suppression during acute malaria and will assist in developing better strategies to harness DC’s immunotherapeutic potential and improve vaccination outcomes.

**RESULTS**

**Study cohort**

42 adult Papuans with acute uncomplicated \textit{Pf} malaria, 25 adult Papuans with acute \textit{Pv} malaria, and 17 uninfected malaria-exposed Papuan adults were included in the study. 10 of the 42 patients with \textit{Pf} malaria were also assessed at days 7 and 28 after antimalarial treatment. There was no significant difference in the age between groups although there were fewer female volunteers in the uninfected group (Table 1). Median peripheral parasitemia was similar in acute \textit{Pf} and \textit{Pv} malaria patients, but only \textit{Pf} patients had detectable plasma histidine-rich protein II (HRP2). No peripheral parasitemia or HRP2 was detected in any \textit{Pf} patient at days 7 or 28 after treatment.

**Subset distribution of DC in patients with malaria**

The blood DC compartment can be identified by flow cytometry as Lin$^{-}$HLA-DR$^+$ cells (Thomas et al., 1993). This population includes two different subsets distinguished into myeloid DC (mDC) and plasmacytoid DC (pDC) lineages (Robinson et al., 1999). Because previous studies suggest dissimilar changes in the frequency of these subsets in acute malaria (Urban et al., 2006; Diallo et al., 2008; Jangpatarapongsa et al., 2008), we set out to carefully analyze the blood DC compartment in a cohort of 45 patients with acute \textit{Pf} or \textit{Pv} malaria (Fig. 1 A). Our data demonstrate a significant reduction in absolute counts of mDC (CD11c$^+$) and pDC (CD123$^+$) concurrent with the marked accumulation of HLA-DR$^+$ immature cells (DR$^{+}$IC) in patients with acute malaria (Fig. 1 B). These immature cells lacked expression of CD11c or CD123 markers yet expressed high levels of the HLA-DR antigen (Pinzon-Charry et al., 2005). Interestingly, this immature population represented only 16.8 ± 2.0% of the blood DC compartment in uninfected donors, while representing a much larger proportion in patients with \textit{Pv} (38.6 ± 3.4%) or \textit{Pf} (46.7 ± 1.8%) infection. The reduction in DC counts was,
however, not generalized to other leucocytes. As such, lymphocyte counts were only mildly (not significantly) reduced, monocyte counts were comparable, and neutrophil counts were only marginally increased (not significantly) compared with uninfected donors (Fig. 1 B).

Given that mDCs can be further subdivided into three subtypes based on their respective expression of CD141, CD16, and CD1c antigens (Piccioli et al., 2007; Jongbloed et al., 2010), numerical characterization of these mDC subsets was also undertaken. Our data confirmed reduced counts of CD141+DC, CD1c+DC, and CD16+DC in patients with acute Pf and Pv malaria (Fig. 2 A). Although individual analyses revealed only significant reductions of CD1c+DC in Pf and CD16+DC in Pv, composite analyses of all malaria patients (Pf plus Pf) confirmed significantly reduced counts (P < 0.05) for all mDC subtypes, suggesting a sample size effect.

To confirm that other DC subpopulations induced during inflammatory settings were not excluded by confining our analyses to the Lin−HLA-DR+ population, characterization of the Lin−HLA-DR+ population was undertaken in five Pv patients (Fig. 2 B) compared with five uninfected controls. This confirmed the minimal proportion of DCs (<2%) and the rather large proportion of B cells (CD79a+ cells) and monocytes (CD11b+ cells) within this gate in malaria patients and uninfected donors (Pv: B cells, 59 ± 18%; monocytes, 30 ± 5% vs. uninfected: B cells, 68 ± 10%; monocytes, 35 ± 8%). These results confirm that in patients with acute malaria, the marked reduction in Lin−HLA-DR+ cells in the peripheral circulation reflects significant reductions in all DC numbers (mDC subsets and pDC) and the concurrent accumulation of immature cells (DR+IC).

**Spontaneous apoptosis of DC in patients with malaria**

To determine whether reduced viability accounted for some of the changes observed in the DC compartment, we assessed spontaneous apoptosis in blood DC ex vivo. To include all cells undergoing apoptosis while eliminating cellular debris, gating was set as described in Fig. 3 A. Blood DCs were identified as Lin−HLA-DR− cells and apoptosis was estimated using Annexin-V. As shown in Fig. 3 B, the minimal proportion of spontaneously apoptotic blood DC in uninfected donors was significantly increased in patients with Pf or Pf infection. Interestingly, apoptosis was mostly evident in DCs (mDC and pDC) as opposed to immature cells (DR+IC), partly explaining the large accumulation of DR+IC in patients with acute malaria (Fig. 3 C). Other antigen-presenting cells, such as B cells (CD19+) or monocytes (CD14+), displayed no significant apoptosis in patients with Pf or Pf infection. Furthermore, CD19+AnnexinV−/− cells and monocytes (CD14+) displayed no significant apoptosis in patients with Pf or Pf infection. However, CD19+AnnexinV−/− cells and monocytes (CD14+) showed markedly reduced ability to up-regulate expression of costimulatory and HLA-DR molecules (Fig. 4, A and B).

**Impaired phenotype and function of DC in patients with malaria**

Next, we set out to determine if the reduced viability of blood DC was associated with phenotypic or functional abnormalities. Because expression of MHC II and costimulatory molecules has been correlated to DC’s immunostimulatory capacity, first we evaluated the expression of CD83, CD86, and HLA-DR in patients with acute Pf or Pf malaria. As shown in Fig. 4 A, ex vivo expression (gray histograms) of CD83, CD86, and HLA-DR in blood DCs from Pf or Pf patients was comparable to uninfected controls. However, upon overnight incubation (black histograms), blood DCs from Pf or Pf patients showed markedly reduced ability to up-regulate expression of costimulatory and HLA-DR molecules (Fig. 4, A and B). Functional assessment also demonstrated significant DC impairment in malaria patients. Here, blood DCs from Pf or Pf patients had a markedly reduced ability to take-up particulate...
antigens (Fig. 4 C) and were poor stimulators of allogeneic CD4 T cell proliferation (Fig. 4 D) and Th1 cytokine secretion (see Fig. 8 B). As shown in Fig. 4 C, impaired antigen uptake was evident in DC (mDC and pDC) as well as in immature cells (DR−IC), although less markedly, explaining the overall dysfunction of all Lin−DC+ populations in patients with malaria. These data demonstrate that the impairment of blood DC in acute malaria affects key aspects of DC function, including maturation (up-regulation of costimulatory and MHC class II molecules), ability to capture antigen, and adequate stimulation of allogeneic CD4 T cell proliferation and cytokine secretion.

Central role for IL-10 in induction of DC apoptosis during malaria

We also set out to assess possible mechanisms responsible for the marked levels of blood DC apoptosis in patients with malaria. Given that no significant apoptosis was observed in uninfected donors and a direct cytopathic effect of the parasite on DC has been excluded (Urban et al., 1999; Skorokhod et al., 2004; Elliott et al., 2007), we hypothesized that apoptosis related to the inflammatory response during infection rather than to the parasite itself. To examine this hypothesis, first we evaluated levels of proinflammatory cytokines in plasma of all patients with acute malaria. We found significantly elevated levels of inflammatory cytokines, including IL-2, IL-4, IFN-γ, TNF, IL-6, and IL-10 in all patients with acute Pv or Pf infection (Fig. 5 A). Interestingly, IL-2, IL-4, and IFN-γ levels corrected to baseline levels by day 7 (at which time parasites had cleared), whereas elevation of TNF, IL-6, and particularly IL-10 persisted beyond this point. Moreover, levels of plasma IL-10 (but not IL-6 or TNF) correlated with the extent of blood DC apoptosis (Fig. 5 B) yet no significant correlation was found between parasitemia or plasma HRP2 and either DC numbers or apoptosis (not depicted). This evidence suggested a key role for IL-10 in blood DC apoptosis during acute infection.

Interestingly, sustained exposure of DC to high levels of IL-10 during their maturation has been associated with induction of apoptosis (Chang et al., 2007). Therefore, we set out to directly evaluate the role of plasma IL-10 from malaria patients on DC survival in vitro. For this purpose, healthy DCs
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were induced to mature with LPS and exposed to recombinant human IL-10 or plasma samples from either uninfected donors containing low levels of IL-10 (mean 58.6 pg/ml, n = 3) or from patients with Pf (n = 3) or Pv (n = 3) containing high levels of IL-10 (Pf: mean 602.6 pg/ml; Pf: mean 353.8 pg/ml).

First, we confirmed the proapoptotic effect of high and sustained levels of rhIL-10 on healthy maturing blood DC (Fig. 6 A) as previously reported (Chang et al., 2007). More importantly, we found that exposure of healthy maturing DC (n = 5) to plasma from Pf or Pv patients resulted in a significant proportion of DC apoptosis (Fig. 6 A). To further confirm the role of IL-10 in this process, specific IL-10 blocking was undertaken. As shown individually in Fig. 6 A, and summarized in Fig. 6 B, blockade of rhIL-10 or infected plasma IL-10 prevented a comparably large proportion (mean rhIL-10: 63% vs. Pf plasma: 53% vs. Pv plasma: 52%) of blood DC from undergoing apoptosis. These data confirmed the central role of IL-10 rather than other plasma cytokines in affecting DC survival and indicate that elevated levels of plasma IL-10 to the extent observed in patients with Pf or Pv can induce apoptosis in a significant proportion of blood DC.

Effect of antimalarial treatment on DC phenotype and function

Finally, to determine whether antimalarial treatment could reverse the impaired phenotype and viability of blood DC, we performed a longitudinal assessment in a cohort of 10 patients with Pf infection. In these patients, blood DCs were analyzed during acute malaria at day 0 and also at days 7 and 28 after successful antimalarial drug treatment. We have demonstrated elsewhere that artemisinin combination therapy drugs do not affect blood DC phenotype or function (Woodberry et al., 2012). Here, blood DCs were analyzed for their subset...
suggesting that malaria DCs were able to activate but not properly stimulate Th1 cell function in vitro. Reversal of such DC impairment, however, was evident in DCs collected by day 28 after treatment (Figs. 7 and 8). Interestingly, plasma IL-10 showed parallel kinetics to DC dysfunction with low IL-10 levels comparable to uninfected donors attained by day 28 after treatment (Fig. 5). Although these results suggest a protracted period of DC impairment, they confirm that full recovery of functional and competent blood DC is only achievable after antimalarial drug treatment and normalization of IL-10 levels.

DISCUSSION

The aim of this study was to evaluate the blood DC compartment in patients with Pf or Pv malaria to identify factors suitable for clinical implementation (i.e., antimalarial treatment) to improve their function. We focused on the blood DC compartment because this population directly reflects the natural biology of immune responses occurring in vivo. Therefore, detailed cross-sectional and longitudinal assessments in 67 patients with acute uncomplicated Pf or Pv, as well as convalescent Pf malaria, were performed to demonstrate significant and protracted impairment in number, function, and viability of blood DC during acute malaria. More importantly, our results

Figure 7. Reversal of DC dysfunction after antimalarial treatment. (A and B) Blood DCs were analyzed during acute Pf malaria at day 0 (D0) and also at days 7 (D7) and 28 (D28) after antimalarial treatment in a cohort of 10 patients and compared with uninfected volunteers (U, n = 12). In all experiments, each patient was tested in parallel with at least one uninfected volunteer. The blood DC compartment was analyzed for absolute counts of mDC, pDC, and DR+IC (10⁶/liter; A) and blood DC subset distribution. (B) Representative dot plots of one uninfected control as well as one patient assessed at days 0 (D0), 7 (D7), and 28 (D28) are shown. Values indicate percentage of cells within respective gates. (C) Summary of blood DC apoptosis data (mean ± SEM). (D) Summary of antigen uptake (FITC-Dextran) data assessed as the difference between uptake at 37°C (test) or 4°C (control) expressed as ΔMFI (mean ± SEM). (E) Representative histograms of apoptosis from one patient at days 0 (D0), 7 (D7), and 28 (D28) compared with one uninfected control. Values indicate percentage of Annexin-V-positive cells. (F) Summary of phenotypic maturation estimated by up-regulation in expression of CD83, CD86, and HLA-DR expressed as ΔMFI (mean ± SEM). (G) Representative histograms of antigen uptake from one patient at days 0 (D0), 7 (D7), and 28 (D28) compared with one uninfected control. Gray histograms indicate uptake at 4°C (control) and black histograms represent uptake at 37°C (test). Values indicate uptake as ΔMFI between cultured and fresh samples. Statistically significant differences compared with uninfected volunteers are indicated as *, P < 0.05; **, P < 0.01; and ***, P < 0.001.
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Figure 8. Recovery of DC allostimulatory capacity after antimalarial treatment. (A) Naive allogeneic CD4 T cells purified from a panel of healthy Australian donors (n = 5) were co-cultured with blood DC from malaria patients at day 0, 7, or 28 (n = 8) or uninfected controls at a 30:1 T/DC ratio (n = 12). Cells were harvested after 96 h of culture and CD4 T cell proliferation estimated by CFSE dilution (x axis). Representative histograms are shown with numbers indicating the percentage of CFSE<sup>dim</sup> CD4 T cells for each stimulatory condition. The representative pairs giving maximal responses for three different T cell donors are shown. In all experiments, each patient was tested in parallel with at least one uninfected volunteer. (B) Supernatants from cultures in A were harvested after 72 h and levels of IL-2, TNF, IFN-γ, IL-6, IL-4, and IL-10 estimated using CBA assay by FACS. Box plots include means, standard deviations, and ranges. Significant differences compared with uninfected controls are indicated as *, P < 0.05. Results are representative of five separate experiments performed.
increased expression of CCR7, CXCR4, and CCR5 in blood DC of patients with Pf or Pv malaria (unpublished data). Although increased migration to lymphoid organs is likely occurring, its effect on peripheral counts is unclear and a definitive answer will only arise from the simultaneous assessment of DC in blood and lymphoid tissues. Myeloid suppression or impaired production of DC progenitors could also be proposed to explain declining blood DC numbers in human malaria. However, our data on the accumulation of immature cells and similar reports of increased immature DC during maternal human infection (Aldebert et al., 2007; Diallo et al., 2008) or CD34+ DC progenitors in blood of children with malaria (Urban et al., 2001a) suggest that myeloid suppression is unlikely to be of significance. Finally, impaired viability of blood DC could contribute to declining counts if a significant proportion of cells are programmed to die while in the circulation. Our results not only confirm the latter hypothesis but suggest that the cytokine milieu occurring in vivo is impacting vigorously on the longevity of all blood DC subpopulations during infection.

The physiological significance of this finding is three-pronged. First, circulating DCs are essential for adequate immunity as they continually replenish the pool of tissue-residing DCs. In fact, most circulating DCs are en route from the bone marrow to peripheral and lymphoid tissues or from nonlymphoid tissues to the regional lymph nodes and spleen (de la Rosa et al., 2003). Given that apoptotic cells are rapidly cleared by the reticulo-endothelial system, increased turnover rate of blood DC is likely occurring in these patients. As infection progresses, continual efforts to replace the pool of blood DC from bone marrow imposes pressure on hematopoietic capacity, resulting in the paucity of functional DC (Urban et al., 2001a; Aldebert et al., 2007; Diallo et al., 2008; Jangapatarapongsa et al., 2008) and the concurrent accumulation of immature cells in the circulation (Aldebert et al., 2007; Diallo et al., 2008). Second, apoptotic DCs are ineffective at inducing immunity (Kitajima et al., 1996), and this can contribute to systemic immune dysregulation and parasite evasion. Third, apoptosis can relate to the immune response against the parasite rather than a direct cytopathic effect of the parasite, and hence it may be amenable to modification through normalization of the suppressive cytokine environment in which DCs are engaged.

In this regard, cytokines that regulate the inflammatory response, and particularly IL–10, have been suggested to affect blood DC during acute malaria (Urban et al., 2006; Diallo et al., 2008). Maturing DCs undergo apoptosis after exposure to high levels of IL–10 (Chang et al., 2007), and a correlation between high IL–10 and reduced DC counts has been suggested for human Pf (Urban et al., 2006; Diallo et al., 2008) and Pv infections (Jangapatarapongsa et al., 2008; Gonçalves et al., 2010). Here, we demonstrate for the first time a direct causal relationship between increased levels of plasma IL–10 and blood DC apoptosis in patients with clinical Pf or Pv infections. In malaria, IL–10 is an important cytokine and immune modulator that strikes a balance between immune protection and immunopathology (Couper et al., 2008). However, sustained exposure of DC to IL–10 can suppress the induction of anti-apoptotic genes like bel-2, bel-x, and bfl-1 at a time of increased sensitivity to viability signals, i.e., during DC maturation (Chang et al., 2007). Additionally, exocrine IL–10 can drive secretion of autocrine IL–10 by DC and other cell types further impacting on cell survival (Corinitti et al., 2001). In human malaria for example, in vitro–derived DCs exposed to infected erythrocytes fail to secrete IL–12 yet produce increasing levels of IL–10 (Urban et al., 1999). Similarly, in rodent malaria, DCs progressively increase their ability to produce IL–10 and induce an IL–10–dominated T cell response (Perry et al., 2005). Therefore, while controlling immunopathology, the scale of IL–10 exposure throughout the maturation process appears to determine the lifespan of blood DC via mechanisms involving cytokine regulation and antiapoptotic gene modulation.

Although apoptosis and high levels of IL–10 appeared central to DC impairment in the present study, other mechanisms have also been proposed. Earlier studies using in vitro–derived DC indicate that Plasmodium can compromise DC via a mechanism involving direct contact through PfEMP1 (Urban et al., 2001b). However, more recent evidence using a similar in vitro approach suggests that modulation is independent of parasite contact and rather depends on parasite dose (Elliott et al., 2007). Because Pv-infected red cells do not express PfEMP1 and are minimally cytoadherent, our finding of comparable DC impairment with either parasite would support the contact-independent nature of DC modulation. Other reports also implicate hemozoin in the modulation of DC through TLR-dependent binding (Coban et al., 2005; Parroche et al., 2007) and suggest that induction of TLR tolerance is central to DC dysregulation (Perry et al., 2005). In our study, sample limitation precluded direct assessment of blood DC–parasite interactions in vivo. However, the observations that DC apoptosis and dysfunction persisted beyond parasite clearance (day 7), was in part IL–10 dependent, and normalized by day 28 upon resolution of the cytokine response suggested that DC impairment during clinical disease was primarily related to the immune response against the parasite rather than to the parasite itself. The lack of correlation between baseline parasitemia or plasma HRP2 and either DC numbers or apoptosis also indicated that by the time of presentation with clinical malaria, DC impairment was cytokine driven rather than parasite driven.

Whereas an alteration in the numerical and maturational phenotype of blood DC in acute malaria had been previously described (Jangapatarapongsa et al., 2008; Gonçalves et al., 2010), there had only been few reports on the function of blood DC in patients with clinical malaria (Arama et al., 2011) and no longitudinal studies in clinical disease had been described to date. Our cross-sectional assessment in 67 Papuan adults with acute malaria allowed us to demonstrate that the marked changes in blood DC viability were associated with significant impairment in all aspects of DC function (maturation, antigen uptake, and presentation) in patients with either type of parasite. In fact, we show that blood DC from Pf and Pv patients display impaired ability to up-regulate costimulatory...
and MHC class II molecules as well reduced antigen uptake and ability to stimulate CD4 T cell proliferation and cytokine secretion. Moreover, upon longitudinal follow up, we demonstrate that parasite clearance and normalization of the cytokine milieu after antimalarial treatment facilitate recovery of fully competent blood DC in patients with malaria.

Therefore, our findings point out that impairment of blood DC number and function, as well as induction of apoptosis, is not species-specific and occurs with the two Plasmodium species causing the majority of global malaria. Consequently, our results have significant implications not only for understanding immune dysfunction during malaria but also for the development of effective interventions to improve vaccination outcomes against this disease. In view of the remarkable diversity of immunosuppressive pathways in malaria, any clinical response achieved by vaccination is already considered an achievement. However, to improve responses to any of the current subunit or whole parasite vaccine formulations (Pinzon-Cherry and Good, 2008), vaccines will need to be combined with other strategies that can offset the suppressive environment in which DCs are primed. Given the protracted nature of the DC dysfunction described here in patients with acute infection and the observation that parasite clearance and normalization of the cytokine milieu after antimalarial treatment facilitate DC recovery, combination strategies will likely be required. Based on the evidence presented here, we propose that vaccination in the context of iterative pre-vaccination antimalarial treatment facilitate DC recovery, combination strategies will be considered to improve vaccination outcomes for malaria.

MATERIALS AND METHODS

Study subjects and samples. 84 highland Papuans were recruited in Timika, a lowland region of Papua, Indonesia, with perennial unstable malaria transmission of both PF and Pv (Karyana et al., 2008). Subjects were enrolled in trials of chloroquine and sulphadoxine-pyrimethamine or artemisinin combination therapy after providing informed consent (Ratcliffe et al., 2007a,b). Individuals with acute uncomplicated malaria—as defined by acute onset of fever within 48 h of enrolment—with no alternative cause identified and parasitemia by microscopically identified PF (n = 42) or Pv (n = 25) were included in the study. No patients with mixed infection were included. For all patients, venous blood was collected at the time of presentation. Additionally, in 10 PF patients with clinical and parasitological cure, venous blood was also collected at 7 and 28 d after successful antimalarial drug treatment with chloroquine plus sulphadoxine-pyrimethamine or artemisinin combination therapy (ACT). Malaria-exposed uninfected subjects (n = 17) served as controls; these were resident in the Timika district for at least 2 yr and had no fever or symptoms of malaria within the preceding 2 wk as previously described (Randall et al., 2010). The studies were approved by the Ethics Committees of the National Institute of Health Research and Development, Ministry of Health, Jakarta, Indonesia; the Menzies School of Health Research, Darwin, Australia; and the Queensland Institute of Medical Research, Brisbane, Australia.

Antibodies and reagents. The following mAbs were used in this study: CD3, CD14, CD19, CD20, CD56, CD34, HLA-DR, CD86, CD25, CD27, CD69, CD79a, and CD11b and IgG1, IgG2a, and IgG2b isotype controls (BD); and HLA-DR, CD83, CD19, and IgG1 isotype control (Beckman Coulter).

Flow cytometry, antigen uptake, and mixed leukocyte reaction. PBMCs were stained with the lineage mixture (CD3, CD14, CD19, CD20, CD56, and CD34) and HLA-DR. Flow cytometry (FACS) was used to evaluate DC numbers, phenotype, antigen uptake, and function. Blood DCs were defined as Lin- HLA-DR+ cells. Blood DC subsets were identified using CD11c (mDC) and CD123 (pDC) antibodies. mDC subsets were further characterized using CD141, CD11c, and CD16 antigens. Antigen uptake was assessed after cells were incubated (10^6 cells/ml) for 60 min with FITC-Dextran at either 37°C (test) or 4°C (control). Antigen uptake was calculated as the difference in mean fluorescence intensity (ΔMFI) between the test and control. To assess allostimulatory capacity, PBMCs from patients or uninfected volunteers were individually tested against naïve allogeneic CD4 T cells obtained from buffy coats from healthy Australian volunteers (n = 5, Australian Red Cross). naïve allogeneic CD4 T cells (>95% CD4) were purified by negative immunoselection using the naïve CD4 T cell isolation kit (Miltenyi Biotech) and labeled using the vibrant CFDA-SE Cell Tracer Kit (Molecular Probes). CD4 T cells were adjusted at 10^5/well and cultured with DCs from malaria patients or uninfected controls at a 30:1 T/DC ratio in PBMC cultures. In all cases, DC numbers were adjusted based on absolute counts estimated by FACS before culture. Cells were harvested after 96 h of culture and CD4 T cell proliferation estimated by CFSE dilution using MODFIT proliferation software (Verity Software). Similar results were found for all T/DC ratios. In all experiments, cells were analyzed within 1 h of staining and 5–10 x 10^6 events were collected within the mononuclear cell gate. Absolute DC counts were calculated from the number of PBMCs/liter of blood as determined by the automated cell counter multiplied by the percentage of DCs determined by FACS. Lymphocytes, monocyte, and neutrophil counts were determined by automated cell counter. Serum and supernatant cytokines were measured using the cytokometric bead array (CBA) for human Th1/Th2 cytokine kit (BD). Data were acquired on a FACS Calibur equipped with CellQuestPro and CBA software (BD) according to the manufacturer’s instructions.

Apoptosis and IL-10 assay. To determine the proportion of apoptotic cells, Annexin-V binding assays were performed according to the manufacturer’s instructions (Annexin-V kit; BD). Briefly, PBMCs were adjusted to 10^6 cells/ml and stained with lineage markers and HLA-DR as above. Cells were washed and resuspended in binding buffer before incubating with Annexin-V and 7-AAD. Absolute DC counts were calculated from the number of PBMCs/liter of blood as determined by the automated cell counter multiplied by the percentage of DCs determined by FACS. Lymphocytes, monocyte, and neutrophil counts were determined by automated cell counter. Serum and supernatant cytokines were measured using the cytokometric bead array (CBA) for human Th1/Th2 cytokine kit (BD). Data were acquired on a FACS Calibur and analyzed using CellQuest 3.1 or Summit (Cytomation) software.

Statistical analysis. All statistical analyses used Prism 5 (GraphPad Software Inc.). Comparisons of samples to establish statistical significance were determined by the two tailed Student’s t test or one way analysis of variance.


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