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To cite this version:
hal-00629378

HAL Id: hal-00629378
https://hal.science/hal-00629378
Submitted on 20 Jul 2022

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Critical role of the neutrophil-associated high-affinity receptor for IgE in the pathogenesis of experimental cerebral malaria

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The role of the IgE–FcεRI complex in malaria severity in Plasmodium falciparum–hosting patients is unknown. We demonstrate that mice genetically deficient for the high-affinity receptor for IgE (FcεR1α-KO) or for IgE (IgE-KO) are less susceptible to experimental cerebral malaria (ECM) after infection with Plasmodium berghei (PbANKA). Mast cells and basophils, which are the classical IgE-expressing effector cells, are not involved in disease as mast cell–deficient and basophil–depleted mice developed a disease similar to wild-type mice. However, we show the emergence of an FcεRI+ neutrophil population, which is not observed in mice hosting a non–ECM-inducing PbNK65 parasite strain. Depletion of this FcεRI+ neutrophil population prevents ECM, whereas transfer of this population into FcεRIα-KO mice restores ECM susceptibility. FcεRI+ neutrophils preferentially home to the brain and induce elevated levels of proinflammatory cytokines. These data define a new pathogenic mechanism of ECM and implicate an FcεRI-expressing neutrophil population in malaria disease severity.

Clinical malaria is associated with high levels of circulating cytokines (Kwitkowski et al., 1990). Although balanced production of IFN-γ, TNF, IL-1, and IL-6 is capable of controlling parasite growth (Stevenson and Riley, 2004), their excessive production exacerbates disease severity (Grau and de Kossodo, 1994; Kwiatkowski, 1995) and contributes to the development of cerebral malaria (Grau et al., 1989; Kwiatkowski et al., 1990).

The inflammatory effector mechanisms remain ill-defined and complex. They involve innate immune responses through members of the mammalian Toll-like receptor (TLR) family that recognize parasite molecules (Coban et al., 2007), or hemoglobin, which is a digestion product of hemoglobin (Coban et al., 2005). Antibody-mediated inflammatory responses may also be critical. Although the role of IgG subclasses has been characterized in some detail (Shi et al., 1996; Metzger et al., 2003), the functional implication of IgE antibodies in malaria pathogenesis needs to be clarified. Past studies have shown that patients with severe malaria show higher IgE levels against P. falciparum than those with uncomplicated malaria (Perlmann et al., 1994, 2000). Other studies reported a reduced risk of severe malaria (Bereczky et al., 2004) and protection from cerebral malaria of IgE antibodies (Nacher et al., 2000). IgE bind to high-affinity
IgE receptors (FcεRI) on mast cells (MCs) and basophils, as well as to low-affinity IgE receptors (FcεRII/CD23) on B cells, granulocytes, and many other cell types. Interaction of CD23 with IgE immune complexes activates iNOS gene transcription leading to nitric oxide production, which is thought to cause cerebral malaria (Maneerat et al., 2000). Activation of basophils (Nyakeriga et al., 2003) and MCs (Furuta et al., 2006) that express FcεRI, but not CD23, may also exacerbate malaria pathogenesis through histamine secretion. High plasma and tissue histamine levels increased disease severity in humans infected with *Plasmodium falciparum* and in several animal models of *Plasmodium berghei* ANKA, an effect that involved binding to H1 and H2 receptors (Beghdadi et al., 2008).

To examine the role of IgE/FcεRI-mediated inflammatory processes in malaria pathogenesis, we studied mice that were genetically deficient for FcεRIα (Dombrowicz et al., 1993b) and IgE (Oettgen et al., 1994) after inoculation of *Pb*ANKA. The present investigations document that both mouse populations are resistant to ECM and control parasite development. Neither MCs nor basophils home to the brain, but a subset of FcεRIα neutrophils that were otherwise shown to emerge in the BM of *Pb*ANKA-hosting mice do home to the brain, disrupting its steady-state features.

**RESULTS**

*FcεRI and IgE deficiency confers protection against ECM*

To examine whether IgE synthesis and FcεRI-expressing cells are involved in ECM, we infected FcεRIα-KO mice that are resistant to IgE-mediated anaphylaxis (Dombrowicz et al., 1993b) with *Pb*ANKA via mosquito bites. The majority (80%) of *Pb*ANKA-infected WT mice died from ECM within 7–12 d (median survival, day 8; Fig. 1 b), whereas 90% of FcεRIα-KO mice survived at day 15 and did not develop ECM. Mice that resisted ECM later died of parasitemia-induced anemia without neurological signs (median survival: day 27; Fig. 1 b). Parasitemia increased over time similarly in C57BL/6 WT and FcεRIα-KO mice until day 15 after infection (Fig. 1 a). After day 15, parasitemia in WT mice that had survived ECM continued to rise, whereas in FcεRIα-KO mice it reached a plateau, indicating that, in contrast to WT mice, they were able to control parasite growth at later stages of infection. Quantitative RT-PCR analysis in brains of WT mice also showed an increase in FcεRIα mRNA over time until day 6, when it became significant, paralleling the appearance of the first signs of ECM (Fig. 1 c).

MC numbers in peritoneum and BM showed no difference between FcεRIα-KO and WT mice, ruling out any defect in MC development and function in FcεRIα-KO mice (Fig. S1 a; Dombrowicz et al., 1993b). Because histamine was previously implicated in malaria pathogenesis (Beghdadi et al., 2008), we measured histamine contents in BM cells and peritoneal MCs and found no differences between the two genotypes (Fig. S1 b). Additionally, plasma histamine levels were similar in FcεRIα-KO mice and WT mice (Fig. S1 c).

ECM resistance in the absence of FcεRIα likely reflects a role of IgE in malaria pathogenesis, as this receptor serves as a signaling relay after ligand binding (Bryce et al., 2004) and after antigen-specific cross-linking of IgE-sensitized cells (Blank and Rivera, 2004). In concordance, IgE-KO mice were less susceptible to ECM after infection with *Pb*ANKA. They survived >3 wk with 60% not developing ECM, whereas 90% of control WT mice died within 8 d. All mice that survived ECM had persistent parasitemia, as determined by real-time PCR analysis (Fig. 1 d), and none reached a plateau of parasitemia (Fig. 1 b).

**Figure 1.** *FcεRI expression and IgE are critical for the pathogenesis of ECM.* C57BL/6N (WT; *n* = 21) mice were infected with *Pb*ANKA through mosquito bites (8–10 mosquitoes per mouse). (a) Parasitemia (Mann-Whitney test; *, *P* < 0.036; **, *P* < 0.008). (b) Kaplan-Meier survival plots (log-rank test, *n* = 52, *P* = 0.0004). Data are from five independent experiments. (c) C57BL/6N (WT) mice were sacrificed at indicated time points after receiving blood-stage parasites of *Pb*ANKA inoculated intraperitoneally (*10^6* infected RBCs), and brain tissues were prepared for mRNA extraction. Transcription of the chain of FcεRI was evaluated by real-time RT-PCR. mRNA expression was normalized to hypoxanthine phosphoribosyltransferase expression. ***, *ANOVA, *P* = 0.0055; followed by an an posteriori Fisher’s PLSD test, *P* = 0.0008. Results were from two independent experiments. (d–i) IgE-KO (*n* = 25) and C57BL/6N (WT; *n* = 21) mice were infected with *Pb*ANKA through intraperitoneal inoculation of blood-stage parasites (*10^6* infected RBCs). (d) Kaplan-Meier survival plots (log-rank test, *P* = 0.035). Survival data are from four independent experiments. (e) Total IgE as measured in the plasma from noninfected (d0) and *Pb*ANKA-infected mice taken at indicated time points. Background value determinations of IgE were performed in sera from IgE-KO mice. * and ** indicate that differences are significant (Mann-Whitney test, *n* = 5–7, 0.01 < *P* < 0.05 and 0.001 < *P* < 0.01, respectively) relative to the basal level. Results are from three independent experiments. (f–i) Serum levels of IFN-γ (f) and IL-6 (h) were quantified by ELISA at day 6 after infection. Transcription of IFN-γ (g) and IL-6 (l) in the brain (n > 6/group) d after infection as evaluated by real-time RT-PCR. Gene mRNA expression is normalized to the endogenous control gene GAPDH, and the relative expression levels were calculated using the uninfected animals as a calibrator. Data are presented as the means ± SD from two independent experiments. **, *P* < 0.02.
whereas 75% of WT controls died of ECM (Fig. 1 d). Together, these data suggest that IgE-mediated signaling via FcεRI is essential for the occurrence of ECM. Considering the role of IgE, we found that total plasma IgE levels became significantly elevated only at day 12 after infection, as measured in surviving WT mice (Fig. 1 e).

In agreement with reports that ECM pathology in PhANKA-infected mice is associated with increased pro-inflammatory IFN-γ (Hunt and Grau, 2003) and IL-6 production (Lou et al., 1998), significantly higher levels were found in plasma and brain tissue of ECM-sensitive C57BL/6 mice than in FcεRIα-KO mice (Fig. 1 f-i). These data demonstrate that IgE and FcεRIα deficiency confers resistance to ECM and that the absence of signaling-competent receptors results in lower inflammatory cytokines in plasma and brain tissue.

Neither MCs nor basophils contribute to the development of ECM

To investigate the role of FcεRI-expressing cells, we first used MC-deficient Wsh/Wsh, which, like the previously used FcεRIα-KO and IgE-KO mice, are on the C57BL/6 background. MC-deficient Wsh/Wsh and WT mice were infected with PhANKA strain via mosquito bites. Parasitemia over time (Fig. 2 a) and survival rates (Fig. 2 b) showed no significant differences between both mouse strains excluding a role of MCs as major pathological effectors. To confirm this, FcεRIα-KO and Wsh/Wsh mice were reconstituted with WT MCs yielding an average of 1.2 and 1.05% FcεRI+ WT MCs, respectively, in the peritoneal fluid 10 wk after reconstitution, as compared with 1.75% in WT animals (Fig. S1 d). No effect was seen in reconstituted Wsh/Wsh mice and reconstituted FcεRIα-KO mice remained resistant to ECM (Fig. S1 e). These data formally rule out MCs as the cellular IgE targets in malaria pathogenesis.

Alternative FcεRI-expressing cells are basophils. To investigate their implication, mice were treated with the basophil-depleting antibody Ba103 1 d before infection. Severe depletion of DX5+/FcεRI+ blood basophils (Fig. S2) did not improve disease susceptibility as compared with control mice and the survival rates were not significantly different compared with FcεRIα-KO or IgE-KO mice (compare Fig. 1, b and d, and Fig. 2 c). Collectively, these data suggest that FcεRI+ cells other than MCs and basophils play a pivotal role in ECM development.

Similar infection outcomes were obtained whether mice were infected via mosquito bites or via infected RBCs (irRBCs). Henceforth, mice were infected via irRBCs. In mice, expression of the FcεRI is thought to be limited to MCs and basophils. However, it has been reported recently that FcεRIα and γ polypeptides are expressed in rat and mouse pinealocytes, the melatonin-secreting cell of the pineal gland (Ganguly et al., 2007). As the brain is a target tissue in ECM, we speculated that FcεRI expressed by pinealocytes contribute to disease expression. To address this, adoptive transfer experiments were performed by injecting BM cells from FcεRIα-KO and C57BL/6 mice into irradiated FcεRIα-KO mice. Only mice that received FcεRI+ BM cells developed ECM (Fig. 2 d), ruling out a significant contribution of pinealocytes in disease expression. Conversely, reconstitution of irradiated C57BL/6 mice with BM from syngeneic mice or from FcεRIα-KO mice showed that only the latter acquired resistance to ECM (unpublished data). Altogether, these data demonstrate that the FcεRIα-expressing cells that contribute to disease expression are of hematopoietic origin.

To exclude functional overlap between MCs and basophils, it was important to test the effect of depleting basophils in the mast cell–deficient Wsh mice. Preliminary data show that depletion of basophils in mast cell–deficient mice did not alter the phenotype of infected mice in regard to the development of ECM (unpublished data), suggesting that both cell lineages are apparently not involved in CM pathogenesis. Given the reported binding of IgE to FcγRI and the major role of FcγRIV in neutrophil activation (Hirano et al., 2007; Mancardi et al., 2008), it was necessary to preclude any possibility of this receptor to contribute to the observed effects associated with the FcεRI. To this end, C57BL/6 mice were inoculated with PhANKA-infected erythrocytes, and then treated with 200 µg of anti-FcγRI mAb (9e9 antibody) every other day from day 2 to day 6 after infection. Binding of the
antibody was assessed throughout the infection period, as shown by FACS analysis of blood leukocytes gated on CD45+ cells (preliminary results; unpublished data). Occurrences of ECM and survival data were strictly similar between mice that received the anti-FcγRIV antibody or the isotype control antibody (preliminary results; unpublished data).

**Identification of neutrophils and eosinophils as novel FcγRI-expressing cells induced during malaria disease**

In search of FcγRI-expressing cells, we surmised that neutrophils and eosinophils might represent inflammatory cells, which under the particular circumstance of *Plasmodium* infection, could express FcγRI and cause the disease. A kinetic analysis of the frequency of 7/4+ Ly6G+ neutrophils, Siglec-F+ eosinophils, and FcγRI+ cells among blood leukocytes showed that neutrophils increased constantly over time, whereas eosinophils remained stable at around 5% (Fig. 3 a). The proportion of total FcγRI+ cells also increased steadily (Fig. 3 a). The most highly represented FcγRI+ cells among examined blood leukocytes were neutrophils reaching up to 6% (Fig. 3 b). FcγRI+ eosinophils peaked at day 4 rising from 0.2% to 4% and then decreased between d6–8 reaching 1.5% (Fig. 3 b).

In the BM, the proportion of neutrophils and eosinophils decreased from day 0 to 4, and then slightly increased until day 8 for neutrophils, while eosinophils decreased again after a short rise (Fig. 3 c). Fig. 3 d shows that naive mice expressed a small but detectable proportion of FcγRI+ neutrophils (1.8%) and eosinophils (1.9%). This proportion peaked at 8.5% and 6% for neutrophils and eosinophils, respectively, at day 4 after infection, whereas at day 6 and 8 after infection, the fraction of FcγRI+ cells declined for the two cell types. In parallel, basophils increased from 0.5% at day 0 to 2% at day 8, whereas the fraction of MCs remained unchanged.

In the brain, no cells were detected until 4 d after infection, which is when both neutrophils (4.9%) and eosinophils (2.3%) appeared, and their proportions reached 14 and 9%, respectively, at 8 d after infection (Fig. 3 e). The proportions of FcγRI+ neutrophils and eosinophils were, however, strikingly different with an accumulation of ~5% of neutrophils at 6–8 d, as compared with 1.3% of FcγRI+ eosinophils (Fig. 3 f). It must be noted that neither mast cells nor basophils were present at any given time (Fig. 3, e and f). An illustration of a FACS analysis of neutrophil populations associated with brain tissue taken at 6 d after infection and showing ECM signs is shown in Fig. 4. Double labeling of leukocyte populations with anti-7/4 and anti-Ly6G antibodies revealed a highly enriched proportion of FcγRI+ 7/4+ Ly6G+ neutrophils (55–61%) associated with brain tissue of mice showing ECM signs at 6 d after infection (Fig. 4, top). To verify whether the increase in receptor expression occurs in the neutrophil population present in the brain, and also to determine whether this increase in expression only occurs in mouse strains susceptible to CM when infected with *Pb*ANKA, mice infected with the non–ECM-inducing PbNK65 parasites did not show any sequestration of FcγRI+ neutrophils in their brain even at 20 d after infection (Fig. 4, bottom). It must also be emphasized that there were small amounts of leukocytes associated with the brain tissue. Indeed, the CD45+ population in the brain of PbNK65-infected mice represents only 0.25% of total cells, whereas the same population was 20-fold higher (5%) in PbANKA-infected mice.

Collectively, these data show that a significant proportion of neutrophils and eosinophils expressed FcγRI during infection with PbANKA parasite.

**Depletion of neutrophils protects mice from ECM**

For depletion experiments, we used the NIPM-R14 mAb, in which staining patterns show a complete overlap between the anti-Ly6G and the 7/4 antibodies. Administration of 200 µg of the antineutrophil mAb NIMP-R14 1 d before infection, which elicited complete depletion of neutrophils up to day 6 (unpublished data), prevented the development of neurological signs of ECM, and protected mice from death as compared with those treated with control IgG isotype (Fig. 5 a). Death occurred on average between day 20–25, without neurological signs from hyperparasitemia-induced anemia (median survival time, 21 d versus 7 d for neutrophil-depleted and control mice, respectively; n = 8; P = 0.006), with no significant difference in final parasitemia (P > 0.05; Fig. 5 b).

To examine the possible contribution of eosinophils to ECM pathogenesis, C57BL/6 mice were treated with eosinophil-depleting anti–mouse Siglec-F antibody 1 d before infection and
at day 4 after infection. No significant differences between eosinophil-depleted and control IgG-treated mice were observed in the development of ECM (Fig. 5 c) and parasitemia (Fig. 5 d). These data demonstrate that neutrophils, but not eosinophils, play a critical role in the pathogenesis of ECM and that cell depletion does not directly affect parasitemia.

To establish if neutrophil depletion was equally effective after infection, we performed a kinetic analysis. Mice were treated before infection or at day 4, 5, or 6 after infection with anti-neutrophil-depleting antibody. Treatment at 4 d after infection was equally effective as depletion 1 d before infection (Fig. 5, a and c). Treatment on day 5 after infection was less protective, although significant (n = 12; P = 0.031; Fig. 5 f) compared with mice treated on day 6 after infection (n = 12; P = 0.074), which is when mice started to develop the first signs of ECM (Fig. 5 g). Thus, late depletion of neutrophils is no longer protective once the pathogenic processes are established, particularly in the brain, where on day 5 these events are already in place (Beghdadi et al., 2008).

To analyze the role of FcεRI+ neutrophils in the initiation of ECM pathology, FcεRIα-KO mice were repleted with BM-derived FcεRI+ neutrophils from PbANKA-infected C57BL/6 mice 6 d after infection. FcεRI+ cells were enriched in the low-density layers of Percoll gradient (50–45% and <45%; Fig. S3) before FACS sorting. Double-positive cells gated on 7/4 and Ly6G expression gave rise to two neutrophil populations: Ly6G+ 7/4+ FcεRI+ neutrophils (9.3%) and Ly6G+ 7/4+ FcεRI− neutrophils. 90.7% were obtained from PbANKA-infected mice, whereas in normal mice the Ly6G+ 7/4+ FcεRI+ neutrophil population represents only 1% (Fig. S4, b and c). Additional morphological analysis of FcεRI+ and FcεRI− neutrophil populations showed that they were phenotypically indistinguishable, as shown by cytospin analysis (Fig. S4, d and e). Sorted triple-positive (Ly6G+ 7/4+ FcεRI+) neutrophils or double-positive (Ly6G+ 7/4+ FcεRI−) neutrophils were injected intravenously into recipient FcεRIα-KO mice. Before injection, these cells were analyzed for their possible contamination with other leukocytes, and as shown in Fig. S4 f, sorted cells consisted of highly pure neutrophil populations with only minor contamination from Siglec-F+ cells, CD11c+ cells, and F4/80+ cells. FcεRIα-KO mice repleted with Ly6G+ 7/4+ FcεRI+ neutrophils acquired susceptibility to ECM, as compared with those reconstituted with FcεRI− neutrophils (n = 15, P = 0.0087; Fig. 5 h). To analyze brain localization, naive or infected FcεRIα-KO or WT C57BL/6 mice (6 d after infection) were injected intravenously with 10⁶ CFSE-labeled sorted neutrophils (7/4+ Ly6G+ FcεRI+) obtained from infected C57BL/6 mice. As shown in Fig. 5 i, a significant proportion of CFSE-labeled neutrophils was found to be associated to brain tissue of both infected recipient FcεRIα-KO (4.9%) and WT C57BL/6 mice (4.5%) compared with noninfected FcεRIα-KO (0.7%) and WT C57BL/6 mice (0.6%), respectively. Similar results were obtained 1 and 24 h after injection, suggesting that 7/4+ Ly6G+ FcεRI+ home rapidly and stably to the brain tissue of infected mice. These data demonstrate that the expression of FcεRI+ in neutrophils is critical for the development of ECM.

Biochemical characterization of FcεRI expressed by neutrophils

As neutrophils ordinarily do not express FcεRI, we further characterized this receptor in cells from PbANKA-infected mice. Highly homogeneous double-positive Ly6G+ 7/4+ cells obtained by FACS sorting (Fig. S4), subjected to analysis using RT-PCR, showed that neutrophils from naive mice expressed low levels of FcεRIα mRNA and IgE expression increased in infected mice (Fig. 6 a). Flow cytometry confirmed that naive mice expressed only low levels of surface FcεRI and IgE-binding (∼1%). On day 6 after infection, ∼9–10% of neutrophils stained positive with anti-FcεRIα and anti-IgE, indicating that they were IgE-sensitized (Fig. 6 b). CD23,
another receptor, which may also account for IgE binding, was not expressed by neutrophils from naive or infected mice (Fig. 6 b). Confocal image analysis also confirmed that FcεRIα was colocalized with the FcεRIγ subunit (Fig. 6 c), whereas FcεRIβ was undetectable (not depicted). Immunoblot analysis of cell lysates confirmed the presence of FcεRIγ and the absence of FcεRIβ, whereas FcεRIβ was readily detected in RBL-2H3 and BMMC lysates (Fig. 6 d). To exclude the possibility that the lack of the FcεRI β chain is caused by a proteolytic degradation, presence of the β chain was assessed at the transcriptional level. Analysis of neutrophils by real time qPCR clearly indicate that sorted FcεRIα neutrophils express the α chain, whereas the β chain is not present (unpublished data). Neutrophils, whether obtained from naive or infected mice also expressed FcεRIγ (Fig. 6 b). Although FcεRIγ has been reported to bind IgEβ (Hirano et al., 2007) or both IgEα and IgEβ allotypes (Mancardi et al., 2008) at high concentrations, we did not detect IgEβ-binding under steady-state conditions in naive mice, and IgE-binding could not be blocked with anti-FcεRIγ antibody in cells from infected mice (unpublished data). We also performed coimmunoprecipitation experiments to analyze the subunit composition of FcεRI. The receptor was directly immunoprecipitated with IgG-Sepharose to avoid precipitation of murine IgG reagents of allotypes (Mancardi et al., 2008) at high concentrations, we did not detect IgEβ-binding under steady-state conditions in naive mice, and IgE-binding could not be blocked with anti-FcεRIγ antibody in cells from infected mice (unpublished data). We also performed coimmunoprecipitation experiments to analyze the subunit composition of FcεRI. The receptor was directly immunoprecipitated with IgG-Sepharose to avoid precipitation of murine IgG receptors through protein G from purified neutrophils, which may contain cell-bound IgG. Co-immunoprecipitation of receptor under mild conditions (0.3% Triton X-100) revealed the specific presence of FcεRIγ, whereas FcεRIβ was absent. Both β and γ chains were readily coimmunoprecipitated from BMMC lysates (Fig. 6 e). The γ chain was also immunoprecipitated in the presence of anti-FcεRIγ blocking antibody (unpublished data) excluding that coinmunoprecipitation of the γ chain was caused by FcεRIγ. Together, these data indicated that the parasite-induced neutrophil population expressed an unconventional FcεRI in the absence of FcεRIβ chain. To assess the functionality of this receptor, neutrophils were passively sensitized with anti-DNP–specific IgE mAb. Stimulation of sensitized cells for 4 h with DNP-HSA elicited significant amounts of TNF and IL-6 release (Fig. 6 f).

DISCUSSION

In this work, we report the implication of molecular and cellular components of the IgE-mediated allergic inflammatory cascade in malaria pathogenesis. Using a murine model of ECM, we show that the inflammatory response elicited by IgE–FcεRI complexes drives development of ECM. This did not involve MCs or basophils. A major finding was that PbANKA-induced expression of FcεRI in neutrophils...
and eosinophils and that depletion of neutrophils, but not eosinophils, had a positive clinical outcome.

In humans, studies aiming at establishing the allergic nature of malaria disease report conflicting results ranging from disease-aggravating to disease-protecting roles of IgE (Perlmann et al., 1997; Bereczky et al., 2004). To clarify this issue, we used genetically deficient animals or antibody-depleted cell populations to examine crucial components of the allergic inflammatory response in malaria pathogenesis. We found that targeted disruption of IgE or the α chain of FcεRI led to resistance to the development of ECM after infection with PbANKA. These results indicate a pathological role of IgE that acts via FcεRI to promote disease development. Interestingly, FcεRI-α-KO mice showed a more marked resistant phenotype than IgE-KO mice, leaving open the possibility for additional disease-aggravating signaling events via FcεRI. This may include galectin 3, an alternative ligand for FcεRI. In agreement, deletion of the galectin-3 gene in susceptible C57BL/6 mice resulted in partial protection from ECM (Oakley et al., 2009). In both FcεRI-α-KO and IgE-KO mice, the observed clinical immunity occurred in the absence of antiparasite immunity. The association of FcεRI with the neuropathological disorders observed during ECM was further emphasized by the constant increase of the receptor α chain expression in the brain.
of infected mice. Conventional effector cells expressing FcεRI in mice consist of MCs and basophils. However, our data using MC-deficient mice or antibody-mediated depletion of basophils excluded MCs and basophils as relevant effector cells. To exclude functional overlap between mast cells and basophils, mast cell–deficient mice treated with the anti–basophil-depleting antibody did not result in any protection against ECM. Previously, MCs and MC-derived TNF were shown to protect against ECM (Furuta et al., 2006). This contradictory result may have been influenced by the different MC–deficient W/Wv mouse strain used, which makes the mice anemic, and thus potentially compromised in controlling a parasite infection. It was also puzzling that TNF was protective in this study, although TNF generally enhances disease severity (Grau et al., 1987).

Searching for alternative FcεRI-expressing cell types, we identified neutrophils and eosinophils, and discovered that the former had a disease enhancing. Although FcεRIα is essentially absent in neutrophils in naive mice, FcεRIα becomes induced during Plasmodium infection as demonstrated by: RT-PCR analysis, the binding of the α chain–specific MAR-1 antibody, and detection of membrane-bound IgE. Additional characterization showed that the receptor was colocalized with the FcεRIγ subunit that could be communoprecipitated with IgE. In contrast, the FcεRI β chain was undetectable in neutrophils. Although FcγRIIV, which is expressed in neutrophils in both naive and infected mice, could potentially bind IgE at high concentration (Hirano et al., 2007; Mancardi et al., 2008), we did not detect significant IgE binding to this receptor. Similarly, another IgE receptor CD23, was not expressed in neutrophils, suggesting that IgE binding to FcεRI was specific. In humans, FcεRI is frequently expressed in neutrophils of atopic asthmatics as a trimeric FcεRIαγγ2 receptor (Saffar et al., 2007), whereas it is absent in healthy individuals. It has therefore been postulated that FcεRI-induced inflammatory signaling and the reported antiapoptotic effect of monomeric IgE may exacerbate the pathogenetic effects of FcεRI+ neutrophils in asthma (Saffar et al., 2007). A parallel can be made in the present work as to the possible implication of FcεRI+ neutrophils in malaria pathogenesis. Indeed, cell type–specific depletion of neutrophils, but not of eosinophils was found to protect mice against ECM and mortality consistent with previous findings using the same neutrophil-depleting antibody (NIMP-R14; Senaldi et al., 1994). Furthermore, transfer of FcεRI+, but not FcεRI−, neutrophils conferred ECM susceptibility to the otherwise resistant FcεRIα-α-KO mice. Likewise, irradiated C57BL/6 mice engrafted with the BM from FcεRIα-α-KO mice acquired resistance to ECM, which was not the case when these mice were reconstituted with the BM from C57BL/6 mice (unpublished data). These results emphasize the critical role of FcεRI+ neutrophils in the disease expression and mortality, as the sequestration properties of this cell population in the brain tissue occurs rapidly, within an hour after cell transfer, in Plasmodium-infected FcεRIα-α-KO mice that are otherwise CM resistant. The fact that the FcεRI+ neutrophils did not sequester in the brain of noninfected mice suggests that the brain tissue of Plasmodium-infected FcεRIα-α-KO mice acquired the potential to recruit FcεRI+ neutrophils. After infection, given the absence of FcεRI in these mice, the pathogenetic effects could not be observed. A subsequent issue relates to the specific induction of FcεRI+ neutrophils by the Plasmodium strain, as this cell population was absent when the non–CM-inducing Plasmodium strain was used. Indeed, it is frequently asked what distinguishes these two parasite strains in terms of their ability to cause ECM or not. One possible explanation is provided by the present work, which establishes a close relationship between the disease–associated FcεRI+ neutrophils and CM-inducing Plasmodium strain. However, it remains to be determined at the molecular level by which mechanism Plasmodium induces the expression of FcεRI.

Collectively, our findings provide a new concept on inflammatory response–driven malaria pathogenesis where neutrophils play a central role in inducing inflammatory responses, reminiscent of the allergic–type reactions implicated in the development of ECM. Inflammatory cytokines IFN-γ and IL–6, which have elevated expression locally in the brain and systemically in the plasma, may represent surrogate markers for this neutrophil–mediated response. Because ECM pathology was found to be associated with increased proinflammatory IFN-γ (Hunt and Grau, 2003), an attenuated production of this cytokine in FcεRIα-α-KO mice raises the possibility that FcεRI+ neutrophils that sequester in the brain of infected C57BL/6 mice may represent an additional source of IFN-γ. Functional studies of FcεRI+ neutrophils via cross-linking of bound IgE results in the production of IL–6 and TNF. In infected mice, the triggering of cytokine release may occur in different tissues, including BM, blood, and brain, giving rise to both systemic and local cytokine induction. Physiologically, several possibilities exist to explain the elevated cytokine levels, such as the possibility that cytokines are released by activated neutrophils subsequent to aggregation of specific IgE antibodies on sensitized neutrophils by parasite–derived antigens. However, this mechanism is uncertain, as we were not able to detect such specific IgE antibodies in infected mice. It is also possible that IgE present in the mouse before infection exerts a priming function when binding to newly expressed FcεRI on a subset of neutrophils, rendering them more responsive to other stimuli.

Several questions remain unresolved. In particular, as mentioned above, the Plasmodium infection–associated signals required for the induction of FcεRI expression in neutrophils are unknown. However, this property seems to be specific to the ECM–inducing Plasmodium parasite, as mice infected with non–ECM–inducing Plasmodium parasite or mice infected with Escherichia coli undergoing septic peritonitis as a result of cecal ligation and puncture did not show any expression of FcεRI in their neutrophils (unpublished data). In humans, it is believed that expression of FcεRI in neutrophils is regulated by Th2 cytokines (Saffar et al., 2007) and GM-CSF. We detected IL–4 in the brain and in the spleen at 6 d after
infection (unpublished data), but a clear relationship with the induction of IgE and FcεRI+ neutrophils during Plasmodium infection was not formally established. Although IgE-KO mice were clinically resistant, our attempts to detect Plasmodium antigen-specific IgE antibodies in the plasma of infected mice have failed. It is possible that within the relatively short period of infection (6–8 d), an effective IgE antibody response may be hardly detectable. A significant increase in total IgE antibodies became detectable in surviving mice only at day 12 after infection (Fig. 1 e). One possibility is that limited amounts of IgE antibodies are sufficient to trigger neutrophil responses. Alternatively, sensitization with parasite antigen-unrelated IgE antibodies may render FcεRI+ neutrophils more prone to fulfill their effector functions. In support of this, an earlier study of MCs highlighted the role of antigen-relevant IgE in positively influencing hapten-specific contact hypersensitivity (Bryce et al., 2004). Therefore, it is possible that IgE present in the mouse before infection binds to newly expressed FcεRI thereby priming these cells for enhanced effector responses.

Our biochemical analysis showed that mouse neutrophils, express FcεRIαγδ trimers in the absence of the β chain (Wang et al., 1992; Maurer et al., 1996). This was surprising, as previous experiments had indicated a requirement of this subunit for cell surface expression in rodents in contrast to the human receptor (Miller et al., 1989), where expression can be observed in several β-less cell types (Bieber, 2007). However, a precedent for the expression of FcεRI in the absence of FcεRIβ in mice has previously been made in lung DCs after infection with Sendai virus (Grayson et al., 2007). It is therefore conceivable that infectious events may enable expression of a trimeric FcεRIαγδ receptor by masking inherent retention signals of the α chain (Blank et al., 1991; Hartman et al., 2008).

Alternatively, they may induce expression of α-like molecules that support receptor expression. Additional studies are necessary to clarify the various aspects leading to the activation of FcεRI+ neutrophils during malaria disease. Collectively, our data provide evidence for the implication of an unconventional FcεRI in neutrophils as being important in the expression of severe malaria mediated by an IgE-mediated inflammatory response.

**MATERIALS AND METHODS**

**Mice.** Female C57BL/6 mice 6–8 wk old were purchased from Charles River Breeding Laboratories. FcεRIαγδ-KO mice have been previously described (Dombrowicz et al., 1993a). IgE single-KO mice were derived from double IgE/CD16-KO mice by backcrosses on C57BL/6 mice (provided by T. Ishino, Department of Medical Zoology, Mae University School of Medicine, Edobashi, Tsu, Japan). FcεRIαγδ-KO mice by backcrosses on C57BL/6 mice (provided by T. Ishino, Department of Medical Zoology, Mae University School of Medicine, Edobashi, Tsu, Japan). FcεRIαγδ-KO mice were derived from mice has previously been made in lung DCs after infection with Sendai virus (Grayson et al., 2007). It is therefore conceivable that infectious events may enable expression of a trimeric FcεRIαγδ receptor by masking inherent retention signals of the α chain (Blank et al., 1991; Hartman et al., 2008). Alternatively, they may induce expression of α-like molecules that support receptor expression. Additional studies are necessary to clarify the various aspects leading to the activation of FcεRI+ neutrophils during malaria disease.

Collectively, our data provide evidence for the implication of an unconventional FcεRI in neutrophils as being important in the expression of severe malaria mediated by an IgE-mediated inflammatory response.

**Parasites and infection.** For all infections, non–ECM-inducing *P. berghei* (strain NK65; PbNK65) or ECM-inducing (ANKA strain) strains expressing the GFP on CS or hsp70 promoter (Ishino et al., 2006), were used allowing the detection of sporozoites and blood stage parasites by fluorescent microscopy. Parasites were provided by Dr. T. Ishino (Department of Medical Zoology, Mae University School of Medicine, Edobashi, Tsu, Japan). Infection of mice with PbANKA induces ECM, characterized by paralysis, ataxia, convulsions, and coma between 7–9 d after infection. PbNK65 induces a lethal malaria around 20–25 d after infection without neurological symptoms and was a gift from R. Menard (Institut Pasteur, Paris, France). The parasites were maintained in a cycle between C57BL/6 mice and *Anopheles stephensi* (Demeure et al., 2005). The erythrocytic stages of the parasites were maintained in liquid nitrogen as iRBC in Asever’s solution (Sigma-Aldrich) containing 10% glycerol. The infection is induced either by exposure to 8–10 infected *An. stephensi* mosquitoes (Beghidi et al., 2008) or by intraperitoneal injection of 10^7 iRBCs.

**Flow cytometry analysis.** Single-cell suspensions from blood or BM obtained at different time points after inoculation of C57BL/6/n mice with 10^7 PbANKA-iRBCs were stained for FACS analysis according to standard protocols in cold PBS containing 2% FCS and 0.01% sodium azide (FACS buffer). Staining was performed as follows: for total neutrophils (PerCP-anti-CD45+ FITC-7/4 PE-anti-Ly6G mAbs), total eosinophils (PerCP-anti-CD45 mAb PE-anti-Siglec-F mAb), and total FcεRIα leukocytes (PerCP-anti-CD45 mAb + PE-anti-FcεRIα chain mAb). To unequivocally define FcεRI+ neutrophil subpopulation by FACS analyses, cells were labeled with PerCP-antiCD45 mAb and counter-stained with antineutrophil FITC-7/4 and anti-Ly6G antibodies, and with APC-anti-FcεRIα chain mAb. Detection of basophils consisted of PerCP-anti-CD45 mAb + APC-Dx5 + PE-anti-FcεRIα chain mAb. FcεRIα+ eosinophils were identified using PerCP-antiCD45 mAb + PE-anti-Siglec-F mAb + FITC-anti-FcεRIα chain mAb, and mast cells were characterized using PerCP-antiCD45 + APC-antiCD117 + PE-anti-FcεRIα chain mAbs. All antibodies were obtained from BD, except FITC-7/4 and anti-FcεRIα chain mAbs (clone MAR-1), which were obtained from Invitrogen and eBioScience, respectively. The hamster anti–mouse FcεRI rabbit antibody (clone 9e9) was provided by J. Ravetch (The Rockefeller University, New York, NY). Analysis was performed using a four-color FACSCalibur flow cytometer with ProCellQuest software (BD). Data were expressed as the percentage of total CD45+ BM or cell subsets, or as the percentage of total FcεRIα+ BM or blood cells.

**Confocal microscopy and immunoprecipitation studies.** For confocal immunofluorescence microscopy, FITC-anti-Ly6G+ neutrophils, FcεRI-expressing cells (~10^4 cells) were first incubated with anti-FcεRI antibody MAR-1 (1 h on ice), followed by incubation with Dylight 649 goat anti–Armenian hamster (BioLegend) before fixation for 15 min in PBS containing 4% parafomaldehyde followed by 2 washes in PBS. Fixed cells were permeabilized in PBS containing 0.025% saponin for 20 min at room temperature, followed by blocking in PBS containing 0.025% saponin and 10% goat serum/0.2% BSA (Invitrogen) for 30 min at room temperature.

Cells were then stained with rabbit anti–FcεRI in PBS containing 0.025% saponin and 10% goat serum/0.2% BSA overnight at 4°C, followed by incubation with anti–rabbit-Alexa Fluor 568 for 60 min in PBS containing 0.012% saponin and 10% goat serum/0.2% BSA. After washing, cells were mounted in Prolong-Gold anti-fading reagent (Invitrogen) and analyzed using a confocal laser-scanning microscope (LSM 510; Carl Zeiss, Inc.). Images were taken using 63× oil immersion objective lens. Colocalization was quantified using LSM 510 image software. A total of 7 cells with a minimum of 10 stacks were quantified.
Real-time RT-PCR and RT-PCR of the α chain of the FceRI. Gene expression in the brains from FceRI-α-KO and C57BL/6 mice at various time points after infection were analyzed by the real-time RT-PCR. RNA used for these assays was isolated by means of a two-step extraction process. First, brains were surgically removed from mice as previously described and placed immediately in RNAzol (QIAGEN) at 4°C overnight. After RNAzol was removed, RNA samples were stored at −80°C until processing. Brains were thawed in 1 ml of TRIzol and subjected to bead disruption in a polytron 3 times for 2 min at a setting of 30 cycles/s. Samples were spun at high speed (10,000 g) for 3 min to remove debris and lipids. Half of the sample was transferred to a new tube and mixed with 500 µl of TRIzol reagent by vortexing. After this step, RNA extraction proceeded according to the manufacturer’s protocol. Precipitated mRNA was resuspended in 100 µl of RNase-free water. The second step of this extraction was followed by QIAGEN’s protocol for RNA clean-up, including steps for removal of protein and DNA (RNasey kit; QIAGEN). Samples were eluted with 50 µl of RNase-free water and quality and quantity assured by photodensitometry. Real-time RT-PCR used primer-probe sets for the α chain of mouse FceRI and standard TaqMan protocols (Applied Biosystems).

Detection of IgE antibodies in sera from Plasmodium-infected mice. For parasite-specific IgE antibodies, 96-well plates were coated with PfANKA freeze-thawed crude lysate in carbonate buffer, pH 9.6, for 2 h at 37°C. After the plates were saturated with 1% bovine serum albumin, each serum was assayed at serial dilutions and incubated overnight at 4°C. Specific binding was detected using biotin-conjugated anti-mouse IgE antibodies (BD) followed by streptavidin–alkaline phosphatase (Mabtech) and pNPP as substrate (Sigma-Aldrich).

To determine total IgE, 96-well plates were coated with rat anti-mouse IgE (clone R35-72; BD) for 2 h at 37°C, and the wells were blocked with 1% BSA for 2 h at 37°C. Serial dilutions of sera were incubated overnight at 4°C and developed using biotinylated rat anti-mouse IgE (e-specific, clone LO-ME-2; Biosys) and streptavidin–alkaline phosphatase (Mabtech). A standard curve was obtained using purified mouse IgE (BD).

Preparation of BM-derived mast cells (BMMCs) and mast cell reconstitution. C57BL/6-Ki67−/−/IL-3−/− (Hab) mice are now used in many instances as a model for studies of mast cell function in vivo (Mallen-St. Clair et al., 2004). W-sash (Ws) is an inversion mutation in the transcriptional regulatory elements upstream of the c-kit transcription start site on mouse chromosome 5 (Nagle et al., 1995). This mutation results in the lack of differentiation of mast cells. Ki67−/−/IL-3−/− and FceRI-KO mice can be transplanted successfully with BM-derived mast cells by injecting 5 × 10⁶ cultured BMMCs intraperitoneally.

BMMCs were prepared as previously described (Razin et al., 1981). After 3 wk of culture of BM cells using RPMI 1640 (BioWhittaker) supplemented with 10% heat-inactivated FCS (Boehringer Mannheim) and 3 U/ml of IL-3, the cells were harvested. They consisted of 98% pure mast cell populations as assessed by toluidine blue staining, and c-Kit and FceRI expression.

Adoptive transfer. Adoptive transfer experiments were performed by injecting BM cells from C57BL/6 mice into irradiated FceRI-KO mice. The reverse adoptive transfer, which consists of the transplantation of BM cells from FceRI-KO KO mice into irradiated C57BL/6 mice was also performed. FceRI-KO mice received myeloablative total-body irradiation (900 Gy; 137Cs source), followed by i.v. injection of 5 × 10⁶ donor BM cells from autologous or C57BL/6 WT mice. BM cell suspensions were prepared by flushing femurs with RPMI 1640 medium supplemented with 10% FCS, nonessential amino acids, l-glutamine, sodium pyruvate, and 2-mercaptoethanol. 6 wk after irradiation, chimeric and control mice were described as.

For short-term reconstitutions with neutrophils, BM cell suspensions, obtained from PbANKA-infected C57BL/6 mice (6 d after infection) were separated over a discontinuous density Percoll gradient as indicated in Fig. S3. Each fraction was labeled with FITC-antineutrophils (clone 7/4), PE-anti-Ly6G, and APC-anti-FceRI antibodies (clone MAR-1). The Percoll density layers corresponding to 50 and 45% were found to be enriched in FceRI+ neutrophil population and were considered for cell sorting. Double-positive cells gated on 7/4 and Ly6G expression isolated from PbANKA-infected mice gave rise to two neutrophil populations: Ly6G+ 7/4 FceRI+ and Ly6G+ 7/4 FceRI− neutrophils (Fig. S4). Sorted triple-positive (Ly6G+ 7/4 FceRI+) neutrophils and the double-positive (Ly6G+ 7/4 FceRI−) neutrophils (2 × 10⁶ neutrophils/mouse) were injected intravenously in recipient FceRI-KO KO mice. Given the short half-life of neutrophils, their injection at day 6 after infection was taken as the optimal proximal time before the manifestation of disease signs.

Neutrophil activation and cytokine release. Purified neutrophils were resuspended at 10⁶ cells/ml in RPMI-1640 medium supplemented with 10% (vol/vol) fetal bovine serum, 2 mM l-glutamine, 100 U/ml penicillin, and 100 mg/ml streptomycin, and then incubated for 1 h with 1 µg/ml of antibody directed against the human β2 integrin (clone 24B1; Sigma-Aldrich) or with 100 µg of an affinity-purified rat monoclonal antibody Ba103, which recognizes the human β2 integrin. After washing, neutrophils were stimulated with PMA, 100 ng/ml IFN-γ, or C57BL/6 WT mice. BM cell suspensions were prepared by flushing femurs with RPMI 1640 medium supplemented with 10% FCS, nonessential amino acids, l-glutamine, sodium pyruvate, and 2-mercaptoethanol. 6 wk after irradiation, chimeric and control mice were described as.

In vivo depletion of basophils, neutrophils, and eosinophils. Basophils represent <1% of peripheral blood leukocytes and have been neglected until recently, when they were found to fulfill critical immunological functions (Karayuzuyama et al., 2009). These cells, which generate large quantities of T helper 2 (Th2) cytokines such as IL-4, provided new insights into their possible role in allergic disorders and immunity to pathogens. A specific antibody has recently been generated, the rat monoclonal antibody Ba103, which recognizes a mouse basophil-associated protein (Obata et al., 2007). For basophil depletion, mice were given intravenous injection of Ba103 1 d before infection with 10⁵ RBCs. A single intravenous administration of 30 µg Ba103 drastically reduced the basophil number in the peripheral blood, and this level remained reduced for ∼10 d after the single injection of Ba103, and thereafter returned to normal. Unlike the number of basophils, no significant reduction in the number of mast cells was observed (Obata et al., 2007). To determine if eosinophils and neutrophils play any role in malaria disease severity, cell-specific depletion experiments were performed. C57BL/6 mice were injected 1 d before infection with PbANKA pRBCs, with 200 µg of a rat anti-mouse neutrophils (clone NIMP-R14; Senaldi et al., 1994) provided by G. Milon (Institut Pasteur, Paris), which was shown to recognize the same neutrophil population as the anti-Ly6G and the 7/4 mAbs, or with 100 µg of an affinity-purified polyclonal antibody raised in sheep against Siglec-F, a specific marker for mouse eosinophils, which was obtained from P. Crocker (Division of Cell Biology and Immunology, The Wellcome Trust Biocentre at Dundee, 2011).
University of Dundee, UK; Zimmermann et al., 2008). A second injection of anti-Siglec-F antibody was provided at day 4 after infection to maintain eosinophils at a minimal level until the expression of clinical signs. At day 6, when the first clinical signs appear, no detectable neutrophils or eosinophils were present in peripheral blood. To verify if NIMP-R14 antibody specifically recognizes neutrophil cells, BM cells obtained 6 d after infection from C57BL/6 mice were first stained with NIMP-R14 mAb followed by anti-rat IgG mAb-PE/Cy7 and positive cells were sorted out. NIMP-R14+ cells were then counter-stained with anti-GR-1-PE, 7/4-FTTC, MAR-1-Alexa Fluor 647, CD11c-PE, DX5-PE, F4/80-PE, CD11b-FTTC, and Siglec-F-PE antibodies.

The pattern of stainings shows a complete overlap between the NIPM-R14 antibody and the anti-Ly6G and 7/4 antibodies.

Statistical analysis. Significant differences in survival were evaluated by generation of Kaplan–Meier plots and log rank analysis. P < 0.05 was considered statistically significant. For other analyses, after verification using a Jarque-Bera test, our data followed a normal distribution; statistical significance was assessed by an ANOVA test followed by a posteriori Fisher PLSD (Protected Least Significant Difference) test. For parasitaemia, after verification using a Jarque-Bera test, our data did not follow normal distribution, and thus, when differences between groups of mice were to be compared at a given time point, the Mann-Whitney test was performed with significance set at P < 0.05.

Online supplemental material. Fig. S1 shows an assessment of mast cell development and function in FcεRIα-KO mice and mast cell reconstitution of FcεRIα-KO mice and Wsh mice. Fig. S2 shows in vivo depletion of basophils. Fig. S3 shows density distribution of FcεRI+ neutrophils. Fig. S4 shows the phenotypic characterization of FcεRI+ neutrophils. Online supplemental material is available at http://www.jem.org/cgi/content/full/jem.20110845/DC1.

We thank Jeffrey V. Ravetch (The Rockefeller University) and Paul Crocker (University of Dundee) for providing anti-mouse FcεRI and anti-Siglec-F antibodies, respectively. We also thank Hans Oettgen (Children’s Hospital, Harvard Medical School) and Sjef J. Verbeek (Leiden University Medical Center) for providing antibodies, respectively. We also thank Hans Oettgen (Children’s Hospital, Harvard Medical School) and Sjef J. Verbeek (Leiden University Medical Center) for providing antibodies, respectively. We also thank Hans Oettgen (Children’s Hospital, Harvard Medical School) and Sjef J. Verbeek (Leiden University Medical Center) for providing antibodies.

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Beglodah, W., A. Porcherie, C. Mathieu, R. Peronet, and U. Blank performed experiments and analyzed the data. H. Kiefer-Biasizzo, and J. Claver gave technical support. G. Milan, H. Karasayuma, M. Dy, J. P. Kinet, and J. Louis developed analytical tools and gave conceptual advice. U. Blank and S. Mécheri wrote the paper. S. Mécheri conceived the study. All authors discussed the results and analytical tools and gave conceptual advice. U. Blank and S. Mécheri wrote the experiments and analyzed the data. H. Kiefer-Biasizzo, and J. Claver gave technical assistance.

The authors declare no competing financial interests.

Online supplemental material is available at http://www.jem.org/cgi/content/full/jem.20110845/DC1.

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The authors declare no competing financial interests.

Submitted: 28 April 2011
Accepted: 29 August 2011

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