

Replication of *Plasmodium* in reticulocytes can occur without hemozoin formation, resulting in chloroquine resistance

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Most studies on malaria-parasite digestion of hemoglobin (Hb) have been performed using *P. falciparum* maintained in mature erythrocytes, in vitro. In this study, we examine *Plasmodium* Hb degradation in vivo in mice, using the parasite *P. berghei*, and show that it is possible to create mutant parasites lacking enzymes involved in the initial steps of Hb proteolysis. These mutants only complete development in reticulocytes and mature into both schizonts and gametocytes. Hb degradation is severely impaired and large amounts of undigested Hb remains in the reticulocyte cytoplasm and in vesicles in the parasite. The mutants produce little or no hemozoin (Hz), the detoxification by-product of Hb degradation. Further, they are resistant to chloroquine, an antimalarial drug that interferes with Hz formation, but their sensitivity to artesunate, also thought to be dependent on Hb degradation, is retained. Survival in reticulocytes with reduced or absent Hb digestion may imply a novel mechanism of drug resistance. These findings have implications for drug development against human-malaria parasites, such as *P. vivax* and *P. ovale*, which develop inside reticulocytes.

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Abbreviations used: AS, artesunate; BP, berghepain; CQ, chloroquine; DV, digestive vacuole; FP, falcipain; Hb, hemoglobin; Hz, hemozoin; iRBC, infected red blood cell; PM, plasmepsin; RBC, red blood cell; RLI, relative light intensity; SD, sulfadiazine; Sz, schizont; Tz, trophozoites.

Clinical symptoms of malaria are associated with *Plasmodium* infection of RBCs. Human *Plasmodium falciparum* parasites catabolize more than half of the hemoglobin (Hb) in the RBCs (Goldberg, 2005). The amino acids derived from Hb proteolysis are used for protein synthesis and energy metabolism. The proteolysis of Hb

is accompanied by the release of free heme, which is cytotoxic for the parasite and is rapidly detoxified and converted into hemozoin (Hz). Therefore, both Hb degradation and heme detoxification are considered to be essential for *P. falciparum* survival (Goldberg, 2005). The digestion of Hb is a conserved and semiordered process, which principally occurs within the acidified digestive vacuole (DV). After the initial cleavage

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by aspartic and papain-like cysteine endoproteases, Hb unfolds and becomes accessible to further proteolysis by downstream proteases. In the *P. falciparum* DV, there are four aspartic proteases (plasmepsins) and two papain-like cysteine proteases (falcipains) capable of hydrolyzing native Hb (Goldberg, 2005; Subramanian et al., 2009). Gene disruption studies of hemoglobins demonstrated that *P. falciparum* has developed redundant and overlapping Hb degradation pathways, demonstrating the importance of Hb digestion for the parasite (Liu et al., 2006; Bonilla et al., 2007). However, Hb is a poor source of methionine, cysteine, glutamine, and glutamate; in addition, human Hb contains no isoleucine and *P. falciparum* blood-stage parasite growth is most effective in culture medium supplemented with these amino acids, especially isoleucine (Liu et al., 2006). These data indicate that *P. falciparum* parasites are not only dependent on Hb digestion, but also import exogenous amino acids (Liu et al., 2006; Elliott et al., 2008).

Most studies on Hb degradation have been performed using *P. falciparum* maintained with mature RBCs (normocytes) in vitro. It is unknown whether observations on *P. falciparum* Hb digestion made in vitro can be directly translated to parasites replicating in vivo or for parasites developing in reticulocytes such as the human parasite *P. vivax* and *P. ovale*. For example, mechanisms of resistance to some drugs that interfere with Hb digestion and heme detoxification (e.g., chloroquine) differ between *P. vivax* and *P. falciparum* (Baird, 2004; Baird et al., 2012) indicating that there may be differences in their Hb digestion pathways.

To obtain a better insight into Hb digestion in parasites developing in vivo we used a rodent malaria parasite, *P. berghei*, which preferentially invades reticulocytes. We show a high level of functional redundancy among the predicted hemoglobins, as 6 of the 8 are dispensable in vivo. Unexpectedly, we were able to create parasite mutants lacking the enzymes known to initiate Hb digestion. These parasites were able to multiply in reticulocytes without Hz formation and were resistant to chloroquine.

RESULTS AND DISCUSSION

High degree of functional redundancy among *Plasmodium* hemoglobins

To determine the essential nature of individual enzymes involved in *P. berghei* Hb digestion, we performed a loss-of-function analysis on eight predicted *P. berghei* hemoglobins. The selection was based on the corresponding *P. falciparum* orthologous proteases with a characterized role in Hb digestion and/or located in the digestive vacuole (DV; Table S1 and Fig. 1 A). These include the aspartic protease, plasmepsin 4 (PM4), a single enzyme equivalent to the 4 *P. falciparum* plasmepsins (PM1–4); berghepains-2 (BP2), equivalent to the 2 *P. falciparum* DV falcipains FP-2 and FP-3; bergheylisin (BLN), the ortholog of *P. falciparum* falcilysin; dipetidyl peptidase 1 (DPAP1); and 4 aminopeptidases (aminopeptidase P [APP], M1-family alanyl aminopeptidase [AAP], M17-family leucyl aminopeptidase [LAP], and M18-family aspartyl aminopeptidase [DAP]). In addition, we included heme detoxification

protein (HDP) and 3 enzymes related to DV proteases with undefined roles in Hb digestion (berghepains 1, the ortholog of *P. falciparum* falcipain 1 and 2 dipetidyl peptidases, DPAP2 and DPAP3). We successfully generated gene-deletion mutants for *pm4*, *bp1*, *bp2*, *dpap1*, *dpap2*, *dpap3*, *app*, *lap*, and *dap*; however, multiple attempts to disrupt *bln*, *aap*, and *hdp* were unsuccessful (Table S2). We previously reported that disruption of *pm4* in *P. berghei* results in the lack of all aspartic protease activity in the DV (Spaccapelo et al., 2010). Similarly, *P. falciparum* has been shown to survive without DV PM activity (Bonilla et al., 2007). We were able to generate mutants lacking BP2, whereas *P. falciparum* blood stages survive without FP2 but not FP3 (Sijwali et al., 2006). We also generated mutants that lack genes encoding DPAP1, APP, and LAP, whereas *P. falciparum* orthologs have been reported to be refractory to disruption (Table S1; Klemba et al., 2004; Dalal and Klemba, 2007). We were unable to select parasites lacking expression of AAP and BLN, and the *P. falciparum* orthologous genes *aap* and *bln* have also been reported to be resistant to disruption and shown to play additional roles outside DV (Dalal and Klemba, 2007; Ponpuak et al., 2007). We were also unable to select mutants lacking HDP expression, suggesting an essential role for *P. berghei* blood stages, as has been proposed for *P. falciparum* HDP (Jani et al., 2008). The successful deletion of 6 of the 8 genes encoding hemoglobinase indicates a high level of redundancy in vivo among these enzymes.

Mutants lacking PM4, DPAP1, BP1, LAP or APP exhibited a significant reduction in asexual multiplication rates (growth rates) compared with WT parasites, whereas growth rates of the other 4 mutants were not significantly reduced (Table 1). In addition, $\Delta pm4$ and Δapp mutants showed a significant reduction in Hz production quantified in mature schizonts (Sz; 8–24 nuclei) using reflection contrast polarized light microscopy (Fig. 1, A and B). Trophozoites (Tz) of Δapp and $\Delta pm4$ have an aberrant morphology as visible on Giemsa-stained smears, exhibiting an accumulation of translucent vesicles inside their cytoplasm (Fig. 1 C). The reduced Hz production in $\Delta pm4$ and Δapp mutants indicate that *P. berghei* blood stages can develop into mature Sz despite significantly reduced Hb digestion. The lower growth rate of mutants lacking downstream hemoglobins DPAP1 and LAP (but with WT Hz levels) indicates that these enzymes are either important in effectively releasing amino acids from Hb peptides or that they have additional functions. Parasites lacking APP unexpectedly also had reduced levels of Hz. However, both APP and LAP are shown to have additional roles, e.g., in cytosolic peptide turnover (Dalal and Klemba, 2007). Although it remains to be investigated, APP may have an indirect effect on the initial steps of Hb digestion, either resulting from its involvement in establishment of the DV or due to feedback mechanisms that inhibit Hb digestion in the absence of APP.

Parasites lacking both PM4 and BP2 are restricted to reticulocytes and produce smaller Sz with less merozoites

Because in *P. berghei* PM4 is the only DV aspartic protease and BP2 is the single syntenic ortholog of the two *P. falciparum*

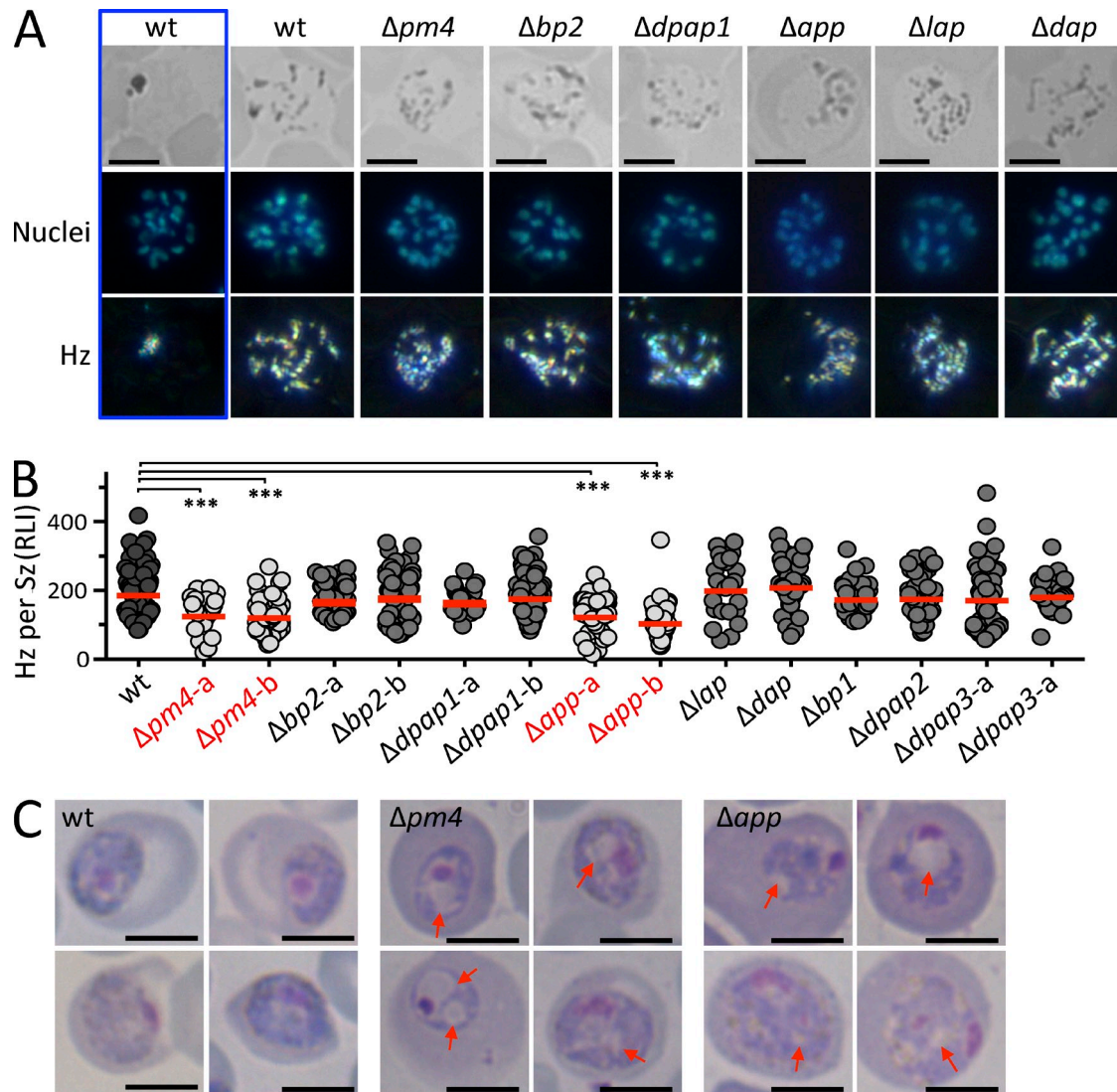


Figure 1. $\Delta pm4$ and Δapp parasites show reduced Hz levels and an aberrant morphology. (A) Reflection contrast polarized light microscopy was used to quantify Hz production inside an iRBC; representative images of Hz in mature Szs are shown. Hz crystals are scattered in Szs and were used for Hz quantification; a single Hz cluster is only observed in fully segmented Szs (blue box); BF, bright field; bars, 5 μ m. (B) Relative light intensity (RLI) of polarized light was measured for individual Szs ($n > 30$; Student's t test; ***, $P < 0.0001$). (C) Aberrant morphology of $\Delta pm4$ and Δapp Tzs exhibiting reduced Hz production and an accumulation of translucent vesicles (indicated by arrows) in their cytoplasm. Bars, 5 μ m. The phenotype was confirmed with two independent mutants.

DV cysteine endoproteases (FP-2 and FP-3), the absence of these enzymes is expected to result in the failure to proteolyse native Hb. Unexpectedly, we were able to generate two independent mutants lacking expression of both PM4 and BP2 ($\Delta pm4\Delta bp2$; Table S2). Blood stages of $\Delta pm4\Delta bp2$ have a severely reduced multiplication rate (2.2–4.6 compared with WT rates of 10; Table 1). After an initial slow rise of parasite numbers in $\Delta pm4\Delta bp2$ -infected mice, parasitemia can reach levels of up to 50% when mice became anemic and the RBCs were principally reticulocytes (unpublished data). At high parasitemias, mature Sz were present in the blood, most of which contained 8–12 merozoites (Fig. 2 A). Even though ring forms of $\Delta pm4\Delta bp2$ were observed in both mature RBCs

and reticulocytes, mature Tz and Sz were exclusively found in reticulocytes (unpublished data), indicating that $\Delta pm4\Delta bp2$ parasites, while retaining their ability to invade all RBCs, are unable to develop in normocytes. This may be related to greater abundance/diversity of amino acids and proteins present in reticulocytes (Allen, 1960), or due to other physical characteristics of reticulocytes, for example, their larger size and reduced Hb content may provide more space for growth in the absence of Hb digestion.

Analysis of Giemsa-stained images revealed $\Delta pm4\Delta bp2$ -Sz to be small, occupying only 25–65% of the RBCs, compared with 60–90% of WT Sz ($n > 30$; Fig. 2 A). This size reduction was confirmed by ImageStream flow cytometry on

Table 1. Growth and virulence characteristics of blood stages of gene deletion mutants

Gene deletion mutant	Day to 0.5–2% parasitemia ^a	Multiplication rate ^b	H ₂ production ^c
WT ^d	8 (0.2); <i>n</i> = 40	10.0 (0.7)	198.8 (69.8)
$\Delta pm4$ -a ^e	9–11; <i>n</i> > 10	5.8 (0.5)–7.0 (1.0) ^f	129.5 (41.7) ^f
$\Delta pm4$ -b	9 (0); <i>n</i> = 2	7.7 (0) ^f	134.5 (47.6) ^f
$\Delta bp2$ -a	8 (0); <i>n</i> = 5	10.0 (0)	177.5 (45.1)
$\Delta bp2$ -b	8 (0); <i>n</i> = 6	10.0 (0)	188.4 (71.5)
$\Delta dpap1$ -a	9.5 (0.7); <i>n</i> = 2	7.0 (1.0) ^f	174.6 (34.0)
$\Delta dpap1$ -b	9 (0); <i>n</i> = 4	7.7 (0) ^f	189.2 (62.7)
Δapp -a	12 (0); <i>n</i> = 1	4.6 (0) ^f	131.8 (50.5) ^f
Δapp -b	12 (0); <i>n</i> = 4	4.6 (0) ^f	111.4 (49.7) ^f
Δdap	8 (0); <i>n</i> = 3	10.0 (0)	223.8 (65.7)
Δlap	15.5 (0.7); <i>n</i> = 2	3.3 (0.2) ^f	213.6 (78.7)
$\Delta bp1$ -a	9.7 (0.6); <i>n</i> = 3	6.8 (0.8) ^f	186.2 (49.2)
$\Delta bp1$ -b	9 (0); <i>n</i> = 1	7.7 (0) ^f	n.d.
$\Delta dpap2$	8.3 (0.4); <i>n</i> = 4	9.4 (1.0)	187.8 (64.6)
$\Delta dpap3$ -a	8.3 (0.6); <i>n</i> = 3	9.2 (1.3)	184.5 (86.3)
$\Delta dpap3$ -b	8 (0); <i>n</i> = 5	10.0 (0)	193.3 (46.8)
$\Delta pm4\Delta bp2$ -a	12, 16, 20; <i>n</i> = 3	3.4 (1.1) ^f	27.2 (36.5) ^f
$\Delta pm4\Delta bp2$ -b	21, 24; <i>n</i> = 2	2.3 (0.1) ^f	46.1 (51.2) ^f

n.d., not determined.

^aThe day on which the parasitemia reaches 2–5% in mice infected with a single parasite in cloning assays. The mean of one cloning experiment and standard deviation are shown (*n* = the number of mice). For the $\Delta pm4\Delta bp2$ mutants, the days for individual clones are shown.

^bThe multiplication rate (mean and SD) of asexual blood stages per 24 h, calculated based on the "day to 0.5–2% parasitemia" in the cloning assay.

^cRelative light intensity (mean and SD) of H₂ crystals in individual Szs, determined by polarized light microscopy. See Fig. 1.

^dWT, wild type *P. berghei* ANKA reference lines (cl15cy1, 676m1cl1, and 1037cl1). Data from >10 independent experiments.

^e*pm4* gene-deletion mutants generated by Spaccapelo et al. (2010).

^fP < 0.0001; Student's *t* test.

live WT and $\Delta pm4\Delta bp2$ Szs expressing GFP under the control of the Sz-specific *ama-1* promoter (Fig. 2 B). Analysis of Giemsa-stained parasites indicated that $\Delta pm4\Delta bp2$ Szs had fewer merozoites (Fig. 2 A). Measuring GFP and Hoechst fluorescence intensity by ImageStream and standard flow cytometry confirmed that mature $\Delta pm4\Delta bp2$ -Sz have 40% reduction in both total DNA and (*ama1*-based) GFP expression levels compared with WT Sz, indicating a significant reduction in the total number of merozoites per Sz (Fig. 2, C and D). Combined, these observations demonstrate that $\Delta pm4\Delta bp$ parasites produce smaller Sz with less daughter merozoites than WT Sz.

Parasites lacking both PM4 and BP2 can form Szs in the absence of detectable H₂

Most $\Delta pm4\Delta bp2$ Tzs have an amoeboid-like appearance with translucent vesicles inside their cytoplasm, and their Tzs and Szs have little or no visible H₂ (Fig. 2 A). Ultrastructural analyses confirmed this, showing that $\Delta pm4\Delta bp2$ Tzs contained a higher number of cytostomes or endocytic vesicles filled with material that had a structural appearance similar to RBC cytoplasm (Fig. 3 A). This indicates that the absence of PM4 and BP2 does not affect the uptake of Hb from the RBC cytoplasm. Electron microscopic images revealed that 37% of the Tzs contained dark-stained (electron-dense) vesicles that are completely absent from WT parasites (Fig. 3 A).

These vesicles are very similar to those that have been described in *P. falciparum* Tz when Hb trafficking or digestion is blocked by inhibitors, and it has been proposed that these vesicles are cytostome derived and contain concentrated undigested and/or denatured Hb (Fitch et al., 2003; Vaid et al., 2010). In addition, although WT Tz contained large numbers of H₂ crystals, >40% of $\Delta pm4\Delta bp2$ Tz had no visible H₂ crystals (Fig. 3 A), reflecting our observations with Giemsa-stained images of Tz and Sz (Fig. 2 A). Next, we used reflection contrast polarized light-microscopy to determine the amount of H₂ in maturing $\Delta pm4\Delta bp2$ -Sz and WT-Sz. The relative light intensity (RLI) values of $\Delta pm4\Delta bp2$ -Sz at all stages of maturation were strongly reduced (78–87% reduction compared with WT Sz; Fig. 3 B and Table 1), and whereas all WT Sz had H₂, a large percentage (35–48%) of $\Delta pm4\Delta bp2$ -Sz had no detectable H₂ (Fig. 3 B), having RLI values the same as uninfected RBCs. The severe reduction in H₂ production was also reflected in vastly reduced H₂ deposition in organs of $\Delta pm4\Delta bp2$ -infected mice compared with WT- and even $\Delta pm4$ -infected mice (Fig. 3 C).

We further quantified the amount of H₂ and undigested Hb in equal numbers of FACS-purified Sz using heme-dependent luminol-enhanced luminescence analysis (Schwarzer et al., 1994). The Hb that remained undigested in $\Delta pm4\Delta bp2$ -Sz iRBCs was twice the amount of that in WT-Sz iRBCs (Fig. 3 D); however, the total heme content in $\Delta pm4\Delta bp2$ -Sz

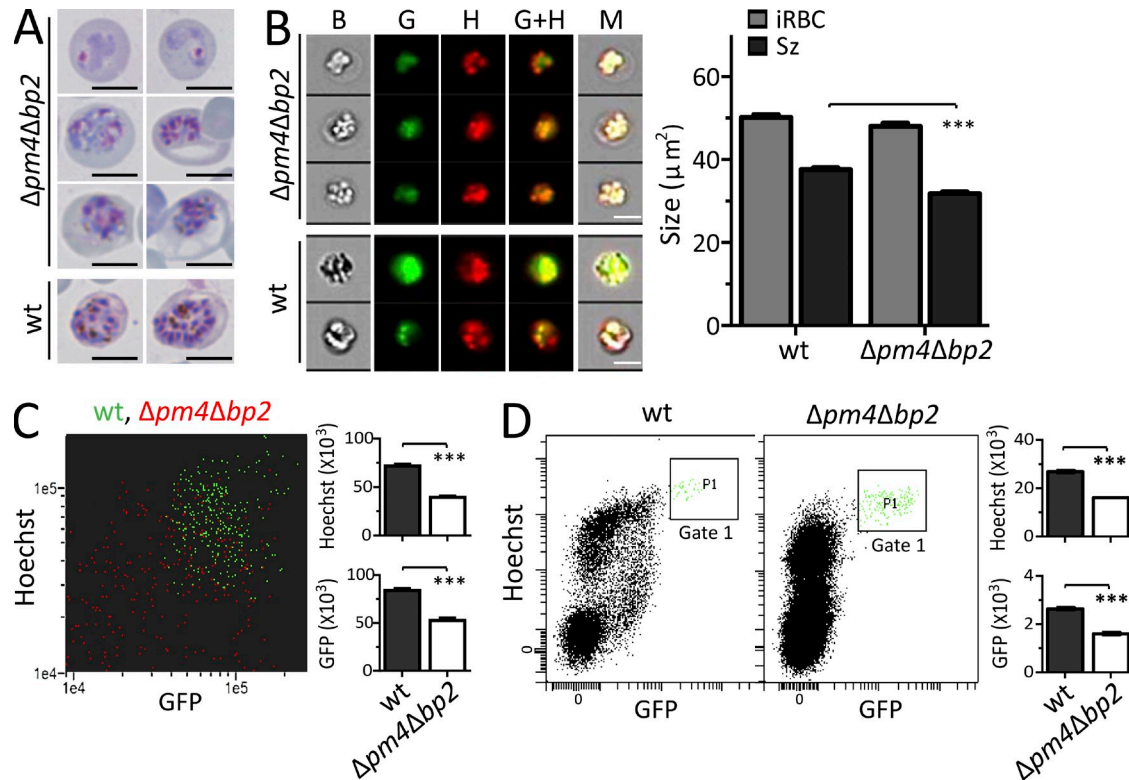


Figure 2. Szs of mutants lacking PM4 and BP2 expression are smaller in size and produce fewer merozoites. (A) Representative Giemsa-stained images showing the difference in size and merozoites production of $\Delta pm4\Delta bp2$ iRBCs relative to WT. Bars, 5 μm . (B) Images of Hoechst stained mature WT and $\Delta pm4\Delta bp2$ Szs expressing GFP under *Sz*-specific *ama1* promoter in their cytoplasm (right) and their size measurement by ImageStream flow cytometry (left). Bars, 5 μm . The size of individual iRBC was determined from bright field images (B) and the size of *Sz* was measured from the combined GFP (G) and Hoechst (H) images (i.e., G+H). M, merged images ($n > 250$; ***, $P < 0.0001$; Student's *t* test). (C) The dot plot (left) generated from ImageStream flow cytometry shows the GFP- and Hoechst-fluorescence of individual WT- (green) and $\Delta pm4\Delta bp2$ - (red) *Sz*, and the GFP expression and DNA content were quantified (right). (D) The GFP and DNA content of mature Szs were measured by standard flow cytometry; mature Szs were selected in Gate 1 (left) and the quantification shown as bar graphs (right). All data are representative of two independent experiments (bar graphs show mean fluorescence intensity with SEM; ***, $P < 0.0001$; Student's *t* test).

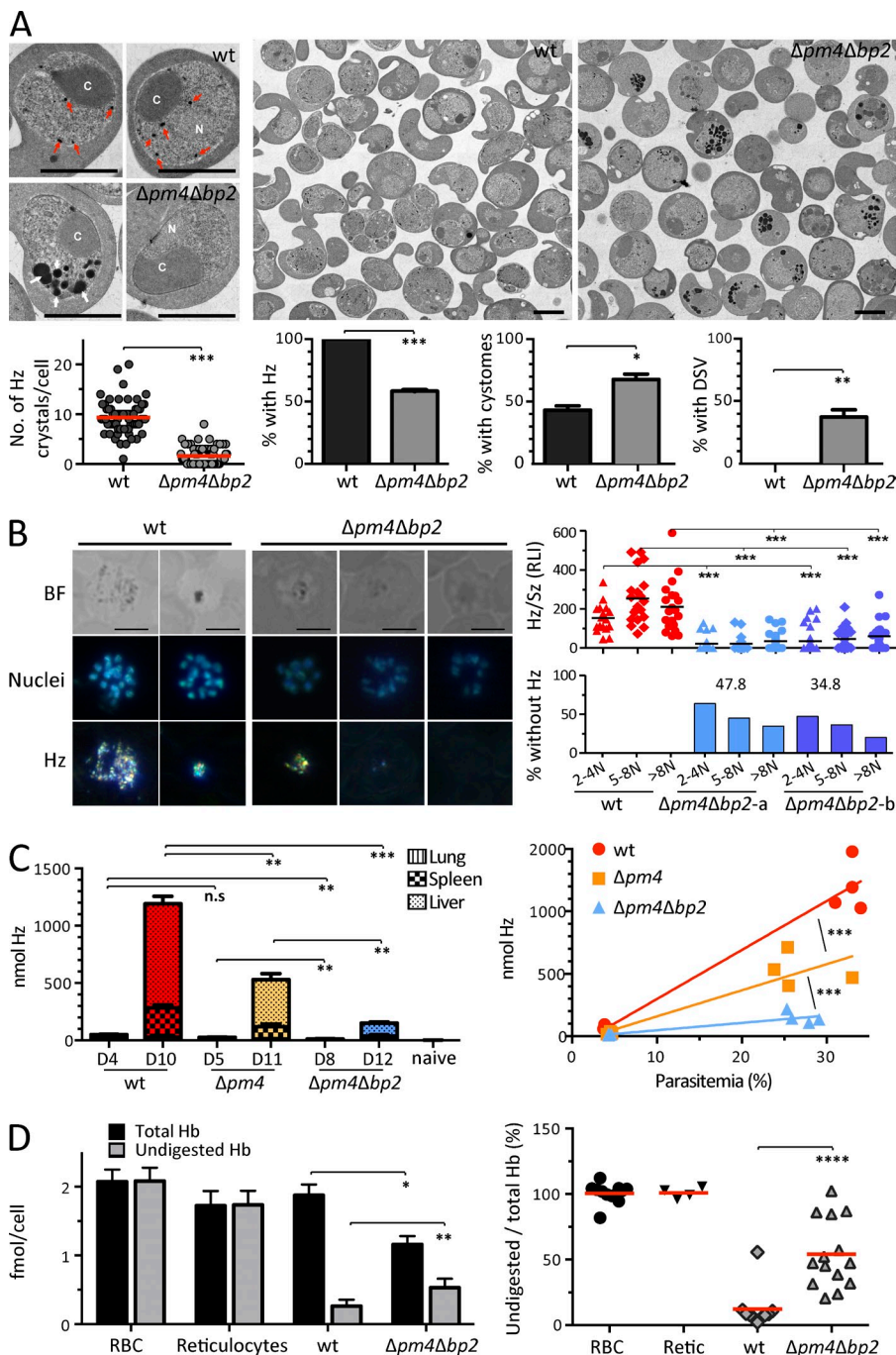
iRBCs was 40% lower than WT-*Sz* iRBCs. On average, 54% (between 20–100%) of Hb remains undigested in $\Delta pm4\Delta bp2$ -*Sz* iRBCs, compared with 12% of WT-*Sz* iRBCs (Fig. 3 D). Combined, the increased number of cytosome inclusions, presence of unusual electron-dense vesicles and severely reduced and often absent Hz crystals indicate that Hb digestion is severely impaired in $\Delta pm4\Delta bp2$ and this is further supported by the high levels of undigested Hb present in RBCs infected with $\Delta pm4\Delta bp2$ *Sz* compared with WT-*Sz*. However, some Hz is still present in a proportion of $\Delta pm4\Delta bp2$ parasites indicating that some heme is released from Hb in the absence of PM4 and BP2. Whether this is the result of a compensatory enzymatic process or a nonspecific disassembly of the Hb tetramer that may occur when Hb accumulates in cytosomes or in the acidified dark-staining vesicles (Fitch et al., 2003) is unknown and requires further investigation.

In *P. falciparum* the PMs and FPs overlap in function and there is extensive functional redundancy within and between these two protease classes (Bonilla et al., 2007; Liu et al., 2006). Our observations on Hz production in the single gene-deletion mutants $\Delta pm4$ and $\Delta bp2$ indicate that also in

P. berghei aspartyl and cysteine endopeptidases overlap in their ability to hydrolyze Hb. Interestingly, the $\Delta bp2$ mutant has a normal growth rate and produces WT levels of Hz, whereas $\Delta pm4$ parasites have a reduced growth and Hz production. These observations demonstrate that although PM4 is able to fully compensate for the function of BP2, BP2 can only partly compensate for the loss of PM4.

Gametocytes of parasite lacking both PM4 and BP2 are fertile despite their smaller size and reduced Hz levels

In mice infected with $\Delta pm4\Delta bp2$ parasites, male and female gametocytes were readily detected. Similar to *Sz*, they were 23% smaller than WT gametocytes, and their cytoplasm had strongly reduced or no Hz crystals (Fig. 4 A). Most $\Delta pm4\Delta bp2$ male gametocytes produced motile gametes ($79.3 \pm 4.6\%$), which are able to fertilize female gametes and produce ookinets; these undergo meiosis and become tetraploid (Fig. 4, B and C). The conversion rates of $\Delta pm4\Delta bp2$ female gametes into ookinets were comparable to those of WT parasites ($60.0 \pm 6.1\%$; Fig. 4 C). Analysis of Hz levels in WT and $\Delta pm4\Delta bp2$ ookinets revealed that they also had reduced



Hz-levels (57%; Fig. 4 C). These observations demonstrate that both asexual and sexual blood-stages can complete development despite the severely impaired Hb digestion.

Parasites lacking both PM4 and BP2 are resistant to chloroquine but retain their sensitivity to artesunate

We tested the sensitivity of the $\Delta pm4\Delta bp2$ parasites to artesunate (AS) and chloroquine (CQ); their mode of action is believed to depend on Hb digestion/Hz formation (Egan et al., 2004; Klonis et al., 2011). As a control we used sulfadiazine (SD), an inhibitor of folic acid synthesis (Kinnamon et al.,

1976). AS and SD treatment of WT- and $\Delta pm4\Delta bp2$ -infected BALB/c mice resulted in rapid clearance of parasites from bloodstream in 3–4 and 4–5 d after start of AS (50 mg/kg body weight, i.p.) and SD (35 mg/liter in drinking water) treatment, respectively (Fig. 5 A). Similarly, BALB/c mice infected with WT parasites rapidly cleared their infection after CQ (288 mg/liter in drinking water) treatment (3–4 d). In contrast, mice infected with $\Delta pm4\Delta bp2$ parasites, first exhibited an increase in parasitemia for 3 d, followed by a slow decline (Fig. 5 A). Parasites with normal morphology were present 6 d after start of CQ treatment (Fig. 5 B). Untreated

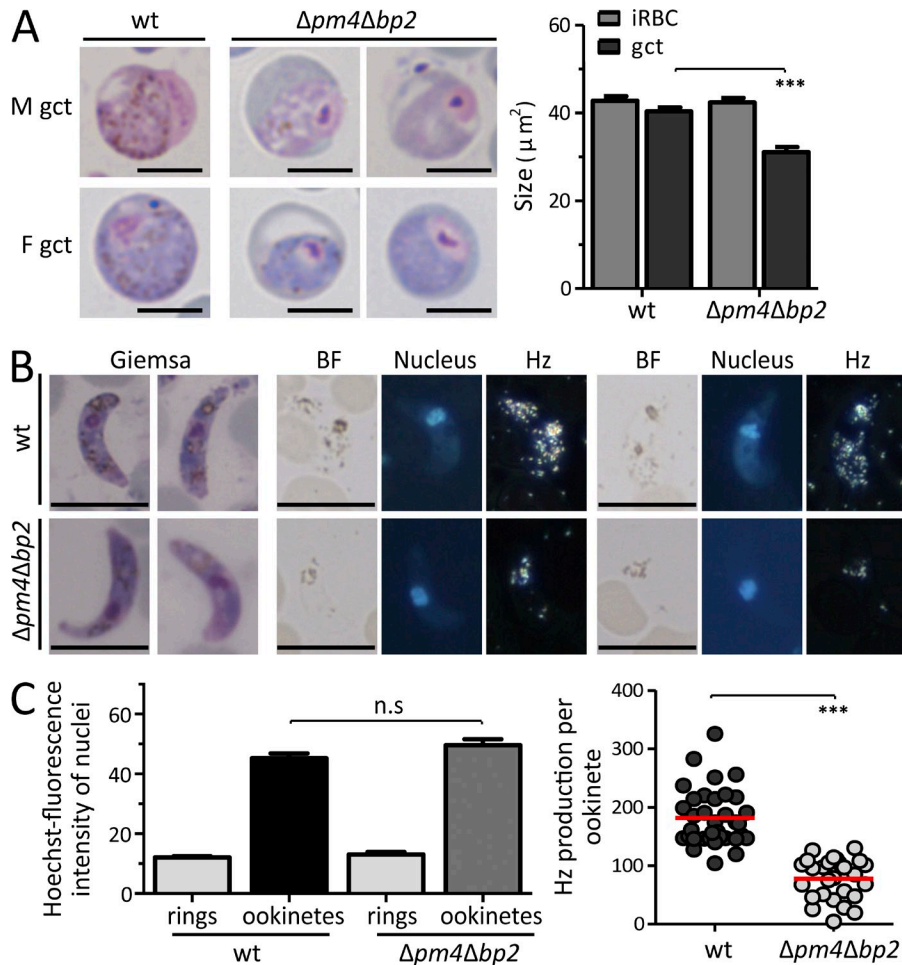


Figure 4. Gametocytes of $\Delta pm4\Delta bp2$ are fertile despite their smaller size and reduced Hz production. (A) Representative Giemsa-stained images of WT and $\Delta pm4\Delta bp2$ gametocytes (left; bars, 5 μm) and the size quantification on these images (right; $n > 30$; ***, $P < 0.0001$; Student's t test). (B) Giemsa-stained images and polarized light microscopy images of ookinetes. BF, bright-field; Nuclei (blue) stained with Hoechst. Bars, 5 μm . (C) Hoechst fluorescence intensity (DNA content) of WT and $\Delta pm4\Delta bp2$ ookinetes, relative to haploid ring-form stages, was quantified (left; $n > 25$; n.s., not significant; Student's t test) indicating that both WT and $\Delta pm4\Delta bp2$ ookinetes are tetraploid. Relative light intensity (RLI) of polarized light (Hz production) measurements of WT and $\Delta pm4\Delta bp2$ ookinetes (right; $n > 25$; ***, $P < 0.0001$; Student's t test).

BALB/c mice also resolved a $\Delta pm4\Delta bp2$ infection 3–4 wk after infection, indicating that host immunity may contribute to the decline of parasitemia in CQ-treated mice. We therefore performed infections and CQ treatment in $Rag2^{-/-}\gamma c^{-/-}$ mice (deficient in B, T, and NK cells). Whereas CQ-treated, WT-infected mice cleared a 2–5% WT infection within 3 d, in $\Delta pm4\Delta bp2$ -infected mice parasites persisted for >20 d of CQ-treatment (Fig. 5 C), during which only Hz-negative $\Delta pm4\Delta bp2$ parasites were observed in circulation (Fig. 5 D). To examine whether $\Delta pm4\Delta bp2$ parasite resistance to CQ is lost at higher concentrations of CQ and conversely if resistance to AS is observed at lower concentrations of AS, we performed drug sensitivity assays using 5 and 10 mg/kg AS (in BALB/c mice) or with 600 mg/liter CQ (in $Rag2^{-/-}\gamma c^{-/-}$ mice). These experiments revealed that, at lower AS doses, drug sensitivity does not significantly differ between $\Delta pm4\Delta bp2$ and WT parasites, and that $\Delta pm4\Delta bp2$ parasites are resistant to CQ even at high doses (Fig. 5 E).

Our observations on the ability of *Plasmodium* parasites to develop without detectable Hz formation that are resistant to CQ indicate a novel mechanism of resistance against drugs that target Hb proteolysis. Interestingly, previous studies on CQ-resistant *P. berghei* lines revealed that parasites are more

restricted to development in reticulocytes and produced less Hz (Platel et al., 1999). It has been proposed that CQ-resistance of parasites with reduced Hz is due to detoxification of heme by elevated levels of glutathione in parasites inside reticulocytes, thus precluding heme-polymerization and preventing CQ activity (Platel et al., 1999; Fidock and DeSilva, 2012). However, our observations may provide a more direct explanation for CQ-resistance and reduced Hz production in these parasites, namely that these parasites, like the $\Delta pm4\Delta bp2$, digest less Hb in reticulocytes.

Our observations may have particular relevance for the human malaria parasite, *Plasmodium vivax*, which is also reticulocyte-restricted. *P. vivax* CQ resistance appears to be different from *P. falciparum* (Suwanarusk et al., 2007; Baird et al., 2012), and no clear association has been found with mutations in the same genes that typify *P. falciparum* CQ resistance (*pfprt* or *pfmdr1*). In addition, DV formation in *P. vivax* appears to resemble more DV formation in *P. berghei* than in *P. falciparum*. Tzs of *P. falciparum* have a large central DV, as Hb-containing cytosomes merge rapidly and Hz formation occurs principally in this single DV. In contrast, *P. berghei* has many small Hb-containing vesicles, in which Hb digestion/Hz formation occurs, resulting in scattered Hz granules throughout

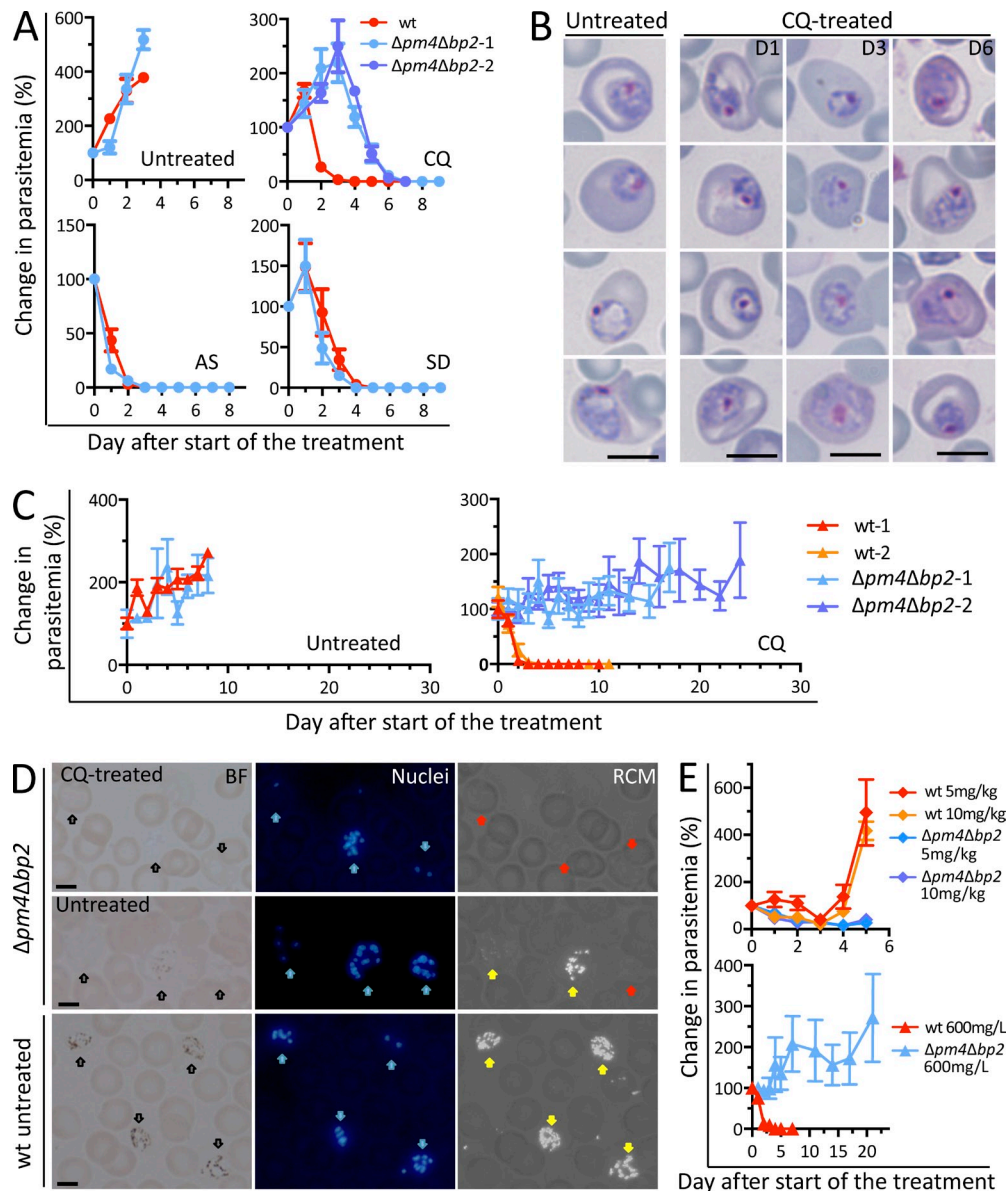


Figure 5. $\Delta pm4\Delta bp2$ parasites are resistant to chloroquine but sensitive to artesunate. (A) Changes in parasitemia of BALB/c mice ($n = 5$) infected with WT or $\Delta pm4\Delta bp2$ parasites after treatment with chloroquine (CQ; 288 mg/liter in drinking water; 2 experiments), artesunate (AS; 50 mg/kg body weight i.p.), or sulfadiazine (SD; 35 mg/liter in drinking water). Data presented as mean with SEM. (B) Representative Giemsa-stained images of $\Delta pm4\Delta bp2$ -Tz in blood of BALB/c mice treated with CQ treatment at different days (D1, 3, 6) after start of CQ treatment. Bars, 5 μm . (C) Changes in parasitemia of Rag2^{-/-} $\gamma c^{-/-}$ ($n = 6$) mice infected with WT or $\Delta pm4\Delta bp2$ parasites either without treatment (left) or after prolonged CQ treatment (right; 288 mg/l in drinking water; 2 experiments). (D) Reflection contrast polarized light microscopy images (RCM) showing the absence of Hz crystals in $\Delta pm4\Delta bp2$ parasites that survived CQ treatment for >20 d in Rag2^{-/-} $\gamma c^{-/-}$ mice; iRBC with no Hz formation are indicated by red arrows. In untreated mice, two populations of $\Delta pm4\Delta bp2$ parasites are present, parasites with no Hz (red arrow), and parasites with Hz crystals (yellow arrows). WT parasites in untreated mice show large amounts of Hz (yellow arrows). Black arrows indicate iRBC in bright field (BF) images. Nuclei of parasites (blue) were stained with Hoechst (blue arrows). Bars, 5 μm . (E) Changes in parasitemia of BALB/c mice (top, $n = 5$) or Rag2^{-/-} $\gamma c^{-/-}$ mice (bottom, $n = 5$) infected with $\Delta pm4\Delta bp2$ and WT parasites exposed to either 5 or 10 mg/kg of AS in or to 600 mg/l CQ in drinking water. Data presented as mean values of changes (%) in parasitemia with SEM.

the cytoplasm of the parasite, these clusters coalesce when schizogony starts (Slomianny et al., 1985). It has been suggested that the uptake of Hb from reticulocytes by the process of micropinocytosis results in multiple small vesicles containing Hb and Hz in both *P. berghei* and *P. vivax* (Jeffers, 2010).

Moreover *P. vivax*, like *P. berghei*, has only 1 DV plasmepsin (PM4) in contrast to *P. falciparum* which encodes 4 DV plasmepsins (Table S1). While *P. vivax* has 3 DV vivapains, 2 of them, VX2 and 3, are syntenic orthologs of FP-2 and 3 the other, VX4, is nonsyntenic with the FPs but shows greater

sequence similarity to BP2 (Na et al., 2010; Table S1). These observations indicate that mechanisms of Hb uptake and digestion in *P. vivax* more closely resembles *P. berghei* than *P. falciparum* and future research is required to see if this also translates into similar mechanisms to resistance to drugs that exclusively target Hb digestion pathways.

Although $\Delta pm4\Delta hp2$ parasites are resistance to CQ, they retain sensitivity to AS. Although the precise mode of action of artemisinin and related derivatives remains contentious, it is believed that their activity results from activation by reduced heme iron in the DV (Eastman and Fidock, 2009). Our results suggest AS activity is not affected by reduced Hb digestion or absence of Hz formation. Alternatively AS activation in $\Delta pm4\Delta hp2$ parasites in reticulocytes may derive from a labile pool of heme that exists in reticulocytes for Hb synthesis. *P. vivax* resistance to artemisinins has not been reported; however, most of the artemisinin-based combination therapies have proven efficacy against chloroquine-resistant strains of *P. vivax* (Price et al., 2014).

We show that, very much counter to expectation, Hb digestion and Hz formation appears not to be essential to parasite survival when parasites develop in reticulocytes. Indeed, our findings support the notion that *Plasmodium* parasites retain multiple modes of development and survival during blood stage development, which has important implications for antimalarial drug design, in particular drugs that target Hb digestion and Hz formation.

MATERIALS AND METHODS

Experimental animals and parasites. Female C57BL/6, BALB/c, Swiss OF1 mice (6–8 wk old; Charles River) and female Rag2^{-/-} $\gamma c^{-/-}$ mice (6–8 wk old, bred in MRC NIMR) were used. All animal experiments performed at the Leiden University Medical Center (LUMC) were approved by the Animal Experiments Committee of the LUMC (DEC 10099; 12042; 12120). All animal experiments performed at the University of Perugia were approved by Ministry of Health under the guidelines D.L. 116/92). All animal experiments performed in MRC NIMR were performed after review and approval by the MRC National Institute for Medical Research Ethical Review Panel in strict accordance to current UK Home Office regulations, and conducted under the authority of UK Home Office Project License PPL 80/2358. The Dutch, Italian, and British Experiments on Animal Act were established under European guidelines (EU directive no. 86/609/EEC regarding the Protection of Animals used for Experimental and Other Scientific Purposes).

Two reference *P. berghei* ANKA parasite lines were used: line cl15cy1 (WT) and reporter line 1037cl1 (WT-GFP-Luc_{schiz}; mutant RMgm-32). This reporter line contains the fusion gene *gfp-luc* gene under control of the Sz-specific *ama1* promoter integrated into the silent 230p gene locus (PBANKA_030600) and does not contain a drug-selectable marker (Spaccapelo et al., 2010).

Generation of *P. berghei* mutants. DNA constructs used to disrupt genes were based on the standard plasmids (pL0001 [MRA-770], pLTgDFHR, and pL0035; [MRA-850]) and by modified PCR methods based on pL0040 and pL0048 (Lin et al., 2011). Targeting sequences for homologous recombination were PCR amplified from *P. berghei* ANKA (cl15cy1) genomic DNA using primers specific for the 5' or 3' end of each gene using primer sets of P1/P2, P3/P4, respectively (see Table S3 for the primer sequences).

The DNA construct targeting *bp1* was provided by P. Sinnis (Johns Hopkins University, Baltimore, MD). Transfection, selection, cloning, and genotyping of transformed parasites was performed using standard genetic modification technologies for *P. berghei* (Janse et al., 2006). To generate

$\Delta pm4\Delta hp2$ mutant, *hdhfr::yfcu* selectable marker was removed by negative selection (Braks et al., 2006) from $\Delta hp2$ -b (based on pL0035) and *pm4* gene was subsequently targeted in $\Delta hp2$ -bsm line. Table S2 provides details of all gene deletion experiments, such as experiment number, targeting construct, parental line for transfection, and RMgmDB IDs (Rodent Malaria Genetically Modified Parasites Database). Details for targeting construct generation (maps and sequences) and genotyping results can be found in RMgmDB and Table S4 includes primers used for genotyping including diagnostic PCR, Southern analyses of chromosomes separated by pulsed-field gel electrophoresis, Northern PCR, and RT-PCR.

In vivo asexual multiplication (growth) rates. The multiplication (growth) rate of asexual blood-stages in mice was determined during cloning of the gene-deletion mutants as described before (Spaccapelo et al., 2010) and was calculated as follows: the percentage of infected erythrocytes (parasitemia) in Swiss OF1 mice injected with a single parasite was determined by counting Giemsa-stained blood films when parasitemias reach 0.5–2%. The mean asexual multiplication rate per 24 h was then calculated assuming a total of 1.2×10^{10} erythrocytes per mouse (2 ml of blood). The percentage of infected erythrocytes in mice infected with reference lines of the *P. berghei* ANKA strain consistently ranged between 0.5–2% at day 8 after infection, resulting in a mean multiplication rate of 10 per 24 h.

Gametocyte and ookinete production. Gametocyte production is defined as the percentage of ring forms developing into mature gametocytes during synchronized infections (Janse and Waters, 1995). Male gamete production (exflagellation) and ookinete production was determined in standard in vitro fertilization and ookinete maturation assays (Janse and Waters, 1995); ookinete production is defined as the percentage of female gametes that develop into mature ookinetes under standardized in vitro culture conditions. Female gamete and mature ookinete numbers were determined on Giemsa-stained blood smears made 16–18 h after activation. Hz level of ookinetes were quantified.

Sz and gametocyte size measurements. For the Giemsa-stained smears, pictures were taken using a Leica microscope from randomly chosen fields of 300–400 RBCs, and all iRBCs were measured in these fields. The sizes of iRBCs and the parasites were measured by ImageJ by gating on the areas of parasites and iRBC. For ImageStream flow cytometry analysis, iRBCs containing Szs of WT-GFP-Luc_{schiz} and $\Delta pm4\Delta hp2$ parasites were collected from infected BALB/c mice with a high parasitemia (10–30%) and enriched by Nycodenz density centrifugation (Janse et al., 2006). Purified parasites were then collected in complete RPMI-1640 culture medium and stained with Hoechst-33258 (2 μ mol/liter; Sigma-Aldrich) for 1 h at room temperature. Cultured, mature Szs of WT *P. berghei* ANKA (cl15cy1) were used as unstained control; Hoechst stained cl15cy1 (Hoechst only) and nonstained WT-GFP-Luc_{schiz} (GFP only) were used as single-color controls. The analyses were performed using an Amnis ImageStream X imaging cytometer (Amnis Corp.) and images were analyzed using the IDEAS image analysis software.

Hz and Hb quantification. Hz was quantified in Szs using different methods. Hz was quantified by measuring the relative light intensity (RLI) of Hz crystals in Szs and ookinetes by reflection contrast polarized light microscopy. Szs were either collected from overnight in vitro blood stage cultures or directly from tail blood when Szs were present in the peripheral circulation. Blood smears were made from cultured parasites or from tail blood and stained with Hoechst-33342 (2 μ mol/liter; Sigma-Aldrich) for 20 min. Szs (8–24 nuclei) with scattered Hz were selected and pictures were taken with a LeicaDM/RB microscope (Leica) which was adapted for reflection contrast polarized light microscopy (Cornelese-ten Velde et al., 1988). The RLI of Hz crystals in the Szs was measured using ImageJ software (NIH).

In addition, Hb and Hz from WT and $\Delta pm4\Delta hp2$ Sz-iRBC were quantified by measuring the heme-dependent luminol-enhanced luminescence (Schwarzer et al., 1994). For these experiments, 10^4 purified Szs were collected by flow sorting from infected blood of BALB/c mice with a high parasitemia

(10–30%) and stained with Hoechst-33258 (2 $\mu\text{mol/liter}$; Sigma-Aldrich) at 37°C in the dark for 1 h. Subsequently, Szs were selected and sorted with a FACSAria II cell sorter (BD; speed 10,000 events/s). Mature Szs were selected by gating on the GFP⁺ population of cells with a DNA content of Szs (Hoechst fluorescence intensity 8–24 N; Fig. 2 D, gate 1). Purified Szs were washed with PBS and concentrated in 10 μl of PBS and kept at -80°C until further analysis. Szs were analyzed for their Hb and H₂ content. Hb-bound heme and alkali-solubilized H₂-heme were assayed by luminol-enhanced luminescence in the untreated or strong alkali-treated lysates prepared as detailed previously (Schwarzer et al., 1994).

To quantify H₂ deposition in organs of infected mice, groups of 8 BALB/c mice were i.p. infected with 10^5 WT, Δpm4 , or $\Delta\text{pm4}\Delta\text{bp2}$ parasites. At different parasitemias, mice were sacrificed and systemically perfused with 20 ml PBS to remove circulating iRBC from the organs. Livers, spleens, and lungs were removed, weighed and stored at -80°C until further analysis. The H₂ extraction from these organs and quantification was performed using an optimized method for H₂ quantification in tissues as described (Deroost et al., 2012).

Electron microscopy analysis. Infected blood was collected from WT or $\Delta\text{pm4}\Delta\text{bp2}$ parasite infected BALB/c mice by heart puncture and enriched by Nycodenz centrifugation (Janse et al., 2006). iRBC (10^7 – 10^8) were collected and fixed overnight in 2 ml of 1.5% glutaraldehyde in 0.1 M sodium cacodylate. After centrifugation, the pellet was rinsed twice with 0.1 M sodium cacodylate and postfixed with 1% osmium tetroxide in 0.1 M sodium cacodylate. After rinsing, samples were dehydrated in a graded ethanol series up to 100% and embedded in epon. 110-nm sections were cut with a microtome and transferred onto standard grids and post-stained with uranyl acetate and lead citrate. Transmission electron microscopy (TEM) data were collected on a FEI Tecnai microscope at 120 kV with a FEI Eagle CCD camera. Virtual slides (Faas et al., 2012) consisting of 759 and 729 unbinned 4kx4k images were collected for the WT and $\Delta\text{pm4}\Delta\text{bp2}$ sample, respectively. The magnification at the detector plane was 12930; the pixel size 1.2 nm square. The resulting slides cover an area of $109 \times 105 \mu\text{m}^2$ and $105 \times 105 \mu\text{m}^2$ for the respective samples. The virtual slides were analyzed by Aperio ImageScope software (Aperio). All statistical tests were performed using GraphPad Prism.

Drug sensitivity assays. Groups of 5–6 BALB/c or Rag2^{-/-} $\gamma\text{c}^{-/-}$ mice were i.p. infected with either 10^4 WT or 10^5 $\Delta\text{pm4}\Delta\text{bp2}$ -parasites. At a peripheral parasitemia of 2–5%, mice were treated with artesunate (AS; Pharmaco; 60 mg powder [a gift from Dafa Pharma International, Turnhout, Belgium], chloroquine [CQ; Sigma-Aldrich], or sulfadiazine [SD; Sigma-Aldrich]) and parasitemia was monitored daily by counting Giemsa-stained blood films of tail blood. AS treatment was performed by i.p. injection of 6.25, 1.25, or 0.625 mg/ml in 5% NaHCO₃ as a single dose for 4 consecutive days (50, 10, or 5 mg/kg body weight). SD was provided at a concentration of 35 mg/liter in drinking water for 7 d, and CQ was provided at a concentration of 288 or 600 mg/liter with 15 g/liter glucose in the drinking water for a period of 7 d in BALB/c or up to 25 d in Rag2^{-/-} $\gamma\text{c}^{-/-}$ mice. The parasitemia was monitored every 1–2 d by Giemsa-stained thin blood smears. All infected mice were sacrificed when the parasitemia reached 50%.

Graphs and statistical analyses. All graphs and statistical analyses were made in GraphPad Prism, all error bars indicate SEM and all p-values were derived from unpaired Student's *t* tests.

Supplemental material. Table S1 shows genes targeted in this study. Table S2 shows details of transfection experiments aiming at deletion of *P. berghei* genes encoding hemoglobins. Table S3 shows gene deletion constructs and primers. Table S4 shows primers for genotyping gene-deletion mutants. Online supplemental material is available at <http://www.jem.org/cgi/content/full/jem.20141731/DC1>.

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