A New Rodent Model to Assess Blood Stage Immunity to the *Plasmodium falciparum* Antigen Merozoite Surface Protein 1\textsubscript{19} Reveals a Protective Role for Invasion Inhibitory Antibodies

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**Abstract**

Antibodies capable of inhibiting the invasion of *Plasmodium* merozoites into erythrocytes are present in individuals that are clinically immune to the malaria parasite. Those targeting the 19-kD COOH-terminal domain of the major merozoite surface protein (MSP)-1\textsubscript{19} are a major component of this inhibitory activity. However, it has been difficult to assess the overall relevance of such antibodies to antiparasite immunity. Here we use an allelic replacement approach to generate a rodent malaria parasite (*Plasmodium berghei*) that expresses a human malaria (*Plasmodium falciparum*) form of MSP-1\textsubscript{19}. We show that mice made semi-immune to this parasite line generate high levels of merozoite inhibitory antibodies that are specific for *P. falciparum* MSP-1\textsubscript{19}. Importantly, protection from homologous blood stage challenge in these mice correlated with levels of *P. falciparum* MSP-1\textsubscript{19}–specific inhibitory antibodies, but not with titres of total MSP-1\textsubscript{19}–specific immunoglobulins. We conclude that merozoite inhibitory antibodies generated in response to infection can play a significant role in suppressing parasitemia in vivo. This study provides a strong impetus for the development of blood stage vaccines designed to generate invasion inhibitory antibodies and offers a new animal model to trial *P. falciparum* MSP-1\textsubscript{19} vaccines.

Key words: malaria • transfection • *P. berghei* • merozoite • invasion inhibition

**Introduction**

It is well established that antibodies targeting merozoite antigens can mediate a degree of immunity to *Plasmodium falciparum* malaria and this knowledge underpins the development of blood stage vaccines against this devastating pathogen (for review see references 1 and 2). Such antibodies are thought to operate by a number of different mechanisms including the prevention of merozoite release (3), the direct neutralization of merozoites (4, 5), and the induction of monocyte-mediated parasite killing (6). However, the relative contribution of these different mechanisms to controlling blood stage parasitaemia remains unclear. A better understanding of this is particularly important for the development of functional “correlate-of-protection” assays for use in clinical trials of malaria vaccine candidates.

A protective role for merozoite invasion inhibitory antibodies, which are those that act in a manner that is independent of complement or other cellular mediators, has been difficult to formally demonstrate and quantify. There are several reasons for this. First, there has been a lack of robust in vitro inhibition assays that account for confounding factors present in serum that can cause non-specific inhibitory, or indeed growth-promoting, effects. Although in vitro inhibition assays have been used for some time to assess antibodies to *P. falciparum* merozoite antigens and have provided a useful guide as to the inhibitory activity of a particular serum or monoclonal antibody, the problems associated with accurate quantification of this activity, especially in whole serum, are well recognized in the field (4, 5, 7, 8). With respect to one important antigen, the 19-kD COOH-terminal domain of *P. falciparum* merozoite surface protein (MSP)-1\textsubscript{19}, this problem has now been overcome with the development of an assay that allows accurate quantification of MSP-1\textsubscript{19}–specific inhibitory antibodies in independent of complement or other cellular mediators.
whole serum (9, 10). This assay involves a comparison of the inhibitory effect of a given serum on two isogenic parasite lines that differ only in MSP-1\textsubscript{19}. One expresses the \textit{P. falciparum} domain and the other expresses an antigenically distinct domain from a rodent malaria parasite \textit{Plasmodium chabaudi}. Using this assay in a previous study, we determined that the invasion inhibitory activity of antibodies present in serum obtained from adults that are clinically immune to malaria, as a result of frequent exposure to \textit{P. falciparum}, is dominated by those targeting MSP-1\textsubscript{19} (9). This finding was consistent with many studies that had implicated a protective role for MSP-1\textsubscript{19}–specific antibodies generated in response to infection or vaccination with recombinant proteins (for review see references 11 and 12). Despite the surprising knowledge that antibodies of this single specificity make such an important contribution to the process of invasion inhibition, it remained uncertain whether these antibodies actually contribute significantly to immunity.

The major remaining obstacle to addressing the protective role of inhibitory antibodies is the lack of a simple and robust in vivo challenge system that can be used in parallel with an in vitro inhibition test. In this paper, we have developed such an in vivo model by generating a rodent malaria parasite line that expresses \textit{P. berghei} MSP-1\textsubscript{19} in place of its own domain. Using this model, we show that the level of MSP-1\textsubscript{19}–specific invasion inhibitory antibodies generated in mice that had been reinfected with the chimeric parasite line correlates with the ability of these animals to control a subsequent blood stage infection. The availability of this novel rodent malaria model also provides an alternative to non-human primates for assessing and monitoring \textit{P. falciparum} MSP-1\textsubscript{19}–based vaccines.

### Materials and Methods

**Plasmids and Plasmodium berghei Transfection.** To create \textit{Pb}–\textit{PfM19}, 1.3 Kb \textit{P. berghei} MSP-1\textsubscript{19} targeting sequence was fused in frame to the MSP-1\textsubscript{19} region of \textit{P. falciparum} (see Fig. 1). PCR was performed on \textit{P. berghei} ANKA and \textit{P. falciparum} D10 genomic DNA (gDNA) using oligonucleotides PbF (5‘-CGGGTACCATCGATAAATACCTTTACCTGAAGCTTCC) and PbR1 (5‘-TACATGCCTAGGTCATACCCTAAATATTCTGATGCAGTAACTGCGTAAAAT) and PfPfF (5‘-GTTATAGACCTAAGCCATGTATGGTATAGACCCTAAGCATGTATG) and PfR (5‘-TGCTCTAGATATACGTAATTATATTGTTGGA) and PfM3’R (5‘-CGCGGATCCTATACAAAACATATACGTAATTATATTGTTGGA) and PfPfF and PfM3’. The resulting fragment was cloned into the KpnI/XbaI sites of pgem4Z (Promega) that harbored the hsp86 3‘ untranslated region (UTR; reference 13). The \textit{PfM1-Pf} 3′ sequence was excised with KpnI/HindIII, the HindIII site filled in with Klenow reagent and the fragment cloned into the KpnI/HincII site of \textit{Pb}–\textit{PfM19}. The 3′ targeting region comprising the \textit{P. berghei} MSP-1 3′ UTR was identified by library screen (15) and PCR amplified from \textit{P. berghei} ANKA gDNA using oligonucleotides PfM3’F (5‘-GGCGATTATCATATAATTGAAATATTTGTTGGA) and PfM3’R (5‘-CGCGGATCCTATACAAAAACATATACGTAATTATATTGTTGGA). The plasmid \textit{Pb}–\textit{PfM19} is analogous to that of \textit{Pb}–\textit{PfM19} with the exception that the entire \textit{P. berghei} MSP-1 targeting sequence was fused in place of its own domain. Using this model, we show that the level of MSP-1\textsubscript{19}–specific invasion inhibitory antibodies generated in mice that had been repeatedly exposed to this chimeric parasite line correlates with the ability of these animals to control a subsequent blood stage infection. The availability of this novel rodent malaria model also provides an alternative to non-human primates for assessing and monitoring \textit{P. falciparum} MSP-1\textsubscript{19}–based vaccines.

**Figure 1.** Schematic representation of \textit{P. berghei} and \textit{P. falciparum} MSP-1 chimeras. The MSP-1 sequences of \textit{P. berghei} (gray), \textit{P. falciparum} (red), and \textit{P. chabaudi} (blue) are represented. The arrows indicate the MSP-1 secondary cleavage site.
The resulting product was ligated into the BamHI site of pGEX-4T-1 and expressed as a GST fusion protein (termed GST-PbM19). Rabbit antisera to GST-PbM19 was derived as previously described (9). Western blot and indirect immunofluorescence assay (IFA) were performed as previously described (9, 19, 20).

**Results**

**Allelic Replacement of P. berghei MSP-1<sub>19</sub> with P. falciparum MSP-1<sub>19</sub>: Functional Complementation of Divergent MSP-1<sub>19</sub> Sequences.** To establish whether P. falciparum MSP-1<sub>19</sub> can complement the in vivo function of the divergent P. berghei MSP-1<sub>19</sub> domain, we created a P. berghei MSP-1 chimaera that expresses P. falciparum MSP-1<sub>19</sub> in place of the endogenous molecule (Fig. 1). The transfection vector pPh-PfM19 was designed to integrate into P. berghei MSP-1<sub>19</sub> and replace the endogenous sequences encoding epidermal growth factor (EGF) domains 1 and 2, and the GPI recognition sequence, with the corresponding P. falciparum (D10 line) sequence (Figs. 1 and 2 A). A second plasmid, pPh-PbM19, designed to integrate in an identical manner but resulting in a homologous MSP-1<sub>19</sub> replacement, was also constructed to generate a control transfectant. Both plasmids were electroporated into the P. berghei (ANKA) line and transgenic parasites were cloned by limiting dilution. Southern blot analysis of gDNA showed that integration had occurred in these parasites by the expected double crossover event into MSP-1<sub>19</sub> (Fig. 2). The resulting P. berghei/P. falciparum chimeric line, which we have termed Pb-PfM19, could be distinguished from a control P. berghei transfection line, termed Pb-PbM19, by digestion with PstI.

**Generation of Semi-immune Mice.** Semi-immune BALB/c mice were generated by the administration of 10<sup>10</sup> erythrocytes infected with either Pb-PbM19 or Pb-PfM19. At 5–10% parasitemia, mice were treated consecutively for 5 d with chloroquine (10 mg/kg body weight, injected i.p.). Recrudescence was typically observed 1 wk after this primary infection, after which mice were administered another five doses of chloroquine. 1 mo later mice were experimentally reinfected and then drug cured as described above. Sera were obtained from individual mice 10 d after the final drug treatment to monitor MSP-1<sub>19</sub> antibodies. For challenge infections, mice were injected i.p with 5 x 10<sup>6</sup> Pb-PbM19– or Pb-PfM19–infected erythrocytes and the course of parasitemia was monitored by microscopy.

**Serology.** Antibodies reacting with recombinant P. berghei or P. falciparum MSP-1<sub>19</sub> were detected by ELISA (9). Blood taken from mice before primary infection were used as negative controls. The ELISA endpoint titres were taken as the highest serum dilution that gave an OD reading five times above that of the control sera. Inhibition of invasion assays were performed as previously described (9).

![Figure 2](https://example.com/figure2.png)
In addition, PCR amplification of gDNA using oligonucleotides specific for the integration events confirmed the expected integration event (unpublished data).

To determine whether the Pb-PfM19 and Pb-PbM19 lines expressed the expected MSP-1\(_{19}\) domains, Western blot analysis was performed on late stage parasite extracts using specific anti-MSP-1\(_{19}\) antibodies (Fig. 3 A). P. falciparum MSP-1\(_{19}\) antibodies recognized both MSP-1\(_{19}\) and an \(\sim 200\)-kD band corresponding to full-length MSP-1 in Pb-PfM19 parasites but not in Pb-PbM19 parasites. In contrast, antibodies specific for P. berghei MSP-1\(_{19}\) only recognized MSP-1\(_{19}\) and full-length MSP-1 in wild-type P. berghei and the transfection control line, Pb-PbM19. This demonstrates that P. falciparum MSP-1\(_{19}\) can be correctly expressed and processed in P. berghei and that the endogenous MSP-1\(_{19}\) gene is no longer expressed in Pb-PfM19 parasites. The localization of MSP-1\(_{19}\) in P. berghei lines was also assessed by double-labeling IFA. Characteristic merozoite surface labeling was observed in both chimeric lines, with Pb-PfM19 parasites reacting only with the P. falciparum–specific monoclonal antibody 4H9/19, whereas P. berghei wild-type and Pb-PbM19 chimeric parasites reacted only with rabbit anti-P. berghei MSP-1\(_{19}\) antibodies (Fig. 3 B). This confirms that the appropriate MSP-1\(_{19}\) domain is correctly localized in both Pb-PbM19 and Pb-PfM19 parasite lines. The growth rates of the transfected lines were also examined and compared with the wild-type parasite line (Fig. 3 C). All mice injected with \(10^4\) parasites succumbed to infection over a similar time frame, regardless of which parasite line they were given. These results extend our previous finding that the function of MSP-1\(_{19}\) during in vitro culture is conserved across divergent Plasmodium species (9, 20) to show that MSP-1\(_{19}\) function is also conserved during the erythrocytic cycle in vivo.

**A Key Role for MSP-1\(_{19}\)–specific Invasion Inhibitory Antibodies in Protection Elicited by Repeated Infection/Drug Cure.** Sera from BALB/c mice that were rendered semi-immune to either Pb-PfM19 or Pb-PbM19 as a result of a low dose infection/drug cure regimen were tested for total MSP-1\(_{19}\)
antibodies in ELISA and for MSP-119–specific invasion inhibitory antibodies. Using MSP-119 GST fusion proteins as antigen in an ELISA, all mice generated a strong MSP-119 antibody response that was specific for the relevant MSP-119 domain (Fig. 4 A). This data highlights the immunogenicity of this domain in the context of a low dose blood stage infection procedure and validates the expression of the appropriate MSP-119 domains in the transfected P. berghei lines.

For the in vitro inhibition assay, the ability of a given serum to inhibit the invasion of RBC by two isogenic P. falciparum lines, D10-PfM3/H11032 and D10-PcMEGF (Fig. 1), was compared. D10-PcMEGF expresses the antigenically diverse P. chabaudi MSP-119 polypeptide and so is not recognized by P. falciparum MSP-119–specific antibodies. This line was used as an alternative to a P. falciparum chimera expressing P. berghei MSP-119 because the latter is currently not available. Hence, P. falciparum MSP-119–specific invasion inhibitory activity of a given serum can be calculated by determining the difference in invasion rates of D10-PfM3/H11032, which uses the wild-type P. falciparum MSP-119 domain for invasion, and D10-PcMEGF in the presence of the test serum. All sera from Pb-PfM19 mice inhibited D10-PfM3/H11032 parasites far more effectively than D10-PcMEGF parasites (Fig. 4 B). Conversely, all sera from Pb-PbM19 immune mice inhibited D10-PcMEGF more effectively than wild-type P. falciparum. Because P. chabaudi and P. berghei are closely related rodent parasites with somewhat conserved MSP-119 domains (73% identity), a degree of antigenic cross-reactivity was expected here. However, because many epitopes differ between the MSP-119 domains of rodent malaria parasites (21), the invasion inhibitory activity of these sera cannot be accurately determined.

To determine if there is an association between the levels of MSP-119–specific invasion inhibitory antibodies present in mouse serum and degree of protection from a subsequent parasite challenge, Pb-PfM19 semi-immune mice were administered a high dose (5 × 10⁶) of Pb-PfM19–infected erythrocytes 3 d after they had been bled for the serological analyses. After challenge, the course of parasitemia was determined and plotted against levels of P. falciparum MSP-119–specific invasion inhibitory antibodies (Fig. 5). Strong evidence of regression was observed (R² = 0.63; P = 0.01 by ANOVA), implicating a substantial role for MSP-119–specific inhibitory antibodies in controlling a blood stage infection. A similarly significant regression curve was evident when invasion inhibition was plotted against cumulative parasitemia in these mice (R² = 0.56; P = 0.02). The apparent linear relationship shown in Fig. 5 might be explained by the fact that P. berghei growth in BALB/c mice in our hands has two periods of almost log phase expansion (see Fig. 3 C). We also performed a two-sided rank correlation test, a more stringent analysis that does not assume a linear relationship between two parameters. This analysis also demonstrated significance for peak parasitemia versus MSP-119–specific invasion inhibition (P = 0.05). Importantly, all mice had very similar anti–PfMSP-19 ELISA antibody endpoint titres when measured against MSP-119 GST fusion proteins (Fig. 4 A) or a baculovirus-expressed P. falciparum MSP-142 antigen (MAD20 allele). The latter antigen is likely to represent MSP-119 in a more appropriate conformation and the reciprocal endpoint titres obtained in this case ranged from 10⁴.5–10⁵ for Pb-PfM19 mice and ≥10² for
MSP-119 antibodies in the control of blood stage parasites. Together, these data are consistent with a significant role for MSP-119 antibodies in the control of blood stage parasites.

Discussion

Although antibodies directed against merozoite antigens are known targets of protective immunity, the relative importance of such antibodies to clinical immunity and their mode of action remain uncertain. In this paper we provide strong evidence implicating a key role for merozoite invasion inhibitory antibodies in reducing the parasite burden in animals previously exposed to blood stage parasites. In addition, consistent with our previous findings (9), we demonstrate that antibodies that are specific for the EGF domains of MSP-119 comprise a large component of the inhibitory activity of the sera from these animals.

This study involved the generation of a P. berghei parasite line (Pb-PfM19) that expresses the P. falciparum MSP-119 domain in place of its own domain and an experiment that demonstrates that the in vivo function of MSP-119 is fully conserved across distantly related Plasmodium species. It is now clear that the extensive amino acid differences between rodent and human (P. falciparum) malaria MSP-119 domains, including an absent disulfide bond in the first EGF domain of the rodent malaria form, are not involved in species-specific erythrocyte invasion events either in vivo (this study) or in vitro (9, 20).

Our observation that the level of inhibitory antibodies specific for MSP-119 correlates with the control of parasitemia upon subsequent blood stage challenge has a number of important implications. First, the dominant protective role for antibodies of this single specificity provides strong support for the development of MSP-119-based vaccines. Second, our findings validate the quantification of MSP-119-specific inhibitory antibodies as a useful correlate-of-protection assay. It should be stressed that the measurement of total MSP-119-specific immunoglobulins is not particularly useful in this regard as some B cell epitopes formed by this protein are not protective (7, 22) and indeed we found no correlation between IgG levels and either invasion inhibition or protection.

The model developed here may prove to be a useful tool to test and monitor the potency of P. falciparum MSP-119-based vaccines. At present there are numerous candidate vaccines based on this domain that are undergoing preclinical testing including different recombinant forms, conformers, and vaccine combinations that incorporate MSP-119 as one component. MSP-119, a protein that incorporates MSP-119 and MSP-133, is the most advanced of these candidates. It appears that the protective antibodies elicited by MSP-119 are directed against the MSP-119 fragment (the MSP-133 fragment may contain T cell epitopes) and hence the animal model developed here should be useful to analyze this vaccine. Currently, the only P. falciparum challenge model available to test MSP-119 antigens involves the use of nonhuman primates. Although vaccine testing in these animals is probably an important precursor to human trials, it is clearly substantially less practical for routine efficacy testing than the simple rodent challenge model described here.

We thank Drs. Chris Janse and Andy Waters for helpful advice on P. berghei transfection and for provision of the P. berghei cloning plasmid, Drs. Carole Long, Anthony Stowers, and Louis Miller for the baculovirus-expressed MSP-119 antigen, and Drs. Louis Schofield and Diana Hanson for helpful discussion. We also acknowledge the expert technical services provided by Lynn Buckingham. We are grateful to the Australian Red Cross Blood Bank for the provision of human blood and serum.
This work was supported by the National Health and Medical Research Council (NHMRC) of Australia. T.F. de Koning-Ward, R.A. O’Donnell, and D.R. Drew are recipients of postdoctoral training awards from the NHMRC. B.S. Crabb is an International Research Scholar of the Howard Hughes Medical Institute.

Submitted: 21 January 2003
Revised: 10 June 2003
Accepted: 1 July 2003

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