

## Materials and Methods

### Experimental animals

Female Swiss Webster mice (6 to 8 weeks old) and female BALB/c mice were purchased from Harlan Company (Indianapolis, IN). Animal handling was conducted according to Institutional Animal Care and Use Committee-approved protocols.

### Generation of *Pys1*<sup>-</sup> parasites

The targeted deletion of *PyS1* by gene replacement was carried out as described in detail by Mikolajczak et al. [1], and the selection of transgenic parasites was carried out as described in Labaied et al. [2]. *PyS1* was replaced with DsRed under the control of the *P. berghei* elongation factor 1 $\alpha$  promoter. All parental populations were cloned using limited dilution. The sequences of all oligonucleotide primers used for this study are listed in Table S1. Similarly, *Pbs1*<sup>-</sup> parasites were created by targeted deletion of *PbS1* by gene replacement.

### Reverse transcriptase PCR (RT-PCR)

To evaluate transcript expression, the following samples were processed for RNA extraction: 8 million PyWT 17XNL oocyst sporozoites were isolated from infected *Anopheles stephensi* midguts 10 days after an infectious blood meal, 1.5 million PyWT 17XNL and *Pys1*<sup>-</sup> salivary gland sporozoites were isolated from infected *Anopheles stephensi* salivary glands 14 days after an infectious blood meal, liver stages were extracted from whole liver lysates of mice injected with 1 million sporozoites and blood stages from 500  $\mu$ l of infected blood. RNA was extracted using TRIzol reagent

(Invitrogen) and treated with DNase (Invitrogen). cDNA synthesis was performed using the Super Script III Platinum 2-step qRT-PCR kit (Invitrogen). *Pys1*<sup>-</sup> and *P. yoelii* circumsporozoite protein (PyCS) specific primers were used in a standard PCR amplification (35 cycles).

#### Phenotypic analysis of *Pys1*<sup>-</sup> parasites in the mosquito

*Anopheles stephensi* mosquitoes were infected with *Pys1*<sup>-</sup> parasites or PyWT 17XNL parasites by blood feeding for 6 min on the first day and 10 min on the following day on infected Swiss Webster mice and subsequently maintained under a cycle of 12.5 h light/11.5 h dark and 70% humidity at 24.5°C. Gametocyte exflagellation capacity was evaluated microscopically before mosquito blood meal. Infected mosquitoes were dissected (20 mosquitoes for each dissection) on day 10 after the first blood meal to determine the mean number of midgut oocyst sporozoites. Similarly, dissections on day 14 after the first blood meal were used to determine the mean number of salivary gland sporozoites.

#### Hepatoma cell line maintenance and cell-traversal assay

All *in vitro* assays were conducted using the human hepatoma cell line HepG2-CD81 [3]. The cell line was cultured in DMEM-F12 medium supplemented with antibiotics and 10% fetal bovine serum (FBS) at 37°C and 5% CO<sub>2</sub>.

HepG2-CD81 cells were seeded in chamber slides (Permanox eight-well chamber slide; Nalge Nunc International, Rochester, NY) at a density of 60 x 10<sup>3</sup> cells per well two

days before the assay. A total of  $20 \times 10^3$  sporozoites per well of PyWT 17XNL or *Pys1*<sup>-</sup>, as well as uninfected mosquito salivary gland extracts (mock), were re-suspended in incomplete DMEM-F12 medium with 3% bovine albumin serum (BSA) and  $2 \text{ mg ml}^{-1}$  fluorescein isothiocyanate (FITC)-dextran (Invitrogen-Molecular Probes, Eugene, OR). Sporozoites and mock suspensions were added to the cells, centrifuged for two min at 199 rcf and incubated for one h at 37°C. Thereafter, the cells were washed thoroughly with PBS and complete DMEM-F12 medium twice to remove any extracellular dextran, and the cells were incubated for a further three h in complete DMEM-F12 medium. Flow cytometric quantitative analysis of dextran-positive cells was conducted using a flow cytometer BD LSR II (BD Biosciences, San Jose CA) and the flow cytometry analysis program FlowJo version 7.2 (TreeStar, Ashland, OR).

#### Mouse infections with PyWT 17XNL and *Pys1*<sup>-</sup>

For sporozoite infection and subsequent liver stage development and onset of blood stage parasitemia, BALB/c mice were injected intravenously (IV) with 100 or 1,000 PyWT 17XNL or *Pys1*<sup>-</sup> sporozoites re-suspended in RPMI 1640. Blood stage patency was monitored daily by evaluation of Giemsa-stained thin blood smears from day 1 to day 5 post sporozoite infection. For blood stage growth experiments, BALB/c mice were injected IV with  $10^3$  or  $10^6$  PyWT 17XNL or *Pys1*<sup>-</sup> erythrocytic asexual stages in RPMI 1640. Blood stage patency was monitored daily by evaluation of Giemsa-stained thin blood smears from day 1 to day 24 post infection.

#### Transgene expression

Expression of DsRed was determined throughout the parasite life cycle by fluorescence microscopy. The different life cycle stages were visualized as follows: blood stage – wet mount; oocysts – dissected mosquito midguts were placed on a microscope slide under a glass cover slip; salivary gland sporozoites – infected salivary glands were dissected and ground to release sporozoites which were placed on a microscope slide under a glass cover slip. For the liver stage, infected cells were fixed at 24 hrs post infection in 4% formalin for 10 min, then blocked and permeabilized in PBS with 10% bovine serum albumin and 0.2% Triton-X 100 (PBS/BSA/Triton) for IFA. IFA was carried out in PBS/BSA. The staining was performed using a rabbit poly-clonal anti-*P. yoelii* UIS4 primary antibody, a parasite parasitophorous vacuole membrane marker. Fluorescent staining was achieved with Alexa Fluor-conjugated secondary antibodies (Invitrogen Corporation, Carlsbad, CA) specific to rabbit (Alexa Fluor 488, green) IgG. Cells were stained with DAPI to visualize the DNA and mounted with FluoroGuard anti-fade reagent (Bio-Rad, Hercules, CA). Preparations were analyzed using a fluorescence inverted microscope (Eclipse TE2000-E; Nikon), and images were acquired using Olympus 1 x 70 Delta Vision deconvolution microscopy.

## References:

- [1] Mikolajczak SA, Aly AS, Dumpit RF, et al. An efficient strategy for gene targeting and phenotypic assessment in the *Plasmodium yoelii* rodent malaria model. *Mol Biochem Parasitol* 2008; 158:213-216.
- [2] Labaied M, Harupa A, Dumpit RF, et al. *Plasmodium yoelii* sporozoites with simultaneous deletion of P52 and P36 are completely attenuated and confer sterile immunity against infection. *Infect Immun* 2007; 75:3758-3768.
- [3] Silvie O, Rubinstein E, Franetich JF, et al. Hepatocyte CD81 is required for *Plasmodium falciparum* and *Plasmodium yoelii* sporozoite infectivity. *Nat Med* 2003; 9:93-96.

**Table S1 PCR oligonucleotide primer sequences used in this study**

| <b>Primer</b>                                       | <b>Sequence</b>                        |
|---|--|
| <b>To test expression throughout the life cycle</b> |  |
| PyS1ORFtest/FWD                                     | GAATACGTCTATTGAAATAAAGC                |
| PyS1ORFtest/RVS                                     | TCCACTGATTCATACATTTT                   |
| <b>To test PyS1 gene structure</b>                  |  |
| PyS1/Exon-1/FWD                                     | CTCTCCAAAAAAGAGAAAATGT                 |
| PyS1/Exon-2/RVS                                     | CGTGAAATAATGCACTTATACA                 |
| PyS1/Intron/RVS                                     | GCCAGTCGATAGAAGAGAAA                   |
| PyS1/postExon-2/RVS                                 | GGGCGAAAATGACACATAAG                   |
| <b>To create PyS1 knockout plasmid</b>              |  |
| SP/pyS1-1   | CGGATATCAGACACTTATAAAGCTAAAGAAG        |
| ASP/pyS1-2  | GAAGAAATATGGGCGCCTACAAATTTTCGATGCACTCA |
| SP/pyS1-3   | GAAATTTGTAGGCGCCCATATTTCTTCTCATTTTCC   |
| ASP/pyS1-4  | ATGCGGCCGCGATGAGAATAATAATATGTAGATAA    |
| <b>To genotype Pys1- parasites</b>                  |  |
| S1 5' test FWD                                      | GATCATAAAAATGTGCAACGTC                 |
| S1 5' test RVS                                      | GTAATACGACTCACTATAG                    |
| S1 3' test FWD                                      | GGCTACGTCCC GCACGGACGAATCCAGATGG       |
| S1 3' test RVS                                      | GTATTTGTTTACATACATATGTGT               |
| S1test FWD  | GATCATAAAAATGTGCAACGTC                 |
| S1test RVS  | CCACAAAGATGATTATTGCAAGGT               |
| <b>To test for presence of PyS1 transcript</b>      |  |
| S1/mRNA/FWD   | ACTGCAACTATGCCCATGTG                   |
| S1/mRNA/RVS   | AAATTTCTCAACTATTTTGTTTCG               |
| PyCS rt for   | AAGAAGTG TACCATTTTAGTTGTAGCGTCAC       |
| PyCS rt rev   | CACTACTGGTTGATTCAATTTATTTTGAGCCTC      |
| <b>To genotype Pbs1- parasites</b>                  |  |
| PbS1 5' test FWD                                    | TACACCCTTAAACAAAAAGCCTAATGGA           |
| PbS1 5' test RVS                                    | CGCATTATATGAGTTCATTTTACACAATCC         |
| PbS1 3' test FWD                                    | GGCTACGTCCC GCACGGACGAATCCAGATGG       |
| PbS1 3' test RVS                                    | CCTATGTATATTATGAACACG                  |
| PbS1test FWD  | TAATGGTACCGTGTATTATGTAGATGTA           |
| PbS1test RVS  | TCCCCGCGGCGAATATTGTTATTCATATCTGTAC     |

## Figure S1

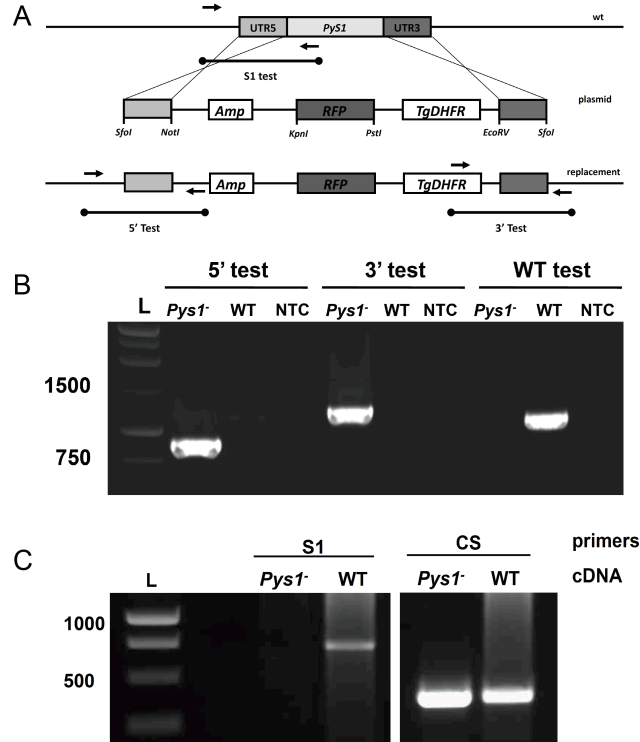


Figure S1: Generation of *P. yoelii* parasites with a deletion in the S1 gene (*Pys1*<sup>-</sup>). *Pys1*<sup>-</sup> parasites were created by replacing *PyS1* with a plasmid containing the *Toxoplasma gondii* dihydrofolate reductase gene and a red fluorescent protein (DsRed) cassette by double crossover homologous recombination. (A) A graphical representation of the double crossover homologous recombination strategy. (B) Gene replacement analysis of the *Pys1*<sup>-</sup> clone G4. 5' test evaluates whether the plasmid has integrated 5' of the ORF; 3' test evaluates whether the plasmid has integrated 3' of the ORF, and WT test evaluates whether the ORF is present. The ladder lane is indicated with an "L" with relevant sizes noted to the left. The gDNA templates, *Pys1*<sup>-</sup>, WT, and no template control (NTC), are indicated below each test. (C) No *PyS1* transcript was detected in *Pys1*<sup>-</sup> parasites. Total RNA was isolated from *Pys1*<sup>-</sup> and WT salivary gland sporozoites and cDNA was generated. The cDNA from *Pys1*<sup>-</sup> or WT was used in a PCR reaction with *PyS1* and circumsporozoite (CS) specific primers. The ladder lane is indicated with an "L" with relevant sizes noted to the left.

**Figure S2**

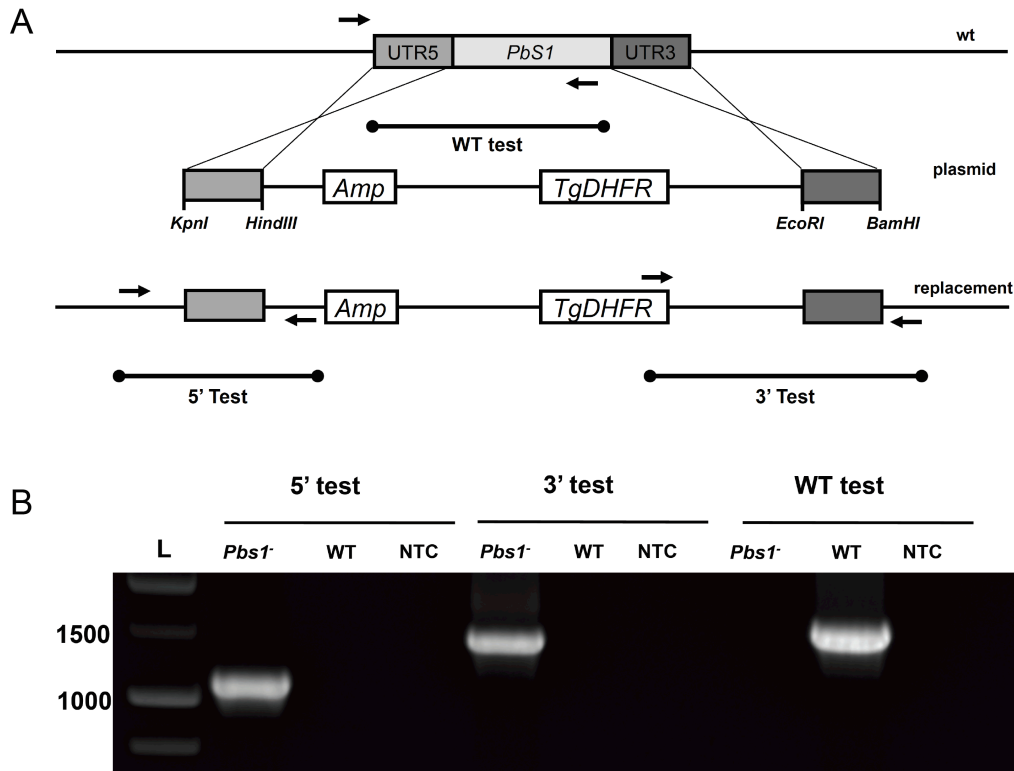


Figure S2: Generation of *P. berghei* parasites with a deletion in the S1 gene (*Pyb1*<sup>-</sup>). *Pbs1*<sup>-</sup> parasites were created by replacing *Pbs1* with a plasmid containing the *Toxoplasma gondii* dihydrofolate reductase gene and a red fluorescent protein (DsRed) cassette by double crossover homologous recombination. (A) A graphical representation of the double crossover homologous recombination strategy. (B) Gene replacement analysis of the *Pbs1*<sup>-</sup> clone 1. 5' test evaluates whether the plasmid has integrated 5' of the ORF; 3' test evaluates whether the plasmid has integrated 3' of the ORF, and WT test evaluates whether the ORF is present. The ladder lane is indicated with an "L" with relevant sizes noted to the left. The gDNA templates, *Pbs1*<sup>-</sup>, WT, and no template control (NTC), are indicated below each test.

**Figure S3**



Figure S3: Phenotypic analysis of *Pbs1*<sup>-</sup> parasites. *Pbs1*<sup>-</sup> and PbWT infected mosquitoes were evaluated for numbers of midgut and salivary gland sporozoites at day 14 and 21, respectively.



**Table S2**     **Determination of *Pbs1*<sup>-</sup> pre-patent period**

|                          | No. positive/No. injected | pre-patant period (days) |
|--------------------------|---------------------------|--------------------------|
| <i>Pbs1</i> <sup>-</sup> | 5/5                       | 3                        |
| Pb WT                    | 5/5                       | 3                        |

Table S2: Determination of *Pbs1*<sup>-</sup> pre-patent period. 10,000 *Pbs1*<sup>-</sup> or PbWT sporozoites were injected IV into 5 C57BL/6 mice. Blood stage parasitemia was followed from day three through five to assess pre-patent period.