

1 – uninfected RBC membrane fraction

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2 – P. yoelii 17X infected reticulocyte membrane fraction

3 – P. yoelii 17X intracellular parasite fraction

c /	PlasmodB acc no.	Protein description	Molecular wt (kDa)	Signal peptide	TM domain	Pf PEXEL motif	P value	Number of peptides
1 2	PY05892	Exported protein-2	31.3	1	0	-	2.92E-06	6
250 -	PY04481	hypothetical protein - (<i>pyst-</i> a family)	32.9	1	0	-	5.27E-06	3
75 -	PY07631	hypothetical protein - (<i>pyst-</i> a family)	31.5	1	0	-	3.25E-11	2
50 -	PY03885	L-lactate dehydrogenase	34.4	1	1	KNLGD	3.70E-11	10
37 -	PY03531	Cof-like hydrolase	32.7	0	0	-	6.74E-04	4
Contraction of the second	PY05001	Heat shock protein 70	79.1	1	3	-	3.10E-10	10
20 -	PY00622	Rhoptry associated protein 1	70.8	1	0	Ę	6.32E-06	5
	PY01557	m1-family aminopeptidase	123.0	1	1	-	3.29E-09	3
	PY00963	ATP synthase F1subunit beta	57.8	0	0	-	8.30E-04	1

Supplemental Figure 1. A. Analysis of *P. yoelii* 17X reticulocyte host cell membrane and parasite associated protein fractions. Proteins associated with the membrane of uninfected (lane 1) or *P. yoelii* 17X infected reticulocytes (lane 2) and intracellular *P. yoelii* 17X parasites (lane 3) were separated by SDS-PAGE and analyzed by immunoblot. A. Coomassie Blue stained gel of each antigen preparation. B. Immunoblot analysis of each preparation using rabbit antisera against r*Py*MSP-8 or normal rabbit sera. C. Silver stained SDS-PAGE gel showing separation of *P. yoelii* 17X reticulocyte membrane fraction (lane 1) and a purified 29-32 kDa protein band (lane 2) from the membrane fraction by a gel electro-elution method. The purified band was subjected to in-gel trypsin digestion followed by mass spectrometric analysis (LC-MS/MS). The experiment was repeated three times and the table on the right shows nine *P. yoelii* proteins obtained at least two out of three times from the analysis. A *p* value <0.001 was set as the threshold for significance (probability of a match in an MS/MS search with equal or better scores than are expected to occur by chance alone). Signal peptides, TM domains and PEXEL motifs were based on bioinformatic data available in PlasmoDB (www.plasmodb.org). A putative PEXEL motif in *Pf*LDH was reported (1).

1. Lanzer M, Wickert H, Krohne G, Vincensini L, Braun Breton C. 2006. Maurer's clefts: a novel multi-functional organelle in the cytoplasm of *Plasmodium falciparum*-infected erythrocytes. Int J Parasitol 36:23-36.



Supplemental Figure 2. The 3' end of the *pyexp2* genomic locus is accessible for manipulation. A. Schematic of pSE02-Exp2-3HA construct and 3' triple HA integration event in the *pyexp2* genomic locus by a single cross-over recombination. **B.** Diagnostic PCR showing integration of triple HA at the 3' end of *pyexp2* gene in two parasite lines (#3, #4) generated by two independent transfections. Parasite genomic DNA isolated from wild type *P. yoelii* 17X (lane 1, 5, 9), *P. yoelii* 17X-*Py*Exp2-3HA transgenic lines #3 (lane 2, 6, 10) and #4 (lane 3, 7, 11) was used for diagnostic PCR using *Tg*DHFR-ts specific primers (A-B), *pyexp2* gene specific primers (C-D), and *pyexp2*-3HA specific primers (C-E). Lanes 4, 8 and 12 represent negative controls for PCR.



Supplemental Figure 3. Expression and purification of rPY04481, a member of the *pyst-a* multigene family and production of rabbit antisera. A. Coomassie-blue stained SDS-PAGE gel showing *E. coli* lysate at the time of IPTG induction (T0), 4 hrs post induction (T4) and rPY04481 (R) (3 μ g) purified by nickel-chelate affinity chromatography. B. Immunoblot analysis of *P. yoelii* 17X parasite antigen lysate (10 μ g) probed with rabbit anti-rPY04481 sera (1) or normal rabbit sera (2). Molecular weight markers in kilodaltons (kDa) are indicated.

Brightfield DAPI (Blue) Exp2 (Green)



Supplemental Figure 4. *Py*Exp2 is localized exclusively to the PVM in lethal *P. yoelii* 17XL infected RBCs. Immunofluorescence image of a representative field showing an overlay of brightfield, *Py*Exp2 (green) and DAPI (blue).



Supplemental Figure 5. CD71 is expressed on the surface of reticulocytes but absent from mature RBCs. Immunofluorescence images showing the labeling of mouse A) reticulocytes or B) mature erythrocytes with anti – mouse CD71 antibodies (red).



Supplemental Figure 6. *PyExp2* vesicles do not co-localize with mouse clathrin in *P. yoelii* 17X infected reticulocytes. Immunofluorescence images showing co-localization of *PyExp2* (green) and mouse clathrin (red) using rabbit anti-r*PyExp2* sera and mouse anti-clathrin heavy chain antibodies respectively. DAPI was used to stain the parasite nuclei (blue).



Supplemental Figure 7. Schematic structure of *P. yoelii exp2* knockout targeting construct and the predicted double crossover homologous recombination in the *pyexp2* genomic locus.

Supplemental Movie Legends

Supplemental movie S1

Rotation of a reconstructed 3D-SIM image showing a *P. yoelii* 17X infected reticulocyte labeled for *Py*Exp2 (green) and parasite nuclei (blue).

Supplemental movie S2

A 3D volume view of de-convoluted z-stacks showing co-localization of *Py*Exp2 (green), BODIPY TR Ceramide (red) and parasite nuclei (blue) in a *P. yoelii* 17X infected reticulocyte.

Supplemental movie S3

Rotation of a reconstructed 3D-SIM image showing the co-localization of *Py*Exp2 (green), BODIPY TR Ceramide (red) and parasite nuclei (blue) in a *P. yoelii* 17X infected reticulocyte.

Supplemental movie S4

Rotation of a reconstructed 3D-SIM image showing the absence of *Py*Exp2 (green) positive vesicles in CD71 (red) negative mature RBC infected with *P. yoelii* 17XL parasite.

Supplemental movie S5

Rotation of a reconstructed 3D-SIM image showing the presence of *Py*Exp2 (green) positive vesicle in a CD71 (red) positive reticulocyte infected with *P. yoelii* 17XL parasite.