Title: Mosquito lipids regulate *Plasmodium* sporogony and infectivity to the mammalian host

Giulia Costa[1], Maarten Eldering[1,2], Randall L. Lindquist[3], Anja E. Hauser[3,4], Robert Sauerwein[2], Christian Goosmann[1], Volker Brinkmann[1] and Elena A. Levashina[1]*

Affiliations:

[1] Max Planck Institute for Infection Biology, Berlin, Germany

[2] Radboud University Medical Center, Nijmegen, The Netherlands

[3] German Rheumatism Research Centre (DRFZ), Berlin, Germany

[4] Charité-Universitätsmedizin Berlin, Germany

* Corresponding author: levashina@mpiib-berlin.mpg.de

Summary

Malaria is a human parasitic disease that is transmitted by a mosquito vector.

Plasmodium parasites, the causative agents, differ in their infectivity and virulence to the

mammalian host, but the mechanistic underpinnings of this variation remain unknown.

As mosquitoes provide a nutrient-rich niche for development of transmissible stages, we

examined the role of lipids in parasite development and infectivity by disrupting lipid

trafficking in mosquito adults. We show that depleting the major mosquito lipoprotein

lipophorin deprives parasites of neutral lipids, arrests oocysts growth and impairs

sporozoite formation. Importantly, lipid deficiency decreases parasite mitochondrial

membrane potential and severely compromises sporozoite infectivity and virulence in the

mammalian host. Our findings demonstrate the requirement of mosquito lipids for

Plasmodium metabolism, and uncover the mitochondrial contribution to parasite

infectivity and virulence. By drawing a connection between vector nutrition and malaria

virulence, our results redefine the paradigm of vector-host-pathogen interactions.

INTRODUCTION

Nutrition plays a key role in host-pathogen interactions, as parasites hijack host metabolites to survive and propagate. *Plasmodium* parasites, the causative agents of malaria, are no exception. Malaria is the deadliest infectious disease transmitted to humans by anopheline mosquitoes. Multiple reports have implicated larval diet and adult blood meals in determining parasite loads within a mosquito (Moller-Jacobs et al., 2014; Okech et al., 2004; Ponnudurai et al., 1989; Shapiro et al., 2016; Takken et al., 2013; Vantaux et al., 2016). Indeed, females produced by undernourished larvae are poor *Plasmodium* hosts (Moller-Jacobs et al., 2014; Shapiro et al., 2016; Takken et al., 2013; Vantaux et al., 2016), although additional blood feedings improve parasite survival (Okech et al., 2004; Ponnudurai et al., 1989). Together with proteins and carbohydrates, lipids constitute important building blocks of nutrition since they provide living organisms with energy, serve as the structural materials of cell and organelle membranes, and function as signaling molecules. In contrast to the defined role of lipids in *Plasmodium* development within a mammalian host (Grellier et al., 1991; Itoe et al., 2014; Lauer et al., 2000), the contributions of mosquito lipids remain unknown. Mosquitoes acquire lipids from their diet and store them in the fat body, an insect equivalent of mammalian liver. Lipid levels in the tissues are maintained by lipophorin (Lp), the hemolymph-circulating transporter that shuffles hydrophobic lipids between the fat body and energy demanding tissues (Atella et al., 2006; Van der Horst et al., 2009). The blood meal brings to the mosquito massive lipid resources that, in the course of the first days, are routed by Lp from the midgut to the developing ovaries for egg development and to the fat body for storage. Disrupting Lp function aborts ovary development and renders the parasites more vulnerable to the mosquito complement-like system (Mendes et al., 2008; Rono et al., 2010). Here we exploited Lp deficiency to examine the role of mosquito lipids in *Plasmodium* sporogonic development, transmission and virulence to the mammalian host.

RESULTS

Disruption of lipid trafficking between mosquito tissues mitigates *Plasmodium* sporogony

We first investigated whether Lp depletion disrupts lipid trafficking between mosquito tissues. To this end, females were injected with *dsRNA* against Lp and then fed on *Plasmodium*-infected blood. Lipid content of the tissues was gauged by Nile Red staining (Rudolf and Curcio, 2009). In control mosquitoes, blood feeding significantly increased levels of the Nile Red signal in the midgut and in the ovaries, but no change was observed in the fat body (Figure 1, A and B). While Lp depletion transiently increased lipid levels in the midgut, it abrogated the feeding-induced increase in lipid levels in the ovaries (Figure 1, A and B). Again, no changes in lipid levels were detected in the fat body. We conclude that blocking the blood meal-induced lipid trafficking by Lp depletion efficiently disrupts lipid transport between mosquito tissues.

We next examined the effects of disruption of lipid trafficking on *Plasmodium* development. To prevent large losses at early stages of parasite development inflicted by the mosquito complement-like system in the absence of Lp (Mendes et al., 2008; Rono et al., 2010), all infection experiments were performed with immune-deficient mosquitoes (Pompon and Levashina, 2015). When mosquitoes were infected with *P. falciparum*, a significant decrease in the size of mature oocysts was observed in Lp-depleted mosquitoes (Figure 1C). Strikingly, inhibition of lipid trafficking led to a 5-fold decrease in the number of salivary gland sporozoites (Figure 1D). Similar effects on sporogony and sporozoite loads were observed for *P. berghei* (Figure 1C and D). Further, the comparable decrease in numbers of midgut and salivary gland sporozoites suggested that Lp depletion inhibited parasite sporogony in the oocysts (Table S1). Taken together, these results show that Lp-mediated lipid trafficking is essential for sporogony of human and rodent *Plasmodium* parasites.

Lp-transported lipids are essential for *Plasmodium* sporogonic development

To investigate how disruption of lipid trafficking affected parasite sporogony, we followed development of *P. berghei* GFP-expressing oocysts by fluorescence microscopy

(Franke-Fayard et al., 2004). A significant decrease in oocyst size was observed in Lp-
deficient mosquitoes 7 days post infection (dpi) (Figure 2A), indicating that Lp
deficiency arrests parasite growth at the onset of sporogony. We next examined whether
oocysts accumulated lipids and the role of Lp in this process. A clear Nile Red signal was
observed in the peripheral cytoplasm and vesicles (Figure 2B). Importantly, this signal
was absent in the oocysts of Lp-depleted mosquitoes (Figure 2B and Figure S1A),
suggesting that Lp is required for parasite provision with mosquito lipids. To investigate
whether Lp was taken up by oocysts together with its lipid cargo, we used antibodies
directed against the protein moiety of the Lp particle (Rono et al., 2010). In controls, The
number of Lp-positive oocysts increased over time (25% and 72% at 7 and 13 dpi,
respectively, Figure 2A). Lp signal was observed on the surface but not inside the oocysts
(Figure 2C). As expected, no signal was detected in Lp-depleted mosquitoes (Figure 2C).
Progressive accumulation of Lp on the parasite surface suggests that *Plasmodium* exploits
Lp particles for lipid delivery to the oocysts rather than for uptake. Transmission electron
microscopy analysis further confirmed that Lp depletion did not impact development of
young oocysts (7 dpi) which displayed normal ultrastructure (Figure 2D and E). Instead,
in Lp-depleted mosquitoes, almost half of the mature oocysts displayed cytoplasmic
vacuolization and lack of classical membrane retractions characteristic of initiation of
sporulation (Figure 2F). Moreover, these aberrant oocysts were surrounded by the
electron-dense actin zones associated with dead ookinetes (Shiao et al., 2006) (Figure 2E
and Figure S2). Collectively, these observations indicate that lipid restriction inhibits
oocyst sporulation and induces the death of mature oocysts. Therefore, mosquito lipids
represent a limiting step in parasite development in the midgut.

Mosquito lipids control *Plasmodium* virulence to the next mammalian host

As some sporozoites were able to complete their development in spite of massive oocyst
die-off (Figure 1D), we examined the effect of lipid starvation on *Plasmodium*
transmission. In these experiments, naïve mice were exposed to the bites of *P. berghei*-
infected control or Lp-deficient mosquitoes. We found that only 20% of mice (n=10)
bitten by Lp-depleted mosquitoes became blood-stage positive, as compared to 90% in

controls (n=10) (Figure 3A and 3B). To assure that this striking difference in infection

levels was not due to the differences in sporozoite loads produced by control and Lp-

deficient mosquitoes (Figure 1D), naïve mice were subcutaneously injected with equal

numbers of sporozoites isolated from control and Lp-depleted mosquitoes. Again, fewer

than 40% of mice (n=18) injected with lipid-deprived sporozoites became infected as

compared to 100% in controls (n=16) (Figure 3C). All mice that became infected with

sporozoites from Lp-deficient mosquitoes displayed a 1-day delay in the onset of

parasitemia (Figure 3D). In addition, only half of the infected mice displayed the severe

neurological symptoms typical of experimental cerebral malaria (ECM), and there was a

significant delay in ECM development (Figure 3E) compared to control mice, which had

100% incidence of ECM. Overall, mosquito lipid deprivation resulted in a cumulative

loss of parasite virulence (Figure 3F). These results strongly suggest that disrupting lipid

transport in the mosquito impacts development of *Plasmodium* liver stages and reduces

the initial burden of blood stage parasites, thereby preventing initiation of severe forms of

the disease.

Supplemental blood feeding rescues parasite infectivity

To obtain direct evidence of the trans-stadial effect of mosquito lipid deficiency on the

Plasmodium liver stages, we gauged development of extra-erythrocytic forms (EEFs) in

the hepatoma HepG2 cell line *in vitro*. Cells were exposed to equal numbers of

sporozoites isolated from control and Lp-depleted mosquitoes (Figure 4A) and the

development of EEFs was analyzed by fluorescence microscopy two days later.

Consistent with the *in vivo* results, lipid restriction reduced sporozoite infectivity in

hepatocytes 4-fold, to levels comparable to those observed after treatment of control

sporozoites with cytochalasin D, a potent inhibitor of actin polymerization and

Plasmodium invasion (Mota et al., 2001) (Figure 4C). Moreover, significantly smaller

EEFs were produced by lipid-deprived sporozoites as compared to controls (Figure 4E

and G, Figure S3), suggesting a trans-stadial effect of lipid deficiency on EEF growth.

Therefore, we hypothesized that providing lipids directly to the midgut at the critical time

of oocyst sporogony might restore sporozoite infectivity and EEF development. To test

this hypothesis, *P. berghei*-infected control and Lp-depleted mosquitoes were blood fed 7

dpi, when the first effects of lipid starvation on oocyst size were observed (Figure 2A).

Strikingly, even in the absence of Lp (Figure S4), this supplemental feeding partially

restored sporozoite numbers in the mosquitoes (Figure 4B), and fully rescued sporozoite

infectivity (Figure 4D) and EEF development (Figure 4F and H). As expected, additional

blood feeding did not restore ovary development (data not shown), confirming the

importance of Lp in lipid trafficking between mosquito organs. Taken together, these

results establish a direct link between lipid starvation at the oocyst stage and *Plasmodium*

infectivity to the next mammalian host.

Mosquito lipids fuel sporozoite mitochondrial membrane potential

We next examined potential mechanisms that attenuate sporozoite infectivity to the next

mammalian host. Microscopic inspection of the overall sporozoite morphology by

scanning electron microscopy failed to detect any major differences between control and

lipid-deficient sporozoites (Figure S5A). Similarly, no major differences were detected in

transcript levels of major regulators of sporozoite development (Figure S5B). Since

neutral lipids such as cholesterol regulate trafficking of GPI-anchored proteins to the

plasma membrane (Zurzolo and Simons, 2016), we gauged surface distribution of the

circumsporozoite protein (CSP), the main surface antigen crucial for sporozoite

morphogenesis and infectivity (Menard et al., 1997). Immunofluorescence analysis

revealed no differences in the distribution of CSP signal at the surface of lipid-deprived

sporozoites compared to controls (Figure S5C). In contrast, a striking effect of lipid

deprivation was observed on the sporozoite mitochondrial membrane potential as

measured by signal intensity of a lipophilic cationic dye (TMRE) whose accumulation in

the mitochondrial membrane matrix space correlates with the mitochondrial membrane

potential (Perry et al., 2011). We first validated TMRE staining of sporozoites by

measuring signal intensity before and after treatment with a mitochondrial uncoupling

drug CCCP and showed that drug treatment abolished TMRE signal (Figure S5D). We

next assessed TMRE intensity by imaging flow cytometry analysis of sporozoites.

Strikingly, a significant decrease in mitochondrial membrane potential was observed in

lipid-deprived sporozoites as compared to controls (Figure 5A, B and D). To examine

whether reduced mitochondrial activity mitigated sporozoite survival, we gauged levels

of transgenic GFP expression as a proxy of parasite live status (Yilmaz et al., 2014).

Although GFP expression levels differed between experiments, absence of significant

differences in GFP signal between the two groups confirmed that all analyzed sporozoites

were alive (Figure 5A, C and E). These results demonstrate that mosquito lipids regulate

the mitochondrial activity of sporozoites, and suggest that the decrease in mitochondrial

membrane potential is responsible for the attenuated infectivity of the lipid-deprived

sporozoites in the mammalian host.

DISCUSSION

Anopheline mosquitoes provide *Plasmodium* parasites a nutritional niche to complete

their life cycle. Here we report the crucial role of mosquito lipids in *Plasmodium*

metabolism that ultimately regulates parasite infectivity and virulence in the mammalian

host. We show that parasites hijack the mosquito nutrient transporter Lp for oocyst

provision with neutral lipids. These results are in line with previous reports that observed

an association of insect Lp particles with Apicomplexan parasites (Atella et al., 2009;

Folly et al., 2003; Ximenes Ados et al., 2015). We demonstrate that mosquito lipids

regulate multiple stages of *Plasmodium* development. First morphological anomalies

were detected during oocyst sporogony and were mainly characterized by electron-light

cytoplasmic vacuolization. Vacuolization is a hallmark of autophagy, a physiological

process occurring in normal conditions in a large proportion of *Plasmodium* liver stages

(Eickel et al., 2013). Indeed, under unfavorable circumstances such as starvation, liver

stage parasites initiate an autophagy-like cell death to reduce competition and ensure the

survival of the fittest progeny (Eickel et al., 2013). As in our experiments, a small

proportion of oocysts also displayed similar abnormalities in controls, we propose that

autophagy is not restricted to the intracellular liver stages, but is a general mechanism of

parasite nutrient sensing, exacerbated in our experiments by lipid restriction. Together

with the data accumulated for mammalian stages (Grellier et al., 1991; Itoe et al., 2014;

Lauer et al., 2000; Sa et al., 2017), our study uncovers the obligatory *Plasmodium*

dependence on host lipids during throughout its life cycle.

In contrast to sporogonic development, lipid restriction did not induce major

morphological or transcriptional changes in the transmissible sporozoite stage. Instead,

we revealed an unexpected association between mosquito lipid transport and sporozoite

mitochondrial membrane potential. Mitochondria are essential eukaryotic organelles that

integrate cellular metabolic signals, generate energy and synthetize intermediates of vital

macromolecules. In line with our results, *Plasmodium* mutants for mitochondrial

pathways are defective in oocyst growth and sporulation (Boysen and Matuschewski,

2011; Goodman et al., 2016; Hino et al., 2012; Oppenheim et al., 2014). Moreover, the

widely used antimalarial drug atovaquone, which targets the cytochrome bc1 complex

and collapses the mitochondrial membrane potential in *Plasmodium* blood stages (Siregar

et al., 2015; Srivastava et al., 1997) also arrests oocyst growth and sporulation, and

reduces the number and size of developing EEFs *in vitro* (Azevedo et al., 2017; Davies et

al., 1993; Fowler et al., 1995). Taken together with these results, our findings establish

the crucial role of mosquito lipids in parasite mitochondrial function, which shapes

Plasmodium sporogonic development and infectivity.

Attenuation of *Plasmodium* sporozoites is a leading strategy for malaria whole-organism

vaccine development (Butler et al., 2012). So far, this has been achieved by irradiation

(Seder et al., 2013) or by genetic manipulation (van Schaijk et al., 2014). The data

presented here add a new paradigm of virulence attenuation by manipulation of mosquito

lipid trafficking. Interestingly, high variability in virulence of *P. falciparum* sporozoites

has been reported under laboratory conditions (March et al., 2013) and in the field (Gupta

et al., 1994; Mackinnon and Read, 2004). We propose that disparity in lipid resources

between larval breeding sites drive fluctuations in mosquito nutritional status (Gillies,

1954), and thereby may account for the observed variability in *Plasmodium* virulence in

the field. Therefore, the demonstrated direct correlation between sporozoite quantities

and transmission efficiency in naïve and vaccinated hosts (Churcher et al., 2017) should

also consider sporozoite quality, both of which depend on the mosquito nutritional status.

Finally, targeting host/vector lipid trafficking may offer new potent and powerful

strategies to block parasite development in the next host, thereby preventing the vicious

cycle of malaria transmission.

AUTHOR CONTRIBUTIONS

GC and EAL conceived the study and designed the experiments. GC, ME, RL, CG, and

VB performed experiments. AEH and RS contributed reagents and expertise. GC, ME,

RL, RS, CG, VB, and EAL analyzed the data. GC and EAL wrote the manuscript.

ACKNOWLEDGEMENTS

This work was supported by EC FP7 EVIMalaR (grant agreement n°242095) and

MALVECBLOK (grant agreement nº223601). The authors thank H. Krüger, M. Andres

and L. Spohr for mosquito rearing, mouse work assistance, and *Plasmodium* infections,

and D. Tschierske and D. Eyermann for *P. falciparum* cultures. Editorial support of Dr.

R. Willmott (Bioscript) is gratefully acknowledged. The authors express their gratitude to

Prof. K. Matuschewski and his group for continuous fruitful discussions and to Dr. M.M.

Mota for helpful comments.

REFERENCES:

Atella, G.C., Bittencourt-Cunha, P.R., Nunes, R.D., Shahabuddin, M., and Silva-Neto,
M.A. (2009). The major insect lipoprotein is a lipid source to mosquito stages of malaria
parasite. Acta Trop *109*, 159-162.

Atella, G.C., Silva-Neto, M.A., Golodne, D.M., Arefin, S., and Shahabuddin, M. (2006).
Anopheles gambiae lipophorin: characterization and role in lipid transport to developing
oocyte. Insect Biochem Mol Biol *36*, 375-386.

Azevedo, R., Markovic, M., Machado, M., Franke-Fayard, B., Mendes, A.M., and
Prudencio, M. (2017). A bioluminescence method for in vitro screening of Plasmodium
transmission-blocking compounds. Antimicrob Agents Chemother.

Boysen, K.E., and Matuschewski, K. (2011). Arrested oocyst maturation in Plasmodium
parasites lacking type II NADH:ubiquinone dehydrogenase. J Biol Chem *286*, 32661-
32671.

Butler, N.S., Vaughan, A.M., Harty, J.T., and Kappe, S.H. (2012). Whole parasite
vaccination approaches for prevention of malaria infection. Trends Immunol *33*, 247-254.

Carroll, R.W., Wainwright, M.S., Kim, K.Y., Kidambi, T., Gomez, N.D., Taylor, T., and
Haldar, K. (2010). A rapid murine coma and behavior scale for quantitative assessment of
murine cerebral malaria. PLoS One *5*.

Churcher, T.S., Sinden, R.E., Edwards, N.J., Poulton, I.D., Rampling, T.W., Brock, P.M.,
Griffin, J.T., Upton, L.M., Zakutansky, S.E., Sala, K.A.*, et al.* (2017). Probability of
Transmission of Malaria from Mosquito to Human Is Regulated by Mosquito Parasite
Density in Naive and Vaccinated Hosts. PLoS Pathog *13*, e1006108.

Coppi, A., Tewari, R., Bishop, J.R., Bennett, B.L., Lawrence, R., Esko, J.D., Billker, O.,
and Sinnis, P. (2007). Heparan sulfate proteoglycans provide a signal to Plasmodium
sporozoites to stop migrating and productively invade host cells. Cell Host Microbe *2*,
316-327.

Davies, C.S., Pudney, M., Nicholas, J.C., and Sinden, R.E. (1993). The novel
hydroxynaphthoquinone 566C80 inhibits the development of liver stages of Plasmodium
berghei cultured in vitro. Parasitology *106 (Pt 1)*, 1-6.

Eickel, N., Kaiser, G., Prado, M., Burda, P.C., Roelli, M., Stanway, R.R., and Heussler,
V.T. (2013). Features of autophagic cell death in Plasmodium liver-stage parasites.
Autophagy *9*, 568-580.

Folly, E., Cunha e Silva, N.L., Lopes, A.H., Silva-Neto, M.A., and Atella, G.C. (2003).
Trypanosoma rangeli uptakes the main lipoprotein from the hemolymph of its
invertebrate host. Biochem Biophys Res Commun *310*, 555-561.

Fowler, R.E., Sinden, R.E., and Pudney, M. (1995). Inhibitory activity of the anti-
malarial atovaquone (566C80) against ookinetes, oocysts, and sporozoites of Plasmodium
berghei. J Parasitol *81*, 452-458.

Franke-Fayard, B., Trueman, H., Ramesar, J., Mendoza, J., van der Keur, M., van der
Linden, R., Sinden, R.E., Waters, A.P., and Janse, C.J. (2004). A *Plasmodium berghei*
reference line that constitutively expresses GFP at a high level throughout the complete
life cycle. Mol Biochem Parasitol *137*, 23-33.

Gillies, M.T. (1954). The recognition of age-groups within populations of *Anopheles*
gambiae by the pre-gravid rate and the sporozoite rate. Ann Trop Med Parasitol *48*, 58-
74.

Goodman, C.D., Siregar, J.E., Mollard, V., Vega-Rodriguez, J., Syafruddin, D.,
Matsuoka, H., Matsuzaki, M., Toyama, T., Sturm, A., Cozijnsen, A.*, et al.* (2016).
Parasites resistant to the antimalarial atovaquone fail to transmit by mosquitoes. Science
352, 349-353.

Grellier, P., Rigomier, D., Clavey, V., Fruchart, J., and Schrevel, J. (1991). Lipid Traffic
Between High Density Lipoproteins and *Plasmodium-falciparum*-Infected Red Blood
Cells. J Cell Biol *112*, 267-277.

Gupta, S., Hill, A.V.S., Kwiatkowski, D., Greenwood, A.M., Greenwood, B., and Day,
K. (1994). Parasite virulence and disease patterns in *Plasmodium falciparum* malaria.
Proc Natl Acad Sci U S A *91*, 3715-3719.

Hino, A., Hirai, M., Tanaka, T.Q., Watanabe, Y., Matsuoka, H., and Kita, K. (2012).
Critical roles of the mitochondrial complex II in oocyst formation of rodent malaria
parasite Plasmodium berghei. J Biochem *152*, 259-268.

Itoe, M.A., Sampaio, J.L., Cabal, G.G., Real, E., Zuzarte-Luis, V., March, S., Bhatia,
S.N., Frischknecht, F., Thiele, C., Shevchenko, A.*, et al.* (2014). Host cell
phosphatidylcholine is a key mediator of malaria parasite survival during liver stage
infection. Cell Host Microbe *16*, 778-786.

Lackner, P., Beer, R., Heussler, V., Goebel, G., Rudzki, D., Helbok, R., Tannich, E., and
Schmutzhard, E. (2006). Behavioural and histopathological alterations in mice with
cerebral malaria. Neuropathol Appl Neurobiol *32*, 177-188.

Lauer, S., VanWye, J., Harrison, T., McManus, H., Samuel, B.U., Hiller, N.L.,
Mohandas, N., and Haldar, K. (2000). Vacuolar uptake of host components, and a role for
cholesterol and sphingomyelin in malarial infection. EMBO J *19*, 3556-3564.

Mackinnon, M.J., and Read, A.F. (2004). Immunity promotes virulence evolution in a
malaria model. PLoS Biol *2*, E230.

March, S., Ng, S., Velmurugan, S., Galstian, A., Shan, J., Logan, D.J., Carpenter, A.E.,
Thomas, D., Sim, B.K., Mota, M.M*., et al.* (2013). A microscale human liver platform
that supports the hepatic stages of *Plasmodium falciparum* and *vivax*. Cell Host Microbe
14, 104-115.

Menard, R., Sultan, A.A., Cortes, C., Altszuler, R., van Dijk, M.R., Janse, C.J., Waters,
A.P., Nussenzweig, R.S., and Nussenzweig, V. (1997). Circumsporozoite protein is
required for development of malaria sporozoites in mosquitoes. Nature *385*, 336-340.

Mendes, A.M., Schlegelmilch, T., Cohuet, A., Awono-Ambene, P., De Iorio, M.,
Fontenille, D., Morlais, I., Christophides, G.K., Kafatos, F.C., and Vlachou, D. (2008).
Conserved mosquito/parasite interactions affect development of *Plasmodium falciparum*
in Africa. PLoS Pathog *4*, e1000069.

Moller-Jacobs, L.L., Murdock, C.C., and Thomas, M.B. (2014). Capacity of mosquitoes
to transmit malaria depends on larval environment. Parasites & vectors *7*, 593.

Mota, M.M., Pradel, G., Vanderberg, J.P., Hafalla, J.C., Frevert, U., Nussenzweig, R.S.,
Nussenzweig, V., and Rodriguez, A. (2001). Migration of *Plasmodium* sporozoites
through cells before infection. Science *291*, 141-144.

Muller, K., Matuschewski, K., and Silvie, O. (2011). The Puf-family RNA-binding
protein Puf2 controls sporozoite conversion to liver stages in the malaria parasite. PloS
one *6*, e19860.

Okech, B.A., Gouagna, L.C., Kabiru, E.W., Beier, J.C., Yan, G., and Githure, J.I. (2004).
Influence of age and previous diet of *Anopheles gambiae* on the infectivity of natural
Plasmodium falciparum gametocytes from human volunteers. Journal of insect science *4*,
33.

Oppenheim, R.D., Creek, D.J., Macrae, J.I., Modrzynska, K.K., Pino, P., Limenitakis, J.,
Polonais, V., Seeber, F., Barrett, M.P., Billker, O*., et al.* (2014). BCKDH: the missing
link in apicomplexan mitochondrial metabolism is required for full virulence of
Toxoplasma gondii and Plasmodium berghei. PLoS Pathog *10*, e1004263.

Perry, S.W., Norman, J.P., Barbieri, J., Brown, E.B., and Gelbard, H.A. (2011).
Mitochondrial membrane potential probes and the proton gradient: a practical usage
guide. BioTechniques *50*, 98-115.

Pompon, J., and Levashina, E.A. (2015). A New Role of the Mosquito Complement-like
Cascade in Male Fertility in *Anopheles gambiae*. PLoS Biol *13*, e1002255.

Ponnudurai, T., Lensen, A.H., van Gemert, G.J., Bensink, M.P., Bolmer, M., and
Meuwissen, J.H. (1989). Sporozoite load of mosquitoes infected with *Plasmodium*
falciparum. Trans R Soc Trop Med Hyg *83*, 67-70.

Rono, M.K., Whitten, M.M., Oulad-Abdelghani, M., Levashina, E.A., and Marois, E.
(2010). The major yolk protein vitellogenin interferes with the anti-*Plasmodium* response
in the malaria mosquito *Anopheles gambiae*. PLoS Biol *8*, e1000434.

Rudolf, M., and Curcio, C.A. (2009). Esterified cholesterol is highly localized to Bruch's
membrane, as revealed by lipid histochemistry in wholemounts of human choroid. J
Histochem Cytochem *57*, 731-739.

Sa, E.C.C., Nyboer, B., Heiss, K., Sanches-Vaz, M., Fontinha, D., Wiedtke, E., Grimm,
D., Przyborski, J.M., Mota, M.M., Prudencio, M.*, et al.* (2017). Plasmodium berghei
EXP-1 interacts with host Apolipoprotein H during Plasmodium liver-stage development.
Proc Natl Acad Sci U S A *114*, E1138-E1147.

Seder, R.A., Chang, L.J., Enama, M.E., Zephir, K.L., Sarwar, U.N., Gordon, I.J.,
Holman, L.A., James, E.R., Billingsley, P.F., Gunasekera, A.*, et al.* (2013). Protection
against malaria by intravenous immunization with a nonreplicating sporozoite vaccine.
Science *341*, 1359-1365.

Shapiro, L.L., Murdock, C.C., Jacobs, G.R., Thomas, R.J., and Thomas, M.B. (2016).
Larval food quantity affects the capacity of adult mosquitoes to transmit human malaria.
Proc Biol Sci *283*.

Shiao, S.H., Whitten, M.M., Zachary, D., Hoffmann, J.A., and Levashina, E.A. (2006).
Fz2 and *cdc42* mediate melanization and actin polymerization but are dispensable for
Plasmodium killing in the mosquito midgut. PLoS Pathog *2*, e133.

Silvie, O., Goetz, K., and Matuschewski, K. (2008). A sporozoite asparagine-rich protein
controls initiation of *Plasmodium* liver stage development. PLoS Pathog *4*, e1000086.

Siregar, J.E., Kurisu, G., Kobayashi, T., Matsuzaki, M., Sakamoto, K., Mi-ichi, F.,
Watanabe, Y., Hirai, M., Matsuoka, H., Syafruddin, D.*, et al.* (2015). Direct evidence for

the atovaquone action on the Plasmodium cytochrome bc1 complex. Parasitol Int *64*,
295-300.

Srivastava, I.K., Rottenberg, H., and Vaidya, A.B. (1997). Atovaquone, a broad spectrum
antiparasitic drug, collapses mitochondrial membrane potential in a malarial parasite. J
Biol Chem *272*, 3961-3966.

Takken, W., Smallegange, R.C., Vigneau, A.J., Johnston, V., Brown, M., Mordue-Luntz,
A.J., and Billingsley, P.F. (2013). Larval nutrition differentially affects adult fitness and
Plasmodium development in the malaria vectors *Anopheles gambiae* and *Anopheles*
stephensi. Parasites & vectors *6*, 345.

Van der Horst, D.J., Roosendaal, S.D., and Rodenburg, K.W. (2009). Circulatory lipid
transport: lipoprotein assembly and function from an evolutionary perspective. Mol Cell
Biochem *326*, 105-119.

van Schaijk, B.C., Ploemen, I.H., Annoura, T., Vos, M.W., Foquet, L., van Gemert, G.J.,
Chevalley-Maurel, S., van de Vegte-Bolmer, M., Sajid, M., Franetich, J.F.*, et al.* (2014).
A genetically attenuated malaria vaccine candidate based on *P. falciparum* b9/slarp gene-
deficient sporozoites. eLife *3*.

Vantaux, A., Lefevre, T., Cohuet, A., Dabire, K.R., Roche, B., and Roux, O. (2016).
Larval nutritional stress affects vector life history traits and human malaria transmission.
Sci Rep *6*, 36778.

Ximenes Ados, A., Silva-Cardoso, L., De Cicco, N.N., Pereira, M.G., Lourenco, D.C.,
Fampa, P., Folly, E., Cunha-e-Silva, N.L., Silva-Neto, M.A., and Atella, G.C. (2015).
Lipophorin Drives Lipid Incorporation and Metabolism in Insect Trypanosomatids.
Protist *166*, 297-309.

Yilmaz, B., Portugal, S., Tran, T.M., Gozzelino, R., Ramos, S., Gomes, J., Regalado, A.,
Cowan, P.J., d'Apice, A.J., Chong, A.S.*, et al.* (2014). Gut microbiota elicits a protective
immune response against malaria transmission. Cell *159*, 1277-1289.

Yuda, M., Iwanaga, S., Shigenobu, S., Kato, T., and Kaneko, I. (2010). Transcription
factor AP2-Sp and its target genes in malarial sporozoites. Mol Microbiol *75*, 854-863.
Zurzolo, C., and Simons, K. (2016). Glycosylphosphatidylinositol-anchored proteins:
Membrane organization and transport. Biochim Biophys Acta *1858*, 632-639.
405
406   Zurzolo, C., and Simons, K. (2016). Glycosylphosphatidylinositol-anchored proteins:
407   Membrane organization and transport. Biochim Biophys Acta *1858*, 632-639.
408
409

Figure 1. Effect of mosquito lipid trafficking on *Plasmodium* sporogony.

Distribution of neutral lipids (Nile Red dye) in the midgut, ovaries, and fat body of

control (Ctrl) and Lp-deficient (*dsLp*) mosquitoes. (**A**) Representative fluorescence

micrographs of female abdomens of control and Lp-depleted mosquitoes dissected before

(unfed), 2, 7 and 13 days post *Plasmodium* infection (dpi). Neutral lipids are stained by

Nile Red (red) and cell nuclei are in blue (DAPI). Scale bar - 100 μm. (**B**) Intensity of the

Nile Red staining was measured in the midgut, ovaries, and fat body of control and Lp-

depleted mosquitoes. Each data point represents the mean intensity of Nile Red signal ±

SEM per midgut (n≥3). Control and Lp-deficient females were infected with *P.*

falciparum (*P.f.)* or *P. berghei* (*P.b.*). (**C**) Sizes of *P.f.* (11 dpi, n=3) and *P.b.* (14 dpi,

n=6) oocysts in control and Lp-depleted mosquitoes. At least 225 oocysts were measured

per condition. The box plots represent medians (horizontal bars) with 10th and 90th percentiles. (**D**) Development of *P.f.* (14 dpi, n=5) and *P.b.* (18 dpi, n=4) salivary gland sporozoites in control and Lp-depleted mosquitoes. Each point represents the mean number of sporozoites per mosquito for each experimental replicate. Asterisks indicate statistically significant differences (Mann-Whitney test and 2-way ANOVA, *p<0.05; **p<0.001; ***p<0.0001).

Figure 2. Disruption of mosquito lipid trafficking impairs *Plasmodium* sporogony.

Control (Ctrl) and Lp-deficient (*dsLp*) females were infected with *P. berghei* and the oocyst sizes, morphology, lipid, and Lp uptake were gauged by fluorescence and transmission electron microscopy. (**A**) Time-series analysis of oocyst development in control (blue) and Lp-depleted (red) mosquitoes. At least 5 mosquitoes were dissected per time point and per condition (n=2). The box plots represent medians (horizontal bars) with 10th and 90th percentiles. (**B**) Neutral lipids (red) detected by the Nile Red dye inside the GFP-expressing *P. berghei* oocysts (green) 14 dpi in control and Lp-depleted mosquitoes. Nuclei are visualized by DAPI (blue). Scale bars - 10 μm. (**C**) Lp accumulation (red) on the GFP-expressing oocysts (green) in the midguts of control *P. berghei*-infected mosquitoes revealed by immunofluorescence analysis using anti-Lp

antibodies at 7, 9, 11, and 13 days post infection (dpi). No Lp signal was observed in Lp-

depleted mosquitoes. Nuclei are visualized by DAPI (blue). Scale bars - 10 µm.

Representative transmission electron micrographs of *P. berghei* oocysts in control and

Lp-depleted mosquitoes 7 (**D**) and 13 (**E**) dpi. White arrowheads point to the

membranous structures in control and to the electron-dense actin-zone in Lp-depleted

mosquitoes. Scale bars - 10 µm. (**F**) Oocysts detected by transmission electron

microscopy were scored according to the developmental stage: non-sporulating oocysts

with normal morphology (immature, white); oocysts with normal plasma membrane

retraction, budding sporoblasts, or formed sporozoites (sporulating, gray); oocysts with

aberrant electron-light intracellular vacuolization (abnormal/dead, black). Proportions of

the categories are shown as pie charts and the total numbers of analyzed oocysts per

condition are indicated in the middle of each chart. Asterisks indicate statistically

significant differences (Kruskal-Wallis test, ***$p < 0.0001$).

Figure 3. Mosquito lipids determine *Plasmodium* virulence in mammalian hosts.

C57BL/6 mice were infected with *P. berghei* and monitored daily for parasite occurrence in the blood by Giemsa staining of thin blood smears and by FACS and experimental cerebral malaria symptoms (ECM) malaria symptoms. (**A**) Kaplan-Meier analysis of time to malaria and (**B**) cumulative health status frequencies of mice infected by control (CTRL, blue line, n=10) or Lp-depleted (*dsLp*, red line, n=10) mosquitoes via direct bite. (**C**) Kaplan-Meier analysis of time to malaria, (D) means and SEM of parasitemia, (E) percentage of experimental cerebral malaria (ECM) incidence and (F) cumulative health status frequencies of mice infected by subcutaneous injection of 5,000 sporozoites dissected from the salivary glands of control (CTRL, blue line, n=18) or Lp-depleted (*dsLp*, red line, n=16) mosquitoes. Asterisks indicate statistically significant differences (log-rank Mantel-Cox test and 2-way ANOVA *p<0.05; **p<0.001, ***p<0.0001.

Figure 4. Mosquito lipids attenuate sporozoite infectivity to hepatocytes.

Lp-depleted mosquitoes (*dsLp*) and controls (CTRL) were infected with *P. berghei* and

offered (**B, D, F and H**) or not (**A, C, E and G**) a supplemental blood meal 7 days post

infection. (**A** and **B**) Salivary gland sporozoites were isolated and counted from control

and Lp-deficient mosquitoes. (**C** and **D**) Human hepatoma HepG2 cells were infected

with 10,000 sporozoites and the number of extra-erythrocytic forms (EEFs) per field was

gauged by microscopy 2 dpi. As a negative control, sporozoites from control mosquitoes

were treated with cytochalasin D (Cyt D). Mean numbers and SEM are shown. (**E** and **F**)

Representative fluorescent micrographs of GFP-expressing EEFs (green) developing in

HepG2 cells. Cell nuclei are stained with DAPI (blue). Scale bar - 10 μm. (**G** and **H**) EEF

485   sizes produced by sporozoites from control and Lp-deficient mosquitoes. The box plots

486   represent 10th and 90th percentiles while the horizontal lines show medians. Asterisks

487   indicate statistically significant differences (n=3, Kruskal-Wallis and Mann-Whitney test,

488   *p<0.05; ***p<0.0001).

490
491
Figure 5. Mosquito lipids regulate sporozoite mitochondrial membrane potential.
(**A**) Sporozoite GFP expression and mitochondrial membrane potential as measured by
TMRE staining were analysed using imaging flow cytometry. Representative images of
control (Ctrl) and lipid-deprived (*dsLp*) sporozoites are shown. Scale bars - 5 μm.
Histograms from one representative experiment (3, 270 events per condition) showing
(**B**) TMRE signal (Bright Detail Intensity R7 of Channel 4) or (**C**) GFP (Intensity MC of
Channel 2) in control (blue) and lipid-deprived (red) sporozoites. Geometrical mean
values of (**D**) Bright Detail Intensity R7 of Channel 4 or (**E**) Intensity MC of Channel 2
from four independent experiments in control (blue, N=1405) and lipid-deprived (red,
N=593) sporozoites. Asterisks indicate statistically significant differences (Paired t test,
*p<0.05).

EXPERIMENTAL PROCEDURES

Mosquito Rearing and Parasite Infections

Anopheles gambiae s.l. mosquitoes were used throughout the study. G3 and 7b lines - an immunocompromised transgenic mosquito line of G3 origin in which expression of the complement-like gene TEP1 is down-regulated (Pompon and Levashina, 2015), were maintained at 29°C 70%–80% humidity 12/12 h day/night cycle. In *P. falciparum* infections, mosquitoes were fed at 37°C for 15 min through a membrane feeder with NF54 gametocytes cultured with O+ human red blood cells (Haema, Berlin), and thereafter kept in a secured S3 laboratory according to the national regulations (Landesamt für Gesundheit und Soziales, project number 411/08). For *P. berghei* experiments, mosquitoes were fed on anesthetized CD1 mice infected with the *P. berghei* GFP-con 259cl2 clone (ANKA strain) that constitutively expresses GFP (Franke-Fayard et al., 2004). Shortly after infections, unfed mosquitoes were removed, while fed mosquitoes were maintained at 26°C for 11-14 days (*P. falciparum*) or at 20°C for 7-21 days (*P. berghei*), and then used for the midgut and/or the salivary gland dissections.

RNAi silencing

Double stranded RNA (dsRNA) against *lipophorin* (*dsLp*) was produced as previously described (Rono et al., 2010). For RNAi silencing, 1-2 day-old females were anesthetized with CO_2 and injected with 69 nl of 3 µg/µl *dsLacZ* (control) or *dsLp* using a Nanoject II Injector (Drummond). Mosquitoes recovered for 3-4 days following injection before infections. Efficiencies of RNAi silencing are summarized in Figure S5.

Immunofluorescence Analysis

Mosquito midguts were dissected in PBS, fixed in 4% formaldehyde and washed in PBS. Tissues were permeabilized with Triton X-100 0.1% and incubated with a 1:1 mix of mouse monoclonal anti-ApoI and anti-ApoII antibodies (1/300, clones 2H5 and 2C6)

(Rono et al., 2010) overnight at 4°C followed by incubation for 40 min at room
temperature with the secondary Cy3-labeled antibodies at 1/1,000 (Molecular Probes), or
with 0.1 µg/ml of the Nile Red dye (Sigma Aldrich). Nuclei were stained with DAPI
(1.25 µg/ml, Molecular Probes) for 40-60 min at room temperature. Images were
acquired using an AxioObserver Z1 fluorescence microscope equipped with an Apotome
module (Zeiss). Oocyst sizes were measured by hand-designing a circular ROI of
randomly selected oocysts (identified by GFP for *P. berghei* or by bright field and DAPI
staining for *P. falciparum*) using ZEN 2012 software (Zeiss). Images were then processed
by FIJI software (ImageJ 1.47m).

Transmission and Scanning Electron Microscopy

Infected midguts were dissected in PBS, embedded in a drop of low melting agarose (4%)
and fixed overnight in 2.5% EM grade glutaraldehyde at 4°C. Midguts were postfixed in
0.5% osmium tetroxide, contrasted with tannic acid and 2% uranyl acetate, dehydrated,
and embedded in epoxy resin. After polymerization, sections were cut at 60 nm and
contrasted with lead citrate. Specimens were analyzed in a Leo 906E transmission
electron microscope at 100KV (Zeiss) using digital camera (Morada).

P. berghei **liver-stage development** *in vitro*

The salivary glands and midguts of *P. berghei* infected mosquitoes were dissected,
sporozoites were collected into RPMI medium (Gibco) 3% bovine serum albumin (Sigma
Aldrich) and enumerated with a hemocytometer. The *P. berghei* liver stages were
cultured *in vitro* in HepG2 hepatoma cells and analyzed using standard techniques (Silvie
et al., 2008). In short, 15,000 - 20,000 HepG2 cells per well (70% confluence) were
plated in the transparent-bottom 96-wells plates (Nalgene International) and incubated for
24 h, then seeded with 10,000 sporozoites and left at 37°C for 2 h. Non-invading
sporozoites were removed by washing. As a negative control, sporozoites isolated from
control mosquitoes were pre-treated with the inhibitor of actin polymerization

Cytochalasin D (Sigma Aldrich) for 10 min. At 48 h post seeding, the cells were fixed for

10 min with 4% formaldehyde, washed with PBS and blocked with 10% fetal calf serum

in PBS. Development of the liver-stage parasites was examined using monoclonal mouse

anti-GFP antibodies (1/1,000, AbCam) and revealed with the secondary AlexaFluor488

conjugated anti-mouse antibody (1/1,000, Molecular Probes). Nuclei were stained with

DAPI (1.25 μg/ml, Molecular Probes). Images were recorded directly on the 96-wells

plate using an AxioObserver Z1 fluorescence microscope equipped with an Apotome

module (Zeiss) and analyzed for number and size of liver forms using the Axio-Vision

ZEN 2012 software (Zeiss).

P. berghei* mouse infections *in vivo

Mice were housed and handled in accordance with the German Animal Protection Law

(§8 Tierschutzgesetz) and both institutional (Max Planck Society) and national

regulations (Landesamt für Gesundheit und Soziales, registration number H 0027/12). To

determine sporozoite infectivity to mice, the sporozoites collected from the mosquito

salivary glands (5,000 sporozoites/mouse) were injected subcutaneously into the tails of

8-10-week-old C57BL/6 females. Bite-back experiments were performed by feeding the

P. berghei-infected mosquitoes (18 dpi) on anesthetized naïve C57BL/6 mice (mean 9

bites/mouse, range 2-15). Blood cell parasitemia was determined by daily Giemsa

staining of thin blood smears and FACS analysis of the red blood cells with the GFP-

expressing blood stage parasites. Infected mice were monitored every 6-12 h for the

appearance of severe neurological and behavioral symptoms typical of experimental

cerebral malaria (ECM) such as hunched body position, grooming alteration, ataxia,

paralysis, or convulsions (Lackner et al., 2006) or by the rapid neurological and

behavioral test (RMCBS) (Carroll et al., 2010). All mice with ECM symptoms or the

RMCBS score equal or below 5/20 were sacrificed immediately.

Sporozoite imaging flow cytometry

Salivary gland sporozoites were purified in RPMI medium (Gibco) 3% bovine serum

albumin (Sigma Aldrich) and kept on ice until staining. Sporozoites were diluted in PBS

to concentrations corresponding to 3 mosquito equivalents and stained in the dark with 5

nM TMRE (Cell Signalling Technology) for 20 min at 20°C. CCCP at 50 µM was used

as a negative control (see Figure S5D). Sporozoite images were acquired without washing

using an ImageStreamX Mk II (Merck Millipore) with a 60x objective over 1 h period.

To avoid a possible bias due to the variable pre-acquisition waiting times on ice, the order

of sample acquisition was swapped in half of the experimental replicates. GFP-expressing

sporozoites were gated by size (Area_M01 or Area_M02) and by GFP intensity

(Intensity_MC_Ch02). The analysis was performed with IDEAS 6.2 (Merck Millipore)

and FCS files were exported and analyzed by FlowJo v10. Given the small size of the

sporozoite mitochondria, the feature finder tool from IDEAS software was used to

improve gating of optimally focused sporozoites. The following parameters were used to

discriminate focused single sporozoites from debris, and to identify sporozoites sharply

focused enough to resolve their mitochondria: H Entropy Std_M01_Ch01_15 over H

Variance Std_M01_Ch01, Aspect Ratio_M02 over Symmetry 4-Object(M02,Ch2)_Ch02,

Gradient RMS-M01-Ch01 over H Correlation Mean-M02-Ch02_3, and Gradient RMS-

M02_Ch02. Briefly, these parameters respectively measure brightfield image texture,

GFP image shape, and brightfield and GFP focus. For measurement of mitochondrial

membrane potential and GFP intensity, each sample was time-gated to exclude events

with prolonged live staining. The parameter corresponding to the lowest background

signal in unstained sporozoites was Bright Detail Intensity R7_M04_Ch04, Geo Mean

which was selected as *bona fide* TMRE intensity readout (see Figure S5D). For GFP

intensity the Intensity_MC_Ch02, Geo. Mean was used.

Statistical analysis

613   Statistical analysis were performed using GraphPad Prism 7 software and p values < 0.05

614   were considered significant (*: $p<0.05$; **: $p<0.001$; ***: $p<0.0001$) and indicated in the

615   figures. The specific tests used are indicated for each figure in the corresponding legend.