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Background: Interventions that interrupt *Plasmodium vivax* transmission or eliminate dormant *P. vivax* liver-stage parasites will be essential for malaria elimination. Development of these interventions has been hindered by the lack of *P. vivax in vitro* culture and could be accelerated by a safe and reproducible clinical model in malaria-naïve individuals.

Method: Healthy, malaria-naïve adults were enrolled in two studies to assess the safety and infectivity and transmissibility of a new *P. vivax* isolate. Participants (Study 1; n=2, Study 2; n=24) were inoculated with *P. vivax*-infected red blood cells to initiate infection, and were treated with artemether-lumefantrine (Study 1) or chloroquine (Study 2). Primary endpoints were safety and infectivity of the new isolate. In Study 2, transmission to mosquitoes was also evaluated using mosquito feeding assays, and sporozoite viability was assessed using in vitro cultured hepatocytes.

Results: Parasitaemia and gametocytemia developed in all participants and was cleared by antimalarial treatment. Adverse events were mostly mild or moderate and none were serious. Participants were infectious to *Anopheles* mosquitoes at peak gametocytemia 69% (11/16). Mosquito infection rates reached 97% following membrane feeding with gametocyte-enriched blood, and sporozoites developed into liver-stage schizonts in culture.

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Abstract

Background: Interventions that interrupt *Plasmodium vivax* transmission or eliminate dormant *P. vivax* liver-stage parasites will be essential for malaria elimination. Development of these interventions has been hindered by the lack of *P. vivax in vitro* culture and could be accelerated by a safe and reproducible clinical model in malaria-naïve individuals.

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Results: Parasitaemia and gametocytemia developed in all participants and was cleared by antimalarial treatment. Adverse events were mostly mild or moderate and none were serious. Participants were infectious to *Anopheles* mosquitoes at peak gametocytemia 69% (11/16). Mosquito infection rates reached 97% following membrane feeding with gametocyte-enriched blood, and sporozoites developed into liver-stage schizonts in culture.

Conclusion: We have demonstrated the safe, reproducible, and efficient transmission of *P. vivax* gametocytes from humans to mosquitoes, and have established an experimental model that will accelerate the development of interventions targeting multiple stages of the *P. vivax* life cycle.

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Key words:

Malaria, *Plasmodium vivax*, CHMI, controlled human malaria infection, volunteer infection study, VIS, induced blood-stage malaria, IBSM, drugs, vaccines, transmission, gametocyte, oocyst, sporozoite, mosquito, transmission-blocking

Introduction

Plasmodium vivax is the most globally widespread human malaria parasite, and the predominant cause of malaria outside of Africa (1). Although a major cause of morbidity, *P. vivax* infection has long been regarded as benign compared to *P. falciparum*. However, it has recently become widely recognised as a cause of severe, life-threatening, and fatal malaria infection (2, 3). As a consequence, there is renewed interest in developing *P. vivax* specific control and elimination strategies (4). *P. vivax* is considered more difficult to control than *P. falciparum* due to the parasite's unique biological features that increase its potential for transmission (5). Unlike *P. falciparum,* the transmissible stages of *P. vivax* (the gametocytes) appear early during blood-stage infection before the onset of symptoms, which increases the likelihood of transmission before treatment. *P. vivax* produces hypnozoites which are dormant liver-stage parasite that cause relapses months to years after initial infection — reported to account for up to 80% of all *P. vivax* infections (6) — thus providing repeated opportunities for onward transmission. In addition, *P. vivax* can be transmitted by a broad range of *Anopheles* vectors, many with exophilic and zoophilic tendencies, thus reducing the efficacy of conventional vector control measures (7). Therefore, as well as treating asexual parasites to control clinical illness, *P. vivax* control strategies must also target hypnozoites and block transmission to have a significant impact on control and elimination (8).

The current recommended treatment for *P. vivax* is chloroquine or artemisinin-based combination therapy to clear asexual parasitaemia, administered with the 8-aminoquinioline, primaquine for 14 days to clear liver-stage hypnozoites (9). A single dose of tafenoquine recently demonstrated equivalent efficacy against hypnozoites with the potential to substantially improve treatment compliance. However, wide scale deployment of these drugs to achieve meaningful public health impact is complicated by the need to screen for glucose-6-phosphate dehydrogenase deficiency, and safer alternatives are needed (10).

A *P. vivax* transmission-blocking vaccine (TBV) could interrupt transmission from primary infections, relapses, and also asymptomatic infections that remain undiagnosed and transmissible for a

prolonged period. A TBV would reduce morbidity and mortality by preventing both new clinical infections and hypnozoite formation (11, 12). The inability to continuously culture *P. vivax* parasites in vitro, and the difficulties in using animal models (8), has hampered development of interventions specifically targeting *P. vivax* hypnozoites and gametocytes. The production of gametocytes for evaluation of TBVs and sporozoites for liver-stage hypnozoite assays is limited to endemic settings where natural gametocyte carriers are available. Thus, a safe and reproducible in vivo model of human to mosquito *P. vivax* transmission in malaria-naïve volunteers would accelerate development and early-clinical evaluation of transmission-blocking interventions. Moreover, sporozoites generated from mosquitoes fed on gametocytes collected from unvaccinated volunteers during these studies could be used to evaluate interventions that target hypnozoites.

P. vivax experimental human infection studies, termed controlled human malaria infection (CHMI) or volunteer infection studies (VIS), have been established where malaria infections are initiated either by sporozoite inoculation or by the induced blood-stage malaria (IBSM) model (13). To date, none of these studies have demonstrated efficient *P. vivax* transmission from humans to mosquitoes. The IBSM model uses cryopreserved and characterised *P. vivax*-infected red blood cells (RBCs) to initiate infection. There have been only two previous *P. vivax* IBSM studies (both conducted at our centre), where a total of 8 adults were infected with a *P. vivax* isolate from the Solomon Islands; however, efficient transmission to mosquito was not achieved (14, 15). These studies were the first experimental infection of humans with blood-stage *P. vivax* using the modern IBSM model (deliberate infection with *P. vivax* was practiced between the 1920s and 1970s when malariotherapy was used for syphilis treatment (16), as well as in experimental studies with US prisoners (17)). Here, we evaluate the safety, tolerability, and infectivity of a new *P. vivax* isolate bank from India and describe a clinical model for evaluating the efficacy of blood-stage schizonticides and transmission-blocking interventions that can be exploited to facilitate the evaluation of *P. vivax* liver-stage interventions.

Results

Twenty-six malaria-naïve volunteers were enrolled in two clinical trials: Study 1 (n=2) undertaken from October 8, 2014 to January 8, 2015 and Study 2 (n=24) undertaken from February 22, 2016 to May 21, 2017 (Figure 1 and 2). Baseline characteristics of participants are presented in Table 1.

All participants were inoculated with an estimated 564 viable *P. vivax* parasites and the experimental infection was generally well tolerated. In Study 1, 14 adverse events (AEs) were reported: 12 attributed to malaria (headache, fever, myalgia, arthralgia, presyncope, rigors), one deemed possibly related to artemether-lumefantrine (somnolence), and one not related to malaria or artemether-lumefantrine (headache 49 days after treatment) (Table 2). Most AEs resolved within 24 h of treatment with paracetamol, except two intermittent headaches that resolved in 4 days and 8 days, and right knee pain that resolved in 4 days. All AEs were mild (n=13/14; 92.9%) or moderate (n=1/14; 7.1%) in severity. In Study 2, 355 AEs were reported (Table 2). A total of 296 (83.4%) were related to malaria, of these, 8 (2.3%) were concurrently deemed possibly related to chloroquine. Eleven (3.1%) AEs were related to direct skin feeding (DFA) (reaction at site of mosquito bite); the remaining AEs were attributed to other causes. Most AEs were mild (250/355; 70.4%) or moderate (98/355; 27.6%) in severity. Four severe AEs occurred and were all attributed to malaria: reduced neutrophil count (0.65×10^9/L), chills, elevated alanine aminotransferase (peak 6.9 ×ULN), and arthralgia. No serious AEs were reported in either trial.

All 26 participants developed blood-stage parasitaemia. In Study 1, parasites were first detected by 18S quantitative PCR (18S qPCR) on Day 5 in both participants. Parasitaemia peaked at 21,836 and 8,949 parasites/mL on the day of treatment (Day 8), and was completely cleared following treatment with artemether-lumefantrine (Figure 3A). In Study 2, parasites were first detected by 18S qPCR in 21/24 participants on Day 4, and in the remaining 3 participants on Day 5. The course of parasite development did not differ between cohorts (Figure 3D+F) and parasitaemia was cleared in all participants in a median of 3 days after initiation of chloroquine treatment, range = 1.5–7.0 days.

Gametocytes were first detected (above 10 gametocytes/mL) on Day 6 in Study 1 (Figure 3A) and between Day 4 and 7 in Study 2, which was an average of 1·5 days (range = 0–3 days) after first detection of asexual parasites (Figure 3D-F). Using the transcript number estimates per gametocyte published by Karl et al., (18) to convert *pvs25* transcripts/mL to gametocytes/mL, the peak gametocyte levels were 5.5% (median) of the peak asexual parasite levels and gametocytemia correlated with asexual parasitemia ($p<0.0001$) (Figure 3C). The course of gametocytemia followed the asexual parasitaemia, but in Study 2 after chloroquine treatment, in contrast to immediate clearance of asexual parasites, clearance of gametocytes was delayed a further 24 h.

In Study 2 cohort 1, median gametocytemia was 136 gametocytes/mL at the time of treatment/last mosquito feeding assay, meaning only 0.14–0.68 gametocytes would be imbibed in a 1–5µL mosquito blood-meal, making transmission extremely unlikely. As a consequence, following review of the safety data and approval from the Safety Monitoring Committee the recommendation was made to delay treatment until Day 10 in cohorts 2 and 3. This resulted in significantly higher median gametocytemia at the time of treatment/last mosquito feeding assay (2,351 gametocytes/mL; $p<0.0001$) compared to participants in cohort 1 (Figure 3B).

The optimal times for mosquito feeding were Day 9 and 10, when 69% (11/16) of participants were infectious to mosquitoes (Table 3 and Table S6). Participants were not infectious on Day 6 and 7 (0/8), and only one participant was infectious on Day 8 (1/8). The rate of mosquito infection was highest on Day 10 (Figure 4A; median on Day 10 = 5.2%; IQR 2.8–8.9). Direct skin feeding resulted in higher mosquito infection rates (median = 3.3%; IQR 2.9–6.1) than direct membrane feeding with whole blood (median = 1.8%; IQR 1.2–2.8; $p = 0.04$), and membrane feeding with serum replacement (median = 8.6%; IQR 2.8–13.9) also resulted in significantly higher mosquito infection rates than membrane feeding with whole blood ($p = 0.02$) (Figure 4B and Table S6). Successful mosquito transmission was associated with gametocyte density, with gametocytemia being significantly higher in the infectious samples (median = 1,993 gametocytes/mL) compared to the non-infectious samples (median = 136 gametocytes/mL; $p<0.0001$) (Figure 4C).

156 To increase mosquito infection rates in this model, we enriched gametocytes over a percoll gradient
157 either ~10 or ~40 fold to increase the density of gametocytes offered to mosquitoes in the membrane
158 feeding assays (19). Very high levels of mosquito infection ranging from 26% (Day 9) to 92% (Day
159 10) were achieved following ~10 fold enrichment (Table 4). When gametocytes were enriched ~40
160 fold, the mosquito infection rate was 97%, with a mean of 7 oocysts (range 1–16) per midgut.
161 Salivary gland sporozoites were detected 15 to 17 days after the feeding assay, with an average of
162 7,635 sporozoites per mosquito following ~40 fold enrichment (Table 4). To assess viability, these
163 sporozoites were collected from the mosquitoes and incubated with HC-04 hepatocyte cells in culture.
164 Following 7 days of incubation, liver-stage schizonts were observed by staining the cells with UIS4
165 monoclonal antibody (Figure 4D).

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Discussion

We have demonstrated for the first time, the safe, reproducible and efficient transmission of gametocytes during experimental *P. vivax* malaria infection in humans, thereby establishing a new clinical model for evaluating *P. vivax* transmission-blocking interventions. Moreover, we have demonstrated the potential to exploit this model to produce viable clonal sporozoites capable of hepatocyte infection that could be used to evaluate interventions targeting *P. vivax* liver-stage parasites.

The new *P. vivax* HMP013 inoculum was safe and well tolerated. The isolate was generated from a donor with blood group O (RhD positive), overcoming the need to match study volunteers' blood group to that of the inoculum. The number and severity of AEs were in line with safety outcomes from published malaria IBSM trials, two of which used *P. vivax* (13). The severity of the single case of elevated alanine aminotransferase is similar to that reported in other *P. vivax* studies (15). A comprehensive analysis of clinically significant transaminase elevations in *P. vivax* IBSM studies will be reported separately.

Gametocytemia was detected in all participants and appeared in circulation early during blood-stage infection — only 1 to 2 days after the first appearance of asexual parasites — consistent with reports of a shorter gametocyte maturation time for *P. vivax* compared to *P. falciparum* (14, 15). The majority of participants (11/16; 68·8%) were infectious to laboratory reared *An stephensi* mosquitoes on Day 9 and 10 after infection. This represents the first report of efficient *P. vivax* gametocyte transmission during experimental malaria infection. Transmission from humans to mosquitoes was previously attempted during a sporozoite induced *P. vivax* experimental malaria infection study but was unsuccessful despite detection of the *pvs25* gametocyte marker (20, 21). In our previous *P. vivax* IBSM study (15) the peak gametocytemia was 43 gametocytes/mL compared to 47,393 gametocytes/mL in this study (Supplementary p 19). Difficulty was experienced during the previous study with verification of mosquito infection by microscopy. Review of the photomicrographs by a number of expert oocyst microscopists from different laboratories indicated a lack of consensus about

which, if any, were true oocysts and which were artefact. This ambiguity about the identification of mosquito infection led us to develop and validate the qPCR assay used here for high-throughput, sensitive, and accurate evaluation of midgut infection (22). It was also followed by a study detailing the difficulty with oocyst identification by microscopy (23). Moreover, similar structures identified later in the same QIMR laboratory were confirmed PCR negative. Although we are unable to verify by PCR the result of the previous study with the Solomon Island isolate, we believe based on the lack of consensus about the identification of oocysts together with the very low gametocytemia during that study that it is likely the mosquito infection rate reported was an overestimate. The study presented here thus demonstrates higher levels of gametocytemia, reliable transmission to mosquitoes, and increased assay validity. The mosquito infection rates we observed in this current study (1–18%) are comparable to those reported from asymptomatic natural gametocyte carriers who had a mean gametocyte density of 1,323 gametocytes/mL and an average mosquito infection rate of 4.2% (21). We also observed increasing mosquito infection rates with increasing gametocytemia, consistent with data from natural infections (21, 24). Transmission was low (on Day 8) or did not occur (on Day 6 and 7) before Day 9, likely due to the low gametocyte densities at the time of feeding. Gametocytemia was so low (less than 397 gametocytes/mL) that the chance of gametocytes being taken up in a 1–5 µL blood meal was extremely unlikely. Membrane feeds performed with gametocytes that had been enriched over a percoll gradient resulted in very high levels of transmission, further demonstrating the observed relationship between gametocyte density and transmission success.

Our model provides a new platform to fully evaluate factors governing efficient transmission, and in accordance with previous *P. vivax* studies, mosquito infection rates were higher via the natural route of infection compared to feeding mosquitoes on whole blood via a membrane (25, 26). This is potentially due to conditions during membrane feeding being suboptimal for efficient transmission, or because gametocytes may localise to subdermal capillaries for more efficient uptake. Consistent with previous reports (19, 26), we observed higher mosquito infection rates from membrane feeding with serum replacement than from direct membrane feeding on whole blood. This suggests a component of

the venous blood sample not present in vivo during skin feeding, such as anticoagulant, may inhibit transmission (19, 26, 27).

Mosquito infection rates were very high after membrane feeding with enriched gametocytes, which further supports the association between gametocyte density and transmission. Midgut oocyst infections developed into salivary gland sporozoites, and these sporozoites were able to infect and develop in human hepatocytes in vitro. This demonstrates the potential application of this model to facilitate the study of *P. vivax* liver-stages.

A limitation of this study is the small sample size; further studies are needed to determine the true variability in *P. vivax* infection characteristics between study participants. An additional limitation is that the IBSM model does not mimic natural infection as it bypasses the liver-stage of infection. However, this offers a safety advantage because it eliminates the risk of hypnozoite formation during liver-stage infections and the potential for relapse. IBSM offers other logistical and safety advantages over *P. vivax* sporozoite induced VIS including i) the ability to readily carry out IBSM studies in non-endemic countries, ii) prior knowledge of *P. vivax* genotype and drug sensitivity, iii) ability to carry out multiple studies with the same strain and dose, and iv) simplified trial design and conduct because all participants develop blood-stage parasitaemia simultaneously.

In conclusion, we have demonstrated the safe, reproducible, efficient transmission of *P. vivax* gametocytes from healthy non-immune participants to mosquitoes during experimental human malaria infection. This experimental model can be used for early-clinical evaluation of drug and vaccine candidates, and could provide a source of sporozoites for the evaluation of *P. vivax* liver-stages. This model will further our understanding of the biology of all stages of *P. vivax* infection and provide critical information for malaria control and elimination agendas.

Methods

Study design and participants

Two single-centre open-label clinical trials were undertaken at Q-Pharm Pty Ltd in Queensland, Australia: a phase 1 first-in-human pilot safety and infectivity study (Study 1), and a phase 1b human to mosquito transmission study (Study 2). Healthy, malaria-naïve males and (non-pregnant, non-lactating) females aged between 18 and 55 years were eligible to participate. Study 1 was conducted with two participants inoculated 24 h apart. Study 2 was undertaken as three cohorts of eight participants. Due to recruitment limitations, cohort 2 was performed as cohort 2a (n=6) and cohort 2b (n=2), conducted separately (Figure 1+2).

Procedures

The *P. vivax* HMP013 isolate was collected in 2014 from a traveller (blood group O, RhD positive) returning to Australia from India who presented with malaria-related symptoms. Informed consent was obtained (under a protocol approved by the QIMR Berghofer and Royal Brisbane Women's Hospital human research ethics committees), and 200 mL of blood was collected. The patient tested negative for blood-borne pathogens using a Red Cross donation protocol and the RBCs were cryopreserved as described previously (14). The cryopreserved bank tested negative for adventitious agents and was subject to whole genome sequencing (28).

Each inoculum was prepared by aseptically thawing and washing a vial of cryopreserved RBCs and diluting to 2 mL with injectable saline. The number of viable parasites per inoculum was retrospectively determined to be 564 parasites (95% CI: 342–930) by quantitative PCR targeting the 18S rRNA gene (18S qPCR) (Supplementary pp 13–15). All participants were inoculated intravenously on Day 0 and monitored daily for AEs and malaria. From Day 4, parasitaemia was measured by 18S qPCR (Supplementary p 13) (14) twice-daily until participants were admitted to the clinic for treatment (Supplementary Table S1 and S2). Gametocyte development was measured by qRT-PCR for *pvs25* mRNA (Supplementary pp 13–14) from Day 4 (14). Curative antimalarial

treatment was administered on Day 8 (Study 1 and Study 2 cohort 1) or Day 10 (Study 2 cohorts 2 and 3, except Participant 205 who was treated on Day 9). Participants in Study 1 received oral artemether-lumefantrine, and participants in Study 2 received oral chloroquine (Supplementary Table S4). All participants were confirmed parasite negative at the end of study (Figure 1+2).

For Study 2, infectivity of gametocytes was evaluated using mosquito feeding assays between Day 6 and 8 (cohort 1) or on Day 9 and 10 (cohorts 2 and 3). All feeding assays were performed before drug treatment was initiated. Gametocytes were fed to *Anopheles stephensi* mosquitoes via direct skin feeding assays (DFAs; 2 per participant), direct membrane feeding assays with whole venous blood in lithium heparin anticoagulant (DMFAs; 2–3 per participant), or membrane feeding assays with serum replacement (MFA-SR) (19). Exploratory membrane feeding assays were performed to investigate mosquito infection rates when fed on gametocytes enriched from participants' blood over a percoll gradient (Supplementary p 17). We determined transmission to mosquitoes by measuring midgut oocyst infections using the 18S qPCR assay (14, 22). Microscopy was used to visually confirm oocysts in a small random selection of midguts prior to qPCR (Figure S3A+B). Salivary gland sporozoite infections were assessed using microscopy 15 to 17 days after mosquito feeding (Figure S3C). Sporozoite viability was determined by adding salivary gland sporozoites to HC-04 cells in culture in liver-stage invasion assays (Supplementary p 18).

Outcomes

Primary endpoints were the safety (both studies) and infectivity (Study 1) of the *P. vivax* isolate in healthy, malaria-naïve adults. Safety endpoint measures were the frequency and severity of AEs, and results of clinical laboratory tests, physical examinations, vital sign assessments, and electrocardiographs. Infectivity endpoint measures were parasitaemia and gametocytemia growth profiles determined by 18S qPCR and *pvs25* qRT-PCR. A secondary endpoint in Study 2 was transmissibility of *P. vivax* gametocytes from humans to mosquitoes. Successful transmission was defined as at least one oocyst-positive mosquito per feeding assay, measured by 18S qPCR. Additional primary and secondary objectives were to characterise the pharmacokinetic-

pharmacodynamic relationship between chloroquine concentration and clearance of blood-stage parasites. These will be reported separately.

Statistics

Both trials were designed to assess the in vivo safety of the *P. vivax* isolate in the IBSM model. The first-in-human pilot study (Study 1) required only 2 participants. Study 2 was designed to assess the parasite-clearing activity of chloroquine. Normative data on log parasite clearance rate was used in sample size estimation from 18 IBSM studies involving 102 individuals with mean decay rate of 0.063 log parasites per hour and SD of 0.019. It was determined that a sample size of 20 participants has 80% power to identify a difference of 20% in mean decay rate compared to a reference standard as significant at 5% two-sided significance based on a one-sample t-test. Statistical analysis was performed using GraphPad Prism version 8.2.1 (infectivity endpoints), and R version 3.3.3 (inoculum size and calibration of 18S qPCR). The D'Agostino–Pearson normality test was used to determine if continuous data were normally distributed. When comparing two groups of nonparametric data the Mann–Whitney test was used. More than two groups of nonparametric data were compared by Kruskal–Wallis test with Dunn's multiple comparison test. P value <0.05 was considered statistically significant.

Study approval

Both studies were approved by the QIMR Berghofer Human Research Ethics Committee. Study 2 was also approved by the Australian Defence Human Research Ethics Committee. All participants met the eligibility criteria (Supplementary pp 3–8) and gave written informed consent before inclusion in the study. The trials were registered with the Australian New Zealand Clinical Trials Registry (ACTRN12614000930684 and ACTRN12616000174482).

Author contributors: Study conception and design of experiment: KAC, JSM, and JJM. Clinical oversight: JSM, SE, AO, and SC. Molecular and entomology experiments: KAC, CYTW, MA, HM, GR, and MR. Liver-stage assays: VMA, LL, TBS, and KAC. Analysed data: KAC, DK, and EB. Wrote manuscript: KAC. All authors reviewed the manuscript and approved the final version.

Conflict of interests: Stephan Chalon and Joerg J Moehrle are employed by Medicines for Malaria Venture. All other authors declare no competing interests.

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Role of funding source

The funders, Bill & Melinda Gates foundation and (Australian) NHMRC had no role in study design, data collection, analysis, interpretation or reporting of data. MMV were involved in study design and safety analysis but had no role in data collection, analysis, interpretation, or reporting of parasitology data. The authors KAC and JSM had full access to all the data in the study and had final responsibility for the decision to submit for publication.

Data sharing statement:

Data collected for the primary and secondary objectives for this study will be available with other supporting documents (e.g., protocol and informed consent) after publication upon reasonable request with a data transfer agreement. Investigators who seek access to data should contact the authors. All methodologies are presented in this manuscript or supplementary. Where details are given in brief the method is already published in the accompanying reference.

References

1. Howes RE, Battle KE, Mendis KN, Smith DL, Cibulskis RE, Baird JK, et al. Global Epidemiology of Plasmodium vivax. *Am J Trop Med Hyg.* 2016;95(6 Suppl):15-34.
2. Price RN, Tjitra E, Guerra CA, Yeung S, White NJ, and Anstey NM. Vivax malaria: neglected and not benign. *Am J Trop Med Hyg.* 2007;77(6 Suppl):79-87.
3. Baird JK. Evidence and implications of mortality associated with acute *Plasmodium vivax* malaria. *Clin Microbiol Rev.* 2013;26(1):36-57.
4. World Health Organization. Geneva, Switzerland; 2015.
5. White MT, Karl S, Battle KE, Hay SI, Mueller I, and Ghani AC. Modelling the contribution of the hypnozoite reservoir to Plasmodium vivax transmission. *eLife.* 2014;3.
6. Ross A, Koepfli C, Schoepflin S, Timinao L, Siba P, Smith T, et al. The Incidence and Differential Seasonal Patterns of Plasmodium vivax Primary Infections and Relapses in a Cohort of Children in Papua New Guinea. *PLoS neglected tropical diseases.* 2016;10(5):e0004582.
7. Bassat Q, Velarde M, Mueller I, Lin J, Leslie T, Wongsrichanalai C, et al. Key Knowledge Gaps for Plasmodium vivax Control and Elimination. *Am J Trop Med Hyg.* 2016;95(6 Suppl):62-71.
8. Mueller I, Galinski MR, Baird JK, Carlton JM, Kochar DK, Alonso PL, et al. Key gaps in the knowledge of Plasmodium vivax, a neglected human malaria parasite. *The Lancet infectious diseases.* 2009;9(9):555-66.

9. Baird JK, Valecha N, Duparc S, White NJ, and Price RN. Diagnosis and Treatment of Plasmodium vivax Malaria. *Am J Trop Med Hyg.* 2016;95(6 Suppl):35-51.

10. Howes RE, Piel FB, Patil AP, Nyangiri OA, Gething PW, Dewi M, et al. G6PD deficiency prevalence and estimates of affected populations in malaria endemic countries: a geostatistical model-based map. *PLoS medicine.* 2012;9(11):e1001339.

11. Mueller I, Shakri AR, and Chitnis CE. Development of vaccines for Plasmodium vivax malaria. *Vaccine.* 2015;33(52):7489-95.

12. Tham WH, Beeson JG, and Rayner JC. *Plasmodium vivax* vaccine research — we've only just begun. *Int J Parasitol.* 2017;47(2-3):111-8.

13. Payne RO, Griffin PM, McCarthy JS, and Draper SJ. *Plasmodium vivax* controlled human malaria infection — progress and prospects. *Trends Parasitol.* 2017;33(2):141-50.

14. McCarthy JS, Griffin PM, Sekuloski S, Bright AT, Rockett R, Looke D, et al. Experimentally induced blood-stage Plasmodium vivax infection in healthy volunteers. *J Infect Dis.* 2013;208(10):1688-94.

15. Griffin P, Pasay C, Elliott S, Sekuloski S, Sikulu M, Hugo L, et al. Safety and reproducibility of a clinical trial system using induced blood stage *Plasmodium vivax* infection and its potential as a model to evaluate malaria transmission. *PLoS Negl Trop Dis.* 2016;10(12):e0005139.

16. Snounou G, and Perignon JL. Malariotherapy — insanity at the service of malariology. *Adv Parasitol.* 2013;81:223-55.

17. Alving AS, Craige B, Jr., and et al. Procedures used at Stateville penitentiary for the testing of potential antimalarial agents. *J Clin Invest.* 1948;27(3 Pt1):2-5.

18. Karl S, Laman M, Koleala T, Ibam C, Kasian B, N'Drewei N, et al. Comparison of three methods for detection of gametocytes in Melanesian children treated for uncomplicated malaria. *Malar J.* 2014;13:319.

19. Collins KA, Wang CY, Adams M, Mitchell H, Rampton M, Elliott S, et al. A controlled human malaria infection model enabling evaluation of transmission-blocking interventions. *J Clin Invest.* 2018;128(4):1551-62.

20. Arevalo-Herrera M, Forero-Pena DA, Rubiano K, Gomez-Hincapie J, Martinez NL, Lopez-Perez M, et al. Plasmodium vivax sporozoite challenge in malaria-naive and semi-immune Colombian volunteers. *PLoS One.* 2014;9(6):e99754.

21. Vallejo AF, Garcia J, Amado-Garavito AB, Arevalo-Herrera M, and Herrera S. Plasmodium vivax gametocyte infectivity in sub-microscopic infections. *Malar J.* 2016;15:48.

22. Wang CYT, McCarthy JS, Stone WJ, Bousema T, Collins KA, and Bialasiewicz S. Assessing Plasmodium falciparum transmission in mosquito-feeding assays using quantitative PCR. *Malar J.* 2018;17(1):249.

23. Musiime AK, Okoth J, Conrad M, Ayo D, Onyige I, Rek J, et al. Is that a real oocyst? Insectary establishment and identification of Plasmodium falciparum oocysts in midguts of Anopheles mosquitoes fed on infected human blood in Tororo, Uganda. *Malar J.* 2019;18(1):287.

24. Kiattibutr K, Roobsoong W, Sriwichai P, Saeseu T, Rachaphaew N, Suansomjit C, et al. Infectivity of symptomatic and asymptomatic Plasmodium vivax infections to a Southeast Asian vector, Anopheles dirus. *International journal for parasitology.* 2017;47(2-3):163-70.

25. Bousema T, and Drakeley C. Epidemiology and infectivity of *Plasmodium falciparum* and *Plasmodium vivax* gametocytes in relation to malaria control and elimination. *Clin Microbiol Rev.* 2011;24(2):377-410.

26. Sattabongkot J, Maneechai N, Phunkitchar V, Eikarat N, Khuntirat B, Sirichaisinthop J, et al. Comparison of artificial membrane feeding with direct skin feeding to estimate the infectiousness of Plasmodium vivax gametocyte carriers to mosquitoes. *Am J Trop Med Hyg.* 2003;69(5):529-35.

27. Solarte Y, Manzano Mdel R, Rocha L, Castillo Z, James MA, Herrera S, et al. Effects of anticoagulants on *Plasmodium vivax* oocyst development in *Anopheles albimanus* mosquitoes. *Am J Trop Med Hyg.* 2007;77(2):242-5.

28. Payne RO, Silk SE, Elias SC, Milne KH, Rawlinson TA, Llewellyn D, et al. Human vaccination against Plasmodium vivax Duffy-binding protein induces strain-transcending antibodies. *JCI Insight.* 2017;2(12).

Figures

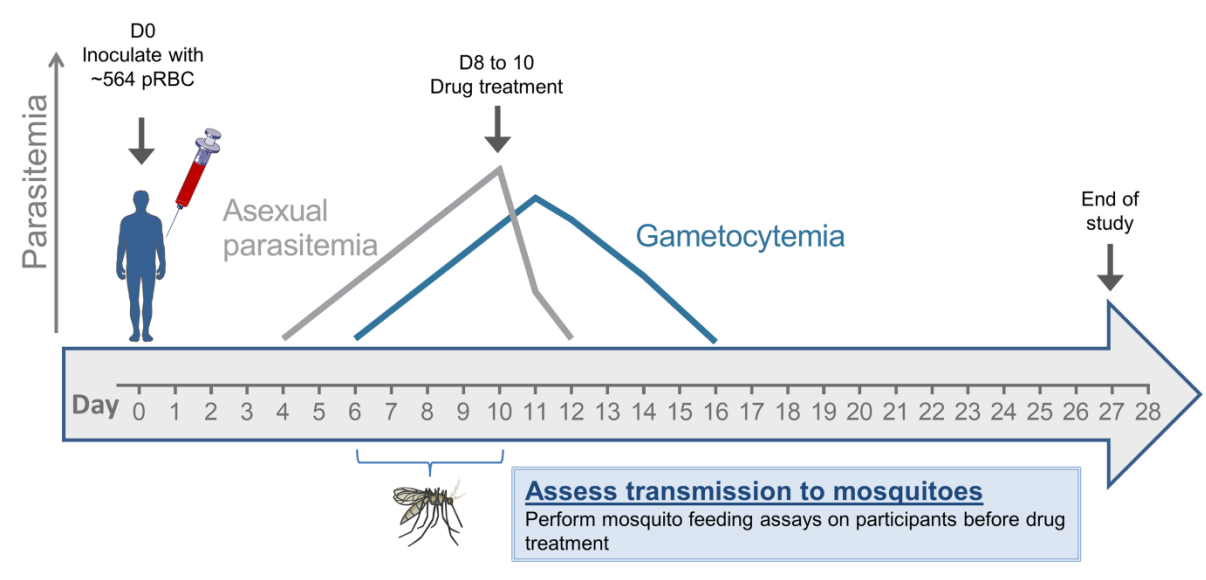

Figure 1: Study design schematic

Malaria-naïve volunteers were inoculated with *P. vivax*-infected RBCs (pRBCs) on day 0 (D0). Asexual parasitaemia and gametocytemia were evaluated from Day 4 and continued until the end of study. Participants in Study 1 started artemether-lumefantrine treatment on Day 8 (n=2). Participants in Study 2 started chloroquine treatment on Day 8 (n=8), Day 9 (n=1), or 10 (n=15). For Study 2, mosquito feeding assays were performed between Day 6 and Day 10 by direct feeding (allowing mosquitoes to feed on participants by live bite), or by membrane feeding on venous blood**.**

D: Day relative to inoculation (Day 0); pRBC: *P. vivax* parasite infected RBCs

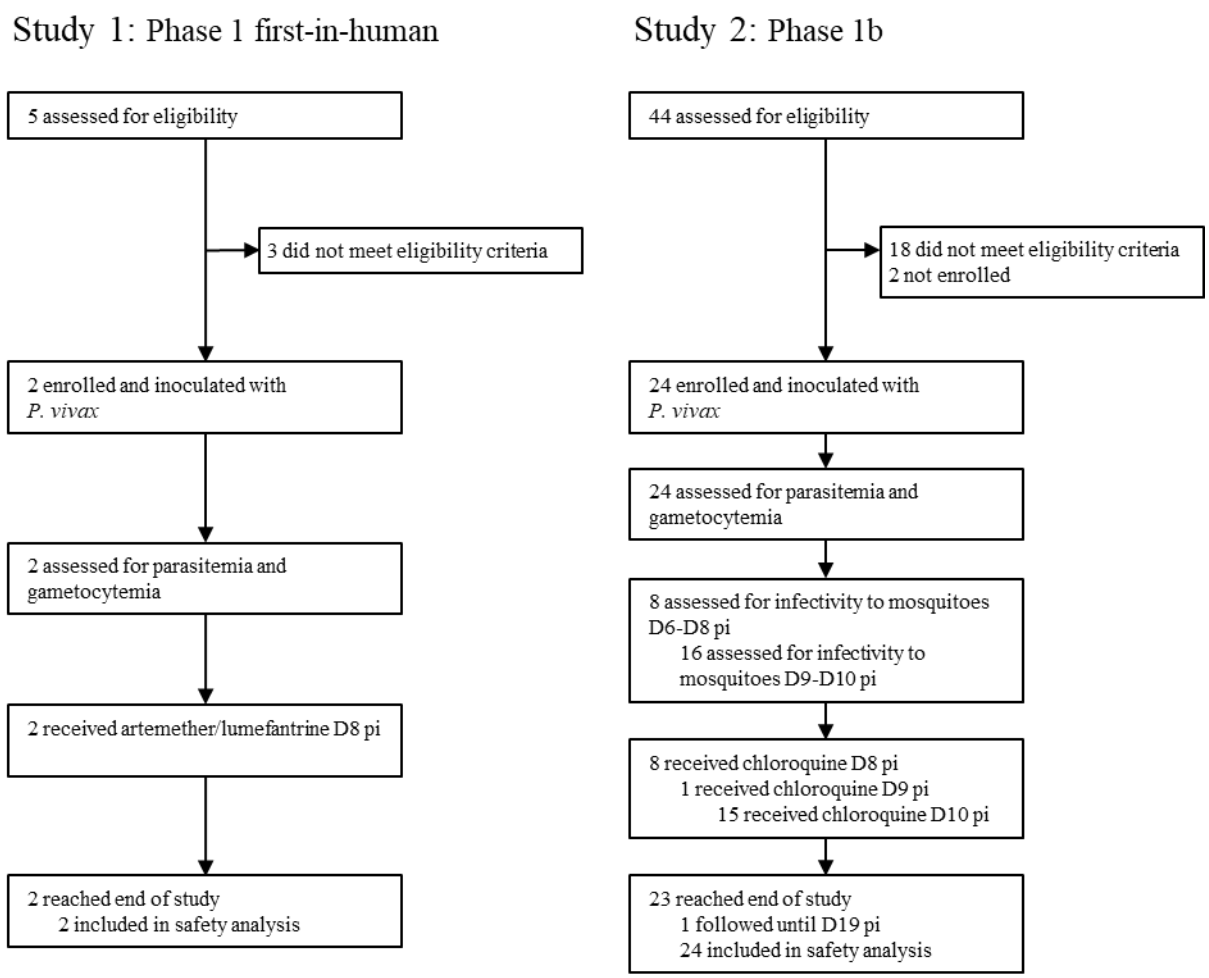

Figure 2: Study profile

All participants were inoculated with *P. vivax* on Day 0.
D=day relative to inoculation; pi=post inoculation

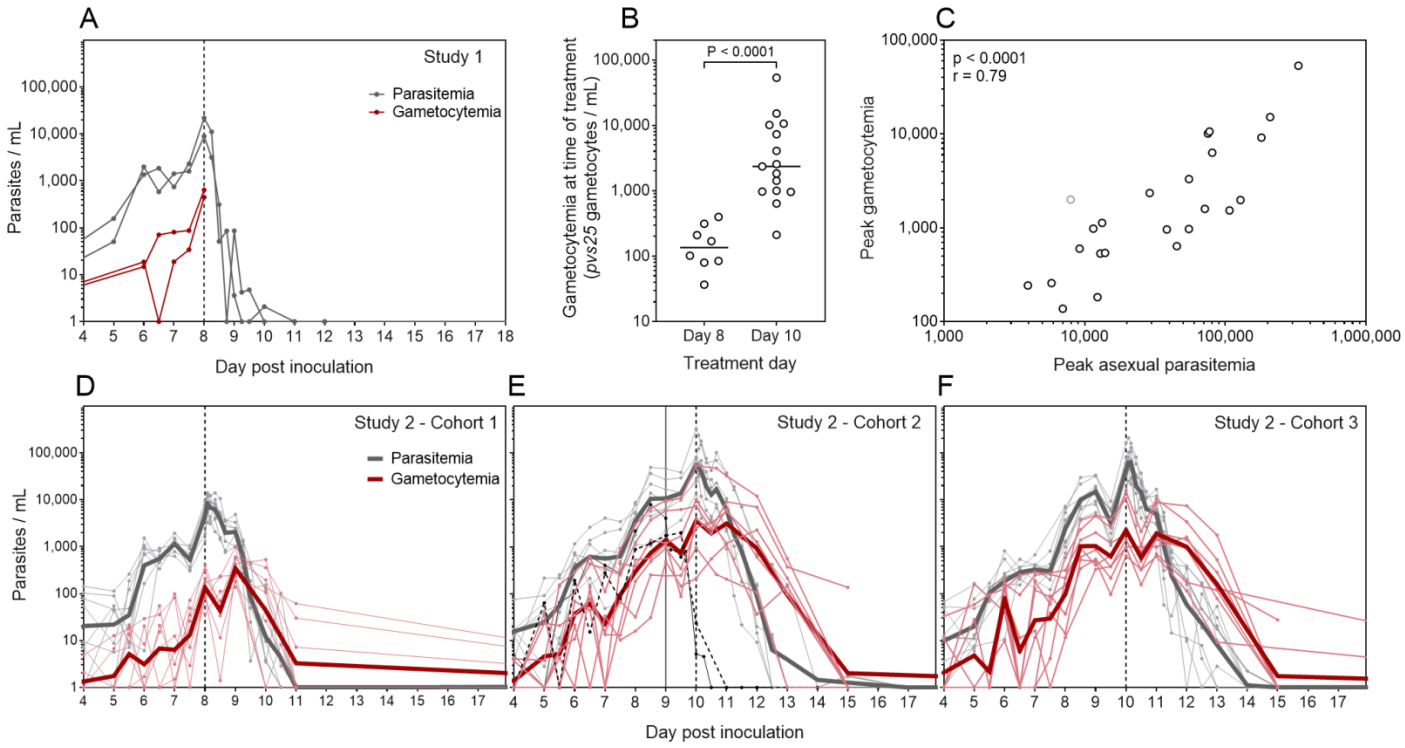

Figure 3: Parasitaemia and gametocytemia

Participants (n=26) were experimentally infected with *P. vivax* on Day 0. Parasitaemia was measured by 18S qPCR and gametocytemia measured by *pvs25* qRT-PCR for Study 1 (n=2) (A), and Study 2 (n=24) (D-F). Grey lines = parasitaemia, red lines = gametocytemia. Thin lines show individual participant data and thick lines show the geometric mean. Initiation of treatment is indicated by the vertical lines. Treatment was initiated on Day 8 for Study 1 (n=2) and Study 2 cohort 1 (n=8), or Day 10 for Study 2 cohorts 2 and 3 (n=15). Participant 205 (cohort 2; black lines) was treated on Day 9 (vertical solid line). (B) Gametocytemia at time of treatment for Study 2 (n=23) (compared by Mann–Whitney test). (C) Spearman correlation of peak asexual parasitaemia and peak gametocytemia (n=24). Participant 205 represented in grey.

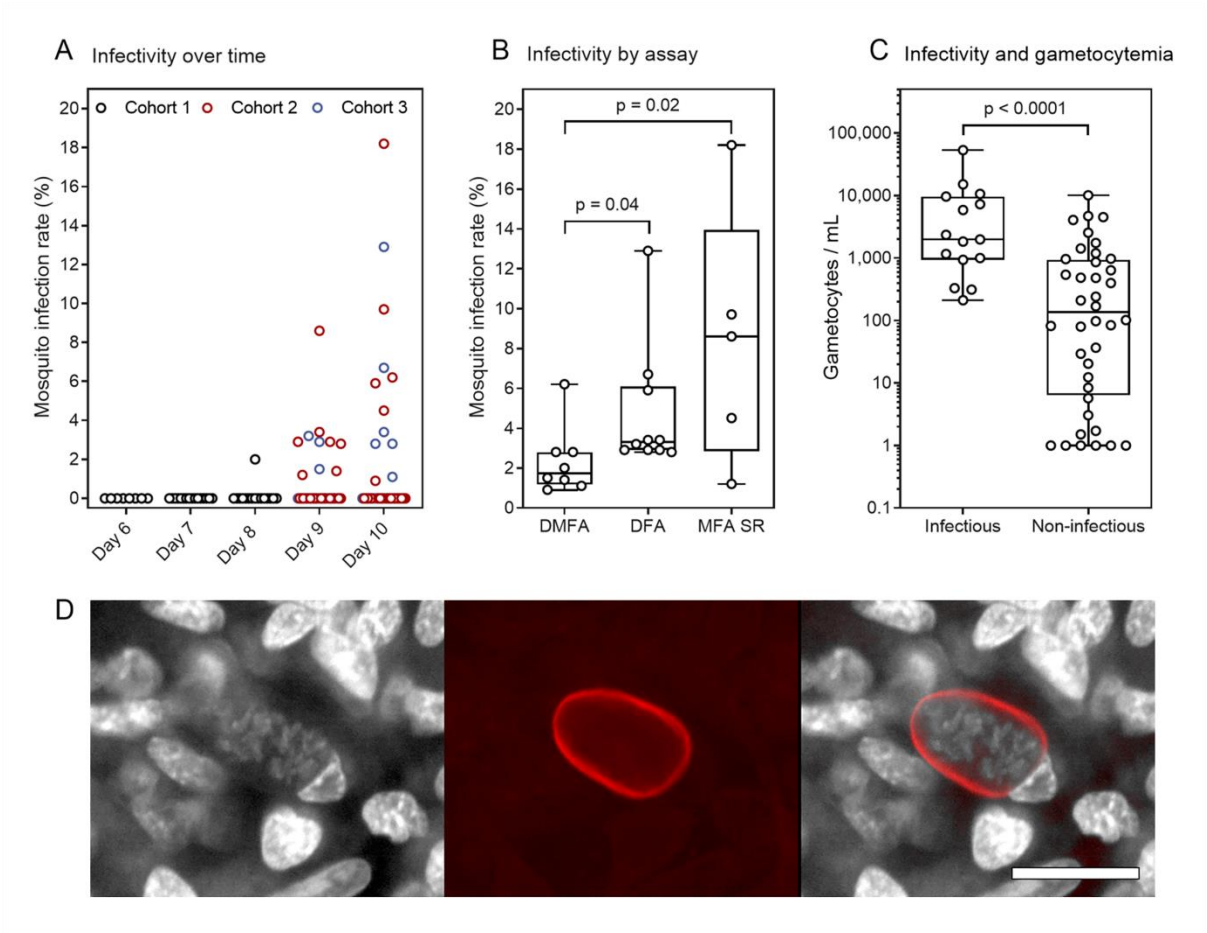

Figure 4: Infectivity to mosquitoes

Successful transmission was defined as at least one oocyst-positive mosquito determined by 18S qPCR. Mosquito infection rate is reported as prevalence of infection (percentage of mosquitoes infected per feeding assay). (A) Prevalence of mosquito infection in all feeding assays in Study 2 at each time point (n=113). (B) Prevalence of mosquito infection in successful feeding assays, by feeding assay type (n=37). Groups compared by Kruskal–Wallis test with Dunn's multiple comparison test. (C) The gametocytemia for participants samples that were infectious compared to samples that were non-infectious (n=54). Groups compared by Mann–Whitney test. Box plots indicate the median and whiskers show the minimum and maximum. (D) Representative image from of a *P. vivax* liver-stage schizont stained with UIS4 and Hoechst33342 following incubation of sporozoites with HC-04 culture for 7 days (Left panel - white channel (Hoechst33342), middle panel - red channel (Alexa fluor 488-conjugated UIS4 antibody), right panel – merge). Image taken at 40× magnification. Scale bar = 20 µm. Sporozoites were obtained by feeding mosquitoes on enriched gametocytes collected on day 10 from participants in cohort 3 (Supplementary pp 18).

DFA = direct skin feeding assay, DMFA = direct membrane feeding assay with whole blood, MFA-SR = membrane feeding assay with serum replacement.

		Study 1 (n=2)	Study 2 (n=24)
Age (years)		20.0 (1.4)	24.8 (6.1)
Sex (male)		**2 (100%)**	13 (54.2%)
Ethnicity n (%)	**White**	1 (50.0%)	21 (87.5%)
	Asian	0	1 (4.2%)
	Asian-European	1 (50.0%)	0
	Indigenous Aboriginal	0	1 (4.2%)
	Latino	0	1 (4.2%)
Height (cm)		179.0 (4.0)	175.8 (9.8)
Body weight (kg)		74.2 (5.7)	73.3 (10.8)
Body mass index (kg/m^2)		23.3 (2.7)	23.7 (2.7)

Table 1: Baseline characteristics of participants

Data are in n (%) or mean (SD)

	Study 1	Study 2			
	(n=2) n (%) or n	Cohort 1 (n=8) n (%) or n	Cohort 2 (n=8) n (%) or n	Cohort 3 (n=8) n (%) or n	Total (n=24) n (%) or n
Number of participants with adverse events					
Participants with AEs	2 (100%)	8 (100%)	8 (100%)	8 (100%)	24 (100%)
Participants with malaria related AEs	10	7 (87.5%)	8 (100%)	8 (100%)	23 (95.8%)
Participants with study drug[a] related AEs	1	3 (37.5%)	2 (25.0%)	1 (12.5%)	6 (25.0%)
Participants with DFA related AEs	NA	1 (12.5%)	4 (50.0%)	3 (37.5%)	8 (33.3%)
Number of adverse events					
Total number of AEs	14	45	157	153	355
Number of mild AEs	13	36	101	113	250
Number of moderate AEs	1	9	53	36	98
Number of severe AEs	0	0	1	3	4
Number of malaria related AEs	12	37	140	119	296
Number of study drug[a] related AEs	1	4	3	1	8
Number of DFA AEs	NA	1	7	3	11

Table 2: Frequency of adverse events by cohort in Study 1 and Study 2

AE severity was recorded in accordance with the Common Terminology Criteria for Adverse Events (CTCAE, version 4, published 28 May 2009). AEs from cohorts 2a and 2b have been combined for reporting in this table. AE=adverse event; DFA=direct feeding assay; NA=not applicable. [a]artemether-lumefantrine (Study 1) or chloroquine (Study 2)

	No. participants infectious to mosquitoes (n/N and %)				
	Cohort				
Day[a]	1	2a	2b	3	Total
6	0/8 (0%)	-	-	-	0/8 (0%)
7	0/8 (0%)	-	-	-	0/8 (0%)
8	1/8 (12.5%)	-	-	-	1/8 (12.5%)
9	-	3/6 (50.0%)	1/2 (50.0%)	2/7 (28.6%)	6/15 (40.0%)
10	-	2/5 (40.0%)	1/2 (50.0%)	5/8 (62.5%)	8/15 (53.3%)

Table 3: Infectivity of participants to mosquitoes in Study 2

[a] Day relative to inoculation (Day 0). Full individual participant infectivity data by assay are displayed in table S6.

Day [a]	Percoll enrichment	% oocyst infected mosquitoes (number positive/number assessed)	Mean no. oocysts/infected mosquito (number assessed)	No. oocysts/infected mosquito *range*	% sporozoite infected mosquitoes (number positive/number assessed)	Sporozoites/ infected mosquito *mean*
Cohort 2a						
10	~10 fold	92.4% (110/119)	4 (n=27)	1–10	93.3% (28/30)	4429
Cohort 2b						
10	~10 fold	71.1% (79/111)	2 (n=19)	1–4	NC	1462
Cohort 3						
9	~10 fold	26.2% (16/61)	NC	NC	NC	NC
10	~10 fold	87.6% (92/105)	2 (n=22)	1–4	50.0% (3/6)	1767
10	~40 fold	97.3% (109/112)	7 (n=30)	1–16	100% (6/6)	7635

Table 4: Infectivity of percoll enriched samples to mosquitoes and development of sporozoites
Membrane feeding assays were performed with gametocytes enriched over a percoll gradient from blood pooled from all participants in a cohort, at the time point specified. Mosquito infection rate is reported as prevalence of infection (% of mosquitoes infected per feeding assay). NC: not counted. [a] Day relative to inoculation (Day 0).