

PEARLS

Developing transmission-blocking strategies for malaria control

Robert E. Sinden*

Department of Life Sciences, Imperial College London, London, United Kingdom

* r.sinden@imperial.ac.uk

Background

Analysis of the varied developmental pathways exploited by malarial parasites as they pass through their differing life stages can be challenging [1–3], the parasites often adopting mechanisms that differ from the conventional norms of their eukaryotic hosts. It is, however, these unexpected differences that provide fascination and drive to the basic research scientist and simultaneously expose potential opportunities to intervene and constrain the terrible impact that these formidable adversaries inflict upon their hosts.

The pressures under which current researchers must compete for finite resources may be contributory factors to the disclosure of each fascinating advance in our understanding of *Plasmodium* being reported as if it were the next magic bullet in management of these amazing parasites. This potentially undervalues the beauty of the science done and observations made. One purpose of this article is to review the biology of malaria transmission and to attempt to provide a rational framework for the discovery, design, and application of measures to reduce the prevalence of human malaria infection in endemic communities—here termed “transmission-blocking (T-B) strategies.” Hopefully, it will still highlight the pure excitement of discovery of new biology whilst simultaneously managing expectations as to the utility of the data to contribute to practical control measures. Where possible, lacunae in current understanding that are inhibiting development of effective and sustainable interventions for elimination/eradication of these cunning and resourceful parasites will be identified.

The purpose and prioritization of T-B strategies

The sole purpose of T-B strategies is to reduce the prevalence of malaria infection in affected populations; it is therefore essential to understand how reductions in each developmental phase of transmission relate to this key endpoint (See Fig 1). It is reassuring that Griffin, using current modelling techniques, recently computed that there is no bistable equilibrium in transmission and therefore that elimination is feasible [4]. The following discussion is, however, founded upon one of the earliest models of malaria transmission, the Ross-MacDonald relationship [5–7], which clearly identifies the impact of key component events regulating malaria case prevalence over time, i.e., the basic reproductive value, R_0 .

$$\text{Ross/MacDonald formula} \dots \dots \dots R_0 = \frac{ma^2bp^n}{-rlog_e p}$$

The component terms can simply be ranked by their descending potential “impact” upon R_0 from the highest, p, the daily survival of the infected mosquito (p^n), where n can be >9, through a, the human biting rate (a^2), to the lowest trio: m, the mosquito number relative to



OPEN ACCESS

Citation: Sinden RE (2017) Developing transmission-blocking strategies for malaria control. PLoS Pathog 13(7): e1006336. <https://doi.org/10.1371/journal.ppat.1006336>

Editor: Laura J Knoll, University of Wisconsin Medical School, UNITED STATES

Published: July 6, 2017

Copyright: © 2017 Robert E. Sinden. This is an open access article distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Funding: The author received no specific funding for this study.

Competing interests: The author has declared that no competing interests exist.

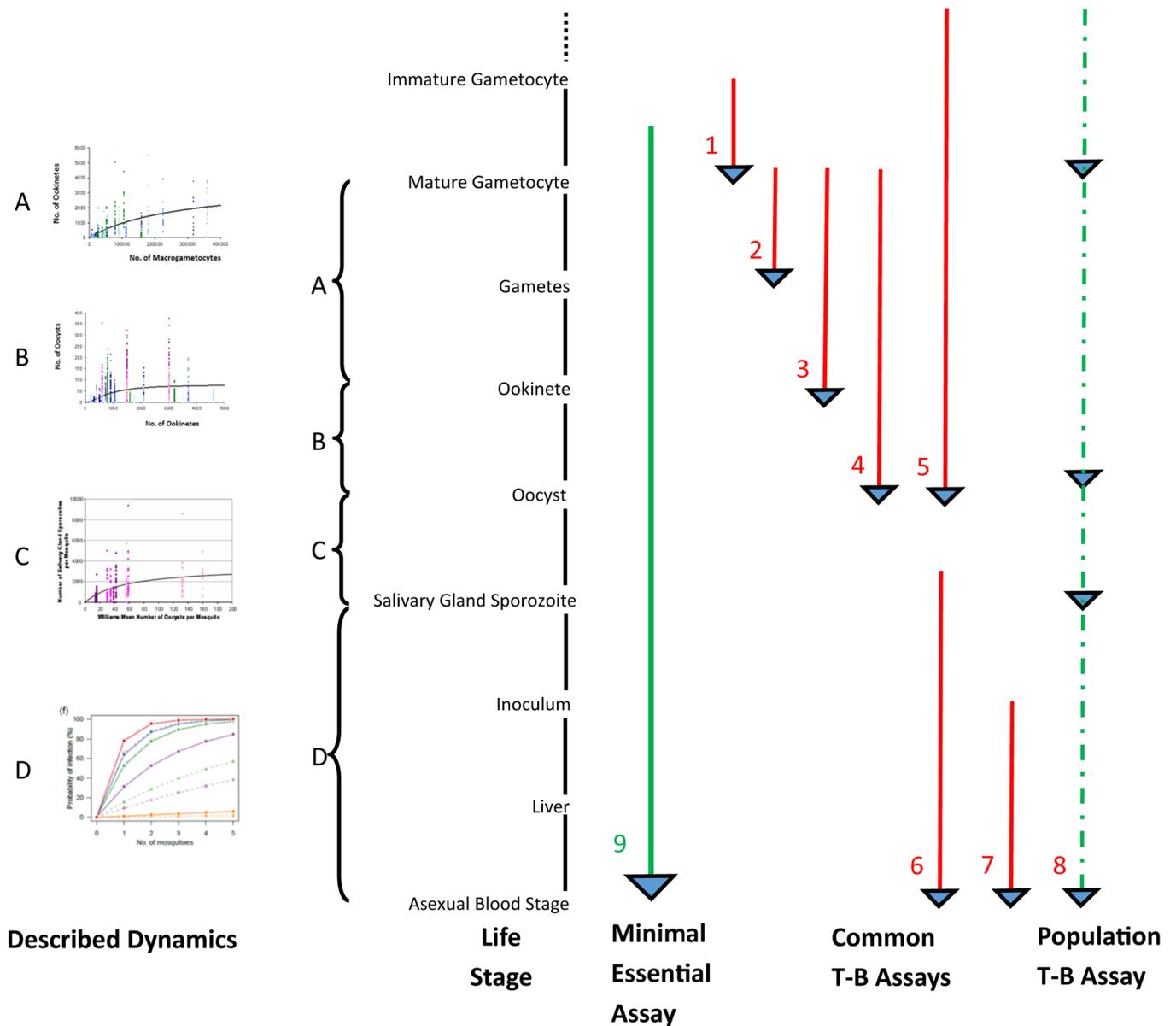


Fig 1. Diagram highlighting the parameters measured by many of the published assays examining the impact of transmission-blocking measures. The biology examined by each assay is indicated by the arrow length; the precise stage enumerated is indicated by the blue arrowheads. The minimal-desired biology to embrace in a directly informative assay is indicated by the solid green arrow; assays measuring less than this ideal are indicated in red. The population assay (dashed green) can be run over repeated cycles of infection measuring multiple desired “endpoints.” The nonlinear dynamic relationships reported between successive transmission life stages are indicated on the left of the diagram. Illustrative references are: A–C [63], D [64], 1 [65, 66], 2 [49, 51], 3–4 [67], 5 [68, 69], 6 [70], 7 [20, 71], 8 [9, 72], 9 [73–75].

<https://doi.org/10.1371/journal.ppat.1006336.g001>

man; b , the probability the infected mosquito will infect a human host; and r , the survival of the infectious human host. Thus, as parasitologists, we must appreciate that reducing either the survival of the infected female anopheline or the mosquito biting rate will have greater impact than reducing either the infectivity to “ r ” or from “ b ,” the mosquito. Interestingly, this 60-year-old prediction was largely endorsed in a recent analysis of the impact of insecticides (long-lasting impregnated bednets, indoor residual spraying [LLIN, IRS]) and antimalarials

(artemisinin combination therapy [ACT]) [8]. Despite the predicted low-ranking impact of targeting “r,” it is encouraging that an intervention described as being only partially effective, i.e., the antimalarial drug (atovaquone), which reduced gametocyte-to-oocyst conversion by only 57%, can eliminate infection in a low-transmission setting (<3 bites/cycle) but notably has no measurable impact in a high-transmission setting (above 4 bites/cycle) [9].

A common feature of parasitic infections is the sheer number of organisms involved, numbers that often overwhelm a host’s ability to control; the asexual blood-stage infections in malaria are 1 example. These vast populations, e.g., 10^{10} – 10^{11} individuals in a single host, have the potential to display such diversity in phenotype that they “outwit” either the human immune response by antigenic variation [10] or antigenic diversity [11], or the pharmaceutical industry by random mutation. When considering malaria transmission, the numbers of parasites (and therefore the variants/mutants challenged) can be reduced by around 7 orders of magnitude (10^3 macrogametocytes/mosquito or 10^3 sporozoites/bite versus 10^{10-11} asexual parasites/human host). Thus, one of the major long-term advantages in developing T-B strategies will lie in the comparatively small populations of parasites actually challenged by the intervention. This fact alone must considerably increase the impact or extend the useful life span of any intervention targeting these bottleneck populations (gametocytes and liver schizonts).

Noting the variation of parasite number “within” the life cycle, it is unclear why we do not make more use of the variations in host or vector numbers to improve the efficiency of our efforts expended on parasite control. Transmission is often seasonal, a pattern imposed by the cyclic changes in the populations of mosquito vectors. Whilst it is unclear whether the parasite is transmitted at all in the “dry” season, overall transmission requires the long-term survival of either or both infected vectors and hosts. Interesting data has recently been presented suggesting that the increased frequency of mosquito feeding itself enhanced the infectivity of “overwintering” parasites by promoting gametocytogenesis [12]. Should we consider attacking the vector (both their abundance and their vectorial capacity), i.e., the potentially infectious reservoir, during the “dry/low” season [13, 14]?

The design and application of T-B measures directly targeting the parasite

The relevant parasite biology extends from the mature gametocyte circulating in peripheral bloodstream until the invasion of the hepatocyte in the subsequent host. With current technologies, vaccines targeting the extracellular parasites (egressed gametocyte, gamete, ookinete) prior to invasion of the mosquito midgut wall [15–18] and the sporozoite in the recipient host [19, 20] are the focus of attention. Whilst the limited duration and partial efficacy of the current pioneering ant sporozoite vaccine (RTSs, which target the circum-sporozoite protein [CSP]) are both frustratingly low [21–23], we should not forget that potential measures that may be partially effective in a single cycle of transmission can, if successfully applied over many cycles of transmission, have significant impact [9]. Thus, the duration of an effective response may prove to be a more useful property than absolute efficacy for a T-B vaccine. Progress on vaccines targeting infection of the mosquito has in recent years moved forward apace, vaccines targeting gametocyte/gamete surface proteins (e.g., pfs230, pfs48/45, HAP2) [9, 16, 17, 24–27] and, notably, pfs25 on the macrogamete and ookinete are already displaying useful efficacy levels [28], and pfs25 has been produced in a wide range of expression systems with diverse utility [29–31]. Noting the practicality of delivery of subunit vaccines (as opposed to live parasites, e.g., [32, 33]) in mass-administration campaigns, if the duration of response can be improved, theoretical and laboratory experiments suggest these vaccines have the most useful contribution to make in elimination campaigns, particularly in combination, e.g., pfs25 and CSP [34, 35].

By contrast, with the slow development of T-B vaccines, the recent focus on the discovery and development of T-B drugs targeting the processes of infection of the mosquito has been remarkable, and the recent decision of MMV to formalise the development of compounds specifically targeting transmission (TCP-5) [36] is to be welcomed. Since “promotion” of the concept [37], the development of assays to identify compounds inhibiting parasite sexual and sporogonic development has flowered [38–53]. Current analyses reinforce conclusions reached some 30 years previously [54–56] as to the limited cellular strategies of some transmission stages. The metabolism of the immature sexual stages (male and female) is largely similar to the asexual parasites [57, 58], whilst the mature gametocytes are metabolically down-regulated (insensitive to many classes of schizonticide) [58], and the mature male and female differ markedly in their drug sensitivity. The female is sensitive to approximately a quarter the number of compounds inactivating the male [49]. By contrast, gametogenesis and microgametogenesis in particular offer numerous potential novel targets for intervention, and the ookinete exhibits a wide range of molecular pathways not seen in the blood-stage parasites (personal communication, M.J. Delves to MJD-RES research group). This knowledge will lead to the rapid identification of new targets.

A person infected with *Plasmodium falciparum* will be prompted to seek treatment at the time of fevers (due to the rising asexual blood-stage infection), but the infectious gametocytes will usually peak 8–10 days later [59]. By contrast, in *P. vivax* and the other 3 species infecting man, these 2 populations are contemporary. Consequently, it is only in the case of *P. falciparum* where the selection of T-B compounds of practical merit will be compromised by the problems of their effective delivery to the slow-maturing gametocyte population. Delivering drugs to kill the parasite in the blood meal or later in the sporogonic period of development (target candidate profile 6 [TCP6] of the MMV portfolio) is even more problematic; neither the time between dispensing the drug to the patient and its uptake by the insect nor the amount ingested by the vector can be controlled, making pharmacokinetics/pharmacodynamics (Pk/Pd) optimisation difficult. So, how does one “package” the effective delivery of drugs to this “late” gametocyte population? One remedy is straightforward: deliver both the schizonticide and a gametocide (with either a very long half-life or, preferably, irreversible activity) simultaneously—the schizonticide will kill all asexuals and young gametocytes up to day 6 of development, and the gametocytocide (here defined as a drug rendering all stage V gametocytes noninfectious to the vector) will sterilize all older gametocytes, which at the time will either be in the peripheral circulation or in the bone marrow [60–62].

The missing pieces in our jigsaw of knowledge and tools

Drugs

Here we are found “between a rock and a hard place!” The most accessible target (the mature gametocyte) is metabolically 1 of the 2 least active stages of the life cycle. We have 2 solutions: (1) we find methods to improve the “longevity” of the T-B drugs such that we can reliably attack the reactivated and highly vulnerable gametocytes when they are undergoing gamete formation and then ookinete formation in the mosquito midgut (a benchmark objective might be to develop a drug active for at least 10 days following delivery to the sick patient) and (b) we analyse in depth the limited targets that may be inhibited irreversibly in the repressed mature stage V gametocytes (only in the past 3 years have modern technologies been applied to this objective [57, 58]). Current functional assays have revealed numerous inhibitory compounds with which to probe the latter question.

The only viable method to inhibit sporozoite development with drugs is to prevent migration from the infected bite to the liver. Whilst automated screens for such drugs exist [76], it must be asked whether their delivery to entire populations at risk is viable.

Vaccines

Vaccines targeting sporozoite transmission are the most advanced currently available, whether as subunit vaccines RTSs [77] or whole/live attenuated parasites [20, 33]. We remain, however, remarkably ignorant of the molecular foundations of sporozoite infection.

On the massive generalization that T-B vaccines act by antibody interference of the biological function of accessible parasite surface molecules in the mosquito midgut, we must candidly admit that we do not yet understand (1) the highly vulnerable biology of fertilization (gamete recognition and fusion), (2) parasite defences against natural attack by host and vector immune factors, nor (3) the mechanisms by which the ookinete recognises and invades the midgut epithelium. Whilst efforts to address these lacunae in our knowledge have been made [78–82], these remain verdant pastures for future study. Whilst the limited spectrum of available vaccine candidates is being pursued successfully, to develop vaccines of high utility in population-wide delivery programmes, we need to improve vaccine immunogenicity and, perhaps more importantly, the longevity of the effective immune responses raised, whatever target we choose.

Novel interventions

Whilst drug and vaccine development provides myriad opportunities for intervention, we need to be alert to novel and disruptive intervention concepts. Currently, such ideas are all based on indirect methodologies acting through the vectors and therefore lie outside the remit of this brief article. They include transgenic approaches to reduce mosquito biting rates (1) by disrupting the vector host-seeking behaviour [83, 84], (2) by up-regulating mosquito factors that suppress parasite infectivity (such as oxidative responses [85–89]), and (3) by impacting mosquito reproduction [13, 14]. Have we asked whether we could similarly seed selectively induced lethal/semilethal phenotypic characters into parasite populations, or does the clonal complexity of parasite population structure preclude this approach [90]? One novel approach has recently been proposed—that of perturbing the pattern of gametocyte sequestration and release into the peripheral bloodstream by (inter alia) modulating the deformability of the maturing gametocytes [91], an approach that will only be feasible when we overcome the problem of sustained-intervention delivery.

Understanding the measurement of impact

If we are ever going to apply T-B measures efficiently, we must understand their performances in the field with respect to the key deliverable in any elimination campaign, namely, the reduction in infection prevalence in the vertebrate host. Those working on the biology of malaria transmission have in the past conducted a wide range of assays to determine the efficacy of parasite transmission to and from the mosquito; these assays have diverse endpoints and often-unappreciated variability (Fig 1). Outputs measured have included gametocyte abundance through ookinete, oocyst, and sporozoite production in the vector, density of exoerythrocytic schizonts in vitro, and, more rarely, blood-stage parasitaemia and prevalence in vivo. Most of the assays, whilst invaluable in the development of our understanding of the biology of transmission, fail to provide the key readout (reduction in infection prevalence) for rational decision making. The fundamental basis for this critique is that the more biology that intervenes between assay readout and the desired endpoint (here, infection prevalence in the

vertebrate population), the more complex the relationship with the parameter measured (see Fig 1). For example, recall the 60-year discussion on the relationship between the limited steps linking gametocyte number/patency and the infectious reservoir [75, 92–100] or between salivary gland sporozoite number and infectious potential [64, 101, 102]. Indeed, a widely used parameter of vector infectious potential, the entomological inoculation rate (EIR), fails to reflect mosquito sporozoite burden at all. Often, it is argued that readily accessible outputs are the best/most cost effective to measure—best, rarely; cost effective, not if they lead to erroneous generalizations! The only current assay for T-B interventions that embraces the entire biology of transmission and provides the desired output is the population transmission assay [9]. Despite measuring the key parameters of parasite infection prevalence over many cycles of transmission, its dependence upon the rodent parasite *P. berghei* does mean the results will need to be fine-tuned for each of the 5 species infecting man [103]. However, we should anticipate that it will provide an understanding of the core qualitative relationships between sequential transmission life stages—relationships that may vary quantitatively between the different parasite species. Importantly, the assay will permit the direct comparison of diverse interventions targeting different life stages of the biology of transmission. With these core relationships identified, it will be possible to ask focussed, rationally prioritised questions in human populations in endemic areas, questions that are orders of magnitude more expensive to address. Amongst the lessons already learnt from the population assay [9] are (1) the saturated nature of malaria transmission means that the magnitude of impact of any intervention declines with increasing transmission intensity. Thus, in human studies, the transmission intensity of the test site must not prejudice the ability to measure meaningfully the impact of the intervention under test; it is possible this has happened in the field evaluation of some antimalarial drugs, (2) even partially effective measures can, over multiple cycles of transmission, eliminate the parasite from the population in low-transmission settings, and (3) the higher the transmission intensity, the higher the efficacy of the intervention required to achieve measurable reductions in transmission in finite periods, e.g., the single cycle of transmission often used.

Combining T-B measures

Recognising that even the limited repertoire of T-B measures attacks different parasite properties by diverse mechanisms, it is logical to ask whether their combined use is additive, competitive, or synergistic. An obvious combination that can be studied today is that of a combined T-B and sporozoite vaccine (Pxs25/CSP) [34, 104] to ask whether there is advantage in hitting both bottleneck populations in the same cycle of transmission. Equally, combinations of drugs or vaccine/drug combinations can be modelled and should be considered.

Concluding remarks

Plasmodium has evolved to be one of the most successful parasites of man. Consequently, it offers one of the most challenging adversaries for the enquiring scientific mind. Success in unravelling these hidden strategies is reward in itself, both for the fortunate investigator and the research community at large. Any aspirational young scientist should be encouraged to share this challenge. However, just a fraction of the discoveries made will lead to the design of successful interventions. To use our limited resources effectively, it is incumbent upon both researchers and developers to identify and, based on secure understanding of the biology of the parasite, dispassionately prioritise those lead concepts. Hopefully, this brief overview may help in setting the agenda for the integration, interpretation, and application of our collective understanding of malaria transmission and to develop what have the promise to be powerful tools in the elimination and perhaps eradication agenda.

References

- Joice R, Narasimhan V, Montgomery J, Sidhu AB, Oh K, Meyer E, et al. Inferring Developmental Stage Composition from Gene Expression in Human Malaria. *PLoS Comput Biol*. 2013; 9(12): e1003392. <https://doi.org/10.1371/journal.pcbi.1003392> PMID: 24348235
- Hall N, Karras M, Raine JD, Carlton JM, Kooij TWJ, Berriman M, et al. A Comprehensive Survey of the *Plasmodium* Life Cycle by Genomic, Transcriptomic, and Proteomic Analyses. *Science*. 2005; 307:82–6. <https://doi.org/10.1126/science.1103717> PMID: 15637271
- Le Roch KG, Zhou Y, Blair PL, Grainger M, Moch K, Haynes D, et al. Discovery of gene function by expression profiling of the malaria parasite life cycle. *Science*. 2003; 301:1503–8. <https://doi.org/10.1126/science.1087025> PMID: 12893887
- Griffin JT, Bhatt S, Sinka ME, Gething PW, Lynch M, Patouillard E, et al. Potential for reduction of burden and local elimination of malaria by reducing *Plasmodium falciparum* malaria transmission: a mathematical modelling study. *Lancet Infect Dis*. 2016; 16:465–72. [https://doi.org/10.1016/S1473-3099\(15\)00423-5](https://doi.org/10.1016/S1473-3099(15)00423-5) PMID: 26809816.
- Macdonald G. Theory of the Eradication of Malaria. *Bulletin of the World Health Organisation*. 1956; 15:369–87.
- Macdonald G. Epidemiological Basis of Malaria Control. *BullWldHlthOrg*. 1956; 15:613–26.
- Macdonald G. The Measurement of Malaria Transmission. *Proceedings of the Royal Society of Medicine*. 1955; 48(4):295–301. PMID: 14371594
- Bhatt S, Weiss DJ, Cameron E, Bisanzio D, Mappin B, Dalrymple U, et al. The effect of malaria control on *Plasmodium falciparum* in Africa between 2000 and 2015. *Nature*. 2015; 526(7572):207–11. <https://doi.org/10.1038/nature15535> PMID: 26375008
- Blagborough AM, Churcher TS, Upton LM, Ghani AC, Gething PW, Sinden RE. Transmission-blocking interventions eliminate malaria from laboratory populations. *Nature Communications*. 2013; 4:1812. <https://doi.org/10.1038/ncomms2840> PMID: 23652000
- Brown KN, Brown IN. Immunity to Malaria: Antigenic Variation in Chronic Infections of *Plasmodium knowlesi*. *Nature*. 1965; 208:1286–8. PMID: 4958335
- Brugat T, Reid AJ, Lin J-w, Cunningham D, Tumwine I, Kushinga G, et al. Antibody-independent mechanisms regulate the establishment of chronic *Plasmodium* infection. *Nature Microbiology*. 2017; 2:16276. <https://doi.org/10.1038/nmicrobiol.2016.276> PMID: 28165471
- Endo N, Eltahir EAB. Environmental determinants of malaria transmission in African villages. *Malaria Journal*. 2016; 15(1):578. <https://doi.org/10.1186/s12936-016-1633-7> PMID: 27903266
- Shaw WR, Marcenac P, Childs LM, Buckee CO, Baldini F, Sawadogo SP, et al. Wolbachia infections in natural *Anopheles* populations affect egg laying and negatively correlate with *Plasmodium* development. *Nat Commun*. 2016; 7:11772. <https://doi.org/10.1038/ncomms11772> PMID: 27243367
- Childs LM, Cai FY, Kakani EG, Mitchell SN, Paton D, Gabrieli P, et al. Disrupting Mosquito Reproduction and Parasite Development for Malaria Control. *PLoS Pathog*. 2016; 12(12):e1006060. <https://doi.org/10.1371/journal.ppat.1006060> PMID: 27977810
- Wu Y, Ellis RD, Shaffer D, Fontes E, Malkin EM, Mahanty S, et al. Phase 1 Trial of Malaria Transmission Blocking Vaccine Candidates Pfs25 and Pvs25 Formulated with Montanide ISA 51. *PLoS ONE*. 2008; 3(7):e2636. <https://doi.org/10.1371/journal.pone.0002636> PMID: 18612426
- Kapulu MC, Da DF, Miura K, Li Y, Blagborough AM, Churcher TS, et al. Comparative Assessment of Transmission-Blocking Vaccine Candidates against *Plasmodium falciparum*. *Scientific reports*. 2015; 5:11193. <https://doi.org/10.1038/srep11193> PMID: 26063320
- Tachibana M, Wu Y, Iriko H, Muratova O, MacDonald NJ, Sattabongkot J, et al. N-terminal pro-domain of Pfs230 synthesized using cell-free system is sufficient to induce the complement dependent malaria transmission-blocking activity. *Clin Vaccine Immunol*. 2011; 18:1343–50. <https://doi.org/10.1128/CVI.05104-11> PMID: 21715579
- Chowdhury DR, Angov E, Kariuki T, Kumar N. A Potent Malaria Transmission Blocking Vaccine Based on Codon Harmonized Full Length *Pfs48/45* Expressed in *Escherichia coli*. *PLoS ONE*. 2009; 4(7):e6352. <https://doi.org/10.1371/journal.pone.0006352> PMID: 19623257
- Chaudhury S, Ockenhouse CF, Regules JA, Dutta S, Wallqvist A, Jongert E, et al. The biological function of antibodies induced by the RTS,S/AS01 malaria vaccine candidate is determined by their fine specificity. *Malaria Journal*. 2016; 15(1):1–12. <https://doi.org/10.1186/s12936-016-1348-9> PMID: 27245446
- Mordmüller B, Surat G, Lagler H, Chakravarty S, Ishizuka AS, Lalremruata A, et al. Sterile protection against human malaria by chemoattenuated PfSPZ vaccine. *Nature*. 2017; 542(Feb 15):445–9. <https://doi.org/10.1038/nature21060> PMID: 28199305

21. Neafsey DE, Juraska M, Bedford T, Benkeser D, Valim C, Griggs A, et al. Genetic Diversity and Protective Efficacy of the RTS,S/AS01 Malaria Vaccine. *N Engl J Med*. 2015; 373(21):2025–37. <https://doi.org/10.1056/NEJMoa1505819> PMID: 26488565.
22. Penny MA, Pemberton-Ross P, Smith TA. The time-course of protection of the RTS,S vaccine against malaria infections and clinical disease. *Malar J*. 2015; 14(1):437. <https://doi.org/10.1186/s12936-015-0969-8> PMID: 26537608;
23. Penny MA, Verity R, Bever CA, Sauboin C, Galactionova K, Flasche S, et al. Public health impact and cost-effectiveness of the RTS,S/AS01 malaria vaccine: a systematic comparison of predictions from four mathematical models. *Lancet*. 2015;(387):367–75. [https://doi.org/10.1016/S0140-6736\(15\)00725-4](https://doi.org/10.1016/S0140-6736(15)00725-4) PMID: 26549466.
24. Simon N, Kuehn A, Williamson KC, Pradel G. Adhesion protein complexes of malaria gametocytes assemble following parasite transmission to the mosquito. *Parasitol Int*. 2016; 65(1):27–30. <https://doi.org/10.1016/j.parint.2015.09.007> PMID: 26408859.
25. MacDonald NJ, Nguyen V, Shimp R, Reiter K, Herrera R, Burkhardt M, et al. Structural and immunological characterization of recombinant 6-cysteine domains of the *Plasmodium falciparum* sexual stage protein Pfs230. *Journal of Biological Chemistry*. 2016; 291:19913–22. <https://doi.org/10.1074/jbc.M116.732305> PMID: 27432885
26. Farrance CE, Rhee A, Jones RM, Musiychuk K, Shamloul M, Sharma S, et al. A Plant-Produced Pfs230 Vaccine Candidate Blocks Transmission of *Plasmodium falciparum*. *Clin Vaccine Immunol*. 2011; 18:1351–7. <https://doi.org/10.1128/CVI.05105-11> PMID: 21715576
27. Williamson KC. Pfs230: from malaria transmission-blocking vaccine candidate toward function. 2003; 25(7):351–9.
28. Janitzek CM, Matondo S, Thrane S, Nielsen MA, Kavishe R, Mwakalinga SB, et al. Bacterial superglue generates a full-length circumsporozoite protein virus-like particle vaccine capable of inducing high and durable antibody responses. *Malaria Journal*. 2016; 15:545. <https://doi.org/10.1186/s12936-016-1574-1> PMID: 27825348
29. Lee S-M, Wu C-K, Plieskatt J, McAdams DH, Miura K, Ockenhouse C, et al. Assessment of Pfs25 expressed from multiple soluble expression platforms for use as transmission-blocking vaccine candidates. *Malaria Journal*. 2016; 15:405. <https://doi.org/10.1186/s12936-016-1464-6> PMID: 27515826
30. Jones RM, Chichester JA, Manceva S, Gibbs SK, Musiychuk K, Shamloul M, et al. A novel plant-produced Pfs25 fusion subunit vaccine induces long-lasting transmission blocking antibody responses. *Human vaccines & immunotherapeutics*. 2014; 11(1):124–32.
31. Talaat KR, Ellis RD, Hurd J, Hentrich A, Gabriel E, Hynes NA, et al. Safety and Immunogenicity of Pfs25-EPA/Alhydrogel[®], a Transmission Blocking Vaccine against *Plasmodium falciparum*: An Open Label Study in Malaria Naïve Adults. *PLoS ONE*. 2016; 11(10):e0163144. <https://doi.org/10.1371/journal.pone.0163144> PMID: 27749907
32. Mikolajczak SA, Lakshmanan V, Fishbaugher M, Camargo N, Harupa A, Kaushansky A, et al. A Next-generation Genetically Attenuated *Plasmodium falciparum* Parasite Created by Triple Gene Deletion. *Molecular therapy: the journal of the American Society of Gene Therapy*. 2014; 22(9):1707–15. <https://doi.org/10.1038/mt.2014.85> PMID: 24827907
33. Lyke KE, Ishizuka AS, Berry AA, Chakravarty S, DeZure A, Enama ME, et al. Attenuated PfSPZ Vaccine induces strain-transcending T cells and durable protection against heterologous controlled human malaria infection. *Proceedings of the National Academy of Sciences*. 2017; 114(10):2711–6. <https://doi.org/10.1073/pnas.1615324114> PMID: 28223498
34. Mizutani M, Iyori M, Blagborough AM, Fukumoto S, Funatsu T, Sinden RE, et al. Baculovirus-Vectored Multistage *Plasmodium vivax* Vaccine Induces Both Protective and Transmission-blocking Immunities against Transgenic Rodent Malaria Parasites. *Infection and immunity*. 2014; 82(10):4348–57. <https://doi.org/10.1128/IAI.02040-14> PMID: 25092912.
35. Zheng L, Pang W, Qi Z, Luo E, Cui L, Cao Y. Effects of transmission-blocking vaccines simultaneously targeting pre- and post-fertilization antigens in the rodent malaria parasite *Plasmodium yoelii*. *Parasit Vectors*. 2016; 9(1):433. <https://doi.org/10.1186/s13071-016-1711-2> PMID: 27502144.
36. Burrows JN, Duparc S, Gutteridge WE, Hooft van Huijsduijnen R, Kaszubska W, Macintyre F, et al. New developments in anti-malarial target candidate and product profiles. *Malaria Journal*. 2017; 16(1):26. <https://doi.org/10.1186/s12936-016-1675-x> PMID: 28086874
37. Drugs TMCGo. A Research Agenda for Malaria Eradication: Drugs. *PLoS Med*. 2011; 8(1):e1000402. <https://doi.org/10.1371/journal.pmed.1000402> PMID: 21311580
38. Lucantoni L, Fidock DA, Avery VM. A Luciferase-Based, High-Throughput Assay For Screening And Profiling Transmission-Blocking Compounds Against *Plasmodium falciparum* Gametocytes. *Antimicrobial Agents and Chemotherapy*. 2016; 60:2097–107. <https://doi.org/10.1128/AAC.01949-15> PMID: 26787698

39. Gonçalves D, Hunziker P. Transmission-blocking strategies: the roadmap from laboratory bench to the community. *Malaria Journal*. 2016; 15(1):1–13. <https://doi.org/10.1186/s12936-016-1163-3> PMID: 26888537
40. Tanaka TQ, Guiguemde WA, Barnett DS, Maron MI, Min J, Connelly MC, et al. Potent *Plasmodium falciparum* Gametocytocidal Activity of Diaminonaphthoquinones, Lead Antimalarial Chemotypes Identified in an Antimalarial Compound Screen. *Antimicrobial Agents and Chemotherapy*. 2015; 59(3):1389–97. <https://doi.org/10.1128/AAC.01930-13> PMID: 25512421
41. Bolscher JM, Koolen KMJ, van Gemert GJ, van de Vegte-Bolmer MG, Bousema T, Leroy D, et al. A combination of new screening assays for prioritization of transmission-blocking antimalarials reveals distinct dynamics of marketed and experimental drugs. *Journal of Antimicrobial Chemotherapy*. 2015; 70:1357–66. <https://doi.org/10.1093/jac/dkv003> PMID: 25667405
42. Reader J, Botha M, Theron A, Lauterbach S, Rossouw C, Engelbrecht D, et al. Nowhere to hide: interrogating different metabolic parameters of *Plasmodium falciparum* gametocytes in a transmission blocking drug discovery pipeline towards malaria elimination. *Malaria Journal*. 2015; 14(1):213. <https://doi.org/10.1186/s12936-015-0718-z> PMID: 25994518
43. Abdul-Ghani R, Basco LK, Beier JC, Mahdy MA. Inclusion of gametocyte parameters in anti-malarial drug efficacy studies: filling a neglected gap needed for malaria elimination. *Malar J*. 2015; 14(1):413. <https://doi.org/10.1186/s12936-015-0936-4> PMID: 26481312;
44. Tanaka TQ, Dehdashti SJ, Nguyen D-T, McKew JC, Zheng W, Williamson KC. A quantitative high throughput assay for identifying gametocytocidal compounds. *Molecular and biochemical parasitology*. 2013; 188(1):20–5. <https://doi.org/10.1016/j.molbiopara.2013.02.005> PMID: 23454872
45. Lucantoni L, Duffy S, Adjalley SH, Fidock DA, Avery VM. Identification of MMV Malaria Box Inhibitors of *Plasmodium falciparum* Early-Stage Gametocytes, Using a Luciferase-based High-Throughput Assay. *Antimicrobial Agents and Chemotherapy*. 2013; 57(12):6050–62. <https://doi.org/10.1128/AAC.00870-13> PMID: 24060871
46. Van Voorhis WC, Adams JH, Adelfio R, Ahyong V, Akabas MH, Alano P, et al. Open Source Drug Discovery with the Malaria Box Compound Collection for Neglected Diseases and Beyond. *PLoS Pathog*. 2016; 12(7):e1005763. <https://doi.org/10.1371/journal.ppat.1005763> PMID: 27467575
47. Upton LM, Brock PM, Churcher TS, Ghani AC, Gething PW, Delves MJ, et al. Lead Clinical and Pre-clinical Antimalarial Drugs Can Significantly Reduce Sporozoite Transmission to Vertebrate Populations. *Antimicrobial Agents and Chemotherapy*. 2015; 59(1):490–7. <https://doi.org/10.1128/AAC.03942-14> PMID: 25385107
48. Baragana B, Hallyburton I, Lee MCS, Norcross NR, Grimaldi R, Otto TD, et al. A novel multiple-stage antimalarial agent that inhibits protein synthesis. *Nature*. 2015; 522(7556):315–20. <https://doi.org/10.1038/nature14451> PMID: 26085270
49. Ruecker A, Mathias DK, Straschil U, Churcher TS, Dinglasan RR, Leroy D, et al. A male and female gametocyte functional viability assay to identify biologically relevant malaria transmission-blocking drugs. *Antimicrobial Agents and Chemotherapy*. 2014; 58(12):7292–302. <https://doi.org/10.1128/AAC.03666-14> PMID: 25267664.
50. White N, Ashley E, Recht J, Delves M, Ruecker A, Smithuis F, et al. Assessment of therapeutic responses to gametocytocidal drugs in *Plasmodium falciparum* malaria. *Malaria Journal*. 2014; 13(1):483. <https://doi.org/10.1186/1475-2875-13-483> PMID: 25486998
51. Delves MJ, Ruecker A, Straschil U, Lelièvre Je, Marques S, López-Barragán MaJ, et al. Male and female *P. falciparum* mature gametocytes show different responses to antimalarial drugs. *Antimicrobial Agents and Chemotherapy*. 2013; 57:3268–74. <https://doi.org/10.1128/AAC.00325-13> PMID: 23629698
52. Delves M, Plouffe D, Scheurer C, Meister S, Wittlin S, Winzeler EA, et al. The Activities of Current Antimalarial Drugs on the Life Cycle Stages of *Plasmodium*: A Comparative Study with Human and Rodent Parasites. *PLoS Med*. 2012; 9(2):e1001169. <https://doi.org/10.1371/journal.pmed.1001169> PMID: 22363211
53. Delves M, Sinden R. A semi-automated method for counting fluorescent malaria oocysts increases the throughput of transmission blocking studies. *Malaria Journal*. 2010; 9(1):35.
54. Sinden RE. The biology of *Plasmodium* in the mosquito. *Experientia*. 1984; 40:1330–43.
55. Sinden RE. Sexual development of malarial parasites. *Advances in Parasitology*. 1983; 22:153–216.
56. Sinden RE. The cell biology of sexual development of malarial parasites. *Parasitology*. 1983; 86:7–28.
57. Lamour S, Straschil U, Saric J, Delves M. Changes in metabolic phenotypes of *Plasmodium falciparum* in vitro cultures during gametocyte development. *Malaria Journal*. 2014; 13(1):468. <https://doi.org/10.1186/1475-2875-13-468> PMID: 25439984

58. Srivastava A, Philip N, Hughes KR, Georgiou K, MacRae JI, Barrett MP, et al. Stage-Specific Changes in Plasmodium Metabolism Required for Differentiation and Adaptation to Different Host and Vector Environments. *PLoS Pathog.* 2016; 12(12):e1006094. <https://doi.org/10.1371/journal.ppat.1006094> PMID: 28027318
59. Field JW, Shute PG. The microscopic diagnosis of human malaria. Study No. 24. Kuala Lumpur. The Institute for Medical Research, Malaya. 1955.
60. Smalley ME, Abdalla S, Brown J. The distribution of *Plasmodium falciparum* in the peripheral blood and bone marrow of Gambian children. *Transactions of the Royal Society of Tropical Medicine and Hygiene.* 1981; 75(1):103–5. PMID: 7022784
61. Dantzler KW, Ravel DB, Brancucci NMB, Marti M. Ensuring transmission through dynamic host environments: host–pathogen interactions in Plasmodium sexual development. *Current Opinion in Microbiology.* 2015; 26(0):17–23.
62. Joice R, Nilsson SK, Montgomery J, Dankwa S, Egan E, Morahan B, et al. *Plasmodium falciparum* transmission stages accumulate in the human bone marrow. *Science translational medicine.* 2014; 6(244):244re5. <https://doi.org/10.1126/scitransmed.3008882> PMID: 25009232
63. Sinden RE, Dawes EJ, Alavi Y, Waldock J, Finney O, Mendoza J, et al. Progression of *Plasmodium berghei* through *Anopheles stephensi* is density-dependent. *PLoS Pathog.* 2008; 3(12):e195.
64. Churcher TS, Sinden RE, Edwards NJ, Poulton ID, Rampling TW, Brock PM, et al. Probability of Transmission of Malaria from Mosquito to Human Is Regulated by Mosquito Parasite Density in Naïve and Vaccinated Hosts. *PLoS Pathog.* 2017; 13(1):e1006108. <https://doi.org/10.1371/journal.ppat.1006108> PMID: 28081253
65. D'Alessandro S, Camarda G, Corbett Y, Siciliano G, Parapini S, Cevenini L, et al. A chemical susceptibility profile of the Plasmodium falciparum transmission stages by complementary cell-based gametocyte assays. *J Antimicrob Chemother.* 2016; 71:1148–58. <https://doi.org/10.1093/jac/dkv493> PMID: 26888912.
66. Lucantoni L, Silvestrini F, Signore M, Siciliano G, Eldering M, Decherig KJ, et al. A simple and predictive phenotypic High Content Imaging assay for Plasmodium falciparum mature gametocytes to identify malaria transmission blocking compounds. *Scientific reports.* 2015; 5:16414. <https://doi.org/10.1038/srep16414> PMID: 26553647.
67. van der Kolk M, de Vlas SJ, Saul A, van de Vegte-Bolmer M, Eling WM, Sauerwein W. Evaluation of the standard membrane feeding assay (SMFA) for the determination of malaria transmission-reducing activity using empirical data. *Parasitology.* 2005; 130:13–22. PMID: 15700753
68. Pasay CJ, Rockett R, Sekuloski S, Griffin P, Marquart L, Peatey C, et al. Piperaquine monotherapy of drug sensitive P. falciparum infection results in rapid clearance of parasitemia but is followed by the appearance of gametocytemia. *Journal of Infectious Diseases.* 2016; 214:105–13. <https://doi.org/10.1093/infdis/jiw128> PMID: 27056954
69. McCarthy JS, Marquart L, Sekuloski S, Trenholme K, Elliott S, Griffin P, et al. Linking Murine and Human Plasmodium falciparum Challenge Models in a Translational Path for Antimalarial Drug Development. *Antimicrobial Agents and Chemotherapy.* 2016; 60(6):3669–75. <https://doi.org/10.1128/AAC.02883-15> PMID: 27044554
70. Douglas AD, Edwards NJ, Duncan CJA, Thompson FM, Sheehy SH, O'Hara GA, et al. Comparison of Modeling Methods to Determine Liver-to-blood Inocula and Parasite Multiplication Rates During Controlled Human Malaria Infection. *Journal of Infectious Diseases.* 2013; 208:340–5. <https://doi.org/10.1093/infdis/jit156> PMID: 23570846
71. Mordmuller B, Supan C, Sim K, Gomez-Perez G, Ospina Salazar C, Held J, et al. Direct venous inoculation of Plasmodium falciparum sporozoites for controlled human malaria infection: a dose-finding trial in two centres. *Malaria Journal.* 2015; 14(1):117. <https://doi.org/10.1186/s12936-015-0628-0> PMID: 25889522
72. Blagborough AM, Delves MJ, Ramakrishnan C, Lal K, Butcher G, Sinden RE. Assessing transmission blockade in Plasmodium spp. *Methods Mol Biol.* 2013; 923:577–600. https://doi.org/10.1007/978-1-62703-026-7_40 PMID: 22990806.
73. Da DF, Churcher TS, Yerbanga RS, Yameogo B, Sangare I, Ouedraogo JB, et al. Experimental study of the relationship between Plasmodium gametocyte density and infection success in mosquitoes; implications for the evaluation of malaria transmission-reducing interventions. *Exp Parasitol.* 2015; 149:74–83. <https://doi.org/10.1016/j.exppara.2014.12.010> PMID: 25541384.
74. Bousema T, Churcher TS, Morlais I, Dinglasan RR. Can field-based mosquito feeding assays be used for evaluating transmission-blocking interventions? *Trends in parasitology.* 2013; 29:53–9. <https://doi.org/10.1016/j.pt.2012.11.004> PMID: 23273727

75. Churcher TS, Bousema T, Walker M, Drakeley C, Schneider P, Ouedraogo AL, et al. Predicting mosquito infection from *Plasmodium falciparum* gametocyte density and estimating the reservoir of infection. *eLife*. 2013; 2:e00626. Epub 2013/05/25. <https://doi.org/10.7554/eLife.00626> PMID: 23705071;
76. Hellmann JK, Münter S, Wink M, Frischknecht F. Synergistic and Additive Effects of Epigallocatechin Gallate and Digitonin on *Plasmodium* Sporozoite Survival and Motility. 2010; 5(1):e8682.
77. Rampling T, Ewer KJ, Bowyer G, Bliss CM, Edwards NJ, Wright D, et al. Safety and High Level Efficacy of the Combination Malaria Vaccine Regimen of RTS,S/AS01(B) With Chimpanzee Adenovirus 63 and Modified Vaccinia Ankara Vected Vaccines Expressing ME-TRAP. *The Journal of infectious diseases*. 2016; 214(5):772–81. <https://doi.org/10.1093/infdis/jiw244> PMID: 27307573
78. Tao D, Ubaida-Mohien C, Mathias DK, King JG, Pastrana-Mena R, Tripathi A, et al. Sex-partitioning of the *Plasmodium falciparum* stage V gametocyte proteome provides insight into falciparum-specific cell biology. *Molecular & Cellular Proteomics*. 2014; 13(10):2705–24. <https://doi.org/10.1074/mcp.M114.040956> PMID: 25056935
79. Talman A, Prieto J, Marques S, Ubaida-Mohien C, Lawniczak M, Wass M, et al. Proteomic analysis of the *Plasmodium* male gamete reveals the key role for glycolysis in flagellar motility. *Malaria Journal*. 2014; 13(1):315. <https://doi.org/10.1186/1475-2875-13-315> PMID: 25124718
80. Mohien CU, Colquhoun DR, Mathias DK, Gibbons JG, Armistead JS, Rodriguez MC, et al. A Bioinformatics Approach for Integrated Transcriptomic and Proteomic Comparative Analyses of Model and Non-sequenced Anopheline Vectors of Human Malaria Parasites. *Molecular & Cellular Proteomics*. 2013; 12(1):120–31.
81. Parish LA, Colquhoun DR, Mohien CU, Lyashkov AE, Graham DR, Dinglasan RR. Ookinete-Interacting Proteins on the Microvillar Surface are Partitioned into Detergent Resistant Membranes of *Anopheles gambiae* Midguts. *Journal of Proteome Research*. 2011; 10(11):5150–62. <https://doi.org/10.1021/pr2006268> PMID: 21905706
82. Wass MN, Stanway R, Blagborough AM, Lal K, Prieto JH, Raine D, et al. Proteomic analysis of *Plasmodium* in the mosquito: progress and pitfalls. *Parasitology*. 2012; 139(9):1131–45. <https://doi.org/10.1017/S0031182012000133> PMID: 22336136;
83. McMeniman CJ. Disruption of mosquito olfaction. In: Adelman ZN, editor. *Genetic control of malaria and dengue*. London: Academic Press; 2016. p. 227–42.
84. Emami SN, Lindberg BG, Hua S, Hill S, Mozuraitis R, Lehmann P, et al. A key malaria metabolite modulates vector blood seeking, feeding, and susceptibility to infection. *Science*. 2017: <https://doi.org/10.1126/science.aah4563> [Epub ahead of print]. PMID: 28183997
85. Blumberg BJ S S.M. Dimopoulos G. Employing the mosquito microflora for disease control. In: Adelman ZN, editor. *Genetic control of malaria and Dengue*. London: Academic Press; 2016. p. 335–53.
86. Dennison NJ, Saraiva RG, Cirimotich CM, Mlambo G, Mongodin EF, Dimopoulos G. Functional genomic analyses of *Enterobacter*, *Anopheles* and *Plasmodium* reciprocal interactions that impact vector competence. *Malaria Journal*. 2016; 15(1):425. <https://doi.org/10.1186/s12936-016-1468-2> PMID: 27549662
87. Delhaye J, Jenkins T, Christe P. *Plasmodium* infection and oxidative status in breeding great tits, *Parus major*. *Malaria Journal*. 2016; 15(1):531. <https://doi.org/10.1186/s12936-016-1579-9> PMID: 27809847
88. Duran-Bedolla J, Tellez-Sosa J, Valdovinos-Torres H, Pavon N, Buelna-Chontal M, Tello-Lopez A, et al. Cellular stress associated with *Plasmodium berghei* ookinete differentiation. *Biochemistry and Cell Biology*. 2016: <https://doi.org/10.1139/bcb-2016-0028> [Epub ahead of print]. PMID: 28177775
89. Siciliano G, Santha Kumar TR, Bona R, Camarda G, Calabretta MM, Cevenini L, et al. A high susceptibility to redox imbalance of the transmissible stages of *Plasmodium falciparum* revealed with a luciferase-based mature gametocyte assay. *Molecular microbiology*. 2017: <https://doi.org/10.1111/mmi.13626> [Epub ahead of print]. PMID: 28118506
90. Wong W, Griggs AD, Daniels RF, Schaffner SF, Ndiaye D, Bei AK, et al. Genetic relatedness analysis reveals the cotransmission of genetically related *Plasmodium falciparum* parasites in Thiès, Senegal. *Genome Medicine*. 2017; 9:5. <https://doi.org/10.1186/s13073-017-0398-0> PMID: 28118860
91. Duez J, Holleran JP, Ndour PA, Loganathan S, Amireault P, François O, et al. Splenic retention of *Plasmodium falciparum* gametocytes to block the transmission of malaria. *Antimicrobial Agents and Chemotherapy*. 2015; 59(7):4206–14. <https://doi.org/10.1128/AAC.05030-14> PMID: 25941228
92. Gonçalves BP, Drakeley C, Bousema T. Infectivity of Microscopic and Submicroscopic Malaria Parasite Infections in Areas of Low Malaria Endemicity. *Journal of Infectious Diseases*. 2016; 213(9):1516–7. <https://doi.org/10.1093/infdis/jiw044> PMID: 26908734
93. Ouédraogo AL, Gonçalves BP, Gnémé A, Wenger EA, Guelbeogo MW, Ouédraogo A, et al. Dynamics of the Human Infectious Reservoir for Malaria Determined by Mosquito Feeding Assays and

- Ultrasensitive Malaria Diagnosis in Burkina Faso. *Journal of Infectious Diseases*. 2016; 213(1):90–9. <https://doi.org/10.1093/infdis/jiv370> PMID: 26142435
94. Stone W, Goncalves BP, Bousema T, Drakeley C. Assessing the infectious reservoir of falciparum malaria: past and future. *Trends in parasitology*. 2015; 31(7):287–96. <https://doi.org/10.1016/j.pt.2015.04.004> PMID: 25985898.
 95. Tusting LS, Bousema T, Smith DL, Drakeley C. Measuring changes in *Plasmodium falciparum* transmission: precision, accuracy and costs of metrics. *Advances in Parasitology*. 2014; 84:151–208. <https://doi.org/10.1016/B978-0-12-800099-1.00003-X> PMID: 24480314.
 96. Muirhead-Thomson RC. The malarial infectivity of an African village population to mosquitoes (*An. gambiae*). *American Journal of Tropical Medicine and Hygiene*. 1957; 6:208–25.
 97. Muirhead-Thomson RC. Factors determining the true reservoir of infection of *Plasmodium falciparum* and *Wuchereria bancrofti* in a West African Village. *Transactions of the Royal Society of tropical Medicine and Hygiene*. 1954; 48(3):208–25. PMID: 13169237
 98. Muirhead-Thomson RC. Low gametocyte thresholds of infection of *Anopheles* with *Plasmodium falciparum*: a significant factor in malaria epidemiology. *British Medical Journal*. 1954; 1 (4893)(Jan. 9):68–70.
 99. Muirhead-Thomson RC, Mercier EC. Factors in Malaria Transmission by *Anopheles albimanus* in Jamaica Part II. *Annals of Tropical Medicine and Parasitology*. 1952; 46((3)):201–13. PMID: 13008349
 100. Muirhead-Thomson RC, Mercier EC. Factors in Malaria Transmission by *Anopheles albimanus* in Jamaica Part I. *Annals of Tropical Medicine and Parasitology*. 1952; 46((2)):103–16. PMID: 12986695
 101. Medica DL, Sinnis P. Quantitative dynamics of *Plasmodium yoelii* sporozoite transmission by infected anopheline mosquitoes. *Infection and immunity*. 2005; 73(7):4363–9. <https://doi.org/10.1128/IAI.73.7.4363-4369.2005> PMID: 15972531
 102. Rosenberg R. Ejection of Malaria Sporozoites by Feeding Mosquitoes. *TransRSocTropMedHyg*. 1992; 86:109.
 103. Garnham PCC. *Malaria parasites and other haemosporidia*. Blackwell. 1966; Oxford.
 104. Li Y, Leneghan DB, Miura K, Nikolaeva D, Brian IJ, Dicks MDJ, et al. Enhancing immunogenicity and transmission-blocking activity of malaria vaccines by fusing Pfs25 to IMX313 multimerization technology. *Scientific reports*. 2016; 6:18848. <https://doi.org/10.1038/srep18848> PMID: 26743316