

Monoclonal antibodies for malaria prevention

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Monoclonal antibodies are highly specific proteins that are cloned from a single B cell and bind to a single epitope on a pathogen. These laboratory-made molecules can serve as prophylactics or therapeutics for infectious diseases and have an impressive capacity to modulate the progression of disease, as demonstrated for the first time on a large scale during the COVID-19 pandemic. The high specificity and natural starting point of monoclonal antibodies afford an encouraging safety profile, yet the high cost of production remains a major limitation to their widespread use. While a monoclonal antibody approach to abrogating malaria infection is not yet available, the unique life cycle of the malaria parasite affords many opportunities for such proteins to act, and preliminary research into the efficacy of monoclonal antibodies in preventing malaria infection, disease, and transmission is encouraging. This review examines the current status and future outlook for monoclonal antibodies against malaria in the context of the complex life cycle and varied antigenic targets expressed in the human and mosquito hosts, and provides insight into the strengths and limitations of this approach to curtailing one of humanity's oldest and deadliest diseases.

INTRODUCTION

Monoclonal antibodies (mAbs), defined as a single antibody (Ab) cloned from a single B cell, have been in use for decades as immune modulators for transplantation, autoimmune diseases, and cancer.¹ Most clinical uses take advantage of the high specificity of Abs which can safely target specific proteins to deplete cells or block receptor-ligand interactions. This specificity and the fact that Abs are naturally occurring proteins rather than foreign molecules make for an excellent clinical safety profile. It is curious, however, that although Abs were first discovered and used in the context of infectious disease, mAbs are only recently seeing a resurgence in their use for this purpose.^{2,3} This review will focus on mAb development for one of the oldest and deadliest infectious diseases that remains without an effective long-term vaccine or chemoprophylactic: malaria.

CONSIDERATIONS FOR MONOCLONAL ANTIBODY DEVELOPMENT FOR INFECTIOUS DISEASES

mAbs are currently being adopted for numerous infectious diseases including respiratory syncytial virus,⁴ anthrax,⁵ HIV,^{6–8} and Ebola.⁹ They have recently been approved for use against Ebola and COVID-19, with the latter proving that mAbs can be a rapid and highly effective means of responding to emerging pathogens. However, as highlighted by the COVID-19 pandemic, developing mAbs for

infectious diseases is not amenable to a one-size-fits-all approach. Special considerations must be taken to consider the host-pathogen immunobiology and epidemiology of each disease as well as the market environment for novel interventions. For example, mAbs can be used as a prophylactic, therapeutic, or both. Which approach is best depends on a number of factors including the likelihood of the mAb in preventing infection or disease, the utility of the mAb at the individual and population level, the underlying cause of disease following infection, and the intended recipient population. In addition, it must be determined whether preventing infection, disease, or transmission is the priority. Finally, mAbs must be considered in the context of available or emerging drugs and/or vaccines which will compete on a public health and market level.

In the context of drugs and vaccines for infectious diseases, mAbs offer a number of potential benefits. They have an excellent safety profile with minimal off-target effects and can be used in combination with little to no interference.¹⁰ They can be delivered at effective doses in a single, directly observed injection or infusion and can persist at effective concentrations in the blood for longer than 1 year when using long-lasting variants.^{6,11,12} Unlike vaccines, mAbs do not depend on the host immune system for production and therefore should have less variability across populations in terms of immediate serum Ab concentration. However, genetic mutations in the Fc receptor can influence the downstream effector mechanisms^{13,14} and half-life¹⁵ of anti-cancer mAbs. How such variations contribute to mAb efficacy in infectious diseases has not been well defined and will be specific for each target pathogen. Finally, unlike vaccines that often require multiple doses and at least weeks to have an effect, mAbs are effective almost immediately upon administration.

Still, the road ahead for mAbs against infectious diseases contains several hurdles. The first and foremost concern is cost. The cost of a course of mAbs depends greatly on the intended market,¹⁶ but using COVID-19 as an example, the mAb therapy REGEN-COV is charged at ~\$2,100/dose to the US Government.¹⁷ This is small compared with the cost of even a short hospital stay but is orders of magnitude above the costs of COVID-19 vaccines. Thus, while COVID-19 has shown that mAbs can offer a cost-effective benefit in the absence of a vaccine, the cost of mAbs will need to decrease significantly before widespread

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use against infectious diseases is possible, particularly in low- and middle-income countries (LMIC). Another consideration is that, typically, tens or hundreds of mAbs need to be screened for function before advancing clinical candidates. This is best achieved using predictive and high-throughput *in vitro* assays (e.g., neutralization assays), which exist for some pathogens such as SARS-CoV-2 but do not exist for other infectious agents such as tuberculosis and for most stages of infection for the parasite that causes malaria. Pathogens are also adept at evolving past even the complex immunity in populations and thus will likely be able to evolve around most individual mAbs and even cocktail combinations of mAbs. Therefore, careful work is required to select either immutable targets or combinations of targets to prevent resistance.¹⁸ While a concern most relevant for dengue virus, the risk of Ab-dependent enhancement of disease due to the presence of non-neutralizing Abs must also be considered. Finally, even fully human monoclonals may be recognized as foreign by the recipient immune system, and “anti-drug antibodies” (ADAs) may form to either clear mAbs or reduce their efficacy. While ADA formation is dependent on many factors, experience with mAbs for infectious diseases have shown little evidence that ADAs will be an issue even following repeated injections.^{7,8,19,20}

CONSIDERATIONS FOR MONOCLONAL ANTIBODY DEVELOPMENT FOR MALARIA

Malaria is the disease caused by infection with eukaryotic pathogens of the genus *Plasmodium*, which have a host range spanning from reptiles and birds to rodents, humans, and other mammals. There are multiple species of *Plasmodium* that infect humans, with the vast majority of disease caused by *Plasmodium falciparum* (*Pf*) common to Sub-Saharan Africa and *Plasmodium vivax* (*Pv*) which dominates in Southeast Asia and South America. *Plasmodium* parasites are transmitted via multiple species of Anopheline mosquitoes, and the mammalian portion of the parasite life cycle begins when an infected mosquito injects tens to hundreds of “sporozoite” forms of the parasite into the dermis. These sporozoites then actively migrate through the skin and into the blood where they will be carried to the liver. Here, the parasites replicate asymptotically and asexually for ~7 days within a single hepatocyte, although at this stage *Pv* also forms dormant stages in the liver called “hypnozoites” that can persist and reactivate for years. At the end of the liver stage the parasites emerge as red blood cell-infectious “merozoites.” These merozoites cyclically infect red blood cells, which rapidly expands the parasite burden and initiates the symptomatic stage of infection. Some parasites also undergo sexual replication to become male and female “gametocytes” which can then be picked up by a new mosquito vector. The invertebrate portion of the parasite life cycle starts in the mosquito midgut where the gametocytes will mate, forming a motile “ookinete” that invades the mosquito midgut, where new sporozoites will develop within the “oocyst” for approximately 2 weeks. These sporozoites will then emerge from the oocyst and migrate into the mosquito salivary gland where they can then be transmitted to a new host and complete the transmission cycle. In this review, we will divide this complex life cycle roughly into three phases: the skin-to-liver or “pre-erythrocytic” stage; the “erythrocytic” or blood stage; and the mosquito stage.

The *Plasmodium* life cycle is more complex than bacterial or viral infections, which, on the one hand, presents a challenge to mAb development but also serves as an opportunity, as Abs can function against each stage of infection (Figure 1). This susceptibility has driven the development of multiple prophylactic Ab-based vaccine candidates which have only recently achieved high levels of protection against disease.²¹ However, protection against infection has been much more difficult to achieve and will be necessary to disrupt the transmission cycle and achieve malaria eradication. Such high levels of infection-blocking protection have been achieved in controlled human malaria infection (CHMI) studies in malaria-naïve volunteers,^{22,23} but this has not translated to field trials in endemic areas.^{24–27} It is hypothesized that this is due in part to pre-existing malaria-specific immune modulation in previously infected persons. In this case, a long-acting prophylactic mAb would be ideal as it does not rely on the recipient immune system to produce Abs. However, parasite fitness and polymorphisms also play a pivotal role in vaccine efficacy,^{28,29} which will need to be considered in developing anti-malarial mAbs.

Finally, it is important to consider that multiple effective and affordable drugs exist to prevent and treat malaria, and that vaccines can be made relatively cheaply if one is developed for malaria. Therefore, the current costs of mAbs would preclude large-scale administration campaigns similar to mass drug administration or mass vaccination. Even at current cost estimates, however, mAbs offer advantages over chemoprophylaxis for members of the military or travelers making multi-week or multi-month visits to endemic areas. This is because long-term chemoprophylaxis is still expensive³⁰ and suffers from low compliance (10%–50%) due to inconvenient schedules and side effects.^{31–33} The high cost of mAbs is also lower than the costs of a medical evacuation and therefore could be cost-effective for visitors at high risk of malaria. Compared with the protracted regimens of vaccines and drugs and the lag time between vaccine administration and efficacy, mAbs would also offer the benefit of a simplified regimen given in a single directly observed administration that has immediate efficacy for unplanned or short-notice trips. While an exact “target product profile” for an anti-malaria mAb will depend on the user and goal, most models suggest that we will need >80% infection-blocking sterile protection for longer than a year to drive malaria toward elimination,^{34–36} similar to what has been proposed for long-lasting injectable chemoprophylactics.³⁶ It is within this context that we will discuss the current state of mAbs for malaria as well as the short-term outlook for achieving the first competitive malaria mAb product capable of achieving high levels of infection-blocking protection. This will be discussed through the lens of the *Plasmodium* life cycle, given the profound impact of the distinct nature of each stage of infection on mAb development (see Figure 1 for summary of life cycle and potential mAb targets).

“PRE-ERYTHROCYTIC” STAGE TARGETED MONOCLONAL ANTIBODIES

As a bottleneck in the life cycle, the numbers of sporozoites injected by the mosquito at the skin-to-liver, or pre-erythrocytic (PE), stages are relatively small^{37–39} and the time between injection, invasion of

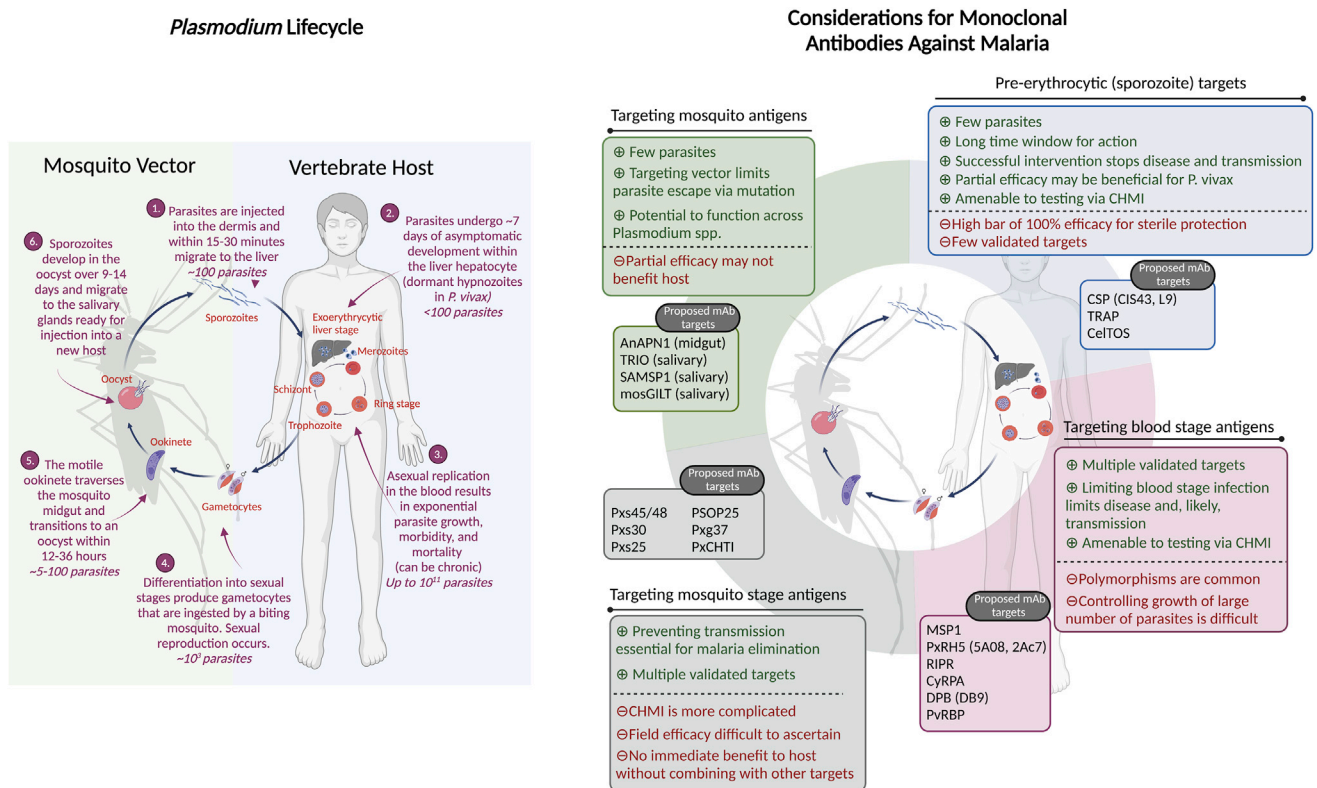


Figure 1. The *Plasmodium* parasite lifecycle and considerations for monoclonal antibodies against malaria

Left: schematic of the *Plasmodium* life cycle, including the approximate number of parasites present in, and duration of, each stage. Right: considerations for monoclonal antibodies against malaria, by life cycle stage. Ab targets that are discussed in this paper are listed by their abbreviation, with specific antibody names included in parentheses where relevant. When the antigen typically includes reference to a specific *Plasmodium* species, x is used instead of species designation. Full antigen names can be found in the text, where relevant. CHMI, controlled human malaria infection. Created with [Biorender.com](https://biorender.com).

the vasculature, and transit to the liver is minutes to hours,^{40–43} which provides a large window for infection-blocking Ab activity. The circumsporozoite protein (CSP) is the most abundant surface antigen present in the sporozoite stage of the *Plasmodium* parasite⁴⁴ and is critical to the normal development of sporozoites in the mosquito salivary gland⁴⁵ as well as their ability to invade and infect hepatocytes once inside the vertebrate host.⁴⁶ The two most successful and advanced malaria vaccines, RTS,S and R21, are both designed to elicit an immune response against CSP⁴⁷ and are thought to provide protection by neutralizing Abs. This is supported by studies showing the capacity of mAbs against *Pf* CSP (PfCSP) and *Plasmodium yoelii* CSP (PyCSP) to prevent hepatocyte invasion both *in vitro* and *in vivo*.^{11,48–53} Using *Pv* infection of liver-humanized mice, Schäfer et al. recently demonstrated that an mAb against PvCSP could also reduce the overall liver burden and in turn relapse infection via reduction of the number of dormant hypnozoites.⁵⁴ This is critical, as the majority of *Pv* disease burden is driven by relapses from dormant liver hypnozoites.⁵⁵

The mechanisms of anti-PfCSP mAbs have been well-studied. The CSP is composed of three domains: an N terminus, a C terminus,

and a central region characterized by a repeating amino acid sequences.⁵⁶ In *Pf*, this repeat region contains a major repeating sequence, NANP, and a minor repeat, NVDP. The CSP-specific mAb CIS43 was recently shown to be a “dual binder” in that it specifically binds to the central repeat region as well as a short junctional sequence that bridges the N terminus and the central repeat region,¹¹ and has been reported to provide sterile protection in two different mouse models following passive transfer.⁴⁸ This may be explained by the ability of CIS43 to bind multiple CSP epitopes, as such dual binding confers potent neutralizing capabilities to a number of other mAbs which target the major repeat and either the minor repeat or the junction sequence.^{49,57} Of note, the introduction of the “LS” mutation into the Fc domain of CIS43 increased the serum half-life of the Ab while maintaining a high level of protection *in vivo*.¹² This modified CIS43LS has been taken into phase I clinical trials in malaria-naïve adults, and this first-in-human study for malaria mAbs showed a very promising safety and pharmacokinetic profile after intravenous or subcutaneous administration.⁵⁸ Furthermore, participants underwent CHMI challenge and all nine were sterilely protected against infection.⁵⁸ However, the numbers of volunteers per dose was small and serum concentration at time of challenge

ranged from ~50 to 500 µg/mL, which is likely higher than what is feasible for long-term protection in the field due to cost. Still, the results from an ongoing field trial in Mali will be critical for understanding the potential for anti-malaria mAbs to perform against natural infection (ClinicalTrials.gov ID: NCT04329104). Encouragingly, a new dual-binding anti-PfCSP mAb, L9, outperformed six published neutralizing mAbs—including CIS43 and other dual binders—in mosquito bite challenges *in vivo* and therefore provides a path to improved potency should results with CIS43LS indicate the need for improvements.⁵³ In summary, mAbs against PfCSP are paving the way to become the first anti-malarial mAb to prevent infection. However, low levels of sterile protection achieved by CSP recombinant vaccines in the field despite high titers of anti-PfCSP Abs^{21,25} and success in CHMI suggest that multiple avenues to improve mAb potency should continue to be pursued.

One such strategy is targeting additional PE antigens. Although no other PE Ab targets have been as well defined or as potent as CSP, the PE stages provide numerous points of possible intervention,⁵⁹ and non-CSP polyclonal Abs have recently been shown as potent inhibitors of parasite liver infection in humanized liver mice.⁶⁰ A leading target for PE mAb development is the thrombospondin-related adhesive protein (TRAP), a transmembrane protein essential for sporozoite motility and successful liver invasion.^{61,62} High levels of anti-TRAP Abs have been correlated with higher protection against malaria in children,⁶³ suggesting that this protein may yield another promising mAb target. The idea of using TRAP in combination with CSP as an Ab target has been considered for decades, but studies have generated mixed results. One vaccine trial using TRAP in combination with RTS,S failed to show any significant protection, perhaps because of immune interference that reduced the anti-CSP Ab titers.⁶⁴ Another clinical trial combining RTS,S with viral-vectored TRAP showed no benefit to adding TRAP, yet interpretation of this is complicated by the combination of vaccine platforms.⁶⁵ This is in contrast to studies in mice where active vaccination with CSP and TRAP suggested the utility of adding TRAP,⁶⁶ and a TRAP/CSP fusion protein conferred sterile protection for 6 months in mice.⁶⁷ Concrete evidence of the utility of additional PE antigens would be best achieved by using passive transfer of polyclonal Abs or mAbs. A recent manuscript in preprint has shed some light on this and has demonstrated that anti-TRAP mAbs can significantly improve the protective efficacy of anti-CSP mAbs in both rodent models and liver-humanized mice to above 80% at low doses.⁶⁸ However, whether this enhancement is additive or synergistic was not addressed and will be critical for determining the utility of such combinations. Together, these data suggest that combinations of PE mAbs may be a pathway to achieving high levels of protection at serum concentrations achievable over extended periods.

A critical part of *Plasmodium* motility and infection at the PE stage is called traversal, where the parasite actively crosses through host cells as it migrates from the skin to the liver in the vertebrate host. Traversal is also utilized during the mosquito stages when the parasite invades the mosquito midgut and salivary glands. This active process

involves several proteins including the cell traversal protein for ookinetes and sporozoites (CelTOS), which is required at multiple stages.⁶⁹ This antigen was first isolated in 2003, is highly immunogenic, and is highly conserved across *Plasmodium* species.^{70,71} Polyclonal Abs against CelTOS are able to suppress parasite motility, inhibit hepatocyte invasion, and provide sterile protection in rodent models.⁷² In addition, passive transfer of anti-CelTOS mAbs has been shown to reduce sporozoite infectivity in mice and decrease oocyst burden in mosquitoes.⁷³ This suggests that multiple functions of CelTOS can be targeted to disrupt multiple points of *Plasmodium* motility within each host, and this may be achievable with a single mAb.

In summary, with CSP leading the way, future studies of PE Ab targets will require improvement of mAbs against existing targets by way of similar detailed mechanistic studies as have been conducted for CSP. This should be supplemented with the identification of additional Ab targets, as we have only begun to explore the >30 sporozoite surface or secreted proteins potentially accessible to Ab binding.

BLOOD STAGE TARGETED MONOCLONAL ANTIBODIES

The gold standard for a prophylactic anti-malarial or vaccine is “sterile protection,” defined as the prevention of blood stage infection. Achieving sterile protection by exclusively targeting the blood stages has proved extremely difficult, as most simply reduce but do not eliminate parasite replication and many blood stage proteins exhibit substantial antigenic polymorphism.⁷⁴ Sterile protection via vaccines has been rare and has been achieved in high proportions thus far only with vaccines and monoclonals targeting the PE stages. Given this difficulty in achieving sterile protection, a vaccine or mAb treatment that targets the asexual blood stages of the parasite could either more quickly alleviate or completely prevent symptomatic blood stage infection. Thus, antigens presented by the infective merozoites as well as those expressed on the red blood cells (RBCs) after infection offer appealing targets for mAbs either alone or in combination with PE targets.

The merozoite surface protein 1 (MSP1) complex is critical to the normal progression of the *Pf* life cycle and has been shown to be necessary for both RBC invasion and merozoite egress from infected erythrocytes.^{75,76} MSP1 is the most abundant protein on the surface of the merozoite, making it a viable target for vaccine and mAb interventions.⁷⁷ It is proteolytically processed as the merozoite matures, resulting in a non-covalently linked complex of the fragments p83, p30, p38, and p42.⁷⁸ It has been shown that MSP1 mediates *Pf* merozoite interactions with human erythrocytes, and Abs targeting various fragments can disrupt parasite growth.^{79,80} However, the prevalent polymorphisms within certain portions of MSP1 and relatively low levels of protection afforded by MSP1-based vaccines has likely limited enthusiasm for MSP1 as a mAb target, although detailed studies using mAbs targeting conserved epitopes are warranted.

A newer and more promising blood stage target with considerable mAb research is the *Pf* reticulocyte-binding protein homolog 5 (PfRH5). This protein binds the surface receptor basiginin on the erythrocyte membrane and has been shown to be essential to merozoite invasion.^{81,82} During invasion, PfRh5 forms a complex with the cysteine-rich protective antigen (CyRPA) and PfRh5 interacting protein (PfRIPR).⁸³ Both CyRPA and PfRIPR are housed within parasite micronemes and are released during merozoite invasion to facilitate entrance into the erythrocyte via their assembly into a trimeric complex with PfRh5.^{83,84} Given the essential nature of this protein to the parasite invasion of RBCs and the association of anti-PfRH5 with protection in field studies, as well as promising data as a vaccine target,^{85,86} PfRh5 is leading the field as an mAb target at the blood stage. A variety of potent neutralizing mAbs targeting PfRH5 have been identified, three of which have been demonstrated to be capable of inhibiting merozoite invasion by >95% at low concentrations *in vitro*.⁸⁷ This work identified 5A08, an Ab that recognizes a highly immunogenic epitope on PfRh5, which has shed light on the mechanism of anti-PfRh5 mAb inhibition.⁸⁷ A more recent study showed that the anti-PfRH5 mAb 2Ac7 can provide sterilizing protection against stringent *Pf* blood stage challenge in non-human primates and also established the *in vitro* growth inhibition assay as predictive of protection *in vivo*.⁸⁸

Still, the concentrations needed to provide protection are too high for direct clinical use, and the potency of anti-PfRh5 mAbs will need to be improved. One path to increasing potency is to disrupt the assembly of the PfRh5/RIPR/CyRPA complex rather than solely targeting PfRH5. This has been achieved using mAbs targeting both Rh5 and CyRPA that prevent the formation of the trimeric complex, and using Abs against PfCyRPA and PfRIPR that act synergistically to reduce merozoite invasion *in vitro*.⁸⁹ These results show the need for further research on these antigens and support mAbs targeting the entire complex as a viable path forward in improving the potency of blood stage mAbs.

Of particular concern in malaria-endemic areas is pregnancy-associated malaria (PAM), which threatens 125 million women per year and is a significant cause of maternal and infant mortality.⁹⁰ *Pf*-infected erythrocytes are known to sequester in the placenta owing to their ability to bind chondroitin sulfate A (CSA), and it has been shown that the parasite protein VAR2CSA, a member of the *Pf* erythrocyte membrane protein 1 (PfEMP1) family,⁹¹ is upregulated in placental infected erythrocytes.^{92,93} One study showed that women with high levels of anti-VAR2CSA immunoglobulin G gave birth to heavier infants and were at a significantly lower risk of delivering low-birth-weight children in comparison with mothers with low levels of circulating Ab.⁹² Therefore, VAR2CSA is a logical vaccine target with the potential to protect pregnant women and their children. However, safety considerations have prevented pregnant women from receiving an experimental malaria immunization, let alone one targeted to preventing PAM.⁹⁴ Furthermore, antigenic variation in VAR2CSA complicates the development of a VAR2CSA vaccine, especially given the difficulty in developing

such a vaccine in a vulnerable population.⁹⁵ This provides an interesting case use for mAbs given their safety profile in pregnant women⁹⁶ with the possibility that a broadly neutralizing mAb could be administered during pregnancy, likely with only a single dose, in the absence of an effective vaccine with an anti-PAM component. Such an mAb could even be administered on top of a partially effective vaccine targeting other stages (e.g., RTS,S) to provide additional protection during pregnancy.

In *Pv*, the blood stage parasites are unique in that they infect immature reticulocytes rather than the mature erythrocytes targeted by *Pf*. Thus, there are unique invasion proteins to consider for *Pv* blood stage mAbs, including the erythrocyte-binding ligand family that is essential for *Pv* merozoite entry into the reticulocyte.⁹⁷ These proteins contain a cysteine-rich binding domain at the N-terminal region called the Duffy binding-like domain, which is the functional portion of the Duffy binding protein (DBP) ligand. This ligand must engage with the Duffy antigen receptor for chemokines (DARC) expressed on the host reticulocyte membrane surface in order for the parasite to begin invasion.⁹⁸ Natural exposure to malaria elicits DBP-specific Abs that inhibit the binding of the parasite⁹⁹ and are associated with clinical protection,¹⁰⁰ possibly due to the highly polymorphic capacity of the molecule that allows it to evade the host immune response.¹⁰¹ Thus, DBP is a logical target for mAb development.

Moreover, an artificial DBP immunogen consisting of the DARC-binding region II of the protein optimized for functional and non-polymorphic targets¹⁰² was used to produce a panel of mAbs in BALB/c mice. A total of ten of these mAbs showed significant inhibition of parasite invasion *in vitro*.¹⁰³ Rawlinson et al. isolated mAbs from volunteers immunized with a PvDBP vaccine candidate and found a promising mAb, DB9, that inhibits parasite invasion *in vitro* and prevents the binding of five variant alleles of PvDBP to DARC.¹⁰⁰ Other groups have successfully isolated mAbs to PvDBP from individuals with natural immunity to *Pv*, which may show enhanced inhibition and can transcend wild-type *Pv* strains.^{104,105} Interestingly, mAbs that bind close to or at the DB9 epitope can provide additive inhibition while mAbs that bind different epitopes elsewhere in the PvDBP molecule are antagonistic.

Pv reticulocyte invasion also requires the interaction between the *Pv* reticulocyte protein (PvRBP) and transferrin receptor on the host reticulocyte.^{106,107} Four anti-PvRBP mAbs have been identified thus far that can prevent reticulocyte invasion *in vitro*, therefore providing another encouraging *Pv* blood stage target.¹⁰⁷ The ability of these mAbs to target unique proteins and invasion pathways to work in additivity or synergy, and the impact of any such mAb *in vivo*, will be critical data. However, this is difficult research to conduct given that blood stage culture of the *Pv* blood stages is limited to using fresh field isolates in short-term assays and that *Pv* blood stage challenge *in vivo* is only possible as a CHMI.^{108–112} However, a manuscript in preprint at the time of this review suggests that a non-human primate model of *Pv* blood stage infection may be near and thus could fill a

significant gap in the preclinical assessment of *Pv* blood stage mAbs.¹¹³

MOSQUITO STAGE TARGETED MONOCLONAL ANTIBODIES

The transmission of parasites between the human host and mosquito vector is an appealing target for Abs, as these stages present another bottleneck in the parasite life cycle^{37,38,114–117} and display minimal polymorphisms, likely due to the lack of evolutionary pressure by the human immune system,^{118–121} and Abs against these stages are especially potent.^{122–124} While Abs targeting solely the transmission of an established blood stage infection to mosquitoes offers no direct benefit to the individual, sufficient coverage of a local population with effective transmission-blocking Abs could have drastic effects on the burden of disease,^{117,125,126} and preliminary data suggest that they may be readily accepted in affected communities.^{127–129} Much of the data available on such transmission-blocking targets concern vaccine development, yet these data have clear applicability to the development of mAbs for passive immunization.

Abs against two proteins expressed on the transmissible gametocyte, Pfs48/45^{121,130} and Pfs230,^{121,131,132} have demonstrated substantial blocking of parasite development in the mosquito at concentrations as low as 1–3 µg/mL.¹²¹ Notably, one such mAb, TB31F, is currently in a clinical trial (ClinicalTrials.gov ID: NCT04238689) aimed to test the safety and pharmacokinetics of intravenous and subcutaneous administration, down to 0.1 mg/kg. Importantly, antigens on the gametocyte may act synergistically as dual-antigen Ab targets that neutralize the gametocyte prior to fertilization in the mosquito midgut.^{132,133} Once the parasite has begun to transition into a zygote and then ookinete, additional proteins, notably Pfs/Pvs25 and Pfs230, are expressed on the surface and can be targeted to prevent subsequent invasion and development within the midgut. These proteins—Pfs25, Pfs230, and Pfs48/45—are the only parasite antigens currently in clinical trials as a transmission-blocking vaccine candidate¹²⁵ (and ClinicalTrials.gov ID: NCT04862416). Additional targets of the parasite at early stages of mosquito development include PSOP25, Pbg37, and PfCHT1, which have yet to be validated for human parasite species, but suggest that the list of potential transmission-blocking candidates may be more extensive than those currently being developed as vaccine candidates.^{134–137}

In addition to targeting the parasite, an intriguing strategy is to target mosquito proteins involved in parasite transmission. While in its infancy, targeting mosquito proteins is an especially appealing avenue because Abs against these proteins could disrupt transmission in a manner that transcends malaria species and is more resistant to evolutionary circumvention by the parasite itself. To this end, the mosquito midgut protein, AnAPN1, shows considerable promise as a nanoparticle vaccine in animal models that functions by blocking ookinete invasion of the mosquito midgut.^{138–140} Another interesting approach targets the other side of mosquito transmission: the saliva proteins that are injected with the parasite during probing. These proteins have a myriad of functions, including immunomodulation

during normal probing feeding.¹⁴¹ Abs against the *Anopheles gambiae* TRIO salivary gland protein can provide partial protection against mosquito bite challenge with multiple *Plasmodium* species and have the potential to work in tandem with anti-sporozoite Abs.¹⁴² Other components of the mosquito saliva, including SAMSP1 and mosGILT, have been shown to affect sporozoite motility to either aid or hinder the progress of the sporozoite,^{143,144} suggesting that Abs raised to novel mosquito saliva proteins may be promising avenues for research. This approach is not unique to malaria control efforts, and ideas can be borrowed from strategies being pursued for arboviruses. For example, Abs to proteins in the *Aedes aegypti* saliva may prevent successful infection by flaviviruses¹⁴⁵ and one construct, AGS-v, has recently been shown to be safe and immunogenic in clinical trials.¹⁴⁶ In summary, mAb approaches to malaria need not be limited to classic parasite antigens, and a combination of both “traditional” and novel targets should be pursued to achieve high levels of protection and eradication.

FUTURE OUTLOOK

As with mAbs for many infectious diseases, mAbs for malaria are poised to become a paradigm-shifting intervention. The numerous lines of research in the preceding discussion indicate that they are indeed a promising avenue for clinical intervention at a number of stages across the parasite life cycle, and the small first-in-human trial is encouraging. Yet for malaria and other diseases that overwhelmingly affect people in LMIC, low investment in research paired with the need for a low cost of goods will be a major impediment. The latter is a technological barrier that is likely easier to overcome than the former, which is an impediment of will and interest by wealthy nations and funders. Optimistically, the COVID-19 pandemic has proved that mAbs can be developed faster, are better tolerated, are as efficacious, and are at least as adaptable compared with vaccines and drugs when it comes to battling infectious diseases. The high demand for and apparent profitability of mAbs in the COVID-19 pandemic will hopefully usher in a new wave of interest in improving the production of mAbs at scale and at lower costs for other diseases. With any luck, these accelerated technological advances to reduce cost will coincide with improved mAb efficacy for malaria that increases potency and reduces the dose required to achieve the high threshold of protection needed.

Such improvements in efficacy are likely to come in both detailed and iterative investigations of structure-function biology as has been performed for PfCSP and PfRh5. Yet it is perhaps too optimistic to assume that a single mAb targeting a single epitope will achieve sufficient efficacy to warrant stand-alone use as a prophylactic or therapeutic. Furthermore, it is likely unwise to use such a single-antigen approach given concerns over resistance and breakthrough infection. Therefore, combinations of mAbs that target multiple epitopes and multiple proteins will likely be needed. Yet the utility of such a combinatorial approach has lacked extensive evidence. Indeed, the blood stage anti-RIPR complex Abs have demonstrated efficacy and even synergy *in vitro*,^{147,148} and combining PE targets such as CSP and TRAP may hold promise despite mixed results. However, it

remains to be seen whether additional gains can be made from combining mAbs targeting different stages. A major hurdle in developing such multi-stage approaches is that the infection cycle spanning the mosquito, PE, and blood stages is impossible to replicate *in vitro*, let alone in a high-throughput manner. Therefore, each mAb targeting each stage will need to be vetted individually in their respective assays and combined for final assessment *in vivo*. The preclinical model that is best poised to assess multiple stages—mosquito bite challenge of humanized liver mice repopulated with exogenous RBCs^{54,149,150}—is tractable but expensive, lacks a gametocyte-transmission component, and is not high throughput. Even CHMI of actively or passively immunized volunteers has yet to be developed for such a multi-stage approach although the PE, blood stages, and transmission can be assessed independently.¹⁵¹ Even with these limitations, whether the existing *in vitro* and *in vivo* models predict clinical success will require clinical testing of both optimal and suboptimal mAb regimens. This will stretch already limited funds which to date have been reserved for only the safest and most highly promising interventions.

In summary, the path to malaria elimination will require a long-lasting, effective, and simple intervention that can prevent infection in a high proportion of people. If this intervention is based on mAbs, it will require: (1) iterative improvements of mAbs against existing targets that can function at lower doses; (2) identification of novel targets and mechanisms that can be incorporated into next-generation mAb regimens; (3) the identification of additive or synergistic combinations of mAbs that improve efficacy and guard against resistance; (4) the improvement of preclinical assays to assess multi-stage interventions; and (5) simultaneous changes in the production of mAbs to make them affordable for global health use. Thus, while the challenges remain large, the components of a path to the first protective mAb product for malaria has been made clear by the impressive work reviewed here and can become a reality with the addition of sufficient interest, financial investment, and time.

REFERENCES

- Liu, J.K. (2014). The history of monoclonal antibody development - progress, remaining challenges and future innovations. *Ann. Med. Surg. (Lond)*, 3, 113–116. <https://doi.org/10.1016/j.amsu.2014.09.001>.
- Pelfrene, E., Mura, M., Cavaleiro Sanches, A., and Cavaleri, M. (2019). Monoclonal antibodies as anti-infective products: a promising future? *Clin. Microbiol. Infect.* 25, 60–64. <https://doi.org/10.1016/j.cmi.2018.04.024>.
- Laustsen, A.H. (2019). How can monoclonal antibodies be harnessed against neglected tropical diseases and other infectious diseases? *Expert Opin. Drug Discov.* 14, 1103–1112. <https://doi.org/10.1080/17460441.2019.1646723>.
- Soto, J.A., Gálvez, N.M.S., Pacheco, G.A., Bueno, S.M., and Kalergis, A.M. (2020). Antibody development for preventing the human respiratory syncytial virus pathology. *Mol. Med.* 26, 1–10. <https://doi.org/10.1186/S10020-020-00162-6>.
- Sparrow, E., Friede, M., Sheikh, M., and Torvaldsen, S. (2017). Therapeutic antibodies for infectious diseases. *Bull. World Health Organ.* 95, 235–237. <https://doi.org/10.2471/BLT.16.178061>.
- Gaudinski, M.R., Coates, E.E., Houser, K.V., Chen, G.L., Yamshchikov, G., Saunders, J.G., Holman, L.A., Gordon, I., Plummer, S., Hendel, C.S., et al. (2018). Safety and pharmacokinetics of the Fc-modified HIV-1 human monoclonal antibody VRC01LS: a Phase 1 open-label clinical trial in healthy adults. *PLoS Med.* 15, e1002493. <https://doi.org/10.1371/JOURNAL.PMED.1002493>.
- Ledgerwood, J.E., Coates, E.E., Yamshchikov, G., Saunders, J.G., Holman, L., Enama, M.E., DeZure, A., Lynch, R.M., Gordon, I., Plummer, S., et al. (2015). Safety, pharmacokinetics and neutralization of the broadly neutralizing HIV-1 human monoclonal antibody VRC01 in healthy adults. *Clin. Exp. Immunol.* 182, 289–301. <https://doi.org/10.1111/CEL.12692>.
- Lynch, R.M., Boritz, E., Coates, E.E., DeZure, A., Madden, P., Costner, P., Enama, M.E., Plummer, S., Holman, L., Hendel, C.S., et al. (2015). Virologic effects of broadly neutralizing antibody VRC01 administration during chronic HIV-1 infection. *Sci. Transl. Med.* 7, 319ra206. <https://doi.org/10.1126/SCITRANSLMED.AAD5752>.
- Maxmen, A. (2019). Two Ebola drugs show promise amid ongoing outbreak. *Nature*. <https://doi.org/10.1038/D41586-019-02442-6>.
- Hansel, T.T., Kropshofer, H., Singer, T., Mitchell, J.A., and George, A.J. (2010). The safety and side effects of monoclonal antibodies. *Nat. Rev. Drug Discov.* 9, 325–338. <https://doi.org/10.1038/NRD3003>.
- Livingstone, M.C., Bitzer, A.A., Giri, A., Luo, K., Sankhala, R.S., Choe, M., Zou, X., Dennison, S.M., Li, Y., Washington, W., et al. (2021). *In vitro* and *in vivo* inhibition of malaria parasite infection by monoclonal antibodies against Plasmodium falciparum circumsporozoite protein (CSP). *Sci. Rep.* 11, 5318. <https://doi.org/10.1038/S41598-021-84622-X>.
- Kisalu, N.K., Pereira, L.D., Ernste, K., Flores-Garcia, Y., Idris, A.H., Asokan, M., Dillon, M., MacDonald, S., Shi, W., Chen, X., et al. (2021). Enhancing durability of CIS43 monoclonal antibody by Fc mutation or AAV delivery for malaria prevention. *JCI Insight* 6, e143958. <https://doi.org/10.1172/JCI.INSIGHT.143958>.
- Musolino, A., Naldi, N., Bortesi, B., Pezzuolo, D., Capelletti, M., Missale, G., Laccabue, D., Zerbini, A., Camisa, R., Bisagni, G., et al. (2008). Immunoglobulin G fragment C receptor polymorphisms and clinical efficacy of trastuzumab-based therapy in patients with HER-2/neu-positive metastatic breast cancer. *J. Clin. Oncol.* 26, 1789–1796. <https://doi.org/10.1200/JCO.2007.14.8957>.
- Musolino, A., Gradishar, W.J., Rugo, H.S., Nordstrom, J.L., Rock, E.P., Arnaldez, F., and Pegram, M.D. (2022). Role of Fcγ receptors in HER2-targeted breast cancer therapy. *J. Immunother. Cancer.* 10, e003171. <https://doi.org/10.1136/JITC-2021-003171>.
- Passot, C., Azzopardi, N., Renault, S., Baroukh, N., Arnoult, C., Ohresser, M., Boisdron-Celle, M., Gamelin, E., Watier, H., Pintaud, G., and Gouilleux-Gruart, V. (2013). Influence of FCGRT gene polymorphisms on pharmacokinetics of therapeutic antibodies. *MAbs* 5, 614–619. <https://doi.org/10.4161/MABS.24815>.
- Hernandez, I., Bott, S.W., Patel, A.S., Wolf, C.G., Hospodar, A.R., Sampathkumar, S., and Shrank, W.H. (2018). Pricing of monoclonal antibody therapies: higher if used for cancer? *Am. J. Manag. Care* 24, 109–112.
- Regeneron Announces New, U.S. (2022). Government Agreement to Purchase Additional Doses of REGEN-COV™ (Casirivimab and Imdevimab) Antibody Cocktail (Regeneron Pharmaceuticals Inc), <https://investor.regeneron.com/news-releases/news-release-details/regeneron-announces-new-us-government-agreement-purchase>.
- Dussupt, V., Sankhala, R.S., Mendez-Rivera, L., Townsley, S.M., Schmidt, F., Wiczorek, L., Lal, K.G., Donofrio, G.C., Tran, U., Jackson, N.D., et al. (2021). Low-dose *in vivo* protection and neutralization across SARS-CoV-2 variants by monoclonal antibody combinations. *Nat. Immunol.* 22, 1503–1514. <https://doi.org/10.1038/S41590-021-01068-Z>.
- Walsh, S.R., and Seaman, M.S. (2021). Broadly neutralizing antibodies for HIV-1 prevention. *Front. Immunol.* 12, 712122. <https://doi.org/10.3389/FIMMU.2021.712122>.
- Mayer, K.H., Seaton, K.E., Huang, Y., Grunenberg, N., Isaacs, A., Allen, M., Ledgerwood, J.E., Frank, I., Sobieszczyk, M.E., Baden, L.R., et al. (2017). Safety, pharmacokinetics, and immunological activities of multiple intravenous or subcutaneous doses of an anti-HIV monoclonal antibody, VRC01, administered to HIV-uninfected adults: results of a phase 1 randomized trial. *PLoS Med.* 14, e1002435. <https://doi.org/10.1371/JOURNAL.PMED.1002435>.
- Dattoo, M.S., Natama, M.H., Somé, A., Traoré, O., Rouamba, T., Bellamy, D., Yameogo, P., Valia, D., Tegneri, M., Ouedraogo, F., et al. (2021). Efficacy of a low-dose candidate malaria vaccine, R21 in adjuvant Matrix-M, with seasonal

- administration to children in Burkina Faso: a randomised controlled trial. *Lancet* 397, 1809–1818. [https://doi.org/10.1016/S0140-6736\(21\)00943-0](https://doi.org/10.1016/S0140-6736(21)00943-0).
22. Epstein, J.E., Paolino, K.M., Richie, T.L., Sedegah, M., Singer, A., Ruben, A.J., Chakravarty, S., Stafford, A., Ruck, R.C., Eappen, A.G., et al. (2017). Protection against *Plasmodium falciparum* malaria by PfSPZ vaccine. *JCI Insight* 2, e89154. <https://doi.org/10.1172/jci.insight.89154>.
 23. Rampling, T., Ewer, K.J., Bowyer, G., Bliss, C.M., Edwards, N.J., Wright, D., Payne, R.O., Venkatraman, N., de Barra, E., Snudden, C.M., et al. (2016). Safety and high level efficacy of the combination malaria vaccine regimen of RTS,S/AS01B with chimpanzee adenovirus 63 and modified vaccinia ankara vectored vaccines expressing ME-TRAP. *J. Infect. Dis.* 214, 772–781. <https://doi.org/10.1093/INFDIS/JIW244>.
 24. Jongo, S.A., Shekalaghe, S.A., Church, L.W.P., Ruben, A.J., Schindler, T., Zenklusen, I., Rutishauser, T., Rothen, J., Tumbo, A., Mkindi, C., et al. (2018). Safety, immunogenicity, and protective efficacy against controlled human malaria infection of *Plasmodium falciparum* sporozoite vaccine in Tanzanian adults. *Am. J. Trop. Med. Hyg.* 99, 338–349. <https://doi.org/10.4269/ajtmh.17-1014>.
 25. Tinto, H., Otieno, W., Gesase, S., Sorgho, H., Otieno, L., Liheluka, E., Valéa, I., Sing'oei, V., Malabeja, A., Valia, D., et al. (2019). Long-term incidence of severe malaria following RTS,S/AS01 vaccination in children and infants in Africa: an open-label 3-year extension study of a phase 3 randomised controlled trial. *Lancet Infect. Dis.* 19, 821–832. [https://doi.org/10.1016/S1473-3099\(19\)30300-7](https://doi.org/10.1016/S1473-3099(19)30300-7).
 26. Tiono, A.B., Nébié, I., Anagnostou, N., Coulibaly, A.S., Bowyer, G., Lam, E., Bougouma, E.C., Ouedraogo, A., Yaro, J.B.B., Barry, A., et al. (2018). First field efficacy trial of the Chad63 MVA ME-TRAP vectored malaria vaccine candidate in 5–17 months old infants and children. *PLoS One* 13, e0208328. <https://doi.org/10.1371/journal.pone.0208328>.
 27. Oneko, M., Steinhardt, L.C., Yego, R., Wiegand, R.E., Swanson, P.A., Kc, N., Akach, D., Sang, T., Gutman, J.R., Nzuu, E.L., et al. (2021). Safety, immunogenicity and efficacy of PfSPZ vaccine against malaria in infants in western Kenya: a double-blind, randomized, placebo-controlled phase 2 trial. *Nat. Med.* 27, 1636–1645. <https://doi.org/10.1038/S41591-021-01470-Y>.
 28. McCall, M.B.B., Wammes, L.J., Langenberg, M.C.C., van Gemert, G.J., Walk, J., Hermsen, C.C., Graumans, W., Koelewijn, R., Franetich, J.F., Chishimba, S., et al. (2017). Infectivity of *Plasmodium falciparum* sporozoites determines emerging parasitemia in infected volunteers. *Sci. Transl. Med.* 9, eaag2490. <https://doi.org/10.1126/scitranslmed.aag2490>.
 29. Shah, Z., Naung, M.T., Moser, K.A., Adams, M., Buchwald, A.G., Dwivedi, A., Ouattara, A., Seydel, K.B., Mathanga, D.P., Barry, A.E., et al. (2021). Whole-genome analysis of Malawian *Plasmodium falciparum* isolates identifies possible targets of allele-specific immunity to clinical malaria. *PLoS Genet.* 17, e1009576. <https://doi.org/10.1371/journal.pgen.1009576>.
 30. Frosch, A.E., Thielen, B.K., Alpern, J.D., Walz, E.J., Volkman, H.R., Smith, M., Wanduragala, D., Holder, W., Boumi, A.E., and Stauffer, W.M. (2021). Antimalarial chemoprophylaxis and treatment in the USA: limited access and extreme price variability. *J. Trav. Med.* taab117. <https://doi.org/10.1093/JTM/TAAB117>.
 31. Saunders, D.L., Garges, E., Manning, J.E., Bennett, K., Schäffer, S., Kosmowski, A.J., and Magill, A.J. (2015). Safety, tolerability, and compliance with long-term antimalarial chemoprophylaxis in American Soldiers in Afghanistan. *Am. J. Trop. Med. Hyg.* 93, 584–590. <https://doi.org/10.4269/ajtmh.15-0245>.
 32. Brisson, M., and Brisson, P. (2012). Compliance with antimalarial chemoprophylaxis in a combat zone. *Am. J. Trop. Med. Hyg.* 86, 587–590. <https://doi.org/10.4269/AJTMH.2012.11-0511>.
 33. Whitman, T.J., Coyne, P.E., Magill, A.J., Blazes, D.L., Green, M.D., Milhous, W.K., Burgess, T.H., Freilich, D., Tasker, S.A., Azar, R.G., et al. (2010). An outbreak of *Plasmodium falciparum* malaria in U.S. Marines deployed to Liberia. *Am. J. Trop. Med. Hyg.* 83, 258–265. <https://doi.org/10.4269/AJTMH.2010.09-0774>.
 34. White, M.T., Verity, R., Churcher, T.S., and Ghani, A.C. (2015). Vaccine approaches to malaria control and elimination: insights from mathematical models. *Vaccine* 33, 7544–7550. <https://doi.org/10.1016/J.VACCINE.2015.09.099>.
 35. Penny, M.A., Camponovo, F., Chitnis, N., Smith, T.A., and Tanner, M. (2020). Future use-cases of vaccines in malaria control and elimination. *Parasit Epidemiol. Control* 10, e00145. <https://doi.org/10.1016/j.parepi.2020.e00145>.
 36. Macintyre, F., Ramachandruni, H., Burrows, J.N., Holm, R., Thomas, A., Möhrle, J.J., Duparc, S., Hooft van Huijsduijnen, R., Greenwood, B., Gutteridge, W.E., et al. (2018). Injectable anti-malarials revisited: discovery and development of new agents to protect against malaria. *Malar. J.* 17, 402. <https://doi.org/10.1186/S12936-018-2549-1>.
 37. Graumans, W., Jacobs, E., Bousema, T., and Sinnis, P. (2020). When is a *Plasmodium*-infected mosquito an infectious mosquito? *Trends Parasitol.* 36, 705–716. <https://doi.org/10.1016/J.PT.2020.05.011>.
 38. Drexler, A.L., Vodovotz, Y., and Luckhart, S. (2008). *Plasmodium* development in the mosquito: biology bottlenecks and opportunities for mathematical modeling. *Trends Parasitol.* 24, 333–336. <https://doi.org/10.1016/J.PT.2008.05.005>.
 39. Ménard, R., Tavares, J., Cockburn, I., Markus, M., Zavala, F., and Amino, R. (2013). Looking under the skin: the first steps in malarial infection and immunity. *Nat. Rev. Microbiol.* 11, 701–712. <https://doi.org/10.1038/nrmicro3111>.
 40. Amino, R., Thiberge, S., Martin, B., Celli, S., Shorte, S., Frischknecht, F., and Ménard, R. (2006). Quantitative imaging of *Plasmodium* transmission from mosquito to mammal. *Nat. Med.* 12, 220–224. <https://doi.org/10.1038/NM1350>.
 41. Yamauchi, L.M., Coppi, A., Snounou, G., and Sinnis, P. (2007). *Plasmodium* sporozoites trickle out of the injection site. *Cell Microbiol.* 9, 1215–1222. <https://doi.org/10.1111/J.1462-5822.2006.00861.X>.
 42. Ejigiri, I., and Sinnis, P. (2009). *Plasmodium* sporozoite-host interactions from the dermis to the hepatocyte. *Curr. Opin. Microbiol.* 12, 401–407. <https://doi.org/10.1016/J.MIB.2009.06.006>.
 43. Hopp, C., and Sinnis, P. (2014). The ins and outs of sporozoite biology in the dermis. *Malar. J.* 13 (Suppl 1), O6. <https://doi.org/10.1186/1475-2875-13-S1-O6>.
 44. Tewari, R., Spaccapelo, R., Bistoni, F., Holder, A.A., and Crisanti, A. (2002). Function of region I and II adhesive motifs of *Plasmodium falciparum* circumsporozoite protein in sporozoite motility and infectivity. *J. Biol. Chem.* 277, 47613–47618. <https://doi.org/10.1074/JBC.M208453200>.
 45. Ménard, 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. <https://doi.org/10.1038/385336A0>.
 46. Rathore, D., Sacci, J.B., De La Vega, P., and McCutchan, T.F. (2002). Binding and invasion of liver cells by *Plasmodium falciparum* sporozoites. Essential involvement of the amino terminus of circumsporozoite protein. *J. Biol. Chem.* 277, 7092–7098. <https://doi.org/10.1074/JBC.M106862200>.
 47. Casares, S., Brumeau, T.D., and Richie, T.L. (2010). The RTS,S malaria vaccine. *Vaccine* 28, 4880–4894. <https://doi.org/10.1016/J.VACCINE.2010.05.033>.
 48. Kisalu, N.K., Idris, A.H., Weidle, C., Flores-García, Y., Flynn, B.J., Sack, B.K., Murphy, S., Schön, A., Freire, E., Franca, J.R., et al. (2018). A human monoclonal antibody prevents malaria infection by targeting a new site of vulnerability on the parasite. *Nat. Med.* 24, 408–416. <https://doi.org/10.1038/NM.4512>.
 49. Tan, J., Sack, B.K., Oyen, D., Zenklusen, I., Piccoli, L., Barbieri, S., Foglierini, M., Fregni, C.S., Marcandalli, J., Jongo, S., et al. (2018). A public antibody lineage that potentially inhibits malaria infection through dual binding to the circumsporozoite protein. *Nat. Med.* 24, 401–407. <https://doi.org/10.1038/nm.4513>.
 50. Oyen, D., Torres, J.L., Cottrell, C.A., Richter King, C., Wilson, I.A., and Ward, A.B. (2018). Cryo-EM structure of *P. falciparum* circumsporozoite protein with a vaccine-elicited antibody is stabilized by somatically mutated inter-Fab contacts. *Sci. Adv.* 4, eaau8529. <https://doi.org/10.1126/sciadv.aau8529>.
 51. Foquet, L., Hermsen, C.C., Van Gemert, G.J., Van Braeckel, E., Weening, K.E., Sauerwein, R., Meuleman, P., and Leroux-Roels, G. (2014). Vaccine-induced monoclonal antibodies targeting circumsporozoite protein prevent *Plasmodium falciparum* infection. *J. Clin. Invest.* 124, 140–144. <https://doi.org/10.1172/JCI70349>.
 52. Sack, B.K., Miller, J.L., Vaughan, A.M., Douglass, A., Kaushansky, A., Mikolajczak, S., Coppi, A., Gonzalez-Aseguinolaza, G., Tsuji, M., Zavala, F., et al. (2014). Model for in vivo assessment of humoral protection against malaria sporozoite challenge by passive transfer of monoclonal antibodies and immune serum. *Infect. Immun.* 82, 808–817. <https://doi.org/10.1128/IAI.01249-13>.
 53. Wang, L.T., Pereira, L.S., Flores-García, Y., O'Connor, J., Flynn, B.J., Schön, A., Hurlburt, N.K., Dillon, M., Yang, A.S.P., Fabra-García, A., et al. (2020). A potent anti-malarial human monoclonal antibody targets circumsporozoite protein minor

- repeats and neutralizes sporozoites in the liver. *Immunity* 53, 733–744.e8. <https://doi.org/10.1016/j.immuni.2020.08.014>.
54. Schäfer, C., Dambrauskas, N., Reynolds, L.M., Trakhimets, O., Raappana, A., Flannery, E.L., Roobsoong, W., Sattabongkot, J., Mikolajczak, S.A., Kappe, S.H.L., and Sather, D.N. (2021). Partial protection against *P. vivax* infection diminishes hypnozoite burden and blood-stage relapses. *Cell Host Microbe* 29, 752–756.e4. <https://doi.org/10.1016/j.chom.2021.03.011>.
 55. White, M., Amino, R., and Mueller, I. (2017). Theoretical implications of a pre-erythrocytic plasmodium vivax vaccine for preventing relapses. *Trends Parasitol.* 33, 260–263. <https://doi.org/10.1016/j.pt.2016.12.011>.
 56. Plassmeyer, M.L., Reiter, K., Shimp, R.L., Kotova, S., Smith, P.D., Hurt, D.E., House, B., Zou, X., Zhang, Y., Hickman, M., et al. (2009). Structure of the Plasmodium falciparum circumsporozoite protein, a leading malaria vaccine candidate. *J. Biol. Chem.* 284, 26951–26963. <https://doi.org/10.1074/JBC.M109.013706>.
 57. Flores-Garcia, Y., Wang, L.T., Park, M., Asady, B., Idris, A.H., Kialu, N.K., Muñoz, C., Pereira, L.S., Francica, J.R., Seder, R.A., and Zavala, F. (2021). The *P. falciparum* CSP repeat region contains three distinct epitopes required for protection by antibodies in vivo. *PLoS Pathog.* 17, e1010042. <https://doi.org/10.1371/journal.ppat.1010042>.
 58. Gaudinski, M.R., Berkowitz, N.M., Idris, A.H., Coates, E.E., Holman, L.A., Mendoza, F., Gordon, I.J., Plummer, S.H., Trofymenko, O., Hu, Z., et al. (2021). A monoclonal antibody for malaria prevention. *N. Engl. J. Med.* 385, 803–814. <https://doi.org/10.1056/NEJMoa2034031>.
 59. Sack, B., Kappe, S.H., and Sather, D.N. (2017). Towards functional antibody-based vaccines to prevent pre-erythrocytic malaria infection. *Expert Rev. Vaccin.* 16, 403–414. <https://doi.org/10.1080/14760584.2017.1295853>.
 60. Fabra-García, A., Yang, A.S.P., Behet, M.C., Yap, X.Z., van Waardenburg, Y., Kaviraj, S., Lanke, K., van Gemert, G.-J., Jore, M.M., Bousema, T., and Sauerwein, R.W. (2022). Human antibodies against non-circumsporozoite proteins block Plasmodium falciparum parasite development in hepatocytes. *JCI Insight* 7, e153524. <https://doi.org/10.1172/JCI.INSIGHT.153524>.
 61. Sultan, A.A., Thathy, V., Frevert, U., Robson, K.J., Crisanti, A., Nussenzweig, V., Nussenzweig, R.S., and Ménard, R. (1997). TRAP is necessary for gliding motility and infectivity of plasmodium sporozoites. *Cell* 90, 511–522. [https://doi.org/10.1016/S0092-8674\(00\)80511-5](https://doi.org/10.1016/S0092-8674(00)80511-5).
 62. Müller, H.M., Reckmann, I., Hollingdale, M.R., Bujard, H., Robson, K.J., and Crisanti, A. (1993). Thrombospondin related anonymous protein (TRAP) of Plasmodium falciparum binds specifically to sulfated glycoconjugates and to HepG2 hepatoma cells suggesting a role for this molecule in sporozoite invasion of hepatocytes. *EMBO J.* 12, 2881–2889. <https://doi.org/10.1002/j.1460-2075.1993.tb05950.x>.
 63. Jimah, J.R., Salinas, N.D., Sala-Rabanal, M., Jones, N.G., Sibley, L.D., Nichols, C.G., Schlesinger, P.H., and Tolia, N.H. (2016). Malaria parasite CelTOS targets the inner leaflet of cell membranes for pore-dependent disruption. *Elife* 5, e20621. <https://doi.org/10.7554/eLife.20621>.
 64. Kester, K.E., Gray Heppner, D., Moris, P., Ofori-Anyinam, O., Krzych, U., Tornieporth, N., McKinney, D., Delchambre, M., Ockenhouse, C.F., Voss, G., et al. (2014). Sequential Phase 1 and Phase 2 randomized, controlled trials of the safety, immunogenicity and efficacy of combined pre-erythrocytic vaccine antigens RTS,S and TRAP formulated with AS02 Adjuvant System in healthy, malaria naïve adults. *Vaccine* 32, 6683–6691. <https://doi.org/10.1016/j.vaccine.2014.06.033>.
 65. Rampling, T., Ewer, K.J., Bowyer, G., Edwards, N.J., Wright, D., Sridhar, S., Payne, R., Powlson, J., Bliss, C., Venkatraman, N., et al. (2018). Safety and efficacy of novel malaria vaccine regimens of RTS,S/AS01B alone, or with concomitant Chad63-MVA-vectored vaccines expressing ME-TRAP. *NPJ Vaccin.* 3, 49. <https://doi.org/10.1038/s41541-018-0084-2>.
 66. Atcheson, E., Bauza, K., Salman, A.M., Alves, E., Blight, J., Viveros-Sandoval, M.E., Janse, C.J., Khan, S.M., Hill, A.V.S., and Reyes-Sandoval, A. (2018). Tailoring a plasmodium vivax vaccine to enhance efficacy through a combination of a CSP virus-like particle and TRAP viral vectors. *Infect. Immun.* 86, e00114-18. <https://doi.org/10.1128/IAI.00114-18>.
 67. Lu, C., Song, G., Beale, K., Yan, J., Garst, E., Feng, J., Lund, E., Catteruccia, F., and Springer, T.A. (2020). Design and assessment of TRAP-CSP fusion antigens as effective malaria vaccines. *PLoS One* 15, e0216260. <https://doi.org/10.1371/JOURNAL.PONE.0216260>.
 68. Wilder, B.K., Vigdorovich, V., Carbonetti, S., Minkah, N., Hertoghs, N., Raappana, A., Cardamone, H., Oliver, B.G., Trakhimets, O., Kumar, S., et al. (2021). Anti-TRAP/SSP2 monoclonal antibodies can inhibit sporozoite infection and I enhance protection of anti-CSP monoclonal antibodies 2 3. Preprint at BioRxiv. <https://doi.org/10.1101/2021.10.15.464611>.
 69. Kariu, T., Ishino, T., Yano, K., Chinzei, Y., and Yuda, M. (2006). CelTOS, a novel malarial protein that mediates transmission to mosquito and vertebrate hosts. *Mol. Microbiol.* 59, 1369–1379. <https://doi.org/10.1111/J.1365-2958.2005.05024.X>.
 70. Bergmann-Leitner, E.S., Legler, P.M., Savranskaya, T., Ockenhouse, C.F., and Angov, E. (2011). Cellular and humoral immune effector mechanisms required for sterile protection against sporozoite challenge induced with the novel malaria vaccine candidate CelTOS. *Vaccine* 29, 5940–5949. <https://doi.org/10.1016/j.vaccine.2011.06.053>.
 71. Doolan, D.L., Southwood, S., Freilich, D.A., Sidney, J., Graber, N.L., Shatney, L., Bebris, L., Florens, L., Dobano, C., Witney, A.A., et al. (2003). Identification of Plasmodium falciparum antigens by antigenic analysis of genomic and proteomic data. *Proc. Natl. Acad. Sci. U S A* 100, 9952–9957. <https://doi.org/10.1073/pnas.1633254100>.
 72. Bergmann-Leitner, E.S., Mease, R.M., de la Vega, P., Savranskaya, T., Polhemus, M., Ockenhouse, C., and Angov, E. (2010). Immunization with pre-erythrocytic antigen CelTOS from Plasmodium falciparum elicits cross-species protection against heterologous challenge with Plasmodium berghei. *PLoS One* 5, e12294. <https://doi.org/10.1371/JOURNAL.PONE.0012294>.
 73. Espinosa, D.A., Vega-Rodríguez, J., Flores-García, Y., Noe, A.R., Muñoz, C., Coleman, R., Bruck, T., Haney, K., Stevens, A., Retallack, D., et al. (2017). The Plasmodium falciparum cell-traversal protein for ookinets and sporozoites as a candidate for preerythrocytic and transmission-blocking vaccines. *Infect. Immun.* 85, e00498-16. <https://doi.org/10.1128/IAI.00498-16>.
 74. Miura, K. (2016). Progress and prospects for blood-stage malaria vaccines. *Expert Rev. Vaccin.* 15, 765–781. <https://doi.org/10.1586/14760584.2016.1141680>.
 75. Das, S., Hertrich, N., Perrin, A.J., Withers-Martinez, C., Collins, C.R., Jones, M.L., Watermeyer, J.M., Fobes, E.T., Martin, S.R., Saibil, H.R., et al. (2015). Processing of plasmodium falciparum merozoite surface protein MSP1 activates a spectrin-binding function enabling parasite egress from RBCs. *Cell Host Microbe* 18, 433–444. <https://doi.org/10.1016/j.chom.2015.09.007>.
 76. Blackman, M.J., Scott-Finnigan, T.J., Shai, S., and Holder, A.A. (1994). Antibodies inhibit the protease-mediated processing of a malaria merozoite surface protein. *J. Exp. Med.* 180, 389–393. <https://doi.org/10.1084/jem.180.1.389>.
 77. Lin, C.S., Uboldi, A.D., Marapana, D., Czabotar, P.E., Epp, C., Bujard, H., Taylor, N.L., Perugini, M.A., Hodder, A.N., and Cowman, A.F. (2014). The merozoite surface protein 1 complex is a platform for binding to human erythrocytes by plasmodium falciparum. *J. Biol. Chem.* 289, 25655–25669. <https://doi.org/10.1074/jbc.M114.586495>.
 78. McBride, J.S., and Heidrich, H.G. (1987). Fragments of the polymorphic Mr 185,000 glycoprotein from the surface of isolated Plasmodium falciparum merozoites form an antigenic complex. *Mol. Biochem. Parasitol.* 23, 71–84. [https://doi.org/10.1016/0166-6851\(87\)90189-7](https://doi.org/10.1016/0166-6851(87)90189-7).
 79. Lin, C.S., Uboldi, A.D., Epp, C., Bujard, H., Tsuboi, T., Czabotar, P.E., and Cowman, A.F. (2016). Multiple plasmodium falciparum merozoite surface protein 1 complexes mediate merozoite binding to human erythrocytes. *J. Biol. Chem.* 291, 7703–7715. <https://doi.org/10.1074/jbc.M115.698282>.
 80. Woelblier, U., Epp, C., Kauth, C.W., Lutz, R., Long, C.A., Coulibaly, B., Kouyaté, B., Arevalo-Herrera, M., Herrera, S., and Bujard, H. (2006). Analysis of antibodies directed against merozoite surface protein 1 of the human malaria parasite Plasmodium falciparum. *Infect. Immun.* 74, 1313–1322. <https://doi.org/10.1128/IAI.74.2.1313-1322.2006>.
 81. Baum, J., Chen, L., Healer, J., Lopatnicki, S., Boyle, M., Triglia, T., Ehlgren, F., Ralph, S.A., Beeson, J.G., and Cowman, A.F. (2009). Reticulocyte-binding protein homologue 5 - an essential adhesin involved in invasion of human erythrocytes by Plasmodium falciparum. *Int. J. Parasitol.* 39, 371–380. <https://doi.org/10.1016/j.ijpara.2008.10.006>.

82. Payne, R.O., Silk, S.E., Elias, S.C., Miura, K., Diouf, A., Galaway, F., de Graaf, H., Brendish, N.J., Poulton, I.D., Griffiths, O.J., et al. (2017). Human vaccination against RH5 induces neutralizing antimalarial antibodies that inhibit RH5 invasion complex interactions. *JCI Insight* 2, e96381. <https://doi.org/10.1172/JCI.INSIGHT.96381>.
83. Wong, W., Huang, R., Menant, S., Hong, C., Sandow, J.J., Birkinshaw, R.W., Healer, J., Hodder, A.N., Kanjee, U., Tonkin, C.J., et al. (2019). Structure of Plasmodium falciparum Rh5-CyRPA-Ripr invasion complex. *Nature* 565, 118–121. <https://doi.org/10.1038/S41586-018-0779-6>.
84. Volz, J.C., Yap, A., Sisquella, X., Thompson, J.K., Lim, N.T., Whitehead, L.W., Chen, L., Lampe, M., Tham, W.H., Wilson, D., et al. (2016). Essential role of the PfRh5/PfRipr/CyRPA complex during plasmodium falciparum invasion of erythrocytes. *Cell Host Microbe* 20, 60–71. <https://doi.org/10.1016/j.chom.2016.06.004>.
85. Douglas, A.D., Baldeviano, G.C., Lucas, C.M., Lugo-Roman, L.A., Crosnier, C., Bartholdson, S.J., Diouf, A., Miura, K., Lambert, L.E., Ventocilla, J.A., et al. (2015). A PfRH5-based vaccine is efficacious against heterologous strain blood-stage plasmodium falciparum infection in Aotus monkeys. *Cell Host Microbe* 17, 130–139. <https://doi.org/10.1016/j.chom.2014.11.017>.
86. Minassian, A.M., Silk, S.E., Barrett, J.R., Nielsen, C.M., Miura, K., Diouf, A., Loos, C., Fallon, J.K., Michell, A.R., White, M.T., et al. (2021). Reduced blood-stage malaria growth and immune correlates in humans following RH5 vaccination. *Med* 2, 701–719.e19. <https://doi.org/10.1016/j.medj.2021.03.014>.
87. Ord, R.L., Caldeira, J.C., Rodriguez, M., Noe, A., Chackerian, B., Peabody, D.S., Gutierrez, G., and Lobo, C.A. (2014). A malaria vaccine candidate based on an epitope of the Plasmodium falciparum RH5 protein. *Malar. J.* 13, 326. <https://doi.org/10.1186/1475-2875-13-326>.
88. Douglas, A.D., Baldeviano, G.C., Jin, J., Miura, K., Diouf, A., Zenonos, Z.A., Ventocilla, J.A., Silk, S.E., Marshall, J.M., Alanine, D.G.W., et al. (2019). A defined mechanistic correlate of protection against Plasmodium falciparum malaria in non-human primates. *Nat. Commun.* 10, 1953. <https://doi.org/10.1038/s41467-019-09894-4>.
89. Healer, J., Wong, W., Thompson, J.K., He, W., Birkinshaw, R.W., Miura, K., Long, C.A., Soroka, V., Søgaard, T.M.M., Jørgensen, T., et al. (2019). Neutralising antibodies block the function of Rh5/Ripr/CyRPA complex during invasion of Plasmodium falciparum into human erythrocytes. *Cell Microbiol.* 21, e13030. <https://doi.org/10.1111/cmi.13030>.
90. Moya-Alvarez, V., Abellana, R., and Cot, M. (2014). Pregnancy-associated malaria and malaria in infants: an old problem with present consequences. *Malar. J.* 13, 271. <https://doi.org/10.1186/1475-2875-13-271>.
91. Srivastava, A., Gangnard, S., Round, A., Dechavanne, S., Juillerat, A., Raynal, B., Faure, G., Baron, B., Ramboarina, S., Singh, S.K., et al. (2010). Full-length extracellular region of the var2CSA variant of PfEMP1 is required for specific, high-affinity binding to CSA. *Proc. Natl. Acad. Sci. U S A* 107, 4884–4889. <https://doi.org/10.1073/pnas.1000951107>.
92. Salanti, A., Dahlbäck, M., Turner, L., Nielsen, M.A., Barfod, L., Magistrado, P., Jensen, A.T., Lavstsen, T., Ofori, M.F., Marsh, K., et al. (2004). Evidence for the involvement of VAR2CSA in pregnancy-associated malaria. *J. Exp. Med.* 200, 1197–1203. <https://doi.org/10.1084/JEM.20041579>.
93. Salanti, A., Staalsøe, T., Lavstsen, T., Jensen, A.T., Sowa, M.P., Arnot, D.E., Hviid, L., and Theander, T.G. (2003). Selective upregulation of a single distinctly structured var gene in chondroitin sulphate A-adhering Plasmodium falciparum involved in pregnancy-associated malaria. *Mol. Microbiol.* 49, 179–191. <https://doi.org/10.1046/J.1365-2958.2003.03570.X>.
94. Healy, S.A., Fried, M., Richie, T., Bok, K., Little, M., August, A., Riley, L., Swamy, G.K., Wylie, B.J., Menendez, C., et al. (2019). Malaria vaccine trials in pregnant women: an imperative without precedent. *Vaccine* 37, 763–770. <https://doi.org/10.1016/J.VACCINE.2018.12.025>.
95. Bockhorst, J., Lu, F., Janes, J.H., Keebler, J., Gamain, B., Awadalla, P., Su, X.Z., Samudrala, R., Jovic, N., and Smith, J.D. (2007). Structural polymorphism and diversifying selection on the pregnancy malaria vaccine candidate VAR2CSA. *Mol. Biochem. Parasitol.* 155, 103–112. <https://doi.org/10.1016/J.MOLBIOPARA.2007.06.007>.
96. Pham-Huy, A., Top, K.A., Constantinescu, C., Seow, C.H., and El-Chaar, D. (2021). The use and impact of monoclonal antibody biologics during pregnancy. *CMAJ* 193, E1129–E1136. <https://doi.org/10.1503/cmaj.202391>.
97. Adams, J.H., Blair, P.L., Kaneko, O., and Peterson, D.S. (2001). An expanding ebl family of Plasmodium falciparum. *Trends Parasitol.* 17, 297–299. [https://doi.org/10.1016/S1471-4922\(01\)01948-1](https://doi.org/10.1016/S1471-4922(01)01948-1).
98. Miller, L.H., Mason, S.J., Dvorak, J.A., Mcginniss, M.H., and Rothman, I.K. (1975). Erythrocyte receptors for (Plasmodium knowlesi) malaria: duffy blood group determinants. *Science* 189, 561–563. <https://doi.org/10.1126/SCIENCE.1145213>.
99. Ceravolo, I.P., Souza-Silva, F.A., Fontes, C.J., Braga, E.M., Madureira, A.P., Krettli, A.U., Souza, J.M., Brito, C.F., Adams, J.H., and Carvalho, L.H. (2008). Inhibitory properties of the antibody response to Plasmodium vivax Duffy binding protein in an area with unstable malaria transmission. *Scand. J. Immunol.* 67, 270–278. <https://doi.org/10.1111/J.1365-3083.2007.02059.X>.
100. Rawlinson, T.A., Barber, N.M., Mohring, F., Cho, J.S., Kosaisavee, V., Gérard, S.F., Alanine, D.G.W., Labbé, G.M., Elias, S.C., Silk, S.E., et al. (2019). Structural basis for inhibition of Plasmodium vivax invasion by a broadly neutralizing vaccine-induced human antibody. *Nat. Microbiol.* 4, 1497–1507. <https://doi.org/10.1038/s41564-019-0462-1>.
101. Tsuboi, T., Kappe, S.H., Al-Yaman, F., Prickett, M.D., Alpers, M., and Adams, J.H. (1994). Natural variation within the principal adhesion domain of the Plasmodium vivax duffy binding protein. *Infect. Immun.* 62, 5581–5586. <https://doi.org/10.1128/IAI.62.12.5581-5586.1994>.
102. Ntumngia, F.B., and Adams, J.H. (2012). Design and immunogenicity of a novel synthetic antigen based on the ligand domain of the Plasmodium vivax duffy binding protein. *Clin. Vaccin. Immunol.* 19, 30–36. <https://doi.org/10.1128/CVI.05466-11>.
103. Ntumngia, F.B., Schloegel, J., Barnes, S.J., McHenry, A.M., Singh, S., King, C.L., and Adams, J.H. (2012). Conserved and variant epitopes of Plasmodium vivax duffy binding protein as targets of inhibitory monoclonal antibodies. *Infect. Immun.* 80, 1203–1208. <https://doi.org/10.1128/IAI.05924-11>.
104. Carias, L.L., Dechavanne, S., Nicolette, V.C., Sreng, S., Suon, S., Amaratunga, C., Fairhurst, R.M., Dechavanne, C., Barnes, S., Witkowski, B., et al. (2019). Identification and characterization of functional human monoclonal antibodies to plasmodium vivax duffy-binding protein. *J. Immunol.* 202, 2648–2660. <https://doi.org/10.4049/jimmunol.1801631>.
105. Urusova, D., Carias, L., Huang, Y., Nicolette, V.C., Popovici, J., Roesch, C., Salinas, N.D., Dechavanne, S., Witkowski, B., Ferreira, M.U., et al. (2019). Structural basis for neutralization of Plasmodium vivax by naturally acquired human antibodies that target DBP. *Nat. Microbiol.* 4, 1486–1496. <https://doi.org/10.1038/s41564-019-0461-2>.
106. Gruszczyk, J., Huang, R.K., Chan, L.J., Menant, S., Hong, C., Murphy, J.M., Mok, Y.F., Griffin, M.D.W., Pearson, R.D., Wong, W., et al. (2018). Cryo-EM structure of an essential Plasmodium vivax invasion complex. *Nature* 559, 135–139. <https://doi.org/10.1038/s41586-018-0249-1>.
107. Gruszczyk, J., Kanjee, U., Chan, L.J., Menant, S., Malleret, B., Lim, N.T.Y., Schmidt, C.Q., Mok, Y.F., Lin, K.M., Pearson, R.D., et al. (2018). Transferrin receptor 1 is a reticulocyte-specific receptor for Plasmodium vivax. *Science* 359, 48–55. <https://doi.org/10.1126/science.aan1078>.
108. Minassian, A.M., Themistocleous, Y., Silk, S.E., Barrett, J.R., Kemp, A., Quinkert, D., Nielsen, C.M., Edwards, N.J., Rawlinson, T.A., Ramos Lopez, F., et al. (2021). Controlled human malaria infection with a clone of Plasmodium vivax with high-quality genome assembly. *JCI Insight* 6, e152465. <https://doi.org/10.1172/JCI.INSIGHT.152465>.
109. Collins, K.A., Abd-Rahman, A.N., Marquart, L., Ballard, E., Gobeau, N., Griffin, P., Chalou, S., Möhrle, J.J., and McCarthy, J.S. (2022). Antimalarial activity of artefenomel against asexual parasites and transmissible gametocytes during experimental blood-stage plasmodium vivax infection. *J. Infect. Dis.* 225, 1062–1069. <https://doi.org/10.1093/INFDIS/JIAA287>.
110. Collins, K.A., Wang, C.Y., Adams, M., Mitchell, H., Rampton, M., Elliott, S., Reuling, I.J., Bousema, T., Sauerwein, R., Chalou, S., et al. (2018). A controlled human malaria infection model enabling evaluation of transmission-blocking interventions. *J. Clin. Invest.* 128, 1551–1562. <https://doi.org/10.1172/JCI98012>.

111. Griffin, P., Pasay, C., Elliott, S., Sekuloski, S., Sikulu, M., Hugo, L., Khoury, D., Cromer, D., Davenport, M., Sattabongkot, J., et al. (2016). 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.* *10*, e0005139. <https://doi.org/10.1371/journal.pntd.0005139>.
112. McCarthy, J.S., Griffin, P.M., Sekuloski, S., Bright, A.T., Rockett, R., Looke, D., Elliott, S., Whiley, D., Sloots, T., Winzeler, E.A., and Trenholme, K.R. (2013). Experimentally induced blood-stage *Plasmodium vivax* infection in healthy volunteers. *J. Infect. Dis.* *208*, 1688–1694. <https://doi.org/10.1093/INFDIS/JIT394>.
113. Ventocilla, J., Tapia, L.L., Sperling, L., Ponce, R., Franco, A., Leelawong, M., Aguiar, J.C., Baldeviano, G.C., and Wilder, B.K. (2021). Analysis of pre-erythrocytic immunity during *Plasmodium vivax* infection reveals a diversity of responses that is partially due to blood stage cross-reactivity. Preprint at *BioRxiv*. <https://doi.org/10.21203/RS.3.RS.518437/V1>.
114. Schneider, P., and Reece, S.E. (2021). The private life of malaria parasites: strategies for sexual reproduction. *Mol. Biochem. Parasitol.* *244*, 111375. <https://doi.org/10.1016/J.MOLBIOPARA.2021.111375>.
115. Smith, R.C., Vega-Rodríguez, J., and Jacobs-Lorena, M. (2014). The *Plasmodium* bottleneck: malaria parasite losses in the mosquito vector. *Mem. Inst. Oswaldo Cruz* *109*, 644–661. <https://doi.org/10.1590/0074-0276130597>.
116. Kuehn, A., and Pradel, G. (2010). The coming-out of malaria gametocytes. *J. Biomed. Biotechnol.* *2010*, 976827. <https://doi.org/10.1155/2010/976827>.
117. Duffy, P.E. (2021). Transmission-blocking vaccines: harnessing herd immunity for malaria elimination. *Expert Rev. Vaccin.* *20*, 185–198. <https://doi.org/10.1080/14760584.2021.1878028>.
118. Miura, K., Tachibana, M., Takashima, E., Morita, M., Kanoi, B.N., Nagaoka, H., Baba, M., Torii, M., Ishino, T., and Tsuboi, T. (2019). Malaria transmission-blocking vaccines: wheat germ cell-free technology can accelerate vaccine development. *Expert Rev. Vaccin.* *18*, 1017–1027. <https://doi.org/10.1080/14760584.2019.1674145>.
119. Niederwieser, I., Felger, I., and Beck, H.P. (2001). Limited polymorphism in *Plasmodium falciparum* sexual-stage antigens. *Am. J. Trop. Med. Hyg.* *64*, 9–11. <https://doi.org/10.4269/AJTMH.2001.64.9>.
120. Vallejo, A.F., Martínez, N.L., Tobon, A., Alger, J., Lacerda, M.V., Kajava, A.V., Arévalo-Herrera, M., and Herrera, S. (2016). Global genetic diversity of the *Plasmodium vivax* transmission-blocking vaccine candidate Pvs48/45. *Malar. J.* *15*, 202. <https://doi.org/10.1186/s12936-016-1263-0>.
121. Patel, P.N., and Tolia, N. (2021). Structural vaccinology of malaria transmission-blocking vaccines. *Expert Rev. Vaccin.* *20*, 199–214. <https://doi.org/10.1080/14760584.2021.1873135>.
122. de Jong, R.M., Meerstein-Kessel, L., Da, D.F., Nsango, S., Challenger, J.D., van de Vegte-Bolmer, M., van Gemert, G.J., Duarte, E., Teyssier, N., Sauerwein, R.W., et al. (2021). Monoclonal antibodies block transmission of genetically diverse *Plasmodium falciparum* strains to mosquitoes. *NPJ Vaccin.* *6*, 101. <https://doi.org/10.1038/S41541-021-00366-9>.
123. de Jong, R.M., Tebeje, S.K., Meerstein-Kessel, L., Tadesse, F.G., Jore, M.M., Stone, W., and Bousema, T. (2020). Immunity against sexual stage *Plasmodium falciparum* and *Plasmodium vivax* parasites. *Immunol. Rev.* *293*, 190–215. <https://doi.org/10.1111/imr.12828>.
124. Singh, S.K., Thrane, S., Chourasia, B.K., Teelen, K., Graumans, W., Stoter, R., van Gemert, G.J., van de Vegte-Bolmer, M.G., Nielsen, M.A., Salanti, A., et al. (2019). Pfs230 and pfs48/45 fusion proteins elicit strong transmission-blocking antibody responses against *Plasmodium falciparum*. *Front. Immunol.* *10*, 1256. <https://doi.org/10.3389/FIMMU.2019.01256>.
125. Challenger, J.D., Olivera Mesa, D., Da, D.F., Yerbanga, R.S., Lefèvre, T., Cohuet, A., and Churcher, T.S. (2021). Predicting the public health impact of a malaria transmission-blocking vaccine. *Nat. Commun.* *12*, 1494. <https://doi.org/10.1038/s41467-021-21775-3>.
126. Teboh-Ewungkem, M.I., Woldegerima, W.A., and Ngwa, G.A. (2021). Mathematical assessment of the impact of human-antibodies on sporogony during the within-mosquito dynamics of *Plasmodium falciparum* parasites. *J. Theor. Biol.* *515*, 110562. <https://doi.org/10.1016/J.JTBI.2020.110562>.
127. McCoy, K.D., Weldon, C.T., Ansumana, R., Lamin, J.M., Stenger, D.A., Ryan, S.J., Bardosh, K., Jacobsen, K.H., and Dinglasan, R.R. (2021). Are malaria transmission-blocking vaccines acceptable to high burden communities? Results from a mixed methods study in Bo, Sierra Leone. *Malar. J.* *20*, 183. <https://doi.org/10.1186/S12936-021-03723-0>.
128. Nunes, J.K., Woods, C., Carter, T., Raphael, T., Morin, M.J., Diallo, D., Lebouilleux, D., Jain, S., Loucq, C., Kaslow, D.C., and Birkett, A.J. (2014). Development of a transmission-blocking malaria vaccine: progress, challenges, and the path forward. *Vaccine* *32*, 5531–5539. <https://doi.org/10.1016/j.vaccine.2014.07.030>.
129. White, S.E., Harvey, S.A., Meza, G., Llanos, A., Guzman, M., Gamboa, D., and Vinetz, J.M. (2018). Acceptability of a herd immunity-focused, transmission-blocking malaria vaccine in malaria-endemic communities in the Peruvian Amazon: an exploratory study. *Malar. J.* *17*, 179. <https://doi.org/10.1186/S12936-018-2328-Z>.
130. Theisen, M., Jore, M.M., and Sauerwein, R. (2017). Towards clinical development of a Pfs48/45-based transmission blocking malaria vaccine. *Expert Rev. Vaccin.* *16*, 329–336. <https://doi.org/10.1080/14760584.2017.1276833>.
131. Williamson, K.C. (2003). Pfs230: from malaria transmission-blocking vaccine candidate toward function. *Parasite Immunol.* *25*, 351–359. <https://doi.org/10.1046/j.1365-3024.2003.00643.x>.
132. Singh, K., Burkhardt, M., Nakuchima, S., Herrera, R., Muratova, O., Gittis, A.G., Kelnhofer, E., Reiter, K., Smelkinson, M., Veltri, D., et al. (2020). Structure and function of a malaria transmission blocking vaccine targeting Pfs230 and Pfs48/45 proteins. *Commun. Biol.* *3*, 395. <https://doi.org/10.1038/S42003-020-01123-9>.
133. Singh, S.K., Plieskatt, J., Chourasia, B.K., Singh, V., Bengtsson, K.L., Reimer, J.M., van Daalen, R.C., Teelen, K., van de Vegte-Bolmer, M., van Gemert, G.J., et al. (2021). Preclinical development of a Pfs230-Pfs48/45 chimeric malaria transmission-blocking vaccine. *NPJ Vaccin.* *6*, 120. <https://doi.org/10.1038/S41541-021-00383-8>.
134. Zheng, W., Liu, F., He, Y., Liu, Q., Humphreys, G.B., Tsuboi, T., Fan, Q., Luo, E., Cao, Y., and Cui, L. (2017). Functional characterization of *Plasmodium berghei* PSOP25 during ookinete development and as a malaria transmission-blocking vaccine candidate. *Parasites Vectors.* *10*, 8–11. <https://doi.org/10.1186/S13071-016-1932-4>.
135. Yang, F., Liu, F., Yu, X., Zheng, W., Wu, Y., Qiu, Y., Jin, Y., Cui, L., and Cao, Y. (2021). Evaluation of two sexual-stage antigens as bivalent transmission-blocking vaccines in rodent malaria. *Parasites Vectors.* *14*, 241. <https://doi.org/10.1186/s13071-021-04743-0>.
136. Langer, R.C., Li, F., Popov, V., Kurosky, A., and Vinetz, J.M. (2002). Monoclonal antibody against the *Plasmodium falciparum* chitinase, PfCHT1, recognizes a malaria transmission-blocking epitope in *Plasmodium gallinaceum* ookinetes unrelated to the chitinase PgCHT1. *Infect. Immun.* *70*, 1581–1590. <https://doi.org/10.1128/IAI.70.3.1581-1590.2002>.
137. Li, F., Patra, K.P., and Vinetz, J.M. (2005). An anti-Chitinase malaria transmission-blocking single-chain antibody as an effector molecule for creating a *Plasmodium falciparum*-refractory mosquito. *J. Infect. Dis.* *192*, 878–887. <https://doi.org/10.1086/432552>.
138. Dinglasan, R.R., Kalume, D.E., Kanzok, S.M., Ghosh, A.K., Muratova, O., Pandey, A., and Jacobs-Lorena, M. (2007). Disruption of *Plasmodium falciparum* development by antibodies against a conserved mosquito midgut antigen. *Proc. Natl. Acad. Sci. U S A* *104*, 13461–13466. <https://doi.org/10.1073/pnas.0702239104>.
139. Atkinson, S.C., Armistead, J.S., Mathias, D.K., Sandeu, M.M., Tao, D., Borhani-Dizaji, N., Tarimo, B.B., Morlais, I., Dinglasan, R.R., and Borg, N.A. (2015). The Anopheles-midgut APN1 structure reveals a new malaria transmission-blocking vaccine epitope. *Nat. Struct. Mol. Biol.* *22*, 532–539. <https://doi.org/10.1038/NSMB.3048>.
140. Howard, G.P., Bender, N.G., Khare, P., López-Gutiérrez, B., Nyasemba, V., Weiss, W.J., Simecka, J.W., Hamerly, T., Mao, H.Q., and Dinglasan, R.R. (2021). Immunopotentiality by lymph-node targeting of a malaria transmission-blocking nanovaccine. *Front. Immunol.* *12*, 729086. <https://doi.org/10.3389/FIMMU.2021.729086>.
141. Titus, R.G., Bishop, J.V., and Mejia, J.S. (2006). The immunomodulatory factors of arthropod saliva and the potential for these factors to serve as vaccine targets to prevent pathogen transmission. *Parasite Immunol.* *28*, 131–141. <https://doi.org/10.1111/j.1365-3024.2006.00807.x>.

142. Dragovic, S.M., Agunbiade, T.A., Freudzon, M., Yang, J., Hastings, A.K., Schleicher, T.R., Zhou, X., Craft, S., Chuang, Y.M., Gonzalez, F., et al. (2018). Immunization with AgTRIO, a protein in Anopheles saliva, contributes to protection against plasmodium infection in mice. *Cell Host Microbe* 23, 523–535.e5. <https://doi.org/10.1016/j.chom.2018.03.008>.
143. Chuang, Y.M., Agunbiade, T.A., Tang, X.D., Freudzon, M., Almeras, L., and Fikrig, E. (2021). The effects of a mosquito salivary protein on sporozoite traversal of host cells. *J. Infect. Dis.* 224, 544–553. <https://doi.org/10.1093/infdis/jiaa759>.
144. Schleicher, T.R., Yang, J., Freudzon, M., Rembisz, A., Craft, S., Hamilton, M., Graham, M., Mlambo, G., Tripathi, A.K., Li, Y., et al. (2018). A mosquito salivary gland protein partially inhibits Plasmodium sporozoite cell traversal and transmission. *Nat. Commun.* 9, 2908. <https://doi.org/10.1038/s41467-018-05374-3>.
145. Manning, J.E., Morens, D.M., Kamhawi, S., Valenzuela, J.G., and Memoli, M. (2018). Mosquito saliva: the hope for a universal arbovirus vaccine? *J. Infect. Dis.* 218, 7–15. <https://doi.org/10.1093/INFDIS/JIY179>.
146. Manning, J.E., Oliveira, F., Coutinho-Abreu, I.V., Herbert, S., Meneses, C., Kamhawi, S., Baus, H.A., Han, A., Czajkowski, L., Rosas, L.A., et al. (2020). Safety and immunogenicity of a mosquito saliva peptide-based vaccine: a randomised, placebo-controlled, double-blind, phase 1 trial. *Lancet* 395, 1998–2007. [https://doi.org/10.1016/S0140-6736\(20\)31048-5](https://doi.org/10.1016/S0140-6736(20)31048-5).
147. Azasi, Y., Gallagher, S.K., Diouf, A., Dabbs, R.A., Jin, J., Mian, S.Y., Narum, D.L., Long, C.A., Gaur, D., Draper, S.J., et al. (2020). Bliss' and Loewe's additive and synergistic effects in Plasmodium falciparum growth inhibition by AMA1-RON2L, RH5, RIPR and CyRPA antibody combinations. *Sci. Rep.* 10, 11802. <https://doi.org/10.1038/S41598-020-67877-8>.
148. Alanine, D.G.W., Quinkert, D., Kumarasingha, R., Mehmood, S., Donnellan, F.R., Minkah, N.K., Dadonaite, B., Diouf, A., Galaway, F., Silk, S.E., et al. (2019). Human antibodies that slow erythrocyte invasion potentiate malaria-neutralizing antibodies. *Cell* 178, 216–228.e21. <https://doi.org/10.1016/j.CELL.2019.05.025>.
149. Schäfer, C., Roobsoong, W., Kangwanrangan, N., Bardelli, M., Rawlinson, T.A., Dambrauskas, N., Trakhimets, O., Parthiban, C., Goswami, D., Reynolds, L.M., et al. (2020). A humanized mouse model for plasmodium vivax to test interventions that block liver stage to blood stage transition and blood stage infection. *iScience* 23, 101381. <https://doi.org/10.1016/j.ISCI.2020.101381>.
150. Foquet, L., Schäfer, C., Minkah, N.K., Alanine, D.G.W., Flannery, E.L., Steel, R.W.J., Sack, B.K., Camargo, N., Fishbaugher, M., Betz, W., et al. (2018). Plasmodium falciparum liver stage infection and transition to stable blood stage infection in liver-humanized and blood-humanized FRGN KO mice enables testing of blood stage inhibitory antibodies (reticulocyte-binding protein homolog 5) in vivo. *Front. Immunol.* 9, 524. <https://doi.org/10.3389/FIMMU.2018.00524>.
151. Cooper, M.M., Loiseau, C., McCarthy, J.S., and Doolan, D.L. (2019). Human challenge models: tools to accelerate the development of malaria vaccines. *Expert Rev. Vaccin.* 18, 241–251. <https://doi.org/10.1080/14760584.2019.1580577>.