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Recent insights into humoral immunity targeting *Plasmodium falciparum* and *Plasmodium vivax* malaria

Michelle J. Boyle^{a,b,*}, Linda Reiling^a, Faith H. Osier^c, Freya J.I. Fowkes^{a,d,e,f}

^aBurnet Institute for Medical Research and Public Health, Melbourne, Victoria 3004, Australia

^bMenzies School of Medical Research, Darwin, Northern Territory 0810, Australia

^cKEMRI Centre for Geographic Medicine Research-Coast, Kilifi, Kenya

^dMelbourne School of Population and Global Health, The University of Melbourne, Melbourne, Victoria 3010, Australia

^eDepartment of Epidemiology and Preventive Medicine, Monash University, Melbourne, Victoria 3004, Australia

^fDepartment of Infectious Diseases, Monash University, Melbourne, Victoria 3004, Australia

Abstract

Recent efforts in malaria control have led to marked reductions in malaria incidence. However, new strategies are needed to sustain malaria elimination and eradication and achieve the World Health Organization goal of a malaria-free world. The development of highly effective vaccines would contribute to this goal and would be facilitated by a comprehensive understanding of humoral immune responses targeting *Plasmodium falciparum* and *Plasmodium vivax* malaria. New tools are required to facilitate the identification of vaccine candidates and the development of vaccines that induce functional and protective immunity. Here we discuss recent published findings, and unpublished work presented at the 2016 Molecular Approaches to Malaria conference, that highlight advancements in understanding humoral immune responses in the context of vaccine development. Highlights include the increased application of ‘omics’ and ‘Big data’ platforms to identify vaccine candidates, and the identification of novel functions of antibody responses that mediate protection. The application of these strategies and a global approach will increase the likelihood of rapid development of highly efficacious vaccines.

Keywords

Malaria; Vaccine; Immunity; *Plasmodium falciparum*; *Plasmodium vivax*; Microarray; Complement; Phagocytosis

*Corresponding author at: Burnet Institute for Medical Research and Public Health, Melbourne, Victoria 3004, Australia. mboyle@burnet.edu.au (M.J. Boyle).

1 Introduction

Since 2000 there have been unparalleled increases in malaria control activities and re-invigorated goals of malaria elimination; there have been substantial increases in bed net usage, indoor residual spraying, chemoprophylaxis and the utilisation of highly efficacious artemisinin derivatives for the treatment of clinical malaria (World Health Organization, 2015). Consequently, infection prevalence has halved and the incidence of clinical disease and malaria mortality has dramatically reduced by more than 40% (Bhatt et al., 2015; World Health Organization, 2015). While the largest reductions have been primarily seen in areas of high stable transmission in Africa, substantial reductions have also been seen in areas of relatively low transmission in Asia. Despite these gains, malaria, caused predominantly by *Plasmodium falciparum* and *Plasmodium vivax*, remains a significant global public health problem causing approximately 200 million clinical cases and half a million deaths in 2015 (World Health Organization, 2015).

Reductions in malaria transmission are accompanied by changes in the epidemiology of malaria. In areas of stable medium–high transmission, the frequency of mild and severe malaria is highest in young children less than 5 years of age (reviewed in (Marsh and Kinyanjui, 2006; Carneiro et al., 2010)), whereas in areas with low transmission, severe malaria continues to occur in older children and adults (Snow et al., 1997; Carneiro et al., 2010). Decreases in transmission are often accompanied by a shift in the peak incidence of mild and severe malaria to later in childhood or adulthood, or rebounds of malaria in previously eliminated areas (Ceesay et al., 2010; Brasseur et al., 2011; Trape et al., 2011; Griffin et al., 2014). These observations have been attributed to declining naturally acquired immunity to malaria, which develops after repeated exposure to malaria in an age-dependent manner (Marsh and Kinyanjui, 2006). Anti-malarial antibody levels have reflected declines in malaria transmission in longitudinal studies spanning less than 5 years (Migot et al., 1993; Ceesay et al., 2010) and in serial cross-sectional studies 10 years apart (Diop et al., 2014). Recent longitudinal sero-epidemiological studies spanning decades have investigated how immunity to malaria changes in areas experiencing substantial reductions in malaria transmission. Recent studies have demonstrated considerable reductions in anti-merozoite immunity over a 10 year period in an area transitioning from low to very low transmission (Ataíde, R. and Fowkes, F., Burnet Institute, Australia, personal communication). In Kenya, which has transitioned from high to low transmission over the past 14 years, studies have demonstrated that in 2000 the magnitude and functional activity of antibodies against merozoite antigens, as quantified by the capacity of antibodies to fix complement to merozoites antigens, or to mediate opsonic phagocytosis, were associated with protection against clinical malaria. However by 2014, after a significant decline in malaria transmission and an increase in the median age of clinical presentation, anti-merozoite immunity had declined to below protective thresholds (Osier, F. and Marsh, K., KEMRI-Centre for Geographic Medicine Research-Coast, Kenya, personal communication). These studies highlight the importance of understanding how immunity to malaria is acquired and maintained over time in populations transitioning from high to low to no malaria transmission. The changes in sero-epidemiology with changing transmission emphasise the need to identify new targets of protective immunity and to understand functional

mechanisms across diverse and changing transmission settings. Further, as studies have used only a few antigens which have not been comprehensively validated either as markers of exposure or as being associated with protection, more studies are needed to validate large numbers of antigens.

2 New strategies to identify targets of *P. falciparum* and *P. vivax* immunity

2.1 'Big data' – large screenings to identify vaccine candidates

Although antibodies have been known to be key components of acquired immunity against *P. falciparum* malaria for over 50 years (Cohen et al., 1961), it still remains unclear which of the thousands of parasite antigens presented to the human immune system induce protective antibodies and should thus be prioritised for malaria vaccine development. Prior to the completion of the genome of *P. falciparum*, a small number of antigens dominated studies aimed at identifying the targets of protective immunity (Fowkes et al., 2010). Now, more than 10 years into the post-genomic era, large panels of antigens and “omic” data sets are being applied to the same question (Davies et al., 2015), with the anticipation that these large-scale screening approaches will rapidly advance the development of highly efficacious malaria vaccines.

Two main strategies have been applied to the search for the targets of protective antibodies. The principle underlying the first approach is an unbiased proteome-wide analysis that has been applied to antigen discovery to guide vaccine development for multiple pathogens (Davies et al., 2005, 2015). A rapid and high-throughput *Escherichia coli* cell-free transcription/translation system is used to express proteins on a genome-wide scale. For malaria, given the size of the proteome, this has required a degree of down-selection based on a range of criteria including stage-specific protein expression and sub-cellular localisation (Doolan et al., 2008; Crompton et al., 2010a; Finney et al., 2014). In subsequent studies, the panels are further down-selected based on the sero-reactivity observed in previous studies (Nnedu et al., 2011; Dent et al., 2015; Helb et al., 2015). The second approach is more directly hypothesis driven, with careful selection of antigens that are either expressed on the merozoite surface or associated with it, or expressed in the apical organelles and secreted at the time of erythrocyte invasion. These platforms include antigens such as the parasite erythrocyte invasion ligands (erythrocyte binding antigens, EBAs) and the *P. falciparum* reticulocyte-binding homologues (PfRh) families of proteins, and are underpinned by the fact that these antigens are all exposed to the host immune system and thus biologically plausible candidates (Richards et al., 2013; Osier et al., 2014b). Individual recombinant proteins can be printed onto microarrays to increase throughput for analysis in sero-epidemiological studies. A bespoke protein microarray containing predominantly merozoite proteins has recently been developed (Tetteh, K. and Drakeley, C., London School of Hygiene and Tropical Medicine, UK, personal communication). In silico tools were used to identify key regions within these proteins that are then expressed in an *E. coli* system before printing onto microarrays. This approach resulted in the expression of regions most likely to be targets of acquired antibodies, avoids other regions such as trans-membrane domains and increases the solubility of expressed proteins. Early results have used this platform to identify a number of novel immune-reactive targets that may be priorities as

putative vaccine candidates (Tetteh, K. and Drakeley, C., London School of Hygiene and Tropical Medicine, UK, personal communication). Similarly, antigens on the surface of the infected erythrocyte are prime targets of protective immunity (Marsh and Howard, 1986; Bull and Marsh, 2002; Chan et al., 2012, 2016) and have been investigated using large scale screening approaches (Barry et al., 2011). In an extension of this approach, 543 *P. falciparum* erythrocyte membrane protein 1 (PfEMP1) variants were analysed in a cohort of young children from Papua New Guinea and it was found that antibodies to specific variants were acquired early in life and were associated with functional immunity against clinical and severe malaria, providing strong candidate biomarkers for protection and possible vaccine candidates (Tessema, S. and Barry, A., Walter and Eliza Hall Institute, Australia, personal communication). While it is thought that many antibodies targeting surface antigens are strain-specific, recent published results indicate that broadly cross-reactive antibodies targeting RIFIN family proteins can be generated, demonstrating the existence of conserved epitopes that may be suitable candidates for malaria vaccine development (Tan et al., 2016).

2.2 Identifying vaccine candidates for *P. vivax* malaria

For *P. vivax*, fewer studies have been done and the data in support of any given target of protective immunity needs strengthening (Cutts et al., 2014; Finney et al., 2014; Hostetler et al., 2015). Additional studies on *P. vivax* immunity were therefore timely, given the burden of disease particularly in central and southeastern Asia, and the more recent appreciation that infection with this species of *Plasmodium* can also result in severe clinical syndromes (Anstey et al., 2012). Studies on responses to a relatively small panel of *P. vivax* antigens but against a large number of patient samples in a low transmission setting in Thailand utilising multiplexed bead-based approaches have been undertaken. Antibodies to pre-erythrocytic antigens *P. vivax* circumsporozoite protein (CSP), thrombospondin-related anonymous protein (TRAP) and cell-traversal protein for ookinetes and sporozoites (CelTOS) were detected and moreover maintained over 1 year in the apparent absence of new *P. vivax* infections (Longley, R. and Sattabongkot, J., Walter and Eliza Hall Institute, Australia and Mahidol University, Thailand, personal communication), confirming previous findings in smaller sero-epidemiological studies within the same geographical region (Longley et al., 2015). Reticulocyte binding proteins in *P. vivax* have been implicated in invasion and are plausible biological targets. Antibodies against this family of proteins were found to be mainly of the IgG1 and IgG3 subclasses, and were associated with a reduced risk of symptomatic malaria as well as high density *P. vivax* infections, identifying these as promising vaccine candidates (He, W.Q. and Tham, W.H., Walter and Eliza Hall Institute, Australia, personal communication). However, a recent large unbiased screening study of 34 exodomain *P. vivax* merozoite proteins identified that a previously un-studied novel hypothetical protein was strongly associated with reduced risk of clinical malaria (França et al., 2016), reiterating the need to investigate a large number of proteins, including those outside the ‘usual suspects’ which have dominated previous work.

2.3 Working together – ‘Big data’ and the future of research

With multiple groups using ‘Big data’ and ‘omics’ approaches to address the central problem of identifying appropriate vaccine candidates against both *P. falciparum* and *P. vivax* malaria, it is essential that analysis and data sharing platforms develop in line with

data generation. One example of this is the recent launch of an additional platform on PlasmoDB (*Plasmodium* genomic resource, <http://plasmodb.org/plasmo/.org>), to share antibody response data generated via micro-array platforms from multiple US National Institutes of Health (NIH) funded International Centers of Excellence for Malaria Research studies. Here, data from Amazonia, Malawi, Uganda, South Pacific, southeastern Asia and southern African field sites can be analysed based on a variety of epidemiological, environmental and clinical parameters by the wider research community. Spanning multiple transmission settings, data sharing such as this is an important step forward in identifying vaccine candidates that are valid in settings of changing transmission intensities. These platforms have implications for not only vaccine candidate identification, but also tracking changes in transmission and evaluating control strategies (King et al., 2015).

3 New assays to identify functional antibodies and protective mechanisms

3.1 Complement fixing antibodies targeting blood stages and beyond

Together with difficulties in vaccine candidate identification, a key issue that hampers the development of an effective antimalarial vaccine is the lack of knowledge about mechanisms of acquired immunity. In order to progress, it is necessary to characterise potential effector mechanisms of antibodies that are associated with protection from malaria, so that vaccines can be developed that induce a functional and protective antibody response. Little is known about how antibodies mediate protection from malaria, but it is thought they act by limiting blood stage replication to avoid high-density parasitaemia (reviewed in Marsh and Kinyanjui, 2006; Mueller et al., 2013; Chan et al., 2014; Beeson et al., 2016). Functional antibody studies to date have focused on a limited number of assays, with the most widely used being growth inhibition in classical growth inhibition assays (Persson et al., 2006; Wilson et al., 2010). These assays quantify antibodies that inhibit parasite erythrocyte invasion by direct disruption of protein–ligand interactions. For example, data by Katherine Wright and colleagues from the University of Oxford, UK shows that antibodies that directly disrupt the binding of the essential parasite invasion ligand PfRh5 (Crosnier et al., 2011) to its erythrocyte receptor have strong growth inhibitory activity (Douglas et al., 2014; Wright et al., 2014). High-throughput assays to measure directly blocking antibodies have also been developed, which are suitable for measuring receptor–ligand binding inhibitory antibodies, in large cohort studies on both *P. falciparum* (Irani et al., 2015) and *P. vivax* malaria (King et al., 2008). However, while affinity-purified antibodies directed against merozoite antigens (Egan et al., 1999; Reiling et al., 2012; Tran et al., 2014) as well as whole sera samples (Nkuo and Deas, 1988; Shi et al., 1999; Wilson et al., 2011) have been shown to limit parasite growth in vitro, the use of serum samples from cohort studies has failed to show consistent or strong protective associations (Marsh et al., 1989; Dent et al., 2008; McCallum et al., 2008; Crompton et al., 2010b). The presence of multiple and redundant invasion pathways, and the parasite’s ability to switch between these and evade invasion inhibitory antibodies have further limited the use of these assays (Persson et al., 2008, 2013; Beeson et al., 2016). The recent development of an invasion inhibition assay using purified merozoites offers the possibility of measuring true invasion inhibition as opposed to growth inhibition (Boyle et al., 2010, 2013). Recently, this method has been used to investigate the function of

naturally acquired and vaccine-induced antibodies in inhibiting invasion and showed that many antibodies targeting the merozoite required complement to inhibit invasion (Boyle et al., 2015). Antibodies fixed the first factor of the classical complement cascade, C1q, on the surface of merozoites, leading to lysis and invasion inhibition (Boyle et al., 2015). This finding is consistent with protective IgG responses against *P. falciparum* antigens being predominantly of the cytophilic IgG1 and IgG3 subtypes (Taylor et al., 1998; Polley et al., 2006; Roussilhon et al., 2007; Stanisic et al., 2009; Reiling et al., 2010; Richards et al., 2010), both of which have high complement fixation capacity.

Following the observation that antibodies bound C1q to inhibit invasion, an ELISA based C1q deposition assay was developed, allowing the examination of cohort sera samples for antibody-dependent fixation of C1q to the merozoite surface, and showed very strong associations with protection from clinical malaria (Boyle et al., 2015). The same ELISA-based assay now allows the dissection of this protective effect and the assessment of protective associations with individual merozoite antigens. Follow-up studies investigated the capacity of individual sera from a longitudinal cohort study to bind C1q on a variety of merozoite surface antigens; results suggest that the ability of acquired antibodies to fix C1q to a broad range of merozoite surface antibodies is strongly associated with protection (Reiling, L. and Beeson, J., Burnet Institute, Australia, personal communication). Encouragingly, antibodies induced by vaccination of human volunteers with recombinant merozoite surface protein 2 (MSP2) (McCarthy et al., 2011) generated antibodies that inhibited invasion in a complement-dependent manner in vitro (Boyle et al., 2015), and these antibodies were shown to specifically fix C1q on MSP2. The role of antibody-complement interactions might also be important in immunity against other parasite stages. For example, antibodies acquired by pregnant women promoted the deposition of complement components on the surface of placental-binding infected red blood cells and the fixation of complement resulted in greatly enhanced phagocytosis by monocytes. (Opi, D.H. and Beeson, J., Burnet Institute, Australia, personal communication). It also appears that naturally acquired antibodies and those generated by vaccination of animals with the major sporozoite antigen, CSP, fix complement to recombinant protein and sporozoites, suggesting a potential role for antibody-complement fixation in immunity against pre-erythrocytic stages (Kurtovic, L. and Beeson, J., Burnet Institute, Australia, personal communication).

3.2 Antibodies that interact with cells to mediate protection

Together with interacting with complement, cytophilic antibodies also interact with Fc Receptors (FcR) on effector cells. In the antibody-dependent cellular inhibition assay (ADCI), antibodies against parasite antigens have been shown to interact with monocytes via FcγRII, resulting in the parasite's uptake and the release of soluble factors that inhibit parasite growth (Bouharoun-Tayoun et al., 1995). This assay has been employed to assess ADCI activity in post vaccination samples, and found vaccine induced antibodies were able to trigger ADCI (McCarthy et al., 2011; Jepsen et al., 2013). Similarly, the uptake of opsonised parasites by neutrophils has been described which results in the respiratory burst that inhibits parasite replication (antibody-dependent respiratory burst, ADRB) (Kumaratilake et al., 1992). In a high-throughput assay, ADRB was found to be associated with protection from clinical malaria (Joos et al., 2010), and ADRB antibodies can be

induced by vaccination (Joos et al., 2015). Interestingly, both ADCI and ADRB were shown to be significantly more efficient after the uptake of opsonised merozoites compared with parasitised red blood cells (Khusmith et al., 1982; Joos et al., 2010). Optimised assays for measuring phagocytosis of both merozoites and parasitised RBCs have been reported (Ataide et al., 2010; Hill et al., 2012). Importantly, protective associations for monocytemediated, opsonic phagocytosis induced by antibodies against the merozoite surface were recently employed in assessing antibody function in longitudinal cohort studies from Papua New Guinea (Hill et al., 2013) and Kenya (Osier et al., 2014a). These studies used a flow-cytometry based assay developed to assess the magnitude of phagocytosis mediated by naturally acquired antibodies against merozoites. It has been suggested that MSP2 vaccine-induced antibodies from rabbits, as well as from human vaccination trials (McCarthy et al., 2011), is revealing how opsonic phagocytosis of merozoites is mediated through interacting with specific Fc γ -receptors on phagocytic cells. Blocking the inhibitory Fc γ R with blocking antibodies enhanced phagocytosis, while mutation of the Fc-region of human IgG inhibited phagocytosis (Feng, G. and Beeson, J., Burnet Institute, Australia, personal communication). These approaches to explore the opsonic activity of merozoite are now being applied to large cohort studies, in a diversity of transmission settings to demonstrate how functional opsonic activity varies according to transmission. Preliminary studies indicate that functional antibody responses vary significantly across transmission settings and set a base line measure to understand how magnitudes of functional antibodies change with decreasing transmission and what that might mean for acquired protective immunity (O'Flaherty, K. and Fowkes, F., Burnet Institute, Australia, personal communication).

3.3 Applying new assays to understand protection and for vaccine development

It is exciting to see the number of tools and assays to assess antibody-mediated functional immunity growing. From data gathered to date it seems that antibodies against different antigens may act by very different modes of action, and that protective immunity may well arise from the complex interplay of different effector mechanisms. It is therefore important to comprehensively assess correlates of protection for each antigen individually, in order to avoid missing important information. For example, MSP2 proved to be an effective part in the combination B vaccine trial, but antibodies failed to consistently show any growth inhibition in traditional assays (Genton et al., 2002; Flück et al., 2004). Recently developed approaches such as the C1q complement deposition assay (Reiling, L. and Beeson, J., Burnet Institute, Australia, personal communication), complement-dependent invasion inhibition assay (Boyle et al., 2015) and the opsonic phagocytosis assays ((Osier et al., 2014a); Feng, G. and Beeson, J., Burnet Institute, Australia, personal communication) are revealing the role of MSP2 vaccine-induced antibodies in mediating immunity. Further, antibodies with strong growth inhibition properties need to be tested in additional assays as growth inhibition per se has traditionally failed to consistently show protective associations. In the future, functional assays need to be standardised in order to produce reliable and comparable results.

4 Conclusions and future directions

While the most advanced anti-malarial vaccine, RTS,S, has recently completed Phase 3 clinical trials (RTS,S Clinical Trials Partnership, 2015), the low efficacy, safety concerns and feasibility of implementation of this vaccine has led to the World Health Organization concluding that it is not appropriate for widespread usage in its current form without further assessment (World Health Organization Secretariat, 2015). As the research community strives towards the development of improved and highly effective vaccines, the use of multiple approaches and collaborative research across centres becomes paramount. With the continued development of ‘omics’ and ‘Big data’ approaches, increased data sharing improves the chances of timely identification of the most likely vaccine candidates suitable across diverse transmission settings. To ensure that vaccine candidates are assessed appropriately, it is of utmost importance that our understanding of the key mechanisms of antibody function against specific antigens continues to improve, and that assays are developed for the screening of functional antibodies in cohort studies and for vaccine evaluation. In combination, it is hoped that these approaches will lead to the development of vaccine approaches to add to the current strategies for malaria control, and contribute to the current World Health Organization goal of a malaria-free world.

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