Minimal Association of Common Red Blood Cell Polymorphisms with *Plasmodium falciparum* Infection and Uncomplicated Malaria in Papua New Guinean School Children

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Abstract. Southeast Asian ovalocytosis (SAO), α^+ -thalassemia, and low expression of complement receptor 1 (CR1) have been associated with protection against severe *Plasmodium falciparum* malaria. In a cohort of children 5–14 years of age the effect of α^+ -thalassemia, SAO (*SLC4A1* Δ 27), CR1 polymorphisms, and Gerbich negativity (*GYPC* Δ ex3) on risk of *P. falciparum* infections and uncomplicated illness were evaluated. The risk of acquiring polymerase chain reaction (PCR)-diagnosed *P. falciparum* infections was significantly lower for α^+ -thalassemia heterozygotes (hazard ratio [HR]: 0.56) and homozygotes (HR: 0.51) than wild-type children. No such differences were seen in light of microscopy diagnosed infections ($P = 0.71$) or were α^+ -thalassemia genotypes associated with a reduced risk of uncomplicated *P. falciparum* malaria. No significant associations between the risk of *P. falciparum* infection or illness were observed for any of the other red blood cell polymorphisms ($P > 0.2$). This suggests that these polymorphisms are not associated with significant protection against *P. falciparum* blood-stage infection or uncomplicated malaria in school-aged children.

INTRODUCTION

A number of red blood cell (RBC) polymorphisms occur at high frequencies in Papua New Guinea (PNG) in geographical areas where malaria is endemic. Throughout the world, epidemiological and clinical studies suggest that these polymorphisms have arisen as a result of positive selection by malaria. Polymorphisms underlying sickle cell anemia (β -globin [*HBB*] amino acid substitution glutamate $\rightarrow$ valine codon 6), α^+ -thalassemia (α -globin [*HBA1*] deletions), southeast Asian ovalocytosis (SAO; [*SLC4A1*] 27-bp deletion), and G6PD deficiency have been associated with protection against severe *Plasmodium falciparum* malaria (reviewed in Reference 1). Additional polymorphisms associated with Gerbich negativity^{2,3} and low levels of complement receptor 1 (CR1, CD35) expression^{4,5} on RBCs may be of additional relevance in PNG. How these RBC-associated polymorphisms influence susceptibility to *P. falciparum* infection and uncomplicated malaria is not clear.

Studies in Africa provide evidence that α^+ -thalassemia does not significantly influence infection rates, multiplicity of infection, or parasite density, whereas only one of three longitudinal studies found a reduction in the incidence of uncomplicated *P. falciparum* malaria.^{6–9} Interestingly, in the later study protective effects were most prominent in children > 5 years of age.⁹ In Melanesia, where both *P. falciparum* and *Plasmodium vivax* are common and where both humans and parasite populations have different genetic backgrounds to Africa, the influence of α -globin polymorphisms on malaria outcomes is more varied. Homozygous α^+ -thalassemia was associated with increased susceptibility to uncomplicated *P. falciparum* and *P. vivax* malaria in Vanuatu in young children.¹⁰ In a case-control study in PNG a significant association between α^+ -thalassemia and mild malaria was only found for homozygote carriers.¹¹ More recently, a serial cross-sectional survey in PNG found there was no significant association between human erythrocyte polymorphisms (α^+ -thalassemia, SAO, CR1, G6PD deficiency, and ABO groups) and *P. falciparum* parasite

prevalence/density or age-specific seroconversion to *P. falciparum* variant surface antigens.¹² The effect of α^+ -thalassemia on risk of uncomplicated disease in older Melanesian children has not been investigated previously.

Studies *in vitro* have shown that Gerbich negativity, caused by an exon 3 deletion of the glycophorin C gene (*GYPC* Δ ex3), and SAO erythrocytes may be less susceptible to invasion by *P. falciparum*.^{13,14} However, cross-sectional and case-control studies have so far not found any significant associations between SAO or *GYPC* genotypes and prevalence or density of *P. falciparum* infections.^{3,12,15} To date, no longitudinal studies, which are less prone to bias and confounding factors, have been performed on either polymorphism and no studies investigating the role of *GYPC* Δ ex3 and symptomatic malaria have been reported. Although expression of CR1 on the erythrocyte surface appears to be involved in rosetting and polymorphisms in CR1 have been associated with resistance to severe malaria,⁴ no studies have yet looked at the relationship between CR1 polymorphisms and uncomplicated malaria.

To address these gaps in our knowledge, we have examined associations of SAO, α^+ -thalassemia, *GYPC* Δ ex3, and CR1 expression polymorphisms with susceptibility to *P. falciparum* infection and uncomplicated malaria episodes = in the context of a prospective longitudinal treatment-reinfection study in children 5–14 years of age in PNG.¹⁶

METHODS

Study design and human subjects. Details of the study design have been previously reported.¹⁶ Briefly, 206 elementary/primary school students (51.5% female; 5 to 14 years of age) from Madang Province (Mugil and Megiar) participated in a treatment-reinfection study from June to December 2004. After an in-depth baseline assessment, all children were treated with a course of 7-day artesunate monotherapy that successfully removed blood stage infections in all but 12 (5.9%) children. Children were actively followed up every 2 weeks at school and passively at the local health center for a total of 6 months. Only children with fever and light microscopy-confirmed malaria infection were treated according to PNG national treatment guidelines with chloroquine plus sulfadoxine-pyrimethamine.

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At every study contact a blood sample was collected for diagnosis of malarial infections by light microscopy (LM) and post-polymerase chain reaction (PCR) ligase detection reaction fluorescent microsphere assay (LDR-FMA).^{17,18} During the follow-up time of the study LM diagnosis found 87.6% of children became reinfected with *P. falciparum* (95.3%, PCR diagnosis), 49.5% with *P. vivax* (82.0%, PCR), 8.3% with *Plasmodium malariae* (29.3%, PCR), and 1.5% with *Plasmodium ovale* (13.6%, PCR). Clinical malaria was defined as a measured fever (axillary temperature $\geq 37.5^{\circ}\text{C}$) or history of febrile illness during the 48 hours preceding examination in conjunction with any malaria infection. The cut-off value for uncomplicated disease was set at 5,000 parasites/ μL for *P. falciparum*¹⁹ and 1,000 parasites/ μL for all other species.²⁰ Of the uncomplicated malaria episodes, 80 were caused by *P. falciparum* (20 study participants had multiple episodes), five to *P. vivax*, two each to *P. malariae* or *P. ovale*, and one to a *P. falciparum*/*P. vivax* mixed infection. This study was approved by the Papua New Guinea Medical Research Advisory Council, and institutional review boards of the Walter and Eliza Hall Institute, Australia, and the Veteran's Affairs Medical Center (Cleveland, OH). Permission for this study was obtained through community-based discussions and written parental consent was obtained for all children who participated in this study.

Diagnosis of *Plasmodium* species infections. Details of blood smear preparation and LM analysis have been provided elsewhere.¹⁶ In short, thick blood films were examined by LM and 100 fields (under a 100 $\times$ oil-immersion lens) were examined before a smear was classified as being infection negative. Slides were scored as LM-positive for an individual *Plasmodium* species if the species was detected independently by at least two microscopists and subsequent PCR-based analysis confirmed the presence of the species. Densities were converted to the number of parasites per microliter of blood assuming 8,000 white blood cells (WBCs)/ μL .

Infection by each of the four human malaria species was assessed in all blood samples collected using a semi-quantitative post-PCR assay. This assay combines PCR amplification of the small subunit (SSU) ribosomal RNA (rRNA) gene (491–500-basepair fragments) using genus-specific primers, followed by a multiplex species-specific ligase detection reaction-fluorescent microsphere assay (LDR-FMA).¹⁷

PCR-based genotyping. Genotyping of common Melanesian 3.7kb ($\alpha^{3.7}$) and 4.2kb ($\alpha^{4.2}$) α -globin (chromosome 16) deletions associated with α^+ -thalassemia was performed as previously described²¹ with some modifications.²² Genotyping of deletion polymorphisms at the band 3 (*SLC4A1* Δ 27; chromosome 17) and glycophorin C (*GYPC* Δ ex3; chromosome 2) loci, associated with SAO and Gerbich negativity, respectively, were determined by PCR.^{23,24} The PCR-reflection fragment length polymorphism (RFLP) analysis was used to genotype the CR1 exon 22 SNP at nucleotide 3650 and the intron 27 HindIII RFLP, as described in Xiang and others.⁵

Enzyme-linked immunosorbent assay (ELISA) assessment of response to *P. falciparum* schizonts. As a marker of the humoral immune response to blood-stage *P. falciparum* antigens, we measured immunoglobulin G (IgG) to *P. falciparum* schizont protein extract by ELISA in pretreatment sera, using established methods.²⁵

Statistical analyses. The associations between different genetic traits and genotypes with prevalence of infections

were assessed using χ^2 and Fisher's exact tests; difference in density of infection at baseline was assessed using analyses of variance. Cox regression was used to test for differences in time-to-first reinfection as detected by LDR-FMA or LM. In these analyses, children were considered at risk start for the first day after completion of the artesunate treatment until they either completed the study or were censored at the time of first (re-) treatment with antimalarial drugs. Poisson regression was used to determine differences in the incidence of uncomplicated malaria during follow-up with children removed from time-at-risk for 4 weeks after each antimalarial treatment. Further details on statistical approaches used are given elsewhere.¹⁶ To control for possible confounding effects of differences in acquired immunity, we included immune status (defined as low, medium, high depending on the tercile of total anti-schizont extract IgG responses) as a covariate in analyses of the association of RBC polymorphism with risk of *P. falciparum* infection or disease. Although small in size, the study had a power of 80% to find protective effects $> 50\%$ for all genotypes except *GYPC* Δ ex3 homozygotes. All statistical analyses were performed using STATA 8 statistical analysis software (Stata Corporation, College Station, TX).

RESULTS

Genotype and allele frequencies in Table 1 are provided for α -globin (wild-type [*wt*], $\alpha^{3.7}$, $\alpha^{4.2}$), band 3 (*wt*, *SLC4A1* Δ 27), *GYPC* (*wt*, *GYPC* Δ ex3), CR1 3650 SNP (A/G), and intron 27 HindIII RFLP (high [H], low [L]). Results showed that 27 children (13.1%) were heterozygous for *SLC4A1* Δ 27, 46 children (22.3%) were heterozygous, and 8 (3.9%) homozygous for *GYPC* Δ ex3. Only 31 children (15.0%) were homozygous wild-type for α -globin ($\alpha\alpha/\alpha\alpha$), 93 (45.2%) were heterozygous ($\alpha\alpha/\alpha-$) and 82 (39.8%) homozygous ($\alpha-/ \alpha-$). The 4.2 deletion accounted for 92.6% of all mutated alleles precluding allele-specific analyses. Thus, all analyses were combined for both alleles. The CR1 alleles distributed into three haplotypes (3650A-HindIII H [0.354], 3650G-HindIII L [0.627], 3650G-HindIII H [0.019]), showing significant linkage disequilibrium ($D' = 1$, $r^2 = 0.9191$, $X^2 = 188.4$, degrees of freedom [df] = 2, $P < 0.001^{26}$). Consequently, associations between CR1 genotype and *P. falciparum* infection and disease were performed only for the SNP at exon 22. While no significant associations were observed between α^+ -thalassemia, *GYPC* Δ ex3, and *CR1*ex22 (Fisher exact tests, $P \geq 0.15$), there was a significant excess of heterozygotes for *CR1*ex22 in SAO children (37.4% versus 63.0%; $P = 0.01$). Genotype frequencies did not differ by age and sex ($P \geq 0.4$). Wild-type and mutant alleles at all loci were present in Hardy-Weinberg equilibrium.

Before treatment, 80 (38.6%) children had microscopically detectable *P. falciparum* infections (trophozoites and/or gametocytes), 17 (8.3%) *P. vivax*, 4 (1.9%) *P. malariae*, and 3 mixed *P. falciparum*/*P. vivax* infections. There were no statistically significant differences either in prevalence ($P > 0.17$) or geometric mean density ($P > 0.2$) of *P. falciparum* infections by light microscopy among children with different genotypes (data not shown). Prevalence of *P. falciparum* infection was higher when assessed by post-PCR LDR-FMA assay with 67.5% of children infected with *P. falciparum*, 34.0% with *P. vivax*, 6.8% with *P. malariae*, and 1.0% with *P. ovale*; with 26.4% children infected with more than one species. Only *GYPC* Δ ex3 homozygosity was associated with a decreased risk of PCR detectable

TABLE 1
Allele and genotype frequencies for common red blood cell (RBC) polymorphisms in Papua New Guinea

Genotype	HBA1* (N = 206)		SLC4A1† (N = 206)		GYPC‡ (N = 206)		CRI ex22§ (N = 206)		CRI HindIII¶ (N = 205)		
	Counts	%	Counts	%	Counts	%	Counts	%	Counts	%	
wt/wt	31	15.0	wt/wt	179	86.9	wt/wt	152	73.8	A/A	35	17.1
wt/α ^{-4.2}	86	41.7	wt/Δ27	27	13.1	wt/Δex3	46	22.3	A/G	83	40.5
wt/α ^{-3.7}	7	3.4	Δ27/Δ27	0	0.0	Δex3/Δex3	8	3.9	G/G	91	44.2
α ^{-4.2} /α ^{-4.2}	71	34.5									
α ^{-4.2} /α ^{-3.7}	10	4.9									
α ^{-3.7} /α ^{-3.7}	1	0.5									

* HBA1 = α-globin locus name, allele names α^{-4.2} and α^{-3.7} refer to the Melanesian deletions (4.2 kb and 3.7 kb, respectively) that eliminate one α-globin gene locus. These deletions are associated with α⁻-thalassaemia.
† SLC4A1 = solute carrier family 4 (anion exchanger), member 1, RBC band 3. Allele name Δ27 refers to the Melanesian 27 nucleotide deletion, codons 400–408.
‡ GYPC = glycophorin C locus name, allele name GYPCΔex3 refers to the Melanesian deletion of GYPC exon 3 associated with Gerbich blood group negativity.
§ CRI ex22 = complement receptor 1 exon 22 SNP at nucleotide 3650, allele names 3650A associated with higher, 3650G associated with lower CRI RBC surface expression.
¶ CRI HindIII = complement receptor 1 intron 27 HindIII RFLP, allele names H (7.4 kb genomic restriction fragment) associated with higher, L (6.9 kb genomic restriction fragment) associated with lower CRI RBC surface expression.

P. falciparum infections when compared with heterozygote and wild-type individuals (2/8 [25.0%] versus 137/198 [69.2%], Fisher's exact test $P = 0.009$).

During the 6 months following treatment, 157/194 (80.9%) and 178/194 (91.8%) became positive for *P. falciparum* as diagnosed by LM and LDR-FMA, respectively, and 80/206 children experienced at least one episode of uncomplicated *P. falciparum* illness, (no children experienced an episode of severe *P. falciparum* malaria¹⁶). When infections were diagnosed by LDR-FMA, the risk of acquiring new *P. falciparum* infections was significantly lower for α⁺-thalassaemia heterozygotes (hazard ratio [HR]: 0.56) and homozygotes (HR: 0.51, Table 2) than wild-type children (likelihood ratio [LR] $X^2 = 7.7$, $df = 2$, $P = 0.02$). However, this association was not seen when infections were diagnosed by LM (LR $X^2 = 0.7$, $df = 2$, $P = 0.71$). No significant association between risk of *P. falciparum* infection and genotype was observed for any of the other RBC polymorphisms ($P > 0.2$). Similarly, there were no significant differences in incidence of uncomplicated *P. falciparum* malaria between genotypes for any of the traits studied (Table 2, $P > 0.2$). The size of the study precluded a thorough analysis of associations between multiple polymorphisms and risk of infection or uncomplicated malaria.

Finally, we evaluated the humoral immune response to *P. falciparum* blood-stage antigens by measuring serum IgG levels against a *P. falciparum* schizont protein extract among samples collected at baseline. In this analysis α-/α- children had significantly lower levels of *P. falciparum*-specific IgG compared with wt/α- and wt/wt children (median optical density 1.28, inter-quartile range [IQR] 0.88–1.46 versus 1.38, IQR 1.20–1.58, respectively; $P = 0.01$). No significant differences in immune status were observed for associations with the other RBC polymorphisms evaluated. We then adjusted for *P. falciparum*-specific antibody levels in analyses examining associations between genotypes and risk of infection or uncomplicated malaria described previously. Following this adjustment, we observed no significant change in the strength of associations between LDR-FMA-diagnosed *P. falciparum* and *GYPC*Δex3 (baseline) or α⁺-thalassaemia (re-infection) (data not shown).

DISCUSSION

In a longitudinal study of school-age children living in a region highly endemic for malaria along the north coast of PNG near Madang, we found only marginal and inconsistent associations between the common RBC polymorphisms and the prevalence of *P. falciparum* infection (measured by LM or LDR-FMA) or uncomplicated disease.

Although children with α⁺-thalassaemia were observed to experience a reduced risk of PCR-diagnosed *P. falciparum* infections during the post-treatment, reinfection phase of the study, we found no association between α⁺-thalassaemia and LM-diagnosed infections or uncomplicated *P. falciparum* malaria. The lack of a protection against uncomplicated *P. falciparum* malaria is in line with both earlier studies in Africa^{6,8} and observations in children > 5 years of age in Vanuatu,¹⁰ but contradicts a more recent study from Tanzania that did find a significant decreased risk in children > 5 years of age.⁹

Given the lack of protection against disease and LM-diagnosed infections, the finding of a significant reduction in risk of PCR-diagnosed infection is surprising. A possible

TABLE 2

Associations between red blood cell (RBC) polymorphisms* and risk of *P. falciparum* infection and disease in Papua New Guinean school-aged children

Phenotype	Gene Locus	Genotype	LDR-FMA†		LM‡		Clinical episode§	
			(MTR = 55 days)¶		(MTR = 99 days)¶		(IR = 1.17/yr)¶	
			HR	CI ₉₅ **	HR	CI ₉₅	IRR††	CI ₉₅
α^+ -Thalassaemia	<i>HBA1</i>	wt/wt						
		wt/ α^-	0.56‡‡	[0.36, 0.87]	1.21	[0.75, 1.97]	0.63	[0.36, 1.10]
		α^-/α^-	0.51‡‡	[0.32, 0.81]	1.12	[0.68, 1.85]	0.84	[0.49, 1.44]
SAO	<i>SLC4A1</i>	wt/wt						
		wt/ $\Delta 27$	1.15	[0.75, 1.76]	1.32	[0.85, 2.04]	0.82	[0.45, 1.52]
Gerbich	<i>GYPC</i>	wt/wt						
		wt/ $\Delta ex3$	0.86	[0.60, 1.24]	1.19	[0.82, 1.71]	0.97	[0.60, 1.55]
		$\Delta ex3/\Delta ex3$	1.8	[0.87, 3.69]	1.11	[0.52, 2.39]	1.6	[0.68, 3.79]
CR1 expression	<i>CR1</i>	3650G/G						
		3650A/G	1.22	[0.89, 1.68]	1.01	[0.72, 1.42]	0.91	[0.59, 1.41]
		3650A/A	0.91	[0.58, 1.43]	0.88	[0.55, 1.40]	1.1	[0.64, 1.89]

* Gene locus, allele names, genotype designations, and phenotypes as described in Table 1.

† LDR-FMA = post-PCR ligase detection reaction-fluorescent microsphere assay for diagnosis of 4 *Plasmodium* parasites of humans.‡ LM = light microscopy, or conventional blood smear, light microscopy diagnosis of four *Plasmodium* parasites of humans.§ Clinical Episode = febrile episode with concurrent *P. falciparum* parasitaemia > 5,000/ μ L.

¶ MTR = median time to re-infection (days), IR = incidence rate (/child/yr) for entire cohort.

|| HR = hazard ratio based on Cox-regression model of time to first infection.

** CI₉₅ = 95% confidence interval.

†† IRR = incidence rate ratio based on Poisson regression—details of the model provided in Michon and others, Reference 16.

‡‡ Statistical significance at $P < 0.05$.

explanation could lie with the reduced level of acquired immunity (as measured by total anti-schizont IgG antibodies) in α^+ -thalassaemia homozygote children. In this cohort high levels of antibodies against different merozoite antigens were associated with better control of *P. falciparum* parasite densities and protection from uncomplicated disease but had no effect on acquisition of new infection.²⁷ It is thus feasible that while α^+ -thalassaemic children acquire less infections, they are less able to control parasite densities at low level and the infections that do occur are more likely to become LM-patent and become symptomatically unwell. This explanation however runs counter to evidence from earlier studies from the Pacific that suggested that the incidence of malaria might be raised in the youngest children with alpha thalassaemia^{10,28} and that α^+ -thalassaemia does not affect the acquisition of antibodies to variant surface antigens (VSA).^{9,12} Further studies of the combined effects of α^+ -thalassaemia and acquired immunity on risk of *P. falciparum* infection and illness are thus warranted.

GYPC $\Delta ex3$ homozygotes had a significantly lower risk of PCR-diagnosed *P. falciparum* infections at baseline, but we did not find any association between *GYPC* $\Delta ex3$ and newly acquired infections or uncomplicated malaria after treatment. We also observed no associations between SAO or CR1 polymorphisms and *P. falciparum* reinfection or uncomplicated *P. falciparum* malaria. The importance of the observed significant association is therefore equivocal as earlier cross-sectional surveys also failed to show any association of *GYPC* $\Delta ex3$ or SAO with prevalence of *P. falciparum* infection.^{3,12,15}

Earlier studies have showed reduced invasion or growth rates of *P. falciparum* in RBC from donors carrying SAO and *GYPC* $\Delta ex3$.^{13,14} The ability of *P. falciparum* to use different invasion pathways, redundancy in the erythrocyte invasion ligands used by *P. falciparum*,²⁹ and the earlier observation that only one of four EBA140/BAEBL variants (VSTK) failed to bind to Gerbich-negative erythrocytes,³⁰ could explain why the expected partial abrogation of the EBA140/BAEBL-GYPC invasion pathway by *GYPC* $\Delta ex3$ was observed to have little effect on infection rates or parasitemias *in vivo*. Whereas results from *in vitro* studies suggest that only a subset of parasite variants can invade SAO RBCs, those that can invade, do

so efficiently.¹⁴ Even if these effects were also present *in vivo*, the high number of new infections¹⁶ and the expected multiplicity of phenotypic variants among these infections, SAO children are likely to be infected with a sufficient number of variants that efficiently infect RBCs to result in comparable numbers of infections and clinical cases as seen in non-SAO children.

Previous studies in PNG have found that α^+ -thalassaemia, SAO, and CR1 genotypes were only associated with protection against severe, but not uncomplicated malaria.^{4,8,11,31,32} The absence of protection against *P. falciparum* infection or complicated disease in our study is thus consistent with these reports. The mechanisms of protection, however, remain unclear. The CR1ex22 SNP and α^+ -thalassaemia could protect against severe malaria from a reduction in CR1 mediated rosetting. Both polymorphisms have been associated with reduced levels of RBC CR1 expression.⁴ Redistribution of sequestered infected RBCs away from the brain may be responsible for the protection of SAO against cerebral malaria. *Plasmodium falciparum* infected SAO RBCs have an increased ability to bind to CD36, an endothelial cell receptor that is largely absent in the brain endothelium, and this might redirect sequestration to non-vital organs where CD36 is expressed.³³

As with the other erythrocyte polymorphisms, our findings that *GYPC* $\Delta ex3$ does not influence risk of *P. falciparum* infection or uncomplicated malaria, does not rule out that *GYPC* $\Delta ex3$ may be associated with protection against severe malaria in younger, less immune children. Studies on associations of *GYPC* $\Delta ex3$ with severe malaria are thus needed to determine if *GYPC* $\Delta ex3$ has been selected for *P. falciparum* or other factors.

The overall lack of associations between genotypes and risk of *P. falciparum* infection and uncomplicated malaria might partly be caused by the significant level of acquired, clinical immunity among these children^{16,27} that may have masked any protective effects of specific genotypes against uncomplicated disease. However, with the exception of α^+ -thalassaemia no differences in immune status as measured by total IgG against schizont protein extract were observed between genotypes or did an earlier study in a neighboring population find an

effect of any of these polymorphism on anti-VSA antibodies¹² and is thus unlikely that differences in immune status could have directly compensated for potential effects of SAO or *GYPC* Δ ex3 polymorphisms. Nevertheless, the relatively high degree of immunity in all children is likely to have reduced possible effects against uncomplicated *P. falciparum* and studies in younger children with a low degree of immunity will be required to conclusively rule out an effect of these RBC polymorphisms on risk of *P. falciparum* infection and uncomplicated malaria.

Using rigorous epidemiological methodology with active follow-up and molecular-based methods for detection of parasitemia, this study did not observe consistent significant associations between common PNG RBC polymorphisms and protection from *P. falciparum* blood-stage infection or uncomplicated malaria. The mechanisms involved in their protection against severe disease are yet to be fully understood.

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REFERENCES

- Williams TN, 2006. Red blood cell defects and malaria. *Mol Biochem Parasitol* 149: 121–127.
- Serjeantson SW, 1989. A selective advantage for the Gerbich-negative phenotype in malarious areas of Papua New Guinea. *PNG Med J* 32: 5–9.
- Patel SS, King CL, Mgone CS, Kazura JW, Zimmerman PA, 2004. Glycophorin C (Gerbich antigen blood group) and band 3 polymorphisms in two malaria holoendemic regions of Papua New Guinea. *Am J Hematol* 75: 1–5.
- Cockburn IA, Mackinnon MJ, O'Donnell A, Allen SJ, Moulds JM, Baisor M, Bockarie M, Reeder JC, Rowe JA, 2004. A human complement receptor 1 polymorphism that reduces *Plasmodium falciparum* rosetting confers protection against severe malaria. *Proc Natl Acad Sci USA* 101: 272–277.
- Xiang L, Rundles JR, Hamilton DR, Wilson JG, 1999. Quantitative alleles of CR1: coding sequence analysis and comparison of haplotypes in two ethnic groups. *J Immunol* 163: 4939–4945.
- Migot-Nabias F, Pelleau S, Watier L, Guitard J, Toly C, De Araujo C, Ngom MI, Chevillard C, Gaye O, Garcia A, 2006. Red blood cell polymorphisms in relation to *Plasmodium falciparum* asymptomatic parasite densities and morbidity in Senegal. *Microbes Infect* 8: 2352–2358.
- Mockenhaupt FP, Ehrhardt S, Otchwemah R, Eggelte TA, Anemana SD, Stark K, Bienzle U, Kohne E, 2004. Limited influence of haemoglobin variants on *Plasmodium falciparum* msp1 and msp2 alleles in symptomatic malaria. *Trans R Soc Trop Med Hyg* 98: 302–310.
- Wambua S, Mwangi TW, Kortok M, Uyoga SM, Macharia AW, Mwacharo JK, Weatherall DJ, Snow RW, Marsh K, Williams TN, 2006. The effect of alpha+-thalassaemia on the incidence of malaria and other diseases in children living on the coast of Kenya. *PLoS Med* 3: e158.
- Enevold A, Lusingu JP, Mmbando B, Alifrangis M, Lemnge MM, Bygbjerg IC, Theander TG, Vestergaard LS, 2008. Reduced risk of uncomplicated malaria episodes in children with alpha+-thalassaemia in northeastern Tanzania. *Am J Trop Med Hyg* 78: 714–720.
- Williams TN, Maitland K, Bennett S, Ganczakowski M, Peto TE, Newbold CI, Bowden DK, Weatherall DJ, Clegg JB, 1996. High incidence of malaria in alpha-thalassaemic children. *Nature* 383: 522–525.
- Allen SJ, O'Donnell A, Alexander ND, Alpers MP, Peto TE, Clegg JB, Weatherall DJ, 1997. alpha+-Thalassemia protects children against disease caused by other infections as well as malaria. *Proc Natl Acad Sci USA* 94: 14736–14741.
- Fowkes FJ, Michon P, Pilling L, Ripley RM, Tavul L, Imrie HJ, Woods CM, Mgone CS, Luty AJ, Day KP, 2008. Host erythrocyte polymorphisms and exposure to *Plasmodium falciparum* in Papua New Guinea. *Malar J* 7: 1.
- Maier AG, Duraisingh MT, Reeder JC, Patel SS, Kazura JW, Zimmerman PA, Cowman AF, 2003. *Plasmodium falciparum* erythrocyte invasion through glycophorin C and selection for Gerbich negativity in human populations. *Nat Med* 9: 87–92.
- Cortes A, Benet A, Cooke BM, Barnwell JW, Reeder JC, 2004. Ability of *Plasmodium falciparum* to invade southeast Asian ovalocytes varies between parasite lines. *Blood* 104: 2961–2966.
- Patel SS, Mehlotra RK, Kastens W, Mgone CS, Kazura JW, Zimmerman PA, 2001. The association of the glycophorin C exon 3 deletion with ovalocytosis and malaria susceptibility in the Wosera, Papua New Guinea. *Blood* 98: 3489–3491.
- Michon P, Cole-Tobian JL, Dabod E, Schoepflin S, Igu J, Susapu M, Tarongka N, Zimmerman PA, Reeder JC, Beeson JG, Schofield L, King CL, Mueller I, 2007. The risk of malarial infections and disease in Papua New Guinean children. *Am J Trop Med Hyg* 76: 997–1008.
- McNamara DT, Kasehagen LJ, Grimberg BT, Cole-Tobian J, Collins WE, Zimmerman PA, 2006. Diagnosing infection levels of four human malaria parasite species by a polymerase chain reaction/ligase detection reaction fluorescent microsphere-based assay. *Am J Trop Med Hyg* 74: 413–421.
- Kasehagen LJ, Mueller I, McNamara DT, Bockarie MJ, Kiniboro B, Rare L, Lorry K, Kastens W, Reeder JC, Kazura JW, Zimmerman PA, 2006. Changing patterns of *Plasmodium* blood-stage infections in the Wosera region of Papua New Guinea monitored by light microscopy and high throughput PCR diagnosis. *Am J Trop Med Hyg* 75: 588–596.
- Smith T, Genton B, Baea K, Gibson N, Taime J, Narara A, Al Yaman F, Beck HP, Hii J, Alpers M, 1994. Relationships between *Plasmodium falciparum* infection and morbidity in a highly endemic area. *Parasitology* 109: 539–549.
- Müller I, Genton B, Rare L, Kiniboro B, Kastens W, Zimmerman P, Kazura J, Alpers M, Smith TA, 2009. Three different *Plasmodium* species show similar patterns of clinical tolerance of malaria infection. *Malar J* 8: 158.
- Chong SS, Boehm CD, Cutting GR, Higgs DR, 2000. Simplified multiplex-PCR diagnosis of common southeast Asian deleterious determinants of alpha-thalassemia. *Clin Chem* 46: 1692–1695.
- Imrie H, Fowkes FJ, Michon P, Tavul L, Hume JC, Piper KP, Reeder JC, Day KP, 2006. Haptoglobin levels are associated with haptoglobin genotype and alpha+-Thalassemia in a malaria-endemic area. *Am J Trop Med Hyg* 74: 965–971.
- Jarolim P, Palek J, Amato D, Hassan K, Sapak P, Nurse GT, Rubin HL, Zhai S, Sahr KE, Liu SC, 1991. Deletion in erythrocyte band 3 gene in malaria-resistant southeast Asian ovalocytosis. *Proc Natl Acad Sci USA* 88: 11022–11026.
- Tavul L, Mueller I, Rare L, Lin E, Zimmerman PA, Reeder J, Siba P, Michon P, 2008. Glycophorin C Δ exon3 is not associated with protection against severe anaemia in Papua New Guinea. *PNG Med J* 51: 149–154.
- Persson KE, McCallum FJ, Reiling L, Lister NA, Stubbs J, Cowman AF, Marsh K, Beeson JG, 2008. Variation in use of erythrocyte

- invasion pathways by *Plasmodium falciparum* mediates evasion of human inhibitory antibodies. *J Clin Invest* 118: 342–351.
26. Gaunt TR, Rodriguez S, Day IN, 2007. Cubic exact solutions for the estimation of pairwise haplotype frequencies: implications for linkage disequilibrium analyses and a web tool “CubeX.” *BMC Bioinformatics* 8: 428.
 27. Stanisic DI, Richards JS, McCallum FJ, Michon P, King CL, Schoepflin S, Gilson PR, Murphy VJ, Anders RF, Mueller I, Beeson JG, 2009. Immunoglobulin G subclass-specific responses against *Plasmodium falciparum* merozoite antigens are associated with control of parasitemia and protection from symptomatic illness. *Infect Immun* 77: 1165–1174.
 28. Oppenheimer SJ, Hill AV, Gibson FD, Macfarlane SB, Moody JB, Pringle J, 1987. The interaction of alpha thalassaemia with malaria. *Trans R Soc Trop Med Hyg* 81: 322–326.
 29. Cowman AF, Crabb BS, 2006. Invasion of red blood cells by malaria parasites. *Cell* 124: 755–766.
 30. Mayer DC, Jiang L, Achur RN, Kakizaki I, Gowda DC, Miller LH, 2006. The glycophorin C N-linked glycan is a critical component of the ligand for the *Plasmodium falciparum* erythrocyte receptor BAEBL. *Proc Natl Acad Sci USA* 103: 2358–2362.
 31. Genton B, Al Yaman F, Mgone CS, Alexander N, Panu MM, Alpers MP, Mokela D, 1995. Ovalocytosis and cerebral malaria. *Nature* 378: 564–565.
 32. Allen SJ, O'Donnell A, Alexander ND, Mgone CS, Peto TE, Clegg JB, Alpers MP, Weatherall DJ, 1999. Prevention of cerebral malaria in children in Papua New Guinea by southeast Asian ovalocytosis band 3. *Am J Trop Med Hyg* 60: 1056–1060.
 33. Cortes A, Mellombo M, Mgone CS, Beck HP, Reeder JC, Cooke BM, 2005. Adhesion of *Plasmodium falciparum*-infected red blood cells to CD36 under flow is enhanced by the cerebral malaria-protective trait south-east Asian ovalocytosis. *Mol Biochem Parasitol* 142: 252–257.