

**Emergence of non-falciparum *Plasmodium* infection despite regular
artemisinin combination therapy in a 18-month longitudinal study of
Ugandan children and their mothers**

Short title: Non-falciparum malaria in Uganda

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SUMMARY: A longitudinal cohort study of multi-species *Plasmodium* infections in mothers and children in Uganda has revealed there to be both persistent and increasing parasitaemia of certain species which has clinical significance despite regular access to frontline antimalarial treatments.

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Abstract

As part of a longitudinal cohort investigation of intestinal schistosomiasis and malaria in Ugandan children and their mothers on the shorelines of Lakes Victoria and Albert, we documented risk factors and morbidity associated with non-falciparum *Plasmodium* infections and the longitudinal dynamics of *Plasmodium* species in children. Host age, household location and *P. falciparum* infection were strongly associated with non-falciparum *Plasmodium* infections, and *P. malariae* infection was associated with splenomegaly. Despite regular artemisinin combination therapy treatment, there was a threefold rise in *P. malariae* prevalence, which was not accountable for by increasing age of the child. Worryingly, our findings reveal the consistent emergence of non-falciparum infections in children, highlighting the complex dynamics underlying multi-species infections here. Given the growing body of evidence that non-falciparum malaria infections cause significant morbidity, we encourage better surveillance for non-falciparum *Plasmodium* infections, particularly in children, with more sensitive DNA detection methods and improved field-based diagnostics.

Key words: malaria, *Plasmodium malariae*, *Plasmodium ovale* spp., Uganda, ACT

Background

Despite progress, control of malaria is a significant challenge in parts of sub-Saharan Africa (SSA) [1]. While *Plasmodium falciparum* is the leading cause of malaria, other species namely *P. vivax*, *P. malariae*, *P. ovale curtisi* and *P. ovale wallikeri*, circulate concurrently, though Duffy negative individuals curtail *P. vivax* distributions [2-5]. Diagnosis of *P. malariae* and *P. ovale* spp. can be problematic by light microscopy as parasitaemias often occur below detection thresholds for expert microscopy or are masked by more visible, concurrent *P. falciparum* infections [6]. Introduction of molecular/serological techniques has revealed that *P. malariae* and *P. ovale* spp. are more common than previously thought [7-11]. In southwestern Uganda nearly half of asymptomatic children with malaria harboured non-falciparum species [12].

Despite often being considered “benign”, a growing body of evidence reports significant disease and morbidity associated with *P. malariae* and *P. ovale* spp. infections [13-17]. In southern Papua, Indonesia, *P. malariae* infection is associated with a high burden of anaemia [18, 19], and in Papua New Guinea, where at least four *Plasmodium* species co-circulate in humans, detrimental epidemiological interactions occur [20]. A number of other studies have suggested that mixed *P. falciparum*/*P. malariae* infections were associated with increased *P. falciparum* gametocytaemia [21-23]. However, evidence of the clinical significance of non-falciparum *Plasmodium* infections can be conflicting; Black *et al.* demonstrated an inverse relationship between mixed infections and fever in Ivory Coast [24] while in Nigeria, anaemia was shown to be more severe in mixed species *Plasmodium* infections [25]. In Malawi, Bruce *et al.* concluded that interactions between *Plasmodium* co-infecting species could protect against certain clinical outcomes but was contingent on the local seasonality and intensity of malaria transmission [8].

Commencing field-surveillance in 2009 in Uganda, a longitudinal cohort study entitled SIMI (Schistosomiasis in Mothers and Infants project) investigated the dynamics of intestinal schistosomiasis and malaria in young children and their mothers during an 18-month period with regular treatment follow-ups [26]. At baseline, while the general prevalence of non-complicated *P. falciparum* in children across the six SIMI villages was high (>75%), *P. malariae* and *P. ovale* spp. could be found in young children at prevalences of up to 15% and 9%, respectively [27].

In the present study, based on a detailed molecular analysis of the SIMI dried-blood spot archive, we identify risk factors for *Plasmodium* species infection, comparing multi-species and single species infections, and assess interactions between species in terms of clinical outcomes. In Bukoba village, where the prevalence of non-falciparum *Plasmodium* infections was highest, we conducted a longitudinal and geospatial analysis of all malaria infections testing for clustering of infection in time and/or space.

Methods

Ethical statement and recruitment

The London School of Hygiene and Tropical Medicine, UK (application no. LSHTM 5538.09) and the Ugandan National Council of Science and Technology approved this study. Before enrolment, informed consent was obtained by mothers on their own behalf or on behalf of their children and was documented in writing or by thumbprint (in cases of illiteracy).

Study sites, participants and sampling

The longitudinal closed-cohort SIMI study was conducted in communities of six villages on the shores of Lakes Albert and Victoria in Uganda [26]. In total 662 mothers were enrolled together with 1211 young children (one or two children per mother) aged from 5 months to 6 years (49.1% were

female). Mothers (or guardians) ranged in age from 15 to 60 years (see Supplementary Table 1). The SIMI study aimed to investigate the infection dynamics of intestinal schistosomiasis, malaria and soil-transmitted helminthiasis over a period of 18 months, with follow-ups at six months, 12 months and 18 months (Lake Victoria communities only). At each time point, a dried blood-spot archive was collected onto Whatman® 3M filter paper. A qualified nurse examined each participant on site, carrying out an abdominal examination to assess hepato-splenomegaly and measuring weight, height and temperature. Each mother was interviewed in the local language to determine their own and their childrens' exposure to risk factors for infection. The GPS coordinates of study participants' households were collected as described [28].

On-site diagnosis and treatment

During each survey, malaria diagnosis was carried out using rapid diagnostic tests (RDTs) (Paracheck-Pf® [Orchid Biomedical Systems, Goa, India] or First Response [Premier Medical Corporation, NJ, USA]) and microscopy on Giemsa-stained blood films [29]. Haemoglobin (Hb) levels were recorded using a HemoCue spectrometer (HemoCue AB, Angelholm, Sweden). Egg-patent *Schistosoma mansoni* and soil-transmitted helminth infections were also diagnosed on-site by microscopic detection of eggs in stool using the Kato-Katz method [26], with diagnosis of intestinal schistosomiasis bolstered by assessing serum antibodies to soluble egg antigen (SEA) by ELISA and circulating cathodic antigen (CCA) in urine using rapid tests [30].

On the basis of a positive malaria RDT or blood film, children were treated with Lonart® (20 mg/120 mg artemether/lumefrantrine; Cipla, Mumbai, India). Praziquantel (40 mg/kg) for treatment of intestinal schistosomiasis was offered to all study participants at baseline and the final survey. For interim surveys, praziquantel was administered on the basis of a positive CCA urine-test. In addition, participants were treated with albendazole (400 mg) at each survey time point. The project nurse supervised all treatment and participants were monitored for side effects [31].

Molecular analysis of dried blood spots

Blood samples on filter paper were stored at 4°C with desiccant prior to genomic DNA extraction using the chelex method [32]. Real-time PCR to detect *Plasmodium* species infections was carried out on all baseline samples. *P. falciparum* infections were detected using a SYBR green-based real-time PCR assay followed by melt-curve analysis [33]. A probe-based real-time PCR assay [34] was employed to detect *P. malariae* and *P. ovale* spp. infections on a Rotorgene RG3000 thermocycler (Corbett, Sydney, Australia). No attempt was made to detect *P. vivax* since analysis of preliminary data demonstrated its absence. For longitudinal analysis of dried blood spots from children in Bukoba village, the probe-based real-time PCR [34] was used to detect *P. falciparum*, *P. malariae* and *P. ovale* spp. infections at baseline, 6 months, 12 months and 18 months, employing the Mx3000P qPCR System (Agilent, Santa Clara, CA, USA).

Epidemiological and statistical analyses

Epidemiological data were analyzed using Stata v9.2 (StatCorp, TX, USA) and R v2.10.1 (The R Foundation for Statistical Computing, Vienna, Austria). Anaemia in children was categorized based on Hb levels as follows: mild 10-11 g/dL, moderate 7-10 g/dL and severe <7 g/dL. Multi-species malaria infections were categorized as either two or more *Plasmodium* species. Intensity of *P. falciparum* infection was either categorised based on Giemsa-stained blood films as high (>5000 parasites/ μ l) or low (\leq 5000 parasites/ μ l) or based on Ct values: negative >40, low 30.46-40, medium 27.22-30.46 and high <27.22 cycles. Univariable regression analysis was performed to identify risk factors associated with *P. falciparum*, *P. malariae* or *P. ovale* spp. infection as detected by real-time PCR. Factors identified as being statistically associated with a malaria infection ($p>0.05$) were incorporated stepwise into a multivariable logistic regression model and likelihood ratio tests were used to compare models. Random effects were included to control for clustering at household (for *P. falciparum* and *P. malariae*) or village level (*P. ovale* spp.) and interactions between variables were

investigated. A similar analysis was carried out to investigate risk factors associated with multi-species malaria versus single species infections and to investigate associations between morbidity markers and infections with different *Plasmodium* species.

A mixed lottery-kind model [35] was used to determine whether there was evidence of a departure from random distribution of single and multi-species malaria infections. A generalised linear mixed model (GLMM) with random intercept to account for within-subject correlation was fitted to the time series data from children in Bukoba village to determine the effects of age, time period and previous infection on current infection *Plasmodium* infection status.

Geospatial analysis

Geospatial analysis of *Plasmodium* species infections among children in Bukoba was carried out, based on household GPS locations. Global tests for clustering were undertaken, using the log ratio of spatial densities method proposed by Kelsall and Diggle (1995) to determine if cases of each species were more clustered than non-cases across the village [36], conducted using the R package `smacpod`. This method was also used to identify and map significant local clusters, using a Monte-Carlo simulation envelope approach. Co-infection of malaria species at baseline were also examined i.e. *P. falciparum* plus *P. malariae* and *P. falciparum* plus *P. ovale* spp.. There were too few co-infections with all three species to explore this spatial structure.

Results

Multi-species malaria infections

Overall malaria infection prevalence as assessed by microscopy or real-time PCR was substantially raised in children compared to mothers (72.2% [95% CI: 69.-74.8] v 24.2% [95% CI: 21.0-27.7] by microscopy; 74.9% [72.4-77.4%] v 38.6% [95% CI: 34.8-42.4%] by real-time PCR) and in children infection prevalence was higher in villages along Lake Victoria than Lake Albert (82.7% [95% CI: 79.5-

85.5%) v 60.5% [95% CI: 56.4-64.6%]) by microscopy; 82.9% [95% CI: 79.8-85.8] v 66.0% [95% CI: 61.9-69.9%] by real-time PCR) (see Supplementary Table 1). *P. falciparum* was the most common species with an overall prevalence of 74.6% [95% CI: 72.1-77.0%] in children and 37.7% [95% CI: 34.0-41.5%] in mothers. Eighty-nine (7.4%) children were infected with *P. malariae* and 34 children (2.8%) with *P. ovale* spp. with a higher prevalence along Lake Victoria than Lake Albert. The majority of children infected with *P. malariae* and/or *P. ovale* spp. were also infected with *P. falciparum*. Only 9 mothers were infected with *P. malariae* and only 2 with *P. ovale* spp. No individual harbored *P. malariae/P. ovale* spp. co-infection in the absence of *P. falciparum*.

The relationship between age and malaria infection prevalence was investigated in children and mothers (Figure 1). The prevalence of slide positive malaria, *P. falciparum* and *P. malariae* infections increased with increasing age in children, however the fold difference between the youngest and oldest age category was substantially larger for *P. malariae* infections than *P. falciparum* infections (15.3 fold v 1.3 fold). In contrast, there was no significant difference in *P. ovale* spp. infection prevalence between the different age groups. The prevalence of highly parasitaemic infections (≥ 5000 parasites/ μ l) peaked in children aged 1-2 years then declined in older age groups. In mothers the prevalence of *P. malariae*, *P. ovale* spp. and highly parasitaemic infections was very low and did not vary between age groups. For slide positive malaria and *P. falciparum* infections, there was a general downwards trend in prevalence with increasing age group in mothers. The prevalence of *P. falciparum* infections as detected by real-time PCR was higher than the prevalence of slide positive malaria, demonstrative of sub-microscopic carriage of *Plasmodium* parasites in the mothers.

Risk factors associated with *Plasmodium* infections

Risk factors associated with *P. falciparum*, *P. malariae* and *P. ovale* spp. infections in children were investigated using logistic regression analysis. This analysis was not carried out in mothers due to the low prevalence of non-falciparum infections. In univariable analysis, infection with one malaria species was associated with infection with each of the other two species and also with hookworm infection (Supplementary Table 2). For both *P. falciparum* and *P. malariae*, there was a strong association with age group, lake system, village and being inside the house at night. For both infections, owning one or more insecticide-treated bednets (ITN) was associated with reduced odds of infection, as was sleeping under a bednet in the case of *P. falciparum*. There was also a positive association between *P. falciparum* infection and living in a household with goats or sheep (Supplementary Table 2). *P. ovale* spp. infection was associated with lake system and living in a household owning goats, sheep or cows. The final multivariable model for *P. falciparum* included age group, village, *P. malariae* infection and *P. ovale* spp. infections (Table 1). The model for *P. malariae* was similar but also included hookworm infection and owning an ITN. In contrast, the model for *P. ovale* spp. contained only lake system, *P. falciparum* infection and *P. malariae* infection (Table 1).

A similar analysis determined whether there were risk factors associated with multi-species versus single species malaria infections. In univariable analysis multi-species infections were associated with age group, lake system, village, hookworm infection and being inside the house at night. Owning one or more ITNs and sleeping under a bednet were associated with single species rather than multi-species malaria infections (Supplementary Table 3). The final multivariable model included age group, village and owning one or more bednets and incorporated random effects to control for clustering at household level (Table 1).

The associations observed between the different malaria species infections (Table 1) suggested that the different species were not randomly distributed. To investigate this in further detail, a multiple lottery-kind analysis was carried out [35]. The numbers of individuals infected with two or three species were greater than expected and the number of single species infections was smaller than expected (Table 2). Overall there was strong evidence of a departure from a random distribution of malaria parasites between infected children ($\chi^2=33.92$; $P<0.0001$).

Clinical measures of malaria

Associations with clinical measures of malaria were then investigated in children. Among parasitaemics, no difference in parasitaemia between single-species and multi-species infections was detected at either Lake Albert (Wilcoxon's $W=-0.602$; $p=0.182$; $N=521$) or Lake Victoria (Wilcoxon's $W=1.33$; $p=0.547$; $N=369$). In multivariable models, infection with *P. falciparum* was associated with moderate anaemia and splenomegaly. In addition, high *P. falciparum* infection levels were associated with fever. Infection with *P. malariae* was associated with an enlarged spleen and multi-species malaria infections were more strongly associated with spleen enlargement than single-species malaria infections (Table 3).

Longitudinal infection dynamics

To investigate the temporal dynamics of multi-species malaria infections over the course of the study, the point prevalence of the different *Plasmodium* species infections was determined at six, 12 and 18 months in children from Bukoba village, where prevalence of non-falciparum malaria infection was highest [27]. There was a consistent and significant rise in *P. malariae* prevalence (Figure 2), whereas *P. falciparum* prevalence did not vary significantly and there was an insignificant

upward trend in *P. ovale* spp. prevalence. In the longitudinal multivariable analysis of risk factors, previous *P. falciparum* infection was associated with current *P. falciparum* infection at each time-point, whereas mixed *P. falciparum/P. malariae* infections were associated with the study time-point, the child's age and previous *P. malariae* infection (Table 4), demonstrating that the rise in *P. malariae* prevalence was not only due to increasing age of the child. This was supported by stratification of the prevalence of *P. malariae* infection by age group for the different study sites (Supplementary Table 4). Mixed *P. falciparum/P. ovale* spp. infections were associated with each time-point.

Geospatial analysis

At baseline, there was no obvious visual pattern of infections of any *Plasmodium* species, and global tests for any clustering were non-significant ($p > 0.05$) (Supplementary Figure 1). However, upon examination of maps of significant log relative risk (Figure 3), the area in the north west of the village appeared to have fewer *P. falciparum*, *P. falciparum/P. malariae* or *P. falciparum/P. ovale* spp. cases than expected by chance ($P = 0.03$).

Discussion

Our analysis of the SIMI dried blood spot archive has provided a much deeper insight into the complex dynamics and significance of multi-species *Plasmodium* infections in children living in lakeshore communities in Uganda. One of the major risk factors identified for *P. malariae* and mixed-species infections was host age: infection with any *Plasmodium* species was much more common in children than in their mothers and older children were more likely to be infected with each of the *Plasmodium* species than younger children. This age-prevalence pattern is well-

established for *P. falciparum* infections and similar results have been reported for *P. malariae* and/or mixed infections in SSA and Papua New Guinea [8, 11, 37, 38], likely reflecting age-related exposure with partial immunity. The fact that no association was found between *P. ovale* spp. infection and age in our study most likely reflects the low prevalence of *P. ovale* spp. infections in the baseline survey and that our diagnostic approach could not differentiate the two sub-species of *P. o. curtisi* and *P. o. wallikeri* which have been reported sympatric within this part of Uganda [39].

Infection prevalence by village varied for all *Plasmodium* species and was more common in children along Lake Victoria than Lake Albert. Children in Bukoba were more at risk of mixed malaria infections than elsewhere. Similarly in Malawi, Bruce *et al.* demonstrated variations in prevalences of different *Plasmodium* species infections between villages [8]. All our survey villages were located in regions of very high malaria endemicity (entomological inoculation rate >100/year) [40], although there is a growing appreciation of local heterogeneities even in high transmission areas, with environmental factors, household factors (e.g. inclusive of domestic control measures) and insecticide resistance in *Anopheles* being implicated [41, 42]. While there was no difference in bednet ownership and use, household construction etc. between villages (Supplementary Table 1 and data not shown), there are climatic factors which differ between lakes that may influence local anopheline biology [42], with potential (un)favorable local microhabitats alluded to in Figure 3.

We found a strong association between *P. falciparum* infection and infection with *P. malariae* and *P. ovale* species infections and the vast majority of *P. malariae* and *P. ovale* spp. infections existed as co-infections with *P. falciparum*. Consistent with this, multiple lottery-kind analysis revealed non-random distributions of *Plasmodium* species. Other studies have reported a frequency of *P. falciparum* and *P. malariae* co-infections higher than would be expected [38, 44-47] but this literature can be somewhat inconsistent, for example, in Papua New Guinea [48] and in Malawi [8].

Our findings here suggest, there may be common exposures and/or susceptibilities to different *Plasmodium* species, an obvious example of which could be shared *Anopheles* vectors. It is not yet known which vectors play a role in natural transmission of *P. malariae* and *P. ovale* spp. in the Ugandan [3, 4].

We did not observe any protective effect of mixed species versus single species *Plasmodium* infections on any of the clinical indicators of malaria, contrasting with other reports [8, 24], although this might benefit from additional assessments over a longer duration and ascertain any other underlying clinical states such as any haemoglobinopathies. Nonetheless, there was an association between mixed *Plasmodium* infection and splenomegaly which, to our knowledge is the first time this observation has been made and adds to the growing body of evidence supporting the clinical significance in children of non-falciparum malaria within mixed species *Plasmodium* infections.

Despite repeated artemisinin combination therapy (ACT) treatments, the dramatic rise in *P. malariae* prevalence seen here is most worrying, notwithstanding an upward trend in *P. ovale* spp. prevalence, and consistently high *P. falciparum* prevalence. The rise in *P. malariae* may be partly explained by the increasing age of the children even though the association between survey time-point and mixed *P. falciparum*/*P. malariae* infections was maintained upon controlling for child age. A four-year longitudinal study of *Plasmodium* infection in children in rural Burkina Faso found a 15-fold increase in *P. malariae* prevalence and a four-fold increase in *P. ovale* spp. prevalence between 2007 and 2010 [22], an indirect consequence perhaps of drug-induced selection. The latter may also be responsible here in Bukoba as, over the 18-month period, 41% of our children ($N=248$) received four ACT treatments, 27% received three treatments and, based on reporting by mothers, 68% of children received further antimalarial treatment between surveys (unpublished data). Consistent with this hypothesis, we have previously demonstrated the persistence of *P. malariae* infections

after ACT treatment in the SIMI cohort, most likely to recrudescence of parasitaemia after treatment rather than relapse *per se* [27].

In certain settings, it has been argued that *P. malariae* may have a relapsing, hepatic hypnozoite stage analogous to *P. vivax* and *P. ovale* spp. or that there is sequestration of quiescent blood-stage form analogous to an arrested lymphatic stage observed in rodent *Plasmodium* species [49]. This argument is based on historical case reports describing an ability to persist for decades and on a contemporary evaluation of imported cases of *P. malariae* infection in China, Sweden and the UK [50]. The latter study demonstrated a delay in onset to symptoms that ranged from one day to one year or more, and was associated with reported chemoprophylactic use by travelers. Thus the dramatic rise in *P. malariae* prevalence is perhaps a combination of the long-term persistence of *P. malariae* parasite processes and drug-induced selection, alongside implementation of more sensitive methods of molecular diagnosis that go beyond the detection thresholds of expert microscopy.

In conclusion, our findings highlight the cryptic burden of non-falciparum malaria infections and indicate that there is a potential for emergence of *P. malariae* (and *P. ovale* spp.) infections in the face of frontline treatment for *P. falciparum*. With efforts increasingly directed towards elimination of falciparum malaria, we encourage better surveillance of non-falciparum *Plasmodium* infections in future, particularly in children, with more sensitive DNA detection methods and improved field-based diagnostics.

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NOTES

Potential conflicts of interest. Authors do not have a commercial or other association which might pose a conflict of interest.

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Figure legends

Figure 1. *Plasmodium* infection prevalence in Ugandan lakeshore communities varies with host age.

A) *Plasmodium* infection prevalence at baseline in children enrolled in the SIMI study. B) *Plasmodium* infection prevalence at baseline in mothers enrolled in the SIMI study. “PCR” refers to infection status determined by real-time PCR performed on DNA extracted from dried blood spots. “Microscopy” refers to presence of parasites in peripheral blood as determined by microscopy on Giemsa-stained blood smears. Error bars represent 95% confidence intervals.

Figure 2. *Plasmodium* infection prevalence in children in Bukoba village at different survey time points. Infection status was determined by real-time PCR performed on DNA extracted from dried blood spots. Error bars represent 95% confidence intervals.

Figure 3. Areas of Bukoba with significant log-transformed relative risk of malaria at baseline, determined using a Monte Carlo simulation envelope approach for A) *P. falciparum* infections, B) *P. falciparum* & *P. malariae* infections and C) *P. falciparum* & *P. ovale* infections. Yellow areas indicate more infections than expected whereas purple areas indicate fewer infections than expected.

Table 1. Multivariable analysis of risk factors for *P. falciparum*, *P. malariae*, *P. ovale* infection, or multi-species malaria infection in children at baseline

Species	Variable	Category	OR	95% CI [§]	p-value	
<i>P. falciparum</i>	Age (years)	<2	1.00	-	-	
		2-4	1.81	1.27-2.57	0.001	
		4-6	2.71	1.70-4.32	<0.0001	
	Village	Bugoigo	1.00	-	-	
		Walukuba	0.89	0.53-1.50	0.670	
		Piida	1.09	0.63-1.90	0.755	
		Bugoto	2.12	1.25-3.57	0.005	
		Bukoba	4.01	2.21-7.29	<0.0001	
		Lwanika	2.11	1.12-3.97	0.021	
	<i>P. malariae</i>	Negative	1.00	-	-	
		Positive	7.32	2.10-25.52	0.002	
	<i>P. ovale</i> spp.	Negative	1.00	-	-	
		Positive	8.24	0.96-70.62	0.054	
<i>P. malariae</i>	Age (years)	<2	1.00	-	-	
		2-4	6.13	2.49-15.09	<0.0001	
		4-6	14.82	5.20-42.25	<0.0001	
	Village	Bugoigo	1.00	-	-	
		Walukuba	6.08	1.27-26.10	0.024	
		Piida	5.03	1.02-24.97	0.048	
		Bugoto	7.86	1.73-35.71	0.008	
		Bukoba	12.07	2.56-56.90	0.002	
		Lwanika	1.74	0.30-10.18	0.540	
	<i>P. falciparum</i>	Negative	1.00	-	-	
		Positive	7.39	1.95-28.03	0.003	
	<i>P. ovale</i> spp.	Negative	1.00	-	-	
		Positive	4.16	1.27-13.57	0.018	
	Hookworm	Negative	1.00	-	-	
		Positive	2.33	0.99-5.48	0.053	
	Houshold owns ≥1 ITN	No	1.00	-	-	
		Yes	0.40	0.20-0.78	0.007	
	<i>P. ovale</i> spp.	Lake	Albert	1.00	-	-
			Victoria	5.24	1.28-21.49	0.021
		<i>P. falciparum</i>	Negative	1.00	-	-
			Positive	6.55	0.87-49.10	0.067
<i>P. malariae</i>		Negative	1.00	-	-	
Positive	2.98	1.30-6.84	0.010			
Multi-species	Age (years)	<2	1.00	-	-	
		2-4	4.64	2.28-9.46	<0.0001	
		4-6	8.04	3.55-18.22	<0.0001	
	Village	Bugoigo	1.00	-	-	
		Walukuba	2.83	0.84-9.53	0.093	
		Piida	1.49	0.40-5.57	0.555	
		Bugoto	3.42	1.10-10.63	0.033	
		Bukoba	11.66	3.68-36.92	<0.0001	
		Lwanika	1.93	0.52-7.18	0.329	
	Household owns ≥1 ITN	No	1.00	-	-	
		Yes	0.46	0.26-0.84	0.009	

[§] 95%CI = 95% confidence interval

Table 2. Multiple lottery kind analysis of the distribution of multi-species infections in children

	Number observed	Number expected	χ^2
1 <i>Plasmodium</i> species	796	841.84	2.50
2 <i>Plasmodium</i> species	101	88.89	1.65
3 <i>Plasmodium</i> species	9	1.87	27.21
Not infected	303	276.40	2.56
Total	1209	1209	33.92*

* df=3; $p < 0.0001$

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Table 3. Multivariable analysis of risk factors for various clinical indicators of malaria in children

Morbidity indicator	Variable	Category	OR	95% CI	P-value	P-value*	P-value ^{&}
Moderate or severe anaemia (≤10g/dL)	<i>P. falciparum</i>	Negative	1.00	-	-	-	-
		Low	1.31	0.70-2.46	0.404	0.127	0.181
		Moderate	3.58	1.91-6.73	<0.0001	0.895	0.002
		High	5.66	3.04-10.56	<0.0001	0.202	0.015
	Age (years)	<2	1.00	-	-	-	-
		2-4	0.19	0.08-0.36	<0.0001	-	-
		4-6	0.48	0.08-0.41	0.140	-	-
	Village	Bugoigo	1.00	-	-	-	-
		Walukuba	0.77	0.45-1.33	0.352	-	-
		Piida	0.31	0.16-0.57	<0.0001	-	-
		Bugoto	0.19	0.10-0.33	<0.0001	-	-
		Bukoba	0.28	0.16-0.50	<0.0001	-	-
		Lwanika	0.17	0.08-0.41	<0.0001	-	-
	Household owns ≥1 animal	No	1.00	-	-	-	-
		Yes	0.63	0.45-0.88	<0.007	-	-
	<i>S. mansoni</i> (by ELISA)	Negative	1.00	-	-	-	-
		Positive	0.69	0.47-1.00	0.050	-	-
Fever	<i>P. falciparum</i>	Negative	1.00	-	-	-	-
		Low	0.58	0.25-1.37	0.217	-	-
		Moderate	0.65	0.29-1.44	0.288	-	-
		High	2.31	1.22-4.37	0.010	-	-
	Age (years)	<2	1.00	-	-	-	-
		2-4	1.21	0.74-1.99	0.441	-	-
		4-6	0.43	0.18-1.06	0.067	-	-
	Lake	Albert	1.00	-	-	-	-
		Victoria	2.25	1.29-3.92	0.008	-	-
	Sleep under a bednet	No	1.00	-	-	-	-
Yes		0.53	0.33-0.84	0.008	-	-	
Enlarged spleen	<i>P. falciparum</i>	Negative	1.00	-	-	-	-
		Low	2.44	1.61-3.68	<0.0001	-	-
		Medium	3.94	2.58-6.02	<0.0001	-	-
		High	4.92	3.18-7.62	<0.0001	-	-
	<i>P. malariae</i>	Negative	1.00	-	-	-	-
		Positive	1.81	1.08-3.05	0.025	-	-
	Village	Bugoigo	1.00	-	-	-	-
		Walukuba	0.75	0.46-1.24	0.266	-	-
		Piida	0.53	0.31-0.92	0.025	-	-
		Bugoto	1.13	0.70-1.80	0.621	-	-
		Bukoba	1.27	0.77-2.07	0.350	-	-
		Lwanika	1.63	0.92-2.89	0.093	-	-
	<i>S. mansoni</i> (ELISA)	Negative	1.00	-	-	-	-
Positive		0.72	0.54-0.98	0.038	-	-	
Enlarged spleen (multi-species)	<i>No. Plasmodium</i> species	1	1.00	-	-	-	-
		>1	1.69	1.04-2.74	0.032	-	-

model)

Village	Bugoigo	1.00	-	-	-	-
	Walukuba	0.84	0.47-1.48	0.546	-	-
	Piida	0.51	0.27-0.94	0.030	-	-
	Bugoto	1.06	0.63-1.79	0.828	-	-
	Bukoba	1.21	0.71-2.08	0.482	-	-
	Lwanika	1.08	0.57-2.03	0.822	-	-
<i>S. mansoni</i> (ELISA)	Negative	1.00	-	-	-	-
	Positive	0.63	0.45-0.88	0.006	-	-

* *P*-value for interaction with age category 2-4 years; & *P*-value for interaction with age category 4-6 years

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Table 4. Longitudinal analysis of risk factors for infection with *P. falciparum* (Pf) only, *P. falciparum* and *P. malariae* (Pf+Pm) or *P. falciparum* and *P. ovale* (Pf+Po) among children in Bukoba village

Species	Variable	OR	95% CI	p-value
Pf only	Previous Pf infection	3.01	1.462, 5.833	0.0015
Pf + Pm	Time point	2.07	1.576, 2.841	<0.0001
	Age	1.19	1.026, 1.407	0.0262
	Previous Pm infection	2.29	1.208, 3.882	0.0001
Pf+Po	Time point	1.42	1.157, 1.755	0.0009

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Figure 1.

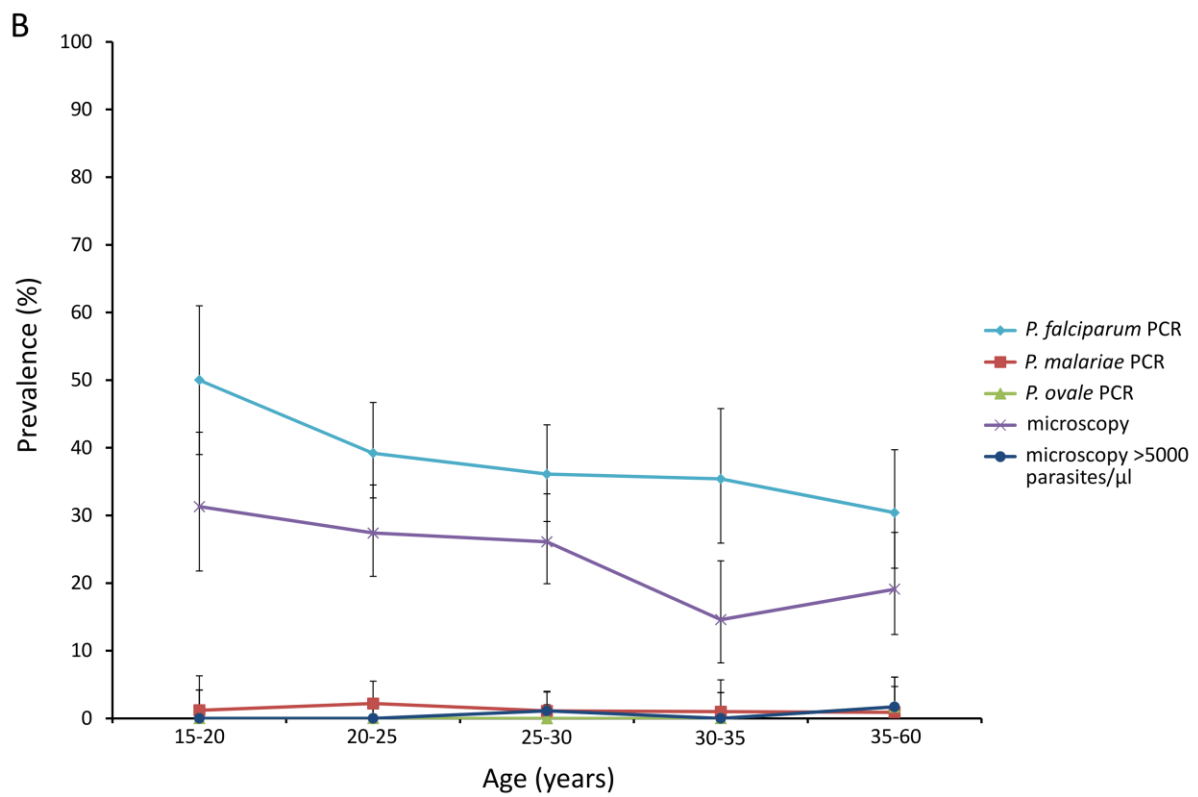
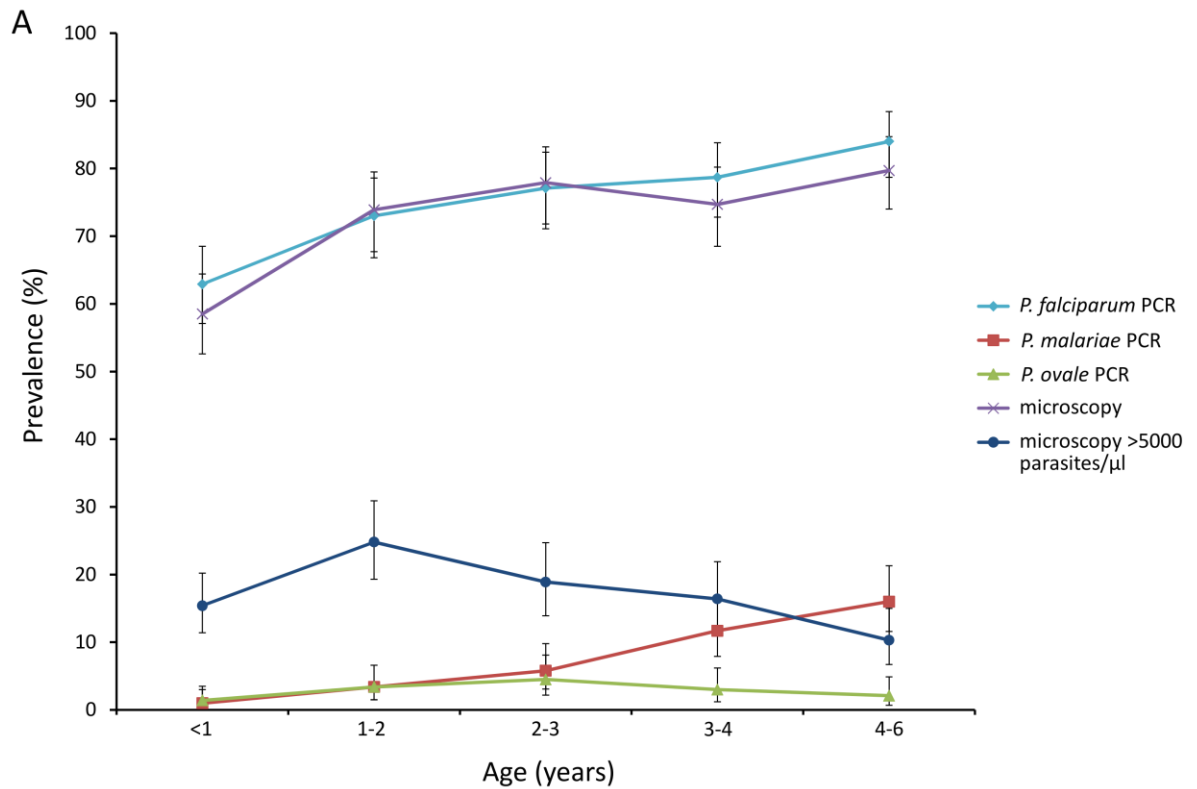
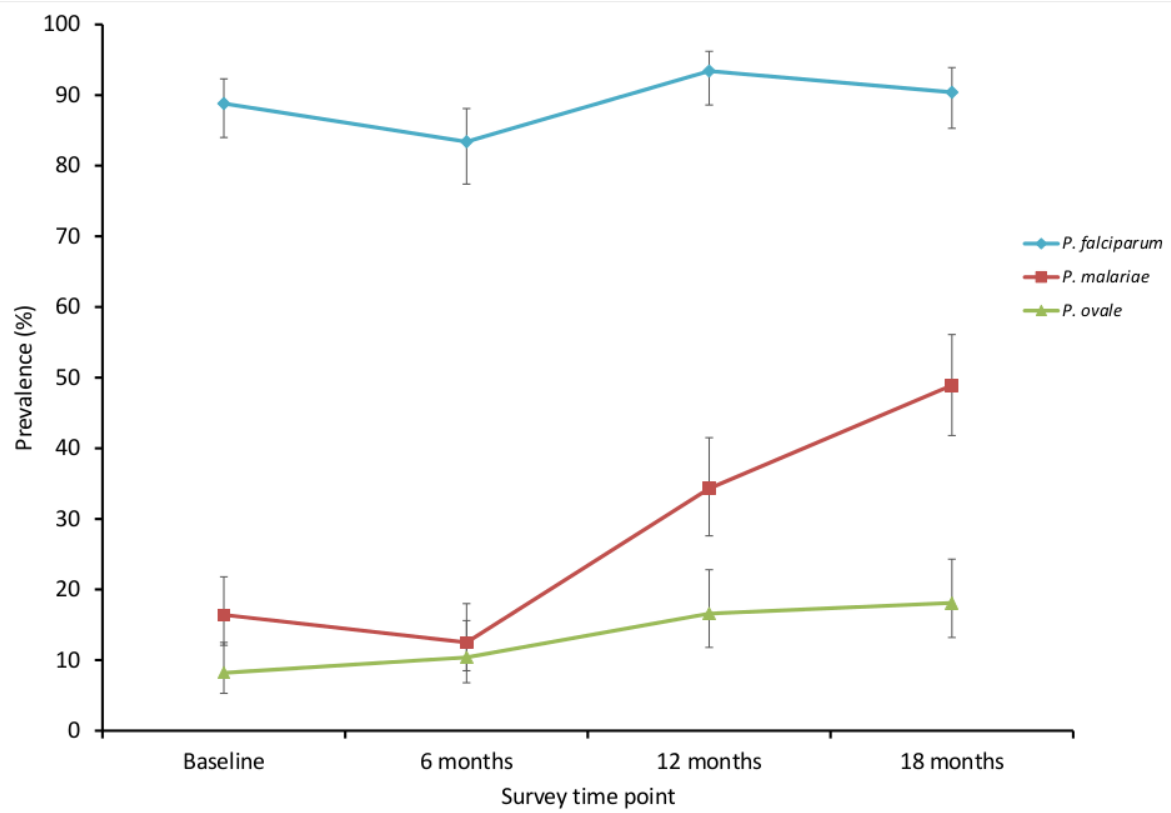


Figure 2.



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Figure 3.

