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Patterns of patent and sub-patent *Plasmodium falciparum* infections in household members of children under seasonal malaria chemoprevention coverage in the health district of Nanoro, Burkina Faso

Sié A. Elisée Kambou[1*], Paul Sondo[1], Bérenger Kabore[1], Ipéné Mylène Carenne Bayala[1], Amélé Fifi Chantal Kouevi[1], Eulalie W. Compaore[1], Kié Solange Millogo[1], Bouda Ismaïla[1], Toussaint Rouamba[1], Adama Kazienga[1], Derra Karim[1], Eli Rouamba[1], Prabin Dahal[2,3,4], Sabina D. Otienoburu[2,4,5], Jaishree Raman[6,7,8], Mehul Dhorda[2,3,4,10], Sanata Bamba[9], Philippe J. Guérin[2,3,4] and Halidou Tinto[1]

Abstract

Background Seasonal Malaria Chemoprevention (SMC) has been adopted since 2014 in Burkina Faso to reduce malaria burden in children under 5 years. However, the intervention's expected potential has not yet been achieved in real-life conditions, suggesting other factors may influence its effectiveness. Asymptomatic carriers, including patent and sub-patent *Plasmodium falciparum* infections in household members seems to be a potential factor maintaining the high malaria burden in children under SMC coverage. This study assessed the patterns of these infections in household members living around children under SMC coverage in Nanoro, Burkina Faso.

Methods A cross-sectional survey nested to a large SMC study named "SMC_RST" was conducted during the 2022 SMC campaign in Nanoro, including 745 participants. Sub-patent infections were defined as *var*ATS qPCR-positive/RDT-negative, and patent infections as positive by both methods. Prevalence of patent and sub-patent malaria infections were presented with 95% confidence intervals (CI), accounting for clustering of individuals within households. Multinomial regression with robust standard errors assessed the effect of age, sex, and locations on risk of malaria infection.

Results Out of 745 participants, diagnostic results regarding malaria status were available for 650 (87.2%). *Plasmodium falciparum* infections in household members were detected in 68.6% (446/650, 95% CI: 64.7–72.5), including 27.4% (178/650, 95% CI: 23.9–30.8) patent and 41.2% (268/650, 95% CI: 37.3–45.2) sub-patent infections. Patent infections declined with age: 37.7%, (95% CI: 31.9–43.5) among 5–14 years, 25% (95% CI: 17.0–33.0) among 15–24 years, and 17.1% (95% CI: 12.6–21.5) among ≥ 25 years. Prevalence of sub-patent infection was 38.0% (95% CI: 32.4–43.7) among 5–14 years, 49.2% (95% CI:40.3–58.1) among 15–24 years and 40.7% (95% CI: 34.5–46.8)

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*Correspondence:
Sié A. Elisée Kambou
eliseekambou96@gmail.com
Full list of author information is available at the end of the article

among ≥ 25 years. No significant difference across villages was observed in terms of prevalence of household members with patent ($\chi^2 = 4.16$, *P*-value = 0.38) or sub-patent infections ($\chi^2 = 3.92$, *P*-value = 0.41).

Conclusion Over two-thirds of the household members living with children under SMC coverage area in Nanoro, Burkina Faso, harboured patent and sub-patent *P. falciparum* infection. Among those aged 15 years and older, asymptomatic carriage was largely sub-patent. This study supports the extension of the SMC intervention to school-aged children and the implementation of interventions such as testing and treatment of household members of children under SMC coverage.

Keywords Malaria, Seasonal malaria chemoprevention, Sub-patent infection, *var*ATS qPCR, Burkina Faso.

Background

As the leading cause of consultation (37.8%), hospitalization (63.16%) and deaths (18%) in health centres, malaria remains a significant health challenge in Burkina Faso [1]. Children under five years represent the most affected age group, with more than 4 million cases and up to 2,925 malaria-related deaths reported in 2022 [1]. In order to reduce malaria burden in children, the World Health Organization (WHO) has recommended seasonal malaria chemoprevention (SMC) which consists of monthly and intermittent administration of treatment with amodiaquine and sulfadoxine-pyrimethamine (AQSP) to children aged 3–59 months (regardless their malaria infection status) during the period of high malaria transmission. These drugs are synergically associated; sulfadoxine–pyrimethamine has a long elimination half-life and is intended to prevent the occurrence of new malaria infections, whereas amodiaquine has a relatively short half-life and represents the curative component expected to rapidly clear existing infections [2]. SMC has been adopted since 2014 in Burkina Faso.

Numerous studies have demonstrated that SMC is a highly effective intervention, offering a high level of protection against clinical malaria and reducing hospitalization and associated mortality rates [3–6]. In addition, high coverage and good adherence to the SMC programme have been reported [3, 7]. However, the expected potential from this intervention is hitherto partially achieved in real-life conditions in Burkina Faso, as the malaria burden remains high among children under five years after several years of implementation. This suggests that beyond the direct determinants of SMC efficacy, other factors could play a role as modifiers of SMC effectiveness in real life conditions which could explain the persistence of malaria transmission in children under SMC coverage. The presence of asymptomatic infections (patent and sub-patent) in household members living around the children under SMC coverage but who are not targeted by any specific intervention seems to be one of these factors [8–10]. These asymptomatic carriers, generally characterized by low parasitaemia, are often untreated and serve as reservoirs of continuous transmission of parasites within the community [11, 12].

Furthermore, it has been reported that parasites from asymptomatic carriers are more infectious to mosquitoes than those from symptomatic carriers and serve as a major source of gametocytes for local mosquito vectors [13, 14]. Moreover, malaria transmission is highly localized within households [15]. A study in Senegal, found a significant association between the presence of an asymptomatic *Plasmodium falciparum* infection within a household and the subsequent clinical malaria episodes in household members [16]. This underlines the critical role of asymptomatic household members in the continuous infection of children under SMC coverage.

Conventional methods, such as microscopy and standard rapid diagnostic tests (RDTs), while effective for detecting symptomatic malaria infections, have low sensitivity in detecting infections with low parasitaemia [17–20]. Sub-patent infections, which account for 50% of cases in asymptomatic carriers are generally not detected by conventional diagnostic methods [11, 21–23]. A real time PCR (qPCR) assay targeting the *var* acidic terminal sequence (*var*ATS) gene exhibits high sensitivity for detecting low level of *P. falciparum* parasitaemia, with a reported limit of detection of 0.03 parasites/microlitre of blood [24, 25]. This high sensitivity makes *var*ATS qPCR particularly suitable for detecting sub-patent infections, often missed by conventional diagnostic tools, thereby providing a more accurate estimation of the asymptomatic malaria reservoir in the community. Such sensitivity is crucial to guide malaria control strategies.

Given all these aspects, the characterization of asymptomatic infected people using highly sensitive methods is crucial to understand the dynamics of *P. falciparum* infections and the contribution of other asymptomatic household members to the persistence of malaria infection in children under SMC coverage. This information is useful for the development of new intervention strategies to enhance the effectiveness of SMC use. This study aims to identify patent and sub-patent *P. falciparum* infections using *var*ATS qPCR among household members living around children under SMC coverage in the health district of Nanoro, Burkina Faso.

Methods

Study area and design

This study was carried out in the Nanoro health district catchment area in Burkina Faso. Malaria is endemic in Burkina Faso, with high seasonal variation resulting in a low transmission period from December to June and a high transmission period from July to November, during which the SMC intervention is deployed. SMC is a community-based intervention conducted in villages located in the catchment area of five health facilities: Soaw, Kolokom, Zoétgomdé, Kokolo and Poéssé.

This study was part of a larger SMC study (called "SMC-RST") described elsewhere [26, 27]. The SMC-RST study was a randomized trial aiming at assessing whether in addition to SMC, screening and treating (if positive) other household members of children under SMC coverage would contribute to better protect these children compare to routine SMC alone. The project included 526 isolated households with a least one child under SMC coverage assigned to one of the 2 study arms (control arm SMC alone, n = 263) or intervention arm (SMC + screening of household members and treatment if positive, n = 263) [26]. The SMC-RST study was implemented exclusively in the Nanoro Health District, Burkina Faso. The present study consisted of a cross-sectional study conducted during the 2022 SMC campaign (July to October). The study population consisted of household members sharing a home with children under SMC coverage and included in the intervention arm of the SMC-RST study. Study participants included asymptomatic members from all 263 households included in the intervention arm of the SMC-RST study. At each monthly visit, only one (1) asymptomatic (other than those included in the previous months) roommate was selected from each household and included in this study. The roommate included at each visit was selected from the asymptomatic carriers presents at the time of the visit in the household, with a random draw if more than one roommate was available and eligible. Moreover, to ensure all eligible housemates were covered before the end of the SMC campaign, two (02) roommates were often selected from certain households. In this study, asymptomatic carrier was defined as a person with no symptoms, with a body temperature < 37.5 °C, and who reported no fever during the 2 days before blood collection. Further details of participants selection process is described elsewhere [27]. Sociodemographic characteristics such as age and sex of participants were collected through an electronic case record form designed on Redcap. Capillary blood samples were taken from each participant for the detection of *P. falciparum* infection by standard rapid diagnostic test (RDT) based on the detection of histidine-rich protein 2 antigen (HRP2) (AdvDx™ Malaria *Pf* test kit, 004ADFEF025KI-1, Advy Chemical Pvt. Ltd, India) and the preparation of dried blood spots (DBS) onto filter paper strips (Whatman no.3, China) for molecular analysis. Each DBS was stored individually in a Ziploc bag containing silica gel desiccant to preserve sample integrity.

DNA extraction and Var ATS qPCR

Molecular analyses were performed at the Laboratory for Antimalarial Resistance Monitoring and Malaria Operational Research at the National Institute for Communicable Diseases in South Africa. Genomic *Plasmodium* DNA isolation from DBS was carried out using the Tween®20-Chelex®100 resin extraction method as previously described [28]. Briefly, a portion of approximately 3-mm-diameter of each DBS was punched and introduced into a sterile 1.5-ml Eppendorf tube. An aliquot of 1 ml of 0.5% Tween-phosphate-buffer saline was added to the tube, vortexed and incubated at 4 °C for at least 12 h and the supernatant was thereafter discarded. Next, 1 ml of fresh phosphate-buffered saline was added to each tube, and incubated at 4 °C for 30 min. The supernatant was aspirated and discarded and 150μL of 10% Chelex® 100 resin solution was added to each tube, followed by a 10-min incubation at 95 °C. During this incubation period, each tube was briefly vortexed (5 to 10 s) at least twice. Finally, the tubes were centrifuged at 13,200 RPM for 5 min and the clear supernatant containing the extracted DNA was collected and transferred to DNA storage tubes for immediate use or stored at −20 °C for later analyses.

The *var*ATS qPCR assay was performed following the protocol described by Hofmann et al. [24]. For the amplification, (total volume of 25μL), 2 μL of 10uM *var*ATS forward primer (5'-CCCATACACAACCAAYTGGA-3'), 2 μl of 10uM and *var*ATS reverse primer (5'- TTCGCA CATATCTCTATGTCTATCT-3'), 1 μl of 10uM a *var*ATS probe (5'- 6-FAM-TTTTCCATAAATGGT-NFQ-MGB −3'), 10 μl of Bioline SensiFAST™ Probe No-ROX kit (Meridian Biosciences, USA), 5 μl of molecular grade water and 5 μl of DNA were used. Amplification was achieved using Bio-Rad CFX Opus (Bio-Rad, Germany) devices and cycling conditions consisting of pre-incubation at 50 °C for 2 min, initial denaturation at 95 °C for 10 min, and 45 cycles of denaturation at 95 °C for 15 s and annealing, and elongation at 55 °C for 1 min. The cut-off threshold (Ct) value of 40 was used to distinguish positive and negative samples. Samples were considered *P. falciparum* negative when Ct ≥ 40 cycles.

Statistical analysis

The study participants were categorized into three groups: (1) those without infection, (2) with patent infection, and (3) with sub-patent infections. Sub-patent infections were defined as infections that tested positive for *P. falciparum* by *var*ATS qPCR but negative for standard RDT (hrp2 based), while patent infections were those testing malaria-positive by both methods. Negative participants were those who were tested malaria-negative by both *var*ATS qPCR and standard RDT. Participants who tested negative by *var*ATS qPCR but positive for standard RDT were considered as false positives and were categorized as negative.

Descriptive statistics were calculated using proportions for qualitative variables. The prevalence of patent and sub-patent *P. falciparum* infections was calculated. Corresponding 95% confidence intervals (95% CI) were estimated by accounting for correlated structure of the data (multiple participants selected within each households) using the method proposed by Fleiss et al. [29] and this was computed across age categories (5–14 years, 15–24 years, ≥ 25 years), sex, and village. The effect of age, village, and the interaction between age and village on the probability of patent and sub-patent infections was assessed using multinomial regression while accounting for the household effect. The results from the regression models were expressed as relative risk ratios (RRR) with 95% CI estimated using robust standard errors. Data were analysed using RStudio (version 4.4) and Stata IC (version 14) software, and a *P*-value < 0.05 was considered statistically significant.

Results

Participant characteristics

A total of 745 asymptomatic household members living around children under SMC coverage were included in this study. *P. falciparum* infection status determined using both *var*ATS qPCR and standard RDT data, was available for 87.2% (650/745) of the participants. Age and sex distribution of the study participants stratified by village are presented in Table 1. A total of 276 (42.5%) participants were aged 5–14 years (school-aged children), 128 (19.7%) were between 15 and 24 years (adolescents and young adults), and 246 (37.8%) were aged ≥ 25 years (adults). The sex distribution was similar across all villages, with females representing 53.3% to 60.4% of the participants (Table 1).

Plasmodium falciparum infections

The overall percentage of asymptomatic *P. falciparum* infections among other household members living with children under SMC coverage detected by *var*ATS qPCR was 68.6% (446/650, 95% CI: 64.7–72.5) (Table 2). Infection prevalence was highest at Kokolo at 86.2% (95% CI: 72.0–100.0), followed by Kolokom (71.4%, 95% CI: 60.9–81.9), Poéssé (70.1%, 95% CI: 61.5–78.8), Soaw (66.9%, 95% CI: 60.9–72.9), and Zoétgomdé (64.5%, 95% CI: 55.8–73.2). Overall, 27.4% (178/650, 95% CI: 23.9–30.8) of the participants harboured patent infections and 41.2% (268/650, 95% CI: 37.3–45.2) had sub-patent infections.

Patent *Plasmodium falciparum* infections by age, sex, and location

The prevalence of patent infections among household members in the study ranged from 21.5% (95% CI: 13.7–29.2) in Zoétgomdé to 28.6% (95% CI: 18.1–38.7) in Kolokom (Table 2). Prevalence of patent infection was 28.7% (95% CI:23.3–34.2%) among males and 26.5% (95% CI: 22.1–30.8%) among females (relative risk ratio (RRR) for males = 1.04, standard error = 0.23, *P*-value = 0.841) (Tables 3 and 4).

Table 1 Demographic characteristics of the study participants per village (n = 650)

Characteristic	Kokolo (n = 29) n[a] (%[b])	Kolokom (n = 63) n (%[b])	Poéssé (n = 164) n (%[b])	Soaw (n = 287) n (%[b])	Zoétgomdé (n = 107) n (%[b])
Age groups (years)					
5–14y[c]	20 (61.0)	23 (36.5)	71 (43.3)	122 (43.5)	40 (37.4)
15–24y[c]	6 (20.7)	14 (22.2)	39 (23.8)	51 (17.8)	18 (16.8)
≥ 25y[c]	3 (10.3)	26 (41.3)	54 (32.9)	114 (39.7)	49 (45.8)
Sex					
Female	17 (58.7)	36 (57.1)	99 (60.4)	165 (57.7)	57 (53.3)
Male	12 (41.4)	27 (42.9)	65 (39.6)	121 (42.3)	50 (46.7)

[a] n = number of positive participants

[b] % = percentage of positive participants

[c] y = years

Table 2 Patent and sub-patent *Plasmodium falciparum* infections per village

	Kokolo (n = 29)	**Kolokom (n = 63)**	**Poéssé (n = 164)**	**Soaw (n = 287)**	**Zoétgomdé (n = 107)**	**Overall (n = 650)**
Patent (%)	27.6	28.6	27.4	29.3	21.5	27.4
95% CI[e]	(12.9–42.3)	(18.1–38.7)	(21.4–33.4)	(23.5–35.1)	(13.7–29.2)	(23.9–30.8)
Sub-patent (%)	58.6	42.9	42.7	37.6	43.0	41.2
95% CI	(43.1–74.1)	(26.4–59.3)	(34.6–50.8)	(32.1–43.2)	(33.4–52.6)	(37.3–45.2)
Overall *P. falciparum* positive (%)	86.2	71.4	70.1	66.9	64.5	68.6
95% CI	(72.0–100)	(60.9–81.9)	(61.5–78.8)	(60.9–72.9)	(55.8–73.2)	(64.7–72.5)

[e] 95% CI = 95% confidence interval for correlated proportions using method by Fleiss et al. [29] as described in the methods section

Table 3 Distribution of *Plasmodium falciparum* infections by sex and age

Variable	**Patent%**	**95% CI**	**Sub-patent%**	**95% CI**	**Overall %**	**95% CI**
Sex						
Male	28.7	(23.3–34.2)	41.5	(35.5–47.4)	70.2	(64.1–76.3)
Female	26.5	(22.1–30.8)	40.9	(35.9–45.9)	67.4	(62.6–72.2)
Age groups (years)						
5–14 y	37.7	(31.9–43.5)	38.0	(32.4–43.7)	75.7	(70.5–80.9)
15–24 y	25.0	(17.0–33.0)	49.2	(40.3–58.1)	74.2	(66.0–82.4)
≥ 25 y	17.1	(12.6–21.5)	40.7	(34.5–46.8)	57.7	(51.2–64.3)

Table 4 Effect of gender, age, location on patent and sub-patent *Plasmodium falciparum* infection using multinomial regression

Variables	**Category**	**Relative risk ratio**	**Standard error†**	***P*-value**
Patent infection (178 positive; n = 650)				
Gender	Female	1(Reference)		
	Male	1.04	0.232	0.841
Age (in years)		0.96	0.008	< 0.0001
Village	Poesse	1 (Reference)		
	Kokolo	1.66	1.211	0.476
	Kolokom	1.22	0.410	0.539
	Soaw	1.05	0.303	0.842
	Zoetgomde	0.77	0.274	0.461
Sub-patent infection (268 positive, n = 650)				
Gender	Female	1(Reference)		
	Male	1.06	0.212	0.731
Age (in years)		0.99	0.005	0.094
Village	Poesse	1(Reference)		
	Kokolo	2.74	1.790	0.122
	Kolokom	1.09	0.472	0.830
	Soaw	0.81	0.220	0.474
	Zoetgomde	0.89	0.282	0.723

† Robust standard errors by taking household clustering into account

Patent infection prevalence was highest in the 5–14 years age-group (37.7%, 95% CI:31.9–43.5) and this declined progressively with increasing age: 25.0% (95% CI:17.0–33.0%) among 15–24 years, and 17.1% (95% CI:12.6%–21.5%) among ≥25 years (Table 3). No significant difference in the prevalence of household members patent infection was observed by sex ($\chi^2 = 0.11$, $P = 0.73$) or villages ($\chi^2 = 4.16$, $P = 0.38$). In a multinomial regression that adjusted for sex and village, every yearly increase in age was found to be associated with a reduction in risk of patent infection by 4% (relative risk ratio (RRR) = 0.96, standard error = 0.008, *P*-value < 0.001) (Figs. 1A, 2A; Table 4). Figure 1 presents the effect of host age and the village on the risk of patent and sub-patent *P. falciparum* infections.

Sub-patent *Plasmodium falciparum* infections by age, sex, and location

The prevalence of sub-patent infection in the study was highest in Kokolo (58.6%, 95% CI: 43.1–74.1) and lowest in Soaw (37.6%, 95% CI: 32.1–43.2). The prevalence was similar between sex: 41.5% (95% CI: 35.5–47.4%) among males and 40.9% (95% CI: 35.9–45.9%) among females (Table 2). No significant differences were observed across sex ($\chi^2 = 0.19$, $P = 0.65$) or village ($\chi^2 = 3.92$, $P = 0.41$). When stratified by age-group, the prevalence was 38.0% (95% CI: 32.4–43.7%) among 5–14 years age-group, 49.2% (40.3–58.1%) in 15–24 years age-group, and 40.7% (95% CI: 34.5–46.8%) among ≥25 years. In a multinomial regression that adjusted for sex and village, the effect of age was less apparent with relative risk ratio close to unity (RRR = 0.99, standard error = 0.005, *P*-value = 0.09) (Figs. 1B, 2B; Table 4).

Discussion

This study reported a high prevalence (over two-thirds) of asymptomatic *P. falciparum* infections detected by *var*ATS qPCR, among household members of children under SMC coverage in the health district of Nanoro, Burkina Faso. Similar findings have been reported from other malaria-endemic areas [30–32]. As all these patent and sub-patent infections were asymptomatic, they

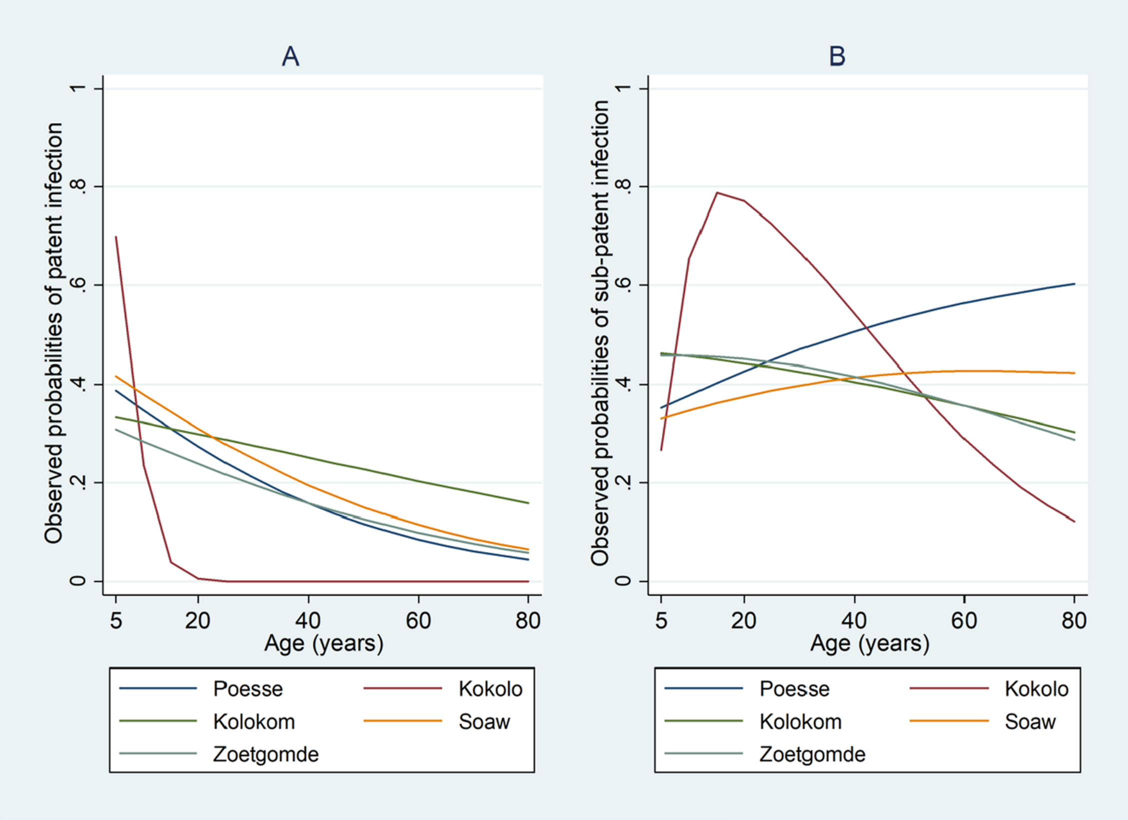

Fig. 1 Probability of patent and sub-patent *Plasmodium falciparum* infections from a multinomial model with interaction between age and village. The figure presents the interaction between participant age and the observed probabilities of patent and sub-patent *Plasmodium falciparum* infections, stratified by village. **A** observed probabilities of patent infections according to age in each village. **B** observed probabilities of sub-patent infections according to age in each village

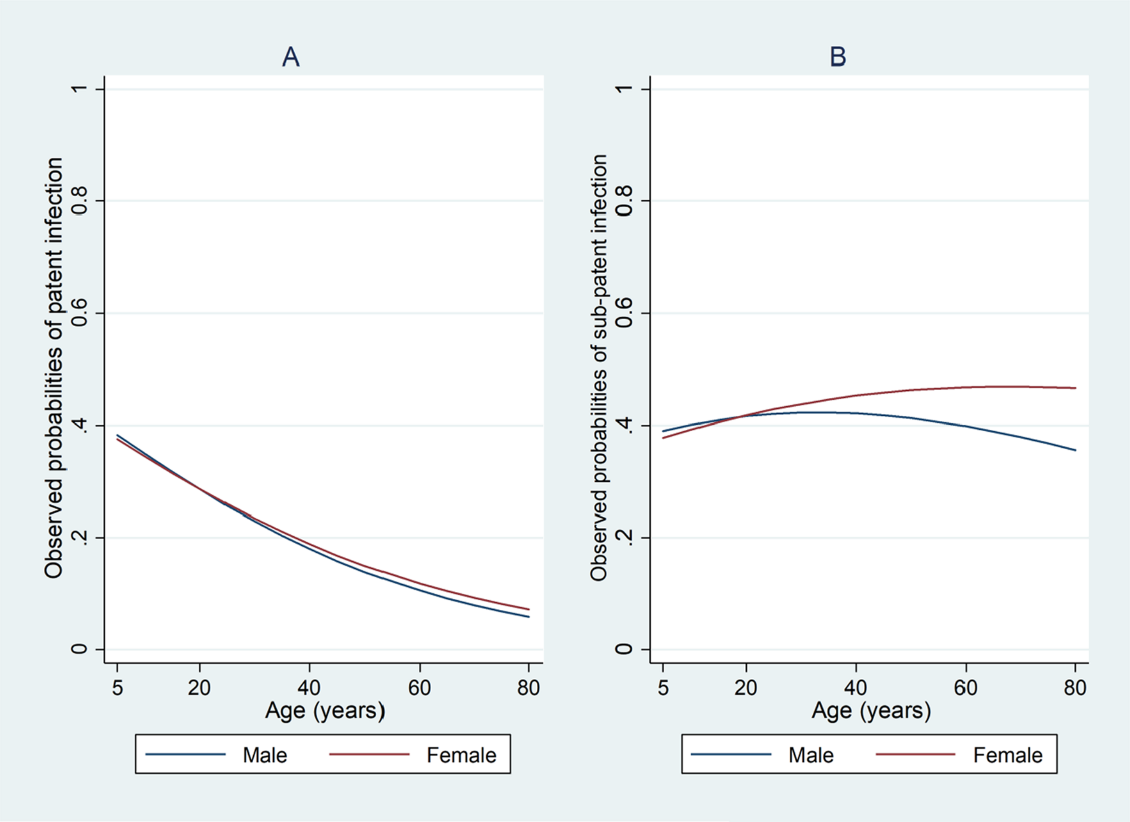

Fig. 2 Probability of patent and sub-patent *Plasmodium falciparum* infections from a multinomial model with interaction between age and sex. This figure presents the interaction between participant age and the observed probabilities of patent and sub-patent *Plasmodium falciparum* infections according to sex. **A** observed probabilities of patent infections. **B** observed probabilities of sub-patent infections

would have likely remained undiagnosed. The gradual acquisition of partial immunity due to repeated *Plasmodium* exposure in high transmission settings explained these phenomena [11, 33, 34]. Consequently, these infections play an important role in the persistence of malaria transmission in the community [13, 14] and constitute a major obstacle for malaria control [35, 36]. In this context, although SMC has proven to be an effective and promising strategy, the presence of silent parasite reservoirs around children under SMC coverage could compromise the effect of this intervention. This is indeed exacerbated by the fact that malaria transmission tends to be highly localized within households [15] and under such circumstances, the presence of patent and sub-patent *P. falciparum* infections within a household would significantly increase the risk of clinical malaria among other household members, especially the vulnerable population of children under five years old [16]. This highlights the central role infected household members play sustaining malaria infections among children under SMC coverage, which might influence the efficacy of SMC interventions. This suggests that the simultaneous testing and treatment of asymptomatic household members is essential to interrupt the infection cycle around children under SMC coverage.

Although no significant difference in the distribution of *P. falciparum* infections was observed across villages, Kokolo had a higher prevalence of sub-patent infections. This could be partially attributable to its proximity to the large dam of Soum, which is a geographical feature of the health district of Nanoro, with intense market farming activities favor the development of mosquitoes. Several studies have reported that villages located near dams with intensive market farming activities constitute micro-geographical hotspots for malaria transmission [37–39]. This suggests that the higher infection rates in Kokolo may be driven by increased local vector density and prolonged exposure to infective bites. These findings underscore the importance of targeted interventions in micro-geographical hotspots to reduce malaria transmission in communities.

Household members aged 5 to 14 years old had a higher prevalence of patent infections while the age-group with largest sub-patent infections were observed in

15–24 years old, as previously reported [40–42]. Moreover, prevalence of participants with patent infections significantly decreased by age. This highlights, on one hand the effect of premunition with increasing age as stated above, but also an increased susceptibility of school-aged children as this asymptomatic carriage trends to be patent in this age group and sub-patent in older adolescents and adults. Moreover, as reported previously, school aged-children are more likely to have low adherence to insecticide-treated nets and other preventive measures, thus favouring malaria infections [41, 43, 44]. In this context, introducing interventions targeting this age group could prevent significant morbidity, reduce the parasite reservoir and thereby contribute to reducing malaria transmission within households. For example, Cissé et al. observed a reduction in transmission when extending SMC in children up to ten years [45]. Similarly, Ahmad et al. reported that interventions that clear persistent asymptomatic infections when targeted at the subpopulation with a high risk of carriage may reduce the infectious reservoir [36]. Therefore, the implementation of intermittent preventive treatment of malaria in school-aged (IPTsc) children, as recommended by the WHO [46], could reduce the parasite reservoir, maximize the effect of SMC and prevent significant morbidity in this age group. However, given the high level of malaria endemicity in settings such as Burkina Faso; the impact of IPTsc on reducing the parasite reservoir could be limited unless this intervention is integrated into a broader set of complementary interventions including strengthened vector control, the use of more sensitive diagnostic tools, malaria vaccination and strong community engagement to support the effective implementation and sustainability of malaria control strategies [27, 47–50]. Furthermore, the high prevalence of sub-patent infections observed among 15–24 years-olds suggests the need to incorporate highly sensitive detection methods into community-based testing and treatment strategies.

A limitation of this study is the lack of data on gametocyte carriage in the asymptomatic individuals detected in this study. It was, therefore, not possible to quantify their contribution to on-going transmission in the study area. However, previous studies reported that asymptomatic patent and sub-patent infections are important gametocyte carriers suggesting that the current study could reflect a similar gametocyte carriage profile [40, 51, 52]. In addition, infections with other malaria species, such as *Plasmodium malariae* and *Plasmodium ovale* are missing in the present study as the *var*ATS qPCR is specific to *P. falciparum*. Another limitation was the cross-sectional design of this study, relying on single time-point testing, which might increase the likelihood of missing sub-patent *P. falciparum* infections [53].

Conclusion

This study found that over two-thirds of the household members living with children under SMC coverage in the health district of Nanoro, Burkina Faso carried asymptomatic *P. falciparum* patent and sub-patent infections. Among school-aged children, adolescents and young adults, asymptomatic carriage occurred equally as patent and sub-patent infections, whereas among those aged 15 years and older, asymptomatic carriage was largely sub-patent, suggesting the acquisition of naturally acquired immunity in older adolescents and adults. This study supports the recommendation of extending the SMC intervention to 5–14 years olds as well as implementing other strategies such as simultaneous testing and treatment of older household members in order to interrupt the transmission cycle around children under SMC coverage.

Abbreviations

DBS	Dried blood spots
SMC	Seasonal malaria chemoprevention
RDT	Rapid diagnostic tests
qPCR	Quantitative polymerase chain reaction
*var*ATS	*Plasmodium falciparum*-Specific acidic terminal sequence of the var genes
CI	Confidence interval
DNA	Deoxyribonucleic acid
RST	Roommates Screening and Treatment
REDCap	Research Electronic Data Capture

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Author contributions

KE, SP and TH designed the study. KE, SP and JR, involved in the laboratory work. KE, SP, RT, KA and PD contributed to data management and statistical analysis. KE, SP, PG, PD, KA, SO, SB and TH contributed to drafting the manuscript and all authors read and approved the manuscript.

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Availability of data and materials

All data generated or analysed during this study are available from the corresponding author upon request.

Declarations

Ethics approval and consent to participate

The study was conducted according to ethical principles for health research. A written informed consent was obtained from all adults, as well as from the parents or legal guardians of children prior to enrollment. For participants aged 10 to 19 years, assent was also obtained in addition to parent or legal guardians consent. The main SMC-RST protocol, as well as the protocol for this ancillary study was reviewed and approved by the Ethics Committee for Health Research of Burkina Faso (*Deliberation N°: 2021-03-059 of March 10, 2021 and Deliberation N°: 2022-03-040 of March 02, 2022* respectively).

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author details

[1]Institut de Recherche en Sciences de La Santé (IRSS), ClinicalResearch Unit of Nanoro (CRUN), Nanoro, Burkina Faso. [2]Infectious Diseases Data Observatory (IDDO), Oxford, UK. [3]Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, UK. [4]WorldWide Antimalarial Resistance Network (WWARN), Oxford, UK. [5]College of STEM, Johnson C. Smith University, Charlotte, NC, USA. [6]Centre for Emerging Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases Johannesburg, Johannesburg, South Africa. [7]Wits Research Institute for Malaria, University of Witwatersrand, Johannesburg, South Africa. [8]Institute for Sustainable Malaria Control, University of Pretoria, Pretoria, South Africa. [9]Institut Supérieur Des Sciences de La Santé (INSSA), Université Nazi Boni, Bobo Dioulasso, Burkina Faso. [10]Tropical Health Network, MORU, Bangkok, Thailand.

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