

discomfort, as well as the regular and permanent follow-up of the patient until recovery of his health. Blood sampling for laboratory examinations was highly appreciated and mentioned by our respondents as the main indicator of the quality of care provided by the research teams.

Conclusion The quality of care according to the criteria the participants and the health workers assigned to it, is intrinsically linked to clinical trials.

PO 8269 **SELECTION OF SEVEN-MUTATION PFCRT-PFMDR1 GENOTYPE AFTER SCALING-UP SEASONAL MALARIA CHEMOPREVENTION WITH SULPHADOXINE-PYRIMETHAMINE AND AMODIAQUINE IN MALI**

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Background WHO recommended seasonal malaria chemoprevention (SMC) in 2012 for Sahel countries in Africa with the aim to reduce malaria among children under 5 years old by using sulphadoxine-pyrimethamine and amodiaquine (SP+AQ). This strategy was scaled up in Mali from 2012. The use of millions of doses of SP+AQ could generate potential *Plasmodium falciparum* resistance in mutant parasites. The aim of this study was to monitor the prevalence of *Pf*dhfr +*Pf*dhps +*pfcrt* +*pfmdr1* mutations in parasites infecting the target population.

Methods Two cross-sectional surveys were conducted before (August 2012, n=662) and after (June 2014, n=670) a pilot implementation of SMC in the health district of Koutiala. Children aged 3–59 months received 3 and 4 rounds of curative doses of SP+AQ over two malaria seasons in 2012 and 2013, respectively. Genotypes of *P. falciparum* *Pf*dhfr codons 51, 59, 108 and 164; *Pf*dhps codons 437 and 540, *Pfcrt* codon 76 and *Pfmdr1* codon 86 were analysed by PCR on DNA of parasites from SMC population blood samples (after and before) and non-SMC patients aged 7 years or above (November 2014, n=500).

Results In the SMC population 191 and 85 children before and after SMC implementation, respectively, were included in the molecular analysis. In the non-SMC patients, 220 were successfully PCR analysed. In the SMC population, the prevalence of the six-mutation *Pfcrt* [*Pf*dhfr-dhps quintuple +*Pfcrt*-76T] genotype increased significantly after SMC implementation, from 0.0% to 7.1% ($p=0.0008$). The post-intervention prevalence of the six-mutation *Pfmdr1* [*Pf*dhfr-dhps quintuple +*Pfmdr1*-86Y] and the seven-mutation *Pfcrt* +*Pfmdr1* [*Pf*dhfr-dhps quintuple +*Pfmdr1*-86Y+*Pfcrt*-76T] genotypes were both 1.2% among the SMC population. No six-mutation and seven-mutation genotypes were observed among SMC population at baseline nor in the non-SMC patient population ($p=0.30$).

Conclusion SMC increased the prevalence of the six-mutation *Pfcrt* genotype of *P. falciparum* that can lead to resistance in a population exposed to SMC with SP+AQ.

PO 8271 **PFHRP2 GENE DELETIONS IN PLASMODIUM FALCIPARUM AND SCHISTOSOMA MANSONI CO-INFECTIONS: AN EMERGING CHALLENGE FOR MALARIA RAPID DIAGNOSTIC TESTS**

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Background Malaria and schistosomiasis are infections that have a great impact in sub-Saharan Africa based on their high morbidity and mortality rates. We suggest the possibility that the microenvironment created from interactions between the parasites involved generates a pressure on the malaria parasite which could in turn favour the parasite's adaptation or escape through *Pfhrp2* gene deletions. Thus, this study aimed at determining the association between the co-infection with both parasites and false-negative *PfHRP2*-based malaria rapid diagnostic tests which occur because of these deletions.

Methods This pilot study was conducted in a total of 149 children aged 7–17 years living in Yororo, located in the Mbam-Inoubou division of the Center region of Cameroon. We collected fresh stool samples from each participant to identify *Schistosoma mansoni* (Sm) eggs by Kato Katz method and blood samples to identify the ring stages of *Plasmodium falciparum* (Pf) by thick smear. Malaria rapid diagnostic test and *Pfhrp2* gene polymerase chain reaction were performed. The association between the co-infection with *Sm/Pf* and the false-negative malaria RDTs was determined by the Fisher's exact test. A p value <0.05 was considered statistically significant.

Results Our results showed that samples were singly infected with *Sm*, *Pf*, co-infected (*Sm/Pf*) and negative for both infections at frequencies of 12%, 43%, 30.2% and 14.8% respectively. False-negative *PfHRP2*-based RDTs were observed in 4.7% of the participants. A higher frequency (5/7) of the cases with false-negative malaria RDTs were co-infected with *Sm/Pf*. A p value of 0.027 showed statistical significance in the association of *Sm/Pf* co-infection and false-negative *PfHRP2*-based RDTs.

Conclusion A significant association of *Plasmodium falciparum* and *Schistosoma mansoni* co-infection with false-negative *PfHRP2*-based RDTs supports the case for a plausible implication of *Pfhrp2* gene deletions, with consequences for malaria rapid diagnostic testing.

PO 8275 **HEPATITIS B VIRUS IMMUNE ESCAPE MUTANTS AMONG APPARENTLY HEALTHY INHABITANTS IN IBADAN, SOUTHWESTERN NIGERIA**

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Background The documentation of circulation of immune escape mutants (IEMs) poses a risk on the continual success of HBV prevention and control. Therefore, this study aimed to determine the possible circulation of IEM among asymptomatic dwellers in southwestern Nigeria.