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 aims of this study was to monitor the prevalence of Pfdhfr-Pfdhps-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 Pfdhfr codons 51, 59, 108 and 164; Pfdhps 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 intervention). Genotyping of Pfcrt and Pfmdr1 post-intervention prevalence of the six-mutation quintuple +pfcrt +pfmdr1 was statistically significant in 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 (57%) 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.