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 *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 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* [*Pfdhfr-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* [*Pfdhfr-dhps* quintuple +*Pfmdr1*–86Y] and the seven-mutation *Pfcrt* +*Pfmdr1* [*Pfdhfr-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 *Pf*hrp2 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 Yorro, 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.

Methods Blood samples collected from consenting 133 males and 305 female participants in Ibadan were tested for HBsAg, HBeAg, HBcIgM, HBcTotal and HBsAb by ELISA technique. Samples positive for HBsAg were further analysed for HBV DNA by amplifying and sequencing the S gene. Isolates were genotyped and subtyped based on amino acid residues at position 122, 127, 134, 160 of the S gene.

Results Of the 438 subjects tested 31 (7.1%) were positive for HBsAg, 2 (6.5%) of which were HBeAg positive. Ninety-nine (22.8%) had detectable HBsAb, 3 (0.7%) were positive for HBcIgM and 195 (44.5%) were HBcTotal positive. HBV DNA was amplified and sequenced in 27 out of 31 and 4 could not be amplified due to low titres. After sequencing, 9 (33.3%) were not exploitable due to the presence of multiple peaks. Of the 18 exploitable isolates, only 15 showed significant similarity to HBV S-gene. Eleven of the 15 isolates were subtyped as ayw4 while others could not due to substitution at s122p. Phylogram showed that the 11 isolates were genotype E. Two of the 4 isolates with R122Q/P substitutions also belonged to genotype E while the other 2 which were >11% divergent from the reference genotype E sequence clustered with an isolate previously described as an Immune Escape Mutant.

Conclusion This study identified high endemicity of HBV infection, presence of markers of infection even in non-detectable HBsAg levels and circulation of genotype E ayw4 and vaccine mutants in south-western Nigeria. It therefore emphasises the risk of development of an indigenous infected population that may not be protected by the current vaccine.

PO 8276 COMMUNITY INDEX CASE APPROACH AND HIV TESTING AND COUNSELING (HTC) FOR SEXUAL PARTNERS OF HIV-POSITIVE PATIENTS LOST TO FOLLOW-UP: THE EXPERIENCE OF WORLD VISION MOZAMBIQUE

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Background HIV-positive patients lost to follow-up (HP-LTFU) represent a challenge for HIV/AIDS control efforts as they are associated with higher risk of HIV transmission to their sexual partners, low viral load suppression and higher risk of morbidity and mortality than adherent patients. The SCIP-Ogumaniha programme implemented by World Vision Mozambique, has been utilising the index case approach together with systematic home-based HIV testing and counseling (hHTC) since August 2016 in 7 districts of the Zambezia province. This abstract outlines an evaluation of the contribution of this approach to HIV/AIDS care and treatment (HACT) of sexual partners of HP-LTFU in alignment with the first and second targets of the 90–90–90 UNAIDS strategy.

Methods The study involved HP-LTFU returned to HACT between October 2016 and September 2017. These patients reported to have sexual partners who had not been tested for HIV and provided informed, written consent for joint hHTC with these individuals. The hHTC package for sexual partners was offered by World Vision project counselors and those who tested HIV-positive were referred to HACT.

Results Of 7.084 patients who returned to HACT and reported to have an untested sexual partner, 63% (4,471) provided informed, written consent for joint hHTC. Of 4264 sexual partners found and tested, 52% was female, 64% was in the 15–34 age groups, and 88% had never been tested for HIV. About 28% (1.205/4.264) was HIV-positive, 56% of the sexual partners who tested HIV-positive, was female and 98% of these was successfully referred to HACT.

Conclusion The index case approach together with hHTC has contributed to the early diagnosis of 28% of new HIV infections among sexual partners of HP-LTFU and 98% of them ensured timely linkage to the HACT. Therefore, broader promotion and adoption of this approach would make a significant contribution to achievement of the first and second targets of the 90–90–90 UNAIDS strategy.

PO 8278 BUILDING CAPACITY IN CONDUCTING CLINICAL RESEARCH IN A VIRTUAL SETTING: EXPERIENCES FROM THE EAST AFRICAN CONSORTIUM FOR CLINICAL RESEARCH (EACCR2)

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Background EACCR2 is an EDCTP-funded, Eastern African-led network established in May 2009, with 23 regional partners from Ehtiopia, Kenya, Sudan, Tanzania, and Uganda, and 8 northern partners from Germany, Netherlands, Norway, Sweden and United Kingdom. The objective is to strengthen capacity to conduct health research to international standards with specific focus on clinical trials on poverty-relevant diseases such as HIV, TB, malaria and neglected infectious diseases. EACCR2 optimises the use of shared research infrastructures and other regional capacity building resources and opportunities.

Activities The activities of the network are implemented in five work packages cutting across 'nodes' in different countries. Capacity building programmes and studies funded by EDCTP are implemented by coordinators at the disease nodes. The Uganda Virus Research Institute (UVRI) hosts the secretariat of the consortium of five nodes located in the following institutions: Malaria Node in Kilifi-Kenya Medical Research Institute Wellcome Trust, Tanzania; Training Node in Kilimanjaro Clinical Research Institute, Tanzania; Tuberculosis Node at the National Institute of Medical Research- Muhimbili, Tanzania; the Neglected and Re-Emerging Tropical Diseases Node at the University of Khartoum, Sudan; and the HIV Node at UVRI, Uganda.

Coordinators form the project implementation committee which meets via skype or teleconference every quarter to assess progress, share best practice and challenges of the network. Scientific and annual meetings are arranged every year in one of the implementing institutions. During such meetings, students, the nodes and steering committee also meet to minimise travel costs while helping teams to network.

EACCR2 learns from the experiences, best practice and challenges of EACCR1 while implementing its current activities. Careful planning and consensus building from all partners has been the driving force to build and implement activities of this virtual network. EACCR2 also works closely with other EDCTP Networks of Excellence, i.e. in Central