

diversity varies according to maternal, placental and umbilical cord blood. Age, gravidity and doses of preventive treatment based on sulfadoxine-pyrimethamine do not interfere with the multiplicity of infections.

PO 8254 LESSONS LEARNT FROM SCALING UP AN ONLINE SYSTEM FOR REVIEW AND MANAGEMENT OF PROTOCOLS IN SUB-SAHARAN AFRICA

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Background The transition from paper-based to online submission of health research protocols using the RHinnO Ethics (RE) platform has been shown to improve efficiency and quality of ethics reviews. However, despite these documented benefits, there are only a total of 40 installations in 12 out of the 54 countries in Africa. We analysed facilitators and barriers to adoption of RE by Research Ethics Committees.

Methods We used a retrospective analysis to identify determinants of adoption or rejection of RE by grouping feedback from users into key emerging themes identified through three stages of RE adoption: 1) contractual 2) trial 3) full implementation.

Results A total of 3947 protocols have been managed through RE by March 2018. Of those reached, 25 per cent adopted and continue to use RE. Of those that rejected, 14 per cent rejected after the trial. At the contractual stage, the key determinants of adoption were the guarantee of sustainable funding, pre-existing good IT infrastructure, and the assurance of technical assistance from the providers. The key determinants of rejection were concerns of cyber security, limited control and ownership by Research Ethics Committees and cost of the annual subscription. At the trial stage, the determinants of continued adoption and use were continued IT support from providers and a proven comparative advantage over the paper-based system. The key determinant of rejection was limited support from organisation leadership. Those who have continued through the implementation stage emphasised financial sustainability and continuous improvement of the RE as key determinants.

Conclusion Accelerated adoption of RE will require increased adaptability of the platform, decrease in cost of annual subscription, improved confidence in security and ownership of data. Developers, Research Ethics Committees and sponsors of RE need to develop a cost-effective funding strategy to increase efficiency, economies of scale and benefits related to harmonised and standardised digital platforms.

PO 8261 CYTOCHROME P450 (CYP2B6*6C.516G>T) VARIANTS IN CONGOLESE INDIVIDUALS WITH HIV AND TB MONO AND DUAL INFECTIONS

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Background The inter-individual genetic polymorphism of cytochrome P450 enzymes (CYP), involved in the metabolism of many drugs, partly modulates drug response and toxicity. Single nucleotide polymorphisms of CYP2B6 for example, G516T have been implicated in high- and sub-therapeutic plasma concentration of the current antimalarial, HIV and TB first-line drugs in various geographical regions and thus undermines effective disease management. At present, there is no data on the frequency of CYP2B6 c.516G>T among the Congolese population, despite a significant number of people undergoing antimalarial, HIV and TB treatment that relies on CYP2B6-based drug clearance or activation.

Methods A total of 418 patients with HIV-1 mono-infection, HIV-1 +TB coinfection and *P. falciparum* infection were genotyped for CYP2B6 c.516G>T polymorphism using PCR-RFLP. The frequencies of the alleles as well as the genotypes (GG, GT and TT) were determined.

Results The frequency of CYP2B6 c.516G>T polymorphism was 69% and frequency of G and T alleles were 45% and 55%, respectively. 17.0% (49/288) of participants were GG (extensive metaboliser), 55.2% (159/288) of participants were GT (intermediate metaboliser) and 27.8% (80/288) of participants were TT (poor metabolisers).

Conclusion This study highlights CYP2B6 c.G516T polymorphism as a potential determinant of drug response and toxicity among the Congolese population, particularly those undergoing antiretroviral, malaria and tuberculosis treatment within the current first-line drug policy framework.

PO 8264 QUALITY CARE CRITERIA IN A CLINICAL TRIAL CONTEXT: PATIENT AND DAFRA AND NANORO CMA HEALTH WORKER PERCEPTIONS IN BURKINA FASO

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Background Participants in clinical trials as well as researchers conducting them, establish a close link between clinical trial and quality care. However, what understanding do they have of the concept of quality of care? This study aimed to answer this question by presenting the criteria which define for them quality care in the context of clinical research.

Methods The data were collected from the participants involved in these clinical trials as well as from the health workers (research teams and other health workers) using a qualitative approach with 70 in-depth interviews. Direct observations of the participants partaking in care activities were also made in both health districts. The data were recorded, transcribed and then analysed on the thematic content basis.

Results For the health workers interviewed, the clinical trials are conducted in optimal conditions which highly contribute to ensure a good quality of care. To them, quality of care in the process of the trial implementation is evident from some availability of qualified human resources, quality medico-technical equipment, as well as good clinical practice strictly adhered to by the researchers.

As for the participants, the quality of care in clinical trials meets specific criteria. To them, quality care delivered by the research team became tangible through laboratory tests before any treatment proposal, the promptness in taking care of any

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 +*pf*cert +*pf*mdr1 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, *Pf*cert codon 76 and *Pf*mdr1 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 *Pf*cert [*Pf*dhfr-dhps quintuple +*Pf*cert-76T] genotype increased significantly after SMC implementation, from 0.0% to 7.1% ($p=0.0008$). The post-intervention prevalence of the six-mutation *Pf*mdr1 [*Pf*dhfr-dhps quintuple +*Pf*mdr1-86Y] and the seven-mutation *Pf*cert +*Pf*mdr1 [*Pf*dhfr-dhps quintuple +*Pf*mdr1-86Y+*Pf*cert-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 *Pf*cert genotype of *P. falciparum* that can lead to resistance in a population exposed to SMC with SP+AQ.

PO 8271 PFCRT 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 *Pf*HRP2-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 *Pf*hrp2 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 *Pf*HRP2-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 *Pf*HRP2-based RDTs.

Conclusion A significant association of *Plasmodium falciparum* and *Schistosoma mansoni* co-infection with false-negative *Pf*HRP2-based RDTs supports the case for a plausible implication of *Pf*hrp2 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.