Conclusion We showed that repeated artesunate-amodiaquine administration inside a 35-day post-treatment frame leads to DEAQ accumulation, the effect being significantly higher in patients carrying the reduced function allele CYP2C8*2, suggesting an increased risk of overexposure and amodiaquine toxicity.

PA-595 HEPATOTOXICITY ASSOCIATED TO N-ACETYLTRANSFERASE TYPE 2 POLYMORPHISMS IN TB PATIENTS WITH MALARIA AT JAMOT HOSPITAL, YAOUNDÉ, CAMEROON

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Background Unlike in developed countries, most infectious diseases such as tuberculosis (TB) and malaria continue to cause deaths in low-income countries. Recent studies have shown that hepatotoxicity during TB treatment may be related to the Arylamine N-Acetyltransferase (NAT2) acetylator polymorphism especially in countries with high TB incidence such as Cameroon. The aim of this study was to determine the NAT2 genetic variation associated with hepatotoxicity in TB/Malaria co-infected patients in Jamot Hospital, Yaoundé-Cameroon.
Methods This was a prospective study from April 2018 - March 2019, aiming to evaluate the genetic variation in NAT2 coding region in TB patients with malaria. A total of 336 pulmonary TB patients with or without malaria infection, aged 15 years and above, were included. Each sputum sample was tested by the Ziehl Neelsen method. Whole blood sample was used for malaria detection using Rapid Diagnostic Test and microscopy. DNA was extracted by chelex method, hepatotoxicity by spectrophotometry, and genotyping done by Polymerase chain reaction followed by restriction fragment length polymorphism analyses with enzymes (KpnI, TaqI, BamHI).
Results Alanine aminotransferase (ALT) and Aspartate aminotransferase (AST) values were significantly higher among TB/malaria co-infected cases compared to TB mono infected patients (p=0.03, p=0.01 respectively). In the group of mono-infected TB patients, a significant difference was found for ALT values between day 1 and day 90 (p=0.021). Similarly, a significant association was found between the development of hepatotoxicity and the presence of a slow acetylator phenotype in TB-malaria co-infected (p=0.026).
Conclusion The study suggests that TB/malaria co-infections and NAT2 variant phenotype are risk factors for hepatoxicity induction. Therefore, for a more efficient care, evaluation of NAT2 genotypes might be essential to reduce drug interactions and liver toxicity in case of coinfections.

PA-597 EXPERIENCES AND LESSONS LEARNT IN THE 13 YEARS OF THE EDCTP FUNDED EACCR RECIPROCAL MONITORING SCHEME

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Background In April 2010, East African Consortium for Clinical Research (EACCR) in partnership with the University of Oxford initiated the Reciprocal Monitoring Scheme (RMS). This is an innovative, practical and affordable monitoring scheme whose main aim is strategic quality management of health research for the 23 institutions that form the consortium. The main role of the RMS is to oversee the progress of clinical trials while ensuring that they are conducted, recorded, reported in accordance with approved Protocols, Standard Operating Procedures (SOPs), applicable local and international regulatory requirements and Good Clinical Practice. We share our experiences and lessons learnt in the past 13 years.
Methods Each institution identified one or two experienced monitors who were paired with unexperienced monitors for mentorship and capacity building. Cross-country pairing was done and monitors were allocated studies to monitor. Physical training was periodically done to refresh skills and brainstorm on experiences.
Results A regional pool of 42 monitors were trained and paired from 6 Eastern Africa countries and 5 Northern countries. Seven sponsors have been supported to monitor thirty three (33) studies so far. The scheme offered an opportunity for cross-site sharing of best practices and networking at a cheaper cost compared to using conventional clinical research associates. Dedicating time for monitoring activities remains a big challenge for the study team and monitors.
Conclusion Paired monitoring fostered capacity building and maximized sharing of best practices for quality management of internationally recognized health research. Cross-country monitoring visits promoted networking and dialogue between researchers, communities and other stakeholders.

PA-604 WHOLE GENOME SEQUENCING CONFIRMED CONTAMINATION OF MYCOBACTERIUM ULCERANS-INFECTED LESIONS BY RHODOCOCCUS ERYTHROPOLIS

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Background We describe two contamination cases of Mycobacterium ulcerans clinically infected lesions by Rhodococcus erythropolis, a bacterium of environmental origin with rare cases of human infection.
Methods Two lesion swabs collected from clinically characterized Buruli ulcer-like patients were submitted to molecular (IS2404-PCR) and biological (OA-decontamination + microscopy + culture) analyses for detection and in-vitro culture of Mycobacterium ulcerans (Buruli ulcer etiological agent) respectively.