positive for *S. haematobium*, and a total of 132 (51%) children developed 230 malaria attacks. Those with schistosomiasis had a 1.5:1 [1.1–2.0] risk to develop malaria compared to their uninfected counterparts. The mean number of malaria episodes per child over the study course was higher among children with schistosomiasis compared to those without (2.03 vs 1.57, p -value=0.015).

Conclusion *S. haematobium* infection was associated with increased susceptibility to develop malaria (by increasing the risk to develop a malaria episode) and, consequently, a higher malaria incidence.

PO 8458 POLYMORPHISM OF THE *PLASMODIUM FALCIPARUM* MSP-2 GENE ASSOCIATED WITH PLACENTAL MALARIA AT THE BORGOU-ALIBORI DEPARTMENTAL HOSPITAL

Dossou Akpéyédjé*, Saadou Issifou. *Fondation pour la Recherche Scientifique, Cotonou, Benin*

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Background In sub-Saharan Africa, malaria during pregnancy is a major health problem because it poses significant risks for the pregnant woman and the foetus. The sequestration of *Plasmodium falciparum*-infected erythrocytes in the placenta has consequences for the mother and the foetus. This study aimed to evaluate the allelic polymorphism of the *Plasmodium falciparum* MSP-2 gene related to the consequences of placental malaria.

Methods It was a cross-sectional study conducted over two periods lasting six months in 2016 and 2017. The maternity center of the Hospital of Borgou-Alibori in Benin served as a framework for the study. From the 98 parturients included, placental blood samples were taken and then genotyped.

Results Using the MSP-2 gene as marker, the prevalence was 17, 34%. The MSP-2 gene was polymorphic with 9 distinct allelic types for both 3D7 and FC27 families (150 bp; 200 bp; 250 bp; 275 bp; 300 bp; 350 bp; 400 bp; 450 bp and 500 bp). The FC27 allelic family was predominant over the 3D7 family with 56, 25% and 43, 75% respectively. The 300 bp allelic type (50%) was predominant in the FC27 family while the 400 bp type was predominant in 3D7 family (35, 71%). 9 women had polyclonality (52,94%). The multiplicity of infection (MOI) was 1, 88. The number of strains ranged 1 to 4 in infected women. In univariate analysis there was no significant relationship between MSP-2 gene polymorphism and maternofoetal consequences. The absence of prenatal consultation ($p=0.0270$), non-taking of IPTp/SP ($p=0.0060$), the occurrence of malaria in the third trimester ($p=0.0364$) and moderate maternal anaemia ($p=0.0277$) were associated with the polymorphism of MSP-2 gene. The MOI was significantly associated with parasite density of infected women.

Conclusion *Plasmodium falciparum* MSP-2 gene was polymorphic in infected women at Parakou. Several factors related to pregnancy monitoring were associated with this genetic diversity. It is therefore essential to ensure correct follow-up of pregnancies.

PO 8460 PANDORA-ID NET (PAN-AFRICAN NETWORK FOR RAPID RESEARCH, RESPONSE, RELIEF AND PREPAREDNESS FOR INFECTIOUS DISEASES EPIDEMICS)

¹Francine Ntoumi*, ²Francine Zumla, ³Giuseppe Ippolito, ³Francesco Vairo. ¹Fondation Congolaise pour la Recherche Médicale, Brazzaville, Republic of the Congo; ²University College of London, London, UK; ³National Institute for Infectious Diseases Lazzaro Spallanzani, Rome, Italy

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Background New and re-emerging infectious disease outbreaks continue to cause much human suffering and loss of life worldwide. Since Africa has experienced repeated outbreaks of zoonotic infections, an important need exists to improve local and regional capacities to identify and respond to zoonotic outbreaks. PANDORA ID-NET is an EDCTP-supported 'ONE Human and Animal HEALTH' multidisciplinary consortium of 24 partner institutions (15 African and 9 European) in 9 African and 4 European countries.

Methods Our overall aim is to strengthen regional and pan-African capacities and systems for enabling a rapid and effective response to infectious diseases with epidemic potential, arising from within Africa or imported from overseas. We aim to build laboratory and public health capabilities for rapid detection and surveillance of pathogens from human and animal sources. This will include obtaining accelerated evidence for optimal clinical management of patients, infection control measures, and public health response during outbreaks. Capacities will be built: a) for performing multisite clinical trials (evaluating rapid diagnostics, biomarkers, a range of treatments, vaccines and operational research studies) and, b) for timely collection, analysis and communication of information.

Conclusion Our activities will be aligned to EDCTP regional Networks of Excellence, Africa CDC and other relevant global and regional initiatives, thus maximizing complementarity and achieving a multiplier effect, facilitating rapid policy implementation of outputs.

PO 8467 IMPACT OF COMMUNITY CASE MANAGEMENT OF MALARIA (CCMM) AMONG CHILDREN UNDER FIVE YEARS OLD: AN EVALUATIVE STUDY IN KABONGA

¹Ciza Bonne*, ²Kagozi Hussen, ³Ciza Josephine Muhigirwa. ¹Health Healing Network Burundi, Bujumbura, Burundi; ²Solidarity of nurses for promotion of maternal and children's health, Burundi; ³Palliative care association of Burundi, Bujumbura, Burundi

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Background In Burundi, malaria is considered a major public health concern and the leading cause of death. Malaria is responsible for up to 25% of all outpatient visits and up to 48% of all deaths in health facilities among children under five years old. Despite efforts made, timely access to health care is still limited, mainly due to geographic inaccessibility and lack of awareness about malaria complications. To increase timely access to malaria treatment, Burundi's Ministry of Health implemented Community Case Management of Malaria (CCMM) since 2015 in Kabonga. We sought to assess the impact of CCMM in improving malaria outcomes following two years of its initiation.

Methods Selected community health workers (CHWs) were initially trained for simple malaria management among children under five years old using artemisinin-based combination therapy (ACT) and to perform rapid diagnostic tests for malaria (RDTs), and then equipped to provide service. This was a retrospective and prospective study using a mixed-methods approach between September–October 2017. Data before CCMM initiation (2013–2014) were collected from the Kabonga health centre, then compared to data from 2015–2016 corresponding to CCMM implementation. Data were from health records and stakeholders and were processed using SPSS.

Results In total, 5922 children were treated for malaria between 2013–2014 and 5249 between 2015–2016, an 11.3% case decrease. CHWs managed in total 1751 children using ACTs between 2015–2016. Of them, 1297 (74%) had a consult within 24 hours of fever onset and the cure rate was approximately 90%. Mortality decreased with up to 75%. Ownership level was encouraging among beneficiary communities and was low among district and health center's staff. Some stock-outs were also reported.

Conclusion Using trained CHWs increased access to timely and appropriate treatment in sampled communities which was associated with improved health outcomes among children under 5 years old. However, regular supply to CHWs and strong ownership is needed.

PO 8468 DETERMINE TB–LAM LATERAL FLOW ASSAY: DOES *M. TUBERCULOSIS* LINEAGE INFLUENCE ITS PERFORMANCE?

¹Willy Ssengooba*, ²Lydia Nakiyingi, ¹Joloba Moses. ¹Department of Medical Microbiology, College of Health Sciences Makerere University Kampala, Uganda; ²Infectious Diseases Institute, College of Health Sciences Makerere University, Kampala, Uganda

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Background Among HIV-positive individuals with CD4 ≤ 100 cells/mm³, *M. tuberculosis* (Mtb) bacteraemia is associated with a positive tuberculosis urine lipoarabinomannan (LAM) test. We conducted a retrospective study, to determine the effect of Mtb lineage on the performance of the Determine TB LAM lateral flow (LF-LAM) assay.

Methods This was nested in a prospective TB diagnostics accuracy study among HIV-positive presumptive TB patients from Mulago National Referral Hospital, Kampala, Uganda, including both inpatients and outpatients. We considered data of 51 HIV-positive individuals with both pulmonary and Mtb bacteraemia. We also evaluated the effect of having mixed Mtb strains using both spoligotyping and MIRU-VNTR 24 loci methods.

Results LF-LAM was; negative among 4 (7.8%; 95% CI, 2.17% to 18.8%), positive among 39 (76.5%; 95% CI, 62.5% to 87.2%) and indeterminate among 8 (15.7%; 95% CI, 7.0% to 28.5%) participants. Mtb lineages from blood samples were: Central Asian Strain (CAS; L3) 10/51 (19.6%) and Euro-American lineage (L4) 41/51 (80.4%). Mtb lineages from sputum samples were 7/51 (13.7%) L3 and 44/51 (86.3%) were L4. Among participants with L3 in blood, LFLAM was positive in 9 (90%; 95% CI, 55.4%–99.7%) whereas those with L4, LF-LAM was positive among 30 (73.2% 95% CI, 57.0% to 85.7%). For those with L3 in sputum, LF-LAM was positive among 7 (100%) and those with L4 was 32 (72.7%;

95% CI 57.2% to 85.0%). Two participants had mixed Mtb strains (all L4) and all LF-LAM positive (2+ and 4+).

Conclusion Our study shows that *M. tuberculosis* lineage 3 may have more sensitivity to LF-LAM assay than lineage 4. The high number of indeterminate results with L4 requires more investigations. Our findings suggest that LF-LAM performance may differ by geographical regions depending on the dominant *M. tuberculosis* lineage.

PO 8470 FIRST INDEPENDENT ASSESSMENT OF PHARMACEUTICAL COMPANY ACTION ON AMR

Jacqueline Kisakyie, Josefien Knoeff, Adrian Ruiz, Dulce Calçada, Jayasree Iyer, J Gabrielle Bruegelmans. Access to Medicine Foundation, Amsterdam, The Netherlands

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Background Antimicrobial resistance (AMR) is one of the most significant threats to public health globally. It will worsen without concerted efforts to spur the development of new antibiotics and ensure access and stewardship of existing ones. Pharmaceutical companies have a critical role to play in these efforts. The Access to Medicine Foundation developed the AMR Benchmark to measure how pharmaceutical companies are responding to AMR and to share and push best practices within the industry.

Methods The AMR Benchmark assessed the AMR activities of 30 pharmaceutical companies in 106 low- and middle-income countries. Survey data on company activities were collected across three research areas: research and development (R&D); manufacturing and production; and access and stewardship. For each research area, specific metrics were developed to evaluate company performance. These metrics were defined through consultation with experts working across the AMR field and represent a broad consensus on where companies can and should be taking action to limit AMR.

Results The Benchmark found that there are good practices in all research areas. Out of 276 R&D projects targeting infectious diseases, 175 target pathogens identified as priority by WHO/CDC. Of these, 88 are in preclinical stage, 87 are in clinical stage, and 54 target gram-negative bacteria. Out of 28 antibiotics in late clinical stage, only two have access and stewardship plans in place. Nearly half of companies evaluated are involved in AMR surveillance and eight companies set limits on antibiotic wastewater discharge. Lastly, four companies separate sales agent bonuses from antibiotics sales volumes to reduce overuse of antibiotics.

Conclusion The Benchmark identified the good ideas being implemented by companies to limit AMR and mapped opportunities to amplify current efforts. Although companies are taking some action, the R&D pipeline needs to be further strengthened and candidates reaching late clinical stage must be supported by concrete plans to ensure access and stewardship.

PO 8471 A SURVEY OF CURRENT CLINICAL DATA MANAGEMENT PRACTICES IN SUB-SAHARAN AFRICA

¹Hanne Landuyt*, ¹Harry Van Loen, ²Bai L Dondeh, ²Badou M Gaye, ¹Yven Van Herreweghe. ¹Institute of Tropical Medicine, Antwerp, Belgium; ²Medical Research Council Unit The Gambia at the London School of Hygiene and Tropical Medicine, London, UK

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