Results Out of 284 participants data for 245 were analysed (Group 1: 27; Group 2: 107; Group 3: 111). Majority were aged 25–29 years and over 60% had primary/lesser education. There were 39 (Group 1: 5; Group 2: 16; Group 3: 18) VFs with a total VF incidence of 8.12 [95% CI (5.96, 11.17)] per 1000 Person months of observation (PMOs). Group 2 had the lowest VF incidence. Baseline CD4 <349 cells/mm$^3$ and initiation/use of TDF/3TC/EFV were associated with virologic failure (VF).

Conclusion Women at risk of VF based on the identified risk factors should be identified and targeted with appropriate intervention. Further studies are needed to verify and understand the mechanisms of association between VF and TDF/3TC/EFV which is a WHO-recommended first-line ART regimen.

ENHANCING LABORATORY DIAGNOSIS OF MYCOBACTERIUM TUBERCULOSIS IN SAMPLES FROM CHILDREN IN THE GAMBIA

PO 8596

1Abigail Ayorinde*, 1Edward G Coker, 1Alieu Mendy, 1Fatoumatta Cole, 1Abdou K Sillah, 1Francis S Mendy, 1Uchendu A Egere, 1Beate Kampmann, 1Ucpop D Tientcheu.
1Medical Research Council Unit The Gambia at London School of Hygiene and Tropical Medicine, The Gambia; 2Imperial College, London, UK; 3Department of Biochemistry, Faculty of Science University of Yaoundé I, Yaoundé, Cameroon

Background Routine laboratory diagnostic methods for M. Tuberculosis complex (MTBC) in induced sputum samples such as smear microscopy, GeneXpert and liquid Mycobacteria growth indicator tube (MGIT) culture are often negative due to the paucibacillary nature of childhood tuberculosis. We hypothesise that prolonged incubation beyond routine culture time could potentially improve MTBC detection in specimens.

Methods Out of over 1000 induced sputum samples collected during our childhood TB contact tracing research programme, we randomly selected 102 MTBC-negative MGIT cultures that had either been reported as contaminated (n=35) or negative (n=67) and further incubated these at 37°C for the duration of one month. Ziehl-Neelsen microscopy, MPT64 Antigen secretion and GeneXpert tests were repeated on all samples to detect MTBC. Bacterial DNA was extracted by CTAB method and genotyped using spoligotyping analysis.

Results Of the 1160 routinely collected induced-sputum samples 12 (1%) were smear-positives; 41 (3.5%) Xpert-positives and genotyped using spoligotyping analysis. Out of over 1000 induced sputum samples collected during our childhood TB contact tracing research programme, we randomly selected 102 MTBC-negative MGIT cultures that had either been reported as contaminated (n=35) or negative (n=67) and further incubated these at 37°C for the duration of one month. Ziehl-Neelsen microscopy, MPT64 Antigen secretion and GeneXpert tests were repeated on all samples to detect MTBC. Bacterial DNA was extracted by CTAB method and genotyped using spoligotyping analysis. Out of 1160 routinely collected induced-sputum samples 12 (1%) were smear-positives; 41 (3.5%) Xpert-positives and Genotyped using spoligotyping analysis. Out of 1160 routinely collected induced-sputum samples 12 (1%) were smear-positives; 41 (3.5%) Xpert-positives and Genotyped using spoligotyping analysis.

Conclusion In summary, these polypeptides could be useful in vaccine design once they are very antigenic and we observed a heterologous neutralising antibody response in naive patients that expressed positive antibody-response anti-peptides.

DETECTION OF PLASMODIUM FALCIPARUM HISTIDINE-RICH PROTEIN 2/3(PFHRP-2/PFHRP-3) GENES DELETION AND AMINO ACID NUCLEOTIDE SEQUENCE VARIABILITY IN NIGERIA

PO 8607

1Roland Funwei*, 1Catheine O Falade, 1Oluosia Ojurongbe. 1Department of Pharmacology and Therapeutics, University of Ibadan, Nigeria; 2Department of Pharmacy Technician Studies, Bayelsa State College of Health Technology, Nigeria; 3Department of Medical Microbiology and Parasitology, Ladoke Akintola University of Technology, Osogbo, Nigeria

Background Prompt diagnosis and appropriate treatment remain the hallmark needed to reduce malaria-related mortality in areas of high transmission. Rapid diagnostic tests (RDTs) that target the Pfhrp-2 gene, are essential in resource-limited settings where microscopy is not available. However,
Pfhrp-2 gene deletion is implicated in limiting RDT sensitivity. Studies evaluating Pfhrp-2 and Pfhrp-3 deletion and the amino acid sequence diversity has not been investigated in Nigeria. We therefore hypothesised that malaria parasites in Nigeria are lacking Pfhrp-2/Pfhrp-3 genes with variable amino acid repeats sequences.

**Methods**
The study was part of a prospective cohort study evaluating RDTs performance. We pooled 66 samples comprising false negatives (n=31) and true positives (n=35) to elucidate Pfhrp-2/Pfhrp-3 gene deletion, RDT cross-reactivity with Pfhrp-3 antigen and amino acid sequence diversity. The 18S rRNA, msp 1, msp2 and glurp genes were amplified to establish active *Plasmodium falciparum* infection and the exon-2 regions of Pfhrp-2 and Pfhrp-3 genes were amplified to determine the presence or absence of Pfhrp-2 and Pfhrp-3 genes. Isolates with conserved Pfhrp-2/Pfhrp-3 were sequenced.

**Results**
All 66 samples were positive for 18S rRNA, msp1, msp2 and glurp, indicating active *P. falciparum* infection. However, 16.7% and 6.0% of the samples were lacking Pfhrp-2 and Pfhrp-3 genes. Of the false negative samples, 25.8% and 12.9% has Pfhrp-2 and Pfhrp-3 deletions. Three Pfhrp-3 conserved antigens cross reacted to give RDT positive results. An extensive diversity in the amino acid sequence was observed.

**Conclusion**
*Plasmodium falciparum* parasites in Nigeria lack Pfhrp-2 and Pfhrp-3 genes. However, the proportion of deletions is low compared to reports from other malaria-endemic regions. In addition, a high amino acid tandem repeat was observed. A combination of pLDH and Pfhrp-2 based RDTs is recommended for accurate malaria diagnosis.

**PO 8608** ESTABLISHED PARTNERSHIPS OF THE UNIVERSITY OF CAPE VERDE WITH THE UNIVERSITY OF LEICESTER, UK AND THE INSTITUTE OF HYGIENE AND TROPICAL MEDICINE, PORTUGAL

1Isabel I Araújo\*\*, 2Sandra Beloaz, 3Maria Do Rosário Martins, 4Faculdade de Ciências e Tecnologia, Universidade de Cabo Verde, Cape Verde; 5Department of Genetics and Genome Biology, University of Leicester, UK; 6Instituto de Higiene e Medicina Tropical, Universidade Nova de Lisboa, Portugal

10.1136/bmjgh-2019-EDC.163

**Background**
The University of Cape Verde (Uni-CV) was founded in 2006 and since then has developed an effective international strategy that is enhancing the teaching and research culture of the university. To build capacity in the public health field, Uni-CV has established collaborations with the University of Leicester (UoL), UK, and with the Institute of Hygiene and Tropical Medicine (IHTM – NOVA University), Portugal. These follow different approaches.

**Methods**
Different type of capacity building initiatives focused on researchers and postgraduate students.

**Results**
The collaboration with UoL was established in 2016 and builds on funded research programmes in infectious disease and evolution of antimicrobial drug resistance (AMR). These programmes have allowed technology development and transfer, which offer the opportunity for undergraduate students to lead laboratory–based research projects at Uni-CV. In these two years, we have successfully characterised the epidemiology and patterns of AMR underlying *Helicobacter pylori* infections in Cape Verde. Beyond the research outputs, we have trained four undergraduates in laboratory-based microbiology at Uni-CV. From this experience, we are currently designing new sustainable higher education programmes aligned with the MSc in Public health at Uni-CV that aim to support Uni-CV lecturers in the supervision of postgraduate students, either independently or in collaboration with UoL researchers.

The collaboration with IHTM was established in 2008 with the main aim of developing the research capacity of Cape Verde researchers and health professionals in infection and vector-born diseases and in bioethics. These activities have also led to collaborative research in these areas. Since then, six training courses were taught that benefited ~20 Uni-CV lecturers and ~100 government professionals.

**Conclusion**
Although these collaborative approaches are different in nature, they have been successful in the training of health professionals, researchers and technicians in Cape Verde and have contributed to the establishment of mutually beneficial research programmes.

**PO 8609** PREVALENCE AND RISK FACTORS FOR GLUCOSE-6-PHOSPHATE DEHYDROGENASE (G6PD) DEFICIENCY IN TWO P. VIVAX MALARIA-ENDEMIC AREAS IN SUDAN

Muzamil Mahdi Abdel Hamid\*1, Musab Albsheer1, Mohamed Muneer1, Lina Altinae1, Andrew A Lover2. 1Institute of Endemic Diseases, University of Khartoum, Sudan; 2Institute for Global Health Sciences, University of California, San Francisco, United States of America

10.1136/bmjgh-2019-EDC.164

**Background**
*Plasmodium vivax* malaria is a major health problem in Sudan and the parasite has become widely distributed in the recent years. The WHO recommends the use of primaquine as radical cure for liver dormant stage, the hypnozoite. However, prior its use, a test for Glucose-6-phosphate Dehydrogenase (G6PD) should be performed. The objective of the current study was to determine prevalence and risk factors for G6PD deficiency in two *P. vivax* malaria-endemic areas in Sudan.

**Methods**
A cross-sectional study recruiting 557 subjects from two malaria-endemic areas in Sudan was conducted. Demographic data and blood samples were collected. G6PD activity was measured by spectrometry using SPINREACT enzymatic UV kit.

**Results**
The measured G6PD activities for both sites ranged from 0.6 to 37.7 U/g Hb, with a median value of 12.8 U/g Hb. There was a significant difference in enzyme activity by study site (p<0.001), but not by sex (p=0.91). Overall, across the two study sites, 22 (3.9%) is G6PDd (<30%). Prevalence of G6PDd (<30%) in Khartoum is 1.8% (4/230) compared to 4.8% (16/327) in New Hafla. In univariate analysis predictors of G6PDd were study site (odds ratio of G6PD activity <3.8, Khartoum relative to New Hafla=0.22 (95% CI: 0.08 to 0.66), p=0.006), and recent antibiotic use (OR=2.45 (95% CI: 1.1 to 5.5), p=0.027). In multivariate analysis, the only factor that was significant was the individual’s weight in kilograms, with an OR of 0.97 (95% CI 0.95 to 0.99, p=0.014).

**Conclusion**
G6PD deficiency is less prevalent among Sudanese population and this indicates that the use of primaquine for radical cure of *P. vivax* malaria is safe.