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.

PO 8596 ENHANCING LABORATORY DIAGNOSIS OF *MYCOBACTERIUM TUBERCULOSIS* IN SAMPLES FROM CHILDREN IN THE GAMBIA

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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 51 (4.4%) MGIT culture MTBC-positives. The remaining MGIT cultures were flagged as contaminated 393 (33.9%) or MTBC-negative 644 (55.5%). After prolonged incubation and retesting of the randomly selected ones, 26/102 (25.5%) were now microscopy-positive, 2/55 (3.63%) were GeneXpert-positive, 8/102 (7.8%) MPT64-Antigen-positive, and 38/102 (37.2%) had readable spoligotyping patterns. The predominant lineages were Mtb-Euro-American 16 (42.1%), Mtb-Indo-Oceanic 11 (28.9%) and *M. africanum* West African type-2 8 (21%).

Conclusion Prolonged incubation of routinely MTBC-negative induced-sputum cultures yielded positive results upon retest, highlighting the low sensitivity of routine diagnosis tools on pauci-bacillary paediatric samples. Spoligotyping was more sensitive to detect MTBC compared to GeneXpert. However, prolonged incubation will cause diagnostic delays and thus better strategies are needed to improve timely childhood TB diagnosis.

PO 8597 NEUTRALISING AND NON-NEUTRALISING ANTIBODIES RESPONSE IN HIV-1-INFECTED INDIVIDUALS FROM MOZAMBIQUE

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Background A vaccine that protects against the different HIV subtypes circulating around the world is essential to control and eliminate HIV infection. The immunogens are the key to develop an effective HIV vaccine. In this study, we characterised the antibody response against recombinant C2V3C3 polypeptides from several HIV-1 subtypes and evaluated the neutralising antibody response.

Methods Plasmas from HIV-1-infected individuals under treatment (n=39) and drugs-naïve individuals (n=8) were tested in an ELISA assay to determine the presence of antibodies against polypeptides from HIV-1 subtypes (CRF02_AG, B, C, G and H). The neutralising activity of plasma was evaluated with a panel of six HIV-1 viruses from a reference panel, [one tier 1 (NL4.3), and five tier 2 (PCH119_CRF07, PCE1176_C, TRO11_B, 246 F3_AC and CRF07_BJOX2000)] in a TZM-bl cells-based assay.

Results Out of 48 plasmas, 44 (89.6%) reacted at least with one polypeptide and four (10.4%) did not react with any polypeptide. Interestingly, 56% of the plasmas recognise ≥3 peptides and 6 reacted with all polypeptides. The polypeptide from virus CRF02_AG was the most antigenic (77%) followed by the polypeptide C (58.3%), G (58.3%), H (50%) and B (35.4%). There was a positive correlation between polypeptides number recognised and binding antibody reactivity (r=0.4895, p=0.0111). All plasmas from drugs-naïve individuals neutralised at least one virus with neutralising activity between 39.3% and 95.7%. Four plasmas showed neutralising activity >50% against five viruses. The virus 249 F3 was the easiest to neutralise (median, 65.7%), whereas PCH119_CRF07 was the most difficult to neutralise (median, 43.6%). Neutralising activity of plasmas from patients under treatment are ongoing.

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 naïve patients that expressed positive antibody-response anti-peptides.

PO 8607 DETECTION OF *PLASMODIUM FALCIPARUM* HISTIDINE-RICH PROTEIN 2/3(PFHRP-2/PFHRP-3) GENES DELETION AND AMINO ACID NUCLEOTIDE SEQUENCE VARIABILITY IN NIGERIA

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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 18SrRNA, 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 18SrRNA, 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

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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

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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 Halfa=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.