

**PA-151** PEP4LEP CASE DETECTION DELAY RELIABILITY OR MEASUREMENT CONSISTENCY TESTING IN MOZAMBIQUE, ETHIOPIA, AND TANZANIA – PRELIMINARY RESULTS

<sup>1,2</sup>Ephrem Gebrehiwot\*, <sup>3</sup>Thomas Hambridge, <sup>4</sup>Anne Schoenmakers, <sup>1</sup>Kidist Bobosha, <sup>2</sup>Mengjistu Legesse, <sup>3</sup>Christa van Wijk, <sup>3</sup>Janhendrick Richardus, <sup>6</sup>Kitesa Debelo, <sup>6</sup>Fufa Daba, <sup>7</sup>Nelly Mwangeni, <sup>8</sup>Abdoulaye Marega, <sup>4</sup>Liesbeth Mieras, <sup>9</sup>Taye Letta, <sup>10</sup>Yuki Stakteas, <sup>11</sup>Blasus Njako, <sup>7</sup>Stephen E Mshana. <sup>1</sup>Armauer Hansen Research Institute, Ethiopia; <sup>2</sup>Aklilu Lemma Institute of Pathobiology (ALIPB), Ethiopia; <sup>3</sup>Department of Public Health, Erasmus MC, University Medical Center, The Netherlands; <sup>4</sup>Medical Technical Department, NLR, The Netherlands; <sup>5</sup>Deutsche Lepra- und Tuberkulosehilfe, Germany; <sup>6</sup>Deutsche Lepra- und Tuberkulosehilfe Ethiopia, Ethiopia; <sup>7</sup>Department of Microbiology and Immunology, Catholic University of Health and Allied Sciences, United Republic of Tanzania; <sup>8</sup>Lúrio University, Mozambique; <sup>9</sup>Ministry of Health Ethiopia, Ethiopia; <sup>10</sup>NLR Mozambique, Mozambique; <sup>11</sup>Deutsche Lepra- und Tuberkulosehilfe e.V. Tanzania, United Republic of Tanzania

10.1136/bmjgh-2023-EDC.104

**Background** Detection delay is defined as the period between onset of first signs and symptoms of leprosy and the time of diagnosis, comprising of a ‘patient delay’ and a ‘health-system delay’ and reliability refers to the consistency of a measure. Three types of consistency are considered: over time (test-retest reliability), across items (internal consistency), and across different researchers (interrater reliability). For the case detection delay (CDD) two are applicable: test-retest reliability and interrater reliability.

**Methods** The study was conducted in Ethiopia, Mozambique and Tanzania. The CDD questionnaire was administered to 79 leprosy patients. One month later, another researcher re-administered the CDD questionnaire with these same patients. Interrater reliability was assessed using the intra class correlation coefficient (ICC). The test-retest reliability was assessed among 69 leprosy patients by determining the CDD at one month difference, both times using the same rater, and then we determined the reliability by looking at the Pearson correlation between the two sets of CDD data.

**Results** Results from 79 leprosy patients show that, 3 (3.8%) were children under 15 years of age and 25 (31.6%) were women. Interrater reliability: the first interviews led to a mean CDD of 24.0 months (95% CI =17.1 - 30.9). The second interviews, also led to a mean CDD of 24.0 months (95% CI =17.7 - 30.3). For the test-retest reliability, the mean CDD of the first and second interviews were 16.5 (95% CI =13.6 - 19.5) and 16.9 (95% CI =13.8 - 20.1) respectively: the interrater reliability measured with ICC was 0.89 (95% CI of 0.84 - 0.93). Test-retest repeatability coefficient was 0.90 (p = 0.01).

**Conclusion** The PEP4LEP CDD tool to determine the case detection delay of newly diagnosed leprosy patients, was validated in the three African countries showing that both test-retest and interrater reliability measurements demonstrated good reliability of the instrument.

**PA-152** EPIGENETIC ALTERATION OF M. TUBERCULOSIS STRAINS DURING EXPOSURE TO CHOLESTEROL REVEAL UNIQUE METHYLOME MOTIFS

Nontobeko Mvubu\*, Kieran Jacoby. University Of KwZulu Natal, South Africa

10.1136/bmjgh-2023-EDC.105

**Background** Mycobacterium tuberculosis, the causative agent of Tuberculosis (TB) is a notorious pathogen that is

responsible for the highest mortalities from a single bacterial pathogen worldwide. Many studies have revealed that cholesterol contribute to M. tuberculosis pathogenesis with unique transcriptome changes implicated to cholesterol metabolism in genetically diverse clinical strains of M. tuberculosis complex (MTBC). Hence, the current study was aimed at investigating epigenetic changes associated with cholesterol metabolism since these changes may provide novel targets for development of TB treatments.

**Methods** The laboratory M. tuberculosis strain, H37Rv together with the recently identified Lineage 8 clinical strain were cultured in 7H9 broth and minimal media supplemented with cholesterol as the main carbon source. DNA was extracted using the Cetyltrimethylammonium bromide method followed by clean-up using Zymo DNA concentrator kit. Long read whole genome sequencing was performed in a PacBio SMART sequencer for complete methylome characterization using the RS Modification and Motif Analysis protocol and annotated further using DistAMo by selecting methylated genes with a significant z score ( $\geq 2$  or  $\leq -2$ ).

**Results** The highest significantly methylated motifs, CTCCAG, CTGGAG and VNCYGVNYR coding for Rv2060, rseA and Rv1175 genes, respectively, were detected in H37Rv grown in normal 7H9 broth while an additional CYGVNYR motif was detected during growth in cholesterol-rich media. This was in contrast to RNCYGVNYR motif detected in the Rv3632 gene for Lineage 8 strain during grown in 7H9 broth compared to CBBV, CTACCCGVC, GATNNNNRTAC, GNCTACSCA, GTAYNNNNATC, GVGGMVCR and CACGCAGHNH motifs detected for pks8, Rv2459, PE\_PGRS16, vapC22, fadD2, sseA, ackA genes, respectively.

**Conclusion** These findings suggest “unique” epigenetic regulation in clinical strains of MTBC compared to the laboratory H37Rv, which may explain their virulence traits. The precise characterization of MTBC methylation profiles in cholesterol-environments could open new avenues for the development of treatments since cholesterol is essential during M. tuberculosis pathogenesis.

Funding: EDCTP

**PA-153** USE OF ANTIBODY-BASED BIOMARKER TO ASSESS THE RISK OF HUMAN EXPOSURE TO AEDES MOSQUITO BITES AND INFECTION OF DENGUE IN NORTH-EASTERN TANZANIA

<sup>1</sup>Debora Charles Kajeguka\*, <sup>1,2</sup>Robert Kaaya. <sup>1</sup>Kilimanjaro Christian Medical University College, Tanzania; <sup>2</sup>Pan-African Malaria Vector Control Consortium, Tanzania

10.1136/bmjgh-2023-EDC.106

**Background** Global expansion of Arboviral diseases transmitted by Aedes mosquitoes is alarming. As seen by the frequent reports of the emergence and re-emergence of dengue, zika and chikununya infection.

There is a growing interest in the use of biomarkers for exposure to mosquito bite, including Aedes Nterm-34 kDa, as a proxy for Aedes-borne diseases risk. The objective of this study was to assess whether IgG antibodies against Nterm-34 kDa peptide was associated with the level of human exposure to Aedes mosquito bites and risk of dengue infection.

**Methods** Three longitudinal surveys were conducted during rainy season (June 2021), dry season (September 2021) and short rainy (January 2022) in three villages in Bondo, Tanga.

The study included children aged between 2–10 years and adolescents/adults aged 11–70 years. Face-to-face interviews were conducted. A pre-tested questionnaire was used to collect information regarding demographic characteristics and mosquito bite prevention measures. The developed questionnaire was uploaded in the system and data was collected electronically using Open Data Kit (ODK) application. Collected blood samples were tested for the presence of IgG antibodies against Aedes Nterm-34kDa using ELISA test.

**Results** Results showed that the medians of specific IgG antibodies levels were significantly different in three seasons ( $p=0.009$ ; Kruskal-Wallis test). Dengue positive participants presented a higher level of anti-salivary IgG compared with dengue negatives ( $p=0.02$ ; non-parametric Mann-Whitney test).

**Conclusion** Anti-Nterm-34kDa IgG antibodies is important correlate of human exposure to mosquito bite, thus the antibodies are important indicator to measure the risk of dengue infection.

**Funding:** This study is part of the EDCTP2 program supported by the European Union (grant number TMA2019PF-2694-SABOT).

#### PA-154 PERCEPTIONS OF FRONTLINE HEALTHCARE WORKERS ON THEIR "DUTY TO CARE" DURING THE COVID-19 PANDEMIC IN MOZAMBIQUE

<sup>1</sup>Angela Maria Alberto Alfaca\*, <sup>1</sup>Graça Salome, <sup>1</sup>Khátia Munguambe, <sup>2</sup>Elizabeth Heitman, <sup>3</sup>Troy Moon, <sup>1</sup>Esperança Sevene. <sup>1</sup>Eduardo Mondlane University, Mozambique; <sup>2</sup>University of Texas Southwestern, USA; <sup>3</sup>Tulane University School of Public Health, USA

10.1136/bmjgh-2023-EDC.106

**Background** The COVID-19 pandemic placed healthcare workers worldwide under significant physical and psychological stress due to increased workplace demands causing fatigue and burnout. In addition, shortages in personal protective equipment (PPE) were commonly, leading to fears for their own personal safety. The pandemic also renewed ethical questions about how to reconcile healthcare workers' duty to care with concern for their personal health, safety, and well-being. Our study aimed to explore this dynamic from the perspectives of frontline healthcare workers.

**Methods** We conducted a mixed-methods, descriptive study in which we carried out semi-structured, in-depth interviews in April-June 2022, with frontline healthcare workers at four hospitals in Maputo Province, Mozambique. Qualitative interviews were audio-recorded, transcribed and entered into Microsoft Excel for content analysis. Quantitative data was entered in REDCap with descriptive analysis in SPSS.

**Results** We interviewed 53 frontline workers (physicians, nurses and assistants). When asked about their ethical responsibility to provide care during a pandemic, 20 (38%) respondents affirmed that, despite the risk, they had an obligation to care for patients with COVID-19, even without PPE, due to their professional commitment. Eighteen participants (34%) stated that they were not obligated to provide patient care, without PPE, due to the risk of contracting the virus. The remaining 15 (28%) said that they would take care of patients in rare situations. Thirteen (25%) respondents reported first-

hand knowledge of examples during the pandemic in which patients were discriminated against in the health care setting, received poor care, or had health workers who refused to provide them care all together.

**Conclusion** Our findings show that frontline healthcare workers in Mozambique were divided as to the limits of their professional responsibility to care for patients with COVID-19. Risk management strategies for highly infectious diseases like COVID-19 must be reformulated to improve service delivery while safeguarding providers.

#### PA-164 ACCEPTABILITY AND FEASIBILITY OF TUBERCULOSIS DIAGNOSTIC SAMPLE COLLECTION IN YOUNG CHILDREN PRESENTING WITH PRESUMPTIVE TUBERCULOSIS IN CAPE TOWN, SOUTH AFRICA

Levern Africa, Michaille Anthony\*, Asanda Mfawze, Asikhangele Mtshabe, Marilyn Mentoor, Margaret Van Niekerk, Graeme Hoddinott, Megan Palmer, Marieke van der Zalm. *Desmond Tutu TB Centre, Stellenbosch University, South Africa*

10.1136/bmjgh-2023-EDC.108

**Background** Due to diagnostic challenges in childhood tuberculosis (TB), the World Health Organization (WHO) has recommended the use of non-sputum-based samples, including stool. This study evaluated the feasibility and acceptability of different TB diagnostic sampling procedures.

**Methods** In a prospective observational cohort study, we collected clinical data from children presenting with presumptive pulmonary tuberculosis (PTB). At enrolment, collection of TB diagnostics samples included respiratory samples (gastric aspirate, induced sputum and expectorated sputum), blood, urine and stool. Questionnaires on the acceptability and feasibility were collected from caregivers and healthcare workers (HCWs). A social scientist observed the collection of samples and performed qualitative interviews with HCWs.

**Results** We conducted 59 diagnostic and acceptability questionnaires of children's experiences of TB diagnostic sample collection. Sample collection was successful in 59% for urine, 36% for stool, 74% for blood and 72% for any respiratory sample. Overall, more than half of the caregivers felt that stool (86%), urine (75%), blood samples (67%) and respiratory samples (57%) were convenient for their children.

We observed sample collection in 32 children. HCWs had specific challenges with collecting urine samples from young girls due to the leaking urine bags. Children of all ages were resistant when collecting respiratory samples. In children aged 7–12 years, HCWs faced difficulties with collecting stool samples. These children felt embarrassed providing stool samples due to increased self-awareness. HCWs found blood samples easiest to collect, followed by respiratory samples, urine and stool. Even though blood sample collection was observed to cause more discomfort and pain.

**Conclusion** Although urine and stool samples seem a good non-invasive alternative sample for TB diagnosis in children, remaining challenges hamper the feasibility and acceptability of these specimens, which will need to be considered for future studies.