

## **CONFERENCES ABSTRACTS**

#### Sub-theme 1: Innovative strategies to fight epidemics and pandemics

## 1. Assessing laboratory capacity for sample collection and referral during the anthrax outbreak response in Amudat district, Uganda in June 2024

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**Background:** Amudat district registered a first suspected anthrax case on December 28, 2023 from Kakworobu village and a surge of cases between January and February 2024. Anthrax outbreak was confirmed on March 15, 2024 and Ministry of Health dispatched a multidisciplinary national rapid response team on June 12, 2024, to support the response. The laboratory team set out to support the coordination of sample collection, transportation and referral to improve turnaround time (TAT).

**Methods:** We conducted a laboratory capacity assessment for two laboratories using the WHO laboratory assessment tool to assess key aspects in laboratory performance such as human resource, sample collection, handling, transportation, bio risk management, partner and stakeholder support, presence of a response plan and sample referral register. Human sample testing was supported by Uganda Virus Research Institute in Arua. Animal and soil samples were tested by National Animal Disease Diagnostics and Epidemiology Centre whereas sample transportation and referral were supported by National Health and Laboratory Diagnostics Service. We tracked the turnaround time for the referred samples to determine the average time for sample collection to results release. We supported the district team in the development a laboratory response plan and a sample referral register.

**Results:** Laboratory capacity to respond to anthrax outbreaks was at an average of 51%. The average indicator scores for Amudat Hospital and Karita HCIV laboratories was 54% and 47%, respectively. Biorisk management had the lowest score (0%) for both laboratories. The district had 100% of referral supplies present, but lacked a laboratory response plan, sample referral register, and had only 13% (2/15) competent staff. Twenty-four samples (16 human, 6 animals, and 2 soil) were collected and referred for testing. Real time PCR revealed 9/16 (56%) human samples were positive while all soil and animal samples tested negative. The average turnaround time from sample collection to result release was 10 days which compared to the target turnaround time of 3 days was too long.

**Conclusion:** Amudat district's capacity to respond to anthrax outbreaks stood at 50% which was below the recommended WHO target of 80%. The district also had long turnaround time which affects public intervention potentially leading to a larger outbreak. The district team should be given security to support timely transportation given the insecurities in the Karamoja region. The district requires routine knowledge and skills improvement to ensure efficient response to future anthrax outbreaks.

## 2. A Comparison of the performance of Sanger and Oxford Nanopore Technology sequencing platforms for the detection of Polioviruses: Kenya's Move Towards Self-Reliance

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**Background:** With the increasing incidence of circulating vaccine-derived poliovirus (cVDPV) infections, particularly in Africa, there's a crucial need for genetic sequencing and analysis capacity at the country level, to improve detection and response timeliness, as part of the poliovirus eradication end-game strategy. Kenya has one WHO-accredited laboratory, at the Kenya Medical Research Institute, responsible for region-wide Poliovirus (PV) diagnosis, but up to quantitative PCR (qPCR). PV2 and discordant Sabin isolates require genetic sequencing according to the WHO protocol, to confirm detection, origin, monitor transmission, and establish the best strategy for vaccination

responses. Sequencing is currently done in a separate laboratory in Atlanta using Sanger method, the gold standard, which takes about 14 days for shipment and analysis. To counter this, in 2023, the KEMRI laboratory was equipped to perform inhouse Oxford Nanopore technology (ONT) sequencing, to reduce this turn-around time. We undertook a comparative study to compare sequencing results similarity between the two platforms.

**Methods:** A cross-sectional, lab-based study design was conducted between August 2023 and November 2024 on stool samples from routine surveillance of suspected AFP cases from Somalia, Kenya and Djibouti. 114 samples were PV positive on culture and purposively sampled to be subjected to qPCR to determine the serotype. Of these, 45 samples were PV2 and thus their VP1 region was sequenced using Sanger and ONT. The percentage of isolates with identical nucleotide differences on both methods was compared on Excel V.2016.

**Results:** 40/45 of the samples had 100% identical VP1 nucleotide differences results on both methods. Of these, 22 were cVDPV2, 23 were Sabin-like 2. The 5 differing sample results had <2 nucleotide differences. ONT results took 3 days to generate while Sanger results took at least 14 days to be received.

**Conclusion:** 88% samples yielded 100% identical VP1 nucleotide differences on both methods, demonstrating that ONT can give reliable results in the absence of Sanger platform. The 12% differing results were mostly due to missed mutations especially around primer binding sites. ONT also allows the identification of multiple polio serotypes in a single sample, and greatly reduces the turn-around time of sequencing results from 14 to 3 days. cVDPV2 identified are indicators of immunity gaps present in the population and hence the need for rapid detection to inform prompt and comprehensive vaccination efforts. We are now working towards meeting the requirements for GPLN approval, including parallel testing and proficiency testing to be fully accredited as a regional sequencing facility.

### 3. First outbreak of Rift Valley fever in Burundi, 2022: field investigation, virus molecular detection and genome characterization

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**Introduction and Objectives:** Rift Valley fever (RVF) is a zoonotic and vector-borne viral disease reported in African countries and the Arabian Peninsula affecting domestic ruminants and humans. In Burundi, RVF was reported and officially confirmed for the first time in may 2022. Field epidemiological investigations were conducted in order to describe the outbreak and for genomic characterization of the viral field isolates.

**Methodology:** In response to the RVF outbreak in Burundi, epidemiological investigation was conducted and a total of 100 samples including sera, tissues, vaginal and nasal swabs were collected from acute and convalescent ruminants.Real-time reverse transcription (RT)-PCR tests were performed. 10 positive samples with a cycle threshold < 30 were selected for genomic sequencing using a targeted amplicon approach that utilizes overlapping primers to recover the entire genome. MAFFT was used for sequence alignment and Bayesian evolutionary analysis by sampling trees was performed to estimate the time of emergence of the virus in Burundi.

**Result:** A total of 1741 cases were reported in livestock with a fatality rate of 41,5% (722). 71.2% of the cases were reported from the northern of the country, along with the fatality rate of 79.8%. The most RVF cases 60.9% were reported in cattle. RVFV genome was detected in 36 of the 100 tested samples. We recovered 9 RVFV genomic sequences with a coverage ranging from 60% to 95%. Out of the 9 strains, we got 5 yielded near complete genome sequences with a coverage rate of >90%. Phylogenetic analysis indicated that the RVFV strain circulating in Burundi in 2022 belongs to lineage C cluster, of the dominant lineage circulating in East Africa and shows a close relationship with RVFV isolates from Rwanda in 2022. The most common recent ancestor of both Burundi and Rwanda 2022 strains are indicated as a cluster of sequences isolated in Uganda 2018/2019.

**Conclusion:** This study generated the first batch of whole genome sequences of the Rift Valley fever virus in Burundi in livestock. The availability of these genomic data is important in the genomic surveillance efforts of RVFV in the region.

### 4. Genomic characterization of *Vibrio cholerae* Isolates from Outbreaks in 2024 in Burundi by Whole Genome Sequencing: Preliminary results

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**Background:** Cholera remains a significant public health concern in East Africa, with recurrent outbreaks causing morbidity and mortality. In 2024, Burundi experienced multiple cholera outbreaks, necessitating an in-depth genomic characterization

of circulating Vibrio cholerae strains. Whole Genome Sequencing (WGS) provides high-resolution insights into pathogen evolution, transmission dynamics, antimicrobial resistance (AMR), and virulence determinants, informing effective outbreak response strategies. The aim of our study was to characterize the genome of Vibrio cholerae isolates from outbreaks in 2024 in Burundi by using Whole Genome Sequencing.

**Methods:** A total of 10 V. cholerae isolates were selected from stored isolated collected from patients presenting with acute watery diarrhea across Bujumbura Mairie hotspots in Burundi in 20024. DNA was extracted by using QIAamp® DNA Mini Kit (Qiagen). Sequencing libraries were prepared using the Native Barcoding kit 24 v14 (Oxford Nanopore Technologies) and sequenced on a MinION<sup>TM</sup> Mk1C using R10.4.1 flowcells. Reads were basecalled with the high accuracy model on Dorado Basecall Server v7.4.13. The generated reads were assembled, annotated, and analyzed for serogroup classification, AMR determinants, virulence factor profiles and comparative phylogenetic relationships with among and with regional V. cholerae genomes.

**Results:** Among 10 isolates sequenced, six were of serogroup 1, three of serogroup 65 and one of serogroup 37. AMR profiling indicated widespread of catB9 (9/10), floR (9/10), almG(10/10), varG(10/10), aph(6)-Id and dfrA1(9/10), sul2, aph(3'')-Ib and aph(6)-Id, and emrD3 resistance determinants conferring resistance to Chloramphenicol, Chloramphenicol/Florfenicol, Colistin, Carbapenems, Trimethoprim, Sulfonamide, Streptomycin and macrolides respectively. Virulence gene analysis confirmed the presence of key virulence factors in all isolates, especially the cholera toxin (ctxA) and toxin-coregulated pilus (tcpA) genes, and other accessory genes associated with environmental persistence and sporadic infections. Phylogenetic analysis showed that the Burundi V cholerae strains are not closely related to any strains from DRC and Tanzania in the tree. They have more than 200 to 1000 SNP difference. Within the Burundi strains, they also have high variability. Among them, they can differ from 200 to 900 SNP difference.

**Conclusion:** Genomic surveillance of V. cholerae in Burundi provides critical insights into strain diversity, virulence factors patterns, and AMR trends. The high prevalence of multidrug resistance underscores the urgent need for revised treatment protocols and enhanced antimicrobial stewardship. Indeed, genomic surveillance should be strengthened for real- time outbreak tracking.

### **5. Genomic monitoring and tracking of** *Mpox virus Clade Ib* **during the ongoing mpox outbreak in Burundi Corresponding author:** Néhémie Nzoyikorera

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**Background:** In October 2023, a large mpox virus (MPXV) Clade Ib outbreak emerged in the province of South Kivu, Democratic Republic of the Congo (DRC), which has spread within the DRC and to bordering countries. Since the first identified case in July 2024, Burundi has been one of the most severely affected countries in this evolving outbreak outside of the DRC. The main objective of this study was to describe the genomic diversity and phylogeny of MPXV during the first months of the outbreak in Burundi.

**Methods:** Cases were detected through the national surveillance system and swab samples were confirmed for MPXV using a generic and Clade Ib specific real-time PCR assay. Samples with sufficient sample volume and viral load were selected for amplicon based whole- genome sequencing. From 96 selected vesicular lesions swabs, genomic DNA was extracted using the QIAamp® DNA Mini Kit (Qiagen). Sequencing libraries were prepared using the Native Barcoding kit 24 v14 (Oxford Nanopore Technologies) and sequenced on a MinION<sup>TM</sup> Mk1C using R10.4.1 flowcells. Reads were basecalled with the high accuracy model on Dorado Basecall Server v7.4.13. Phylogenetic analysis and Bayesian phylogenetic inference analysis was performed.

**Results:** Real-time PCR and WGS confirmed all positive MPXV samples as Clade Ib. In total, 98 genome sequences from cases diagnosed during the first three months of the outbreak were generated. Phylogenetic analysis based on the alignment generated using Squirrel with the masking as advised by the WHO showed that the branch containing all Burundi sequences was rooted to cases notified in the DRC. From there, a few different branches with sequences from Burundi were observed. This observed pattern suggests several introductions, one of which mainly seeded the ongoing outbreak. Of note, sample number 362 showed alternative clustering suggesting a different introduction into the country which was supported by recorded recent travel history to the DRC. The increasing number of observed APOBEC-3 style mutations provided further support for the epidemiological observation that the transmission was mainly driven by human-to-human spread. Bayesian evolutionary analysis on the shaded sequences showed that there were at least three different clusters identified in Burundi.

**Conclusion:** Here we show several different introductions and sustained circulation of Clade Ib MPXV in Burundi, most likely after initial introduction from the bordering province of South Kivu (DRC). The virus acquired several additional APOBEC-3 mediated mutations, in line with reported evidence of ongoing human-to-human transmission.

### 6. Laboratory based evaluation of the diagnostic accuracy of three commonly used MPOX diagnostic PCR tests in the EAC region for detection of the *Clade Ib* variant in EAC region

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**Background:** In October 2023, a large mpox virus (MPXV) outbreak emerged in the province of South Kivu, Democratic Republic of the Congo (DRC), which has spread within the DRC and subsequently expanded to other areas within and outside the DRC, including Burundi, Kenya, Rwanda and Uganda. The first sequence data generated and shared showed that the South Kivu outbreak was caused by a novel sublineage of Clade I, not previously seen in any of the public databases. It also showed the virus has a genomic deletion, affecting the fit of commonly used molecular assays for detection of clade I viruses, therefore potentially affecting the ability to diagnose such cases as well as surveillance. As such, there is a risk of false negatives with the widely used MPXV diagnostic PCR tests. To address this challenge, the EAC Mobile Laboratory project proposes to conduct an MPXV diagnostic PCR validation study with the National Public Health Institue of Burundi (INSP), to identify which MPXV PCR diagnostic assay provides the best sensitivity and specificity for identifying the Clade Ib sublineage.

**Method:** This is a retrospective study to evaluate the diagnostic accuracy of the commonly used MPOX diagnostic PCR tests in the EAC region based on a selection of cases from the national surveillance database. Archived samples, previously identified by RT PCR and stored in the Burundian National Reference Laboratory of Burundi were used. DNA extraction and purification were carried out by using Qiagen kit. The amplification was done on CFX-96 thermocycler by using Altona Diagnostics FlexStar, Seegene MPXV and Viasure Certest MPXV kits following the manufacturers protocol. All samples were based sequenced to confirm the presence or absence of MPXV in the samples. The sensitivity and specificity value were determined for all the tests.

**Results:** In total, 75 lesion swabs samples were analyzed within 53,3% were collected from male patients and 46,7% were from female patients. With regards to the age group repartition, 22,7% were from children under 5 years while 77,3% were from adult patients. The sequencing analysis confirmed the positive and negative samples. All positive were of clade Ib. All kits were of 100% of specificity and 100% of sensitivity compared to the sequencing results, as reference test.

**Conclusion:** In conclusion, we showed the potential of three rapid, and high-performance real-time PCR assay for the detection of MPXV clade Ib in lesion swabs sample types, with 100% of specificity and sensitivity.

## 7. Resilience to Ebola importation: A case study of priority-1 risk, neighboring Yei River State, South Sudan Corresponding author: John Rumunu

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**Introduction:** Outbreak of Ebola Virus Disease (EVD) which was declared in the Democratic Republic of the Congo (DRC) in August 2018 has been elevated to a Public Health Emergency of International Concern (PHEIC) in July 2019; and priority-1 risk, countries were advised to "improve their preparedness for detecting and managing imported or locally- acquired cases". South Sudan, a country bordering DRC implemented preparedness in high risk States, including Yei River State (YRS) that, borders EVD-affected Ituri Province, in the DRC. This study highlights health system capacity in YRS to rapidly detect suspected EVD cases. The main study question is what is the capacity of Yei River State health system to rapidly detect and respond to suspected EVD cases?

**Method:** We conducted a two-steps study to measure capacity of the state: (1) Desk-review was conducted to find alerts recorded in the Public Health Emergency Operation Center (PHEOC) since the declaration of outbreak in DRC in September 2018 to October 2019; the proportion of alerts that met the standard case definition of EVD suspect was calculated and the value (in percentage) was construed as capacity to detect Ebola suspect case. (2) Preparedness interventions were assessed by extracting activities from State Task Force (STF) owned mapping of partners' data using the 4Ws tool- (who, what, when, where) interpreted as capacity to detect and manage EVD suspect in the four counties.

**Result:** During the study period, seven (7) EVD suspect alerts were raised to Public Health Emergency Operation Centre (PHEOC), through toll-free number '6666' made available to the public: 4 (57%) of the alerts met case definition; 2 (29%) did not; and 1 (14%) could not be traced. The alerts that met case definition were reported from Yei County 3 (75%) and

Lainya 1 (25%). Alerts that met standard case definition are attributed to health system capacity (e.g. frontline facility screening and community-based surveillance) to detect EVD suspect cases.

**Conclusion:** The study concludes that, there was some capacity to rapidly detect should Ebola virus be imported or locally contracted. Therefore, scaling-up frontline health facility screening and community-based surveillance is key to securing areas where the virus might migrate.

#### 8. The role of the laboratory in the effective response and control of a viral conjunctivitis outbreak, Kampala, Uganda, March 2024

#### Corresponding author: Wilfred Opeli

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**Background:** On March 7, 2024, the Public Health Emergency Operations Center, Ministry of Health received reports of a suspected conjunctivitis outbreak in Uganda Prisons Service (UPS) and two schools in Kampala Metropolitan area (KMA). We assessed five laboratories in UPS, Luzira and 2 laboratories, Kisenyi and Kisugu, in KMA for testing capacity, supply availability, laboratory surveillance, data management, sample management, human resources, facility suitability and equipment functionality. We also investigated the conjunctivitis causative agent and monitored turnaround time (TAT) from sample collection to return of test results to the requester.

**Methods:** The World Health Organization Laboratory capacity assessment tool was used to assess laboratory capacity. Capacity scores in these areas were compared against a WHO standard for laboratory capacity to Public Health Emergencies of 80%. We collected and referred 142 eye swab samples from 85 suspected cases. A total of 116 samples were referred to the Uganda National Health Laboratory and Diagnostic Services Laboratory for culture and sensitivity testing. We also collected and referred 26 samples to the Arbo-virus Laboratory at Uganda Virus Research Institute for genomic sequencing using the Miseq platform and RT PCR using the ABI 7500 fast RT PCR System. We tracked and calculated the average TAT and range in days from the date of sample collection return of results to the requester.

**Results:** Overall laboratory capacity to respond to the conjunctivitis outbreak was at an average of 43%, below the WHO-recommended 80%. All laboratories lacked testing and bio- risk management capacity. Only 38% of the supply was available in the laboratories for sample collection and referral. Access to the National Hub Sample Transportation Network was available to all the requesting laboratories. Culture and sensitivity testing for 116 (100%) samples showed no significant bacterial growth. We identified Enterovirus C as the causative agent for the conjunctivitis outbreak. The average TAT was 5 days (range:3-7) from the date of sample collection to result returned to the requester.

**Conclusion:** The outbreak was caused by Enterovirus C. Following the assessment, we conducted onsite mentorship training at UPS and KMA laboratories on outbreak response and sample management. The findings highlight the importance of timely laboratory response and genomic sequencing in outbreak investigations before mass antibiotic usage to inform public health interventions. We recommended strengthening the UPS and KMA laboratory systems for effective detection and sample management of future public health emergencies.

## 9. Use of regionalized laboratory services in supporting response to the cholera outbreak: case of cholera in Kasensero landing site in Lake Victoria, Kyotera District, May 2024

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**Background:** Cases of cholera were detected in Kasensero landing site in Kyotera District in Central Uganda in late April 2024. The Ministry of Health in Uganda investigated and confirmed the outbreak on May 8, 2024. The laboratory was part of the investigation and response team to support real-time and accurate diagnosis, which is crucial for managing outbreaks, monitoring transmission, and guiding public health responses. The team aimed at assessing Masaka Regional Referral Hospital (RRH) laboratory emergency response mechanism for timely public health intervention.

**Methods:** We used a customized checklist from the World Health Organization to assess human capacity, infrastructural standards, equipment functionality and cholera logistics at the regional laboratory for cholera outbreak response and management. We then collected data on time and number of verified alerts sampled and results returned to track timely sample collection and result return. Isolated organisms were shipped to the Uganda National Health Laboratories and Diagnostics Services (UNHLDS) for interlaboratory QA/QC.

**Results:** The Masaka RRH laboratory met human and infrastructural standards with functional equipment and a qualified microbiologist. Shortages of cholera rapid test kits and some cholera culture media were noted. National sample transportation ensured timely movement from Kasensero to regional and national labs, with samples delivered to testing labs within 24 hours. Samples from 47 verified alerts were collected and tested. Out of these: 33 alerts (70%) were tested by rapid diagnostic

tests (RDT), with 15 (45%) testing positive for cholera antigens. All 47 alerts (100%) were cultured, with 23 (49%) returning positive for Vibrio cholerae. Lake Victoria water samples tested negative for V. cholerae. Results were received by the requester within an average of six days (range: 5-7 days) from sample collection.

**Conclusion:** There was timely sample collection, testing and result return for patient management and public health intervention with robust support from the regional laboratory team highlighting the importance of decentralizing emergency response.

#### Sub-theme 2: Strengthen one health approach to address communicable and non-communicable diseases

#### 10. Development and validation of novel test system for serodiagnosis of louse-borne relapsing fever in Nairobi Kenya

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**Background:** Louse-borne relapsing fever (LBRF) caused by Borrelia recurrentis is a poverty-related and a neglected bacterial infection. It is endemic in the Horn of Africa. There is a critical need for development of cheaper and rapid point of care sero-logical test that can be deployed for routine diagnoses of LBRF in resource scarce settings lacking the molecular diagnostic tools. Aims: This study hoped to develop and validated two novel immunoassays for rapid serodiagnosis of LBRF.

**Methods:** Bioinformatic and cloning approaches we used to screen and identify candidate genes encoding B. recurrentis immunogenic proteins using B. recurrentis strain A17. The promising genes were then cloned into pQE-30 Xa expression vector. The resulting recombinant vectors were then transformed and expressed in E. coli M15. The purification of recombinant proteins was done using Ni-metal affinity chromatography. After quality testing of the antigens, line immunoblots were prepared and ELISA plates coated. Evaluation of the diagnostic performance of the two immunoassays was performed using culture/ polymerase chain reaction confirmed banked sera and sera from clinically suspected patients in Kenya and a panel of human sera from patients infected with closely related spirochetes such as Treponema pallidum and Leptospira spp. and Borrelia burgdorferi. Sensitivity and specificity analysis was then determined using culture/PCR confirmed samples as gold standards.

**Results:** Two genes encoding two immunoreactive antigens (complement- inhibiting protein CihC and the glycerophosphodiester phosphodiesterase GlpQ of B. recurrentis) were found to be the most promising target candidates leading to the diagnostic evaluation of two immunoassays (line immunoblot and ELISA) for IgM and IgG. By utilizing a N-terminal CihC fragment, the sensitivity and specificity of both immunoassays (CihC and GlpQ) were high (IgM: sensitivity 100%, specificity of 89.9%, IgG: sensitivity 100%, specificity 99.2%).

**Conclusion:** The findings indicate the diagnostic potential of CihC and GlpQ as valuable markers for the serodiagnosis of LBRF even at early time points of infection thus, providing strong evidence for the utilization of these immunoassays as reliable tools in clinical practice.

## 11. I stopped to prove them wrong:" Accounts for discontinuing oral HIV pre-exposure prophylaxis among women at high risk of HIV in Tanzania. A mixed-method study

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**Introduction:** High discontinuation from HIV pre-exposure prophylaxis (PrEP) among at-risk populations undermines its effectiveness in preventing HIV infection. However, evidence is scarce on the reasons attributed to a high rate of discontinuation among female sex workers in sub-Saharan Africa. This study examined reasons for PrEP discontinuation among female sex workers in Tanzania.

**Methods:** We conducted a convergent mixed-method study involving female sex workers from February 2022 to June 2023 in the city of Tanga, Tanzania. The quantitative data on PrEP use and reasons for PrEP discontinuation were collected at months 1, 6 and 12 from female sex workers who were recruited by respondent-driven sampling. In-depth interviews were simultaneously conducted (along with the 12-month survey) with purposely sampled female sex workers who reported discontinuation from PrEP. The quantified reasons for discontinuation were mutually exclusive. The qualitative findings were interpreted in the light of the Health Believe Model. Separate descriptive and thematic analyses for the quantitative and qualitative data were conducted and the results were triangulated to generate meta-themes.

**Results:** We enrolled 313 female sex workers with a median age of 27 (IQR: 23-32) years. At 6 months 61.5% (95%CI: 54.3-68.4) had stopped taking PrEP in the last 3 months or more, increasing to 67.4% (95%CI: 60.2-74.0) at 12 months. Perceiving oneself to be at "medium" to "high" HIV risk was associated with a 20% reduced risk of stopping PrEP use for more than 3

months than perceiving oneself to be at low or no HIV risk (aRR 0.8, 95% CI: 0.783-0.896). Six meta-themes emerged on the reasons for stopping PrEP, namely: medical and pharmacological challenges; perceived negative social norms and societal pressure on PrEP discontinuation; perceived unfavorable pill characteristics and dosing schedule; low self-assessed own HIV risk; perceived low benefit to PrEP and; low self- efficacy to PrEP.

**Conclusion:** Female sex workers discontinued PrEP care due to complex interactions of clinical and negative experiences, self-perceived low risk of HIV, changing priorities and low self-efficacy, and social pressure. This suggests the need for a multiple-component intervention strategy to support PrEP retention, such as combining behavioural change strategy with education and awareness campaigns or psychological and social support.

#### 12. Nanoformulation and Preclinical Evaluation of a Triple Combination Antimalarial Therapy: Dihydroartemisinin-Lumefantrine with Primaquine

#### Corresponding author: Jeremiah Gathirwa

**Co-authors:** Pesila Odera, Geoffrey Otieno, Joab Onyango, James Owour, Florence Oloo, Martin Ongas, Hulda Swai, Bernards Ogutu

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**Background:** The World Health Organization recommends artemisinin-based combinations for uncomplicated malaria treatment. Artemether and lumefantrine (LUM) are the first-line treatments, with artemether serving as a prodrug of dihydroartemisinin (DHA) while primaquine (PQ) is primarily used as a prophylactic drug. However, these drugs face challenges such as toxicity, low bioavailability and poor aqueous solubility. The advent of nanomedicine offers solutions by improving drug pharmacokinetic and pharmacodynamic profiles, thereby enhancing therapeutic efficacy. This study aimed to improve the efficacy of DHA, LUM and PQ through nano- formulation using solid lipid nanoparticles (SLNs).

**Methodology:** These nanoparticles were prepared using a modified solvent extraction method based on a water-in-oil-in-water (W/O/W) double emulsion. Obtained nanoparticles were characterized and antimalarial efficacy evaluated in vivo in a mouse model.

**Results:** The resulting nanoparticles had a mean particle size of  $357.1\pm57.14$  nm, a polydispersity index of  $0.657\pm0.091$ , and a zeta potential of  $-35.7\pm1.25$  mV. The encapsulation efficiencies of DHA, LUM and PQ were  $93.98\pm0.41\%$ ,  $42.03\pm9.46\%$  and  $87.60\pm0.64\%$ , respectively with drug loading capacities of  $11.87\pm0.04\%$ ,  $24.10\pm2.88\%$ , and  $8.01\pm0.09\%$ . The drugs followed Kors-Peppas and Higuchi drug release models and were released progressively over 68 hours. The nanoparticles were spherically shaped, and Fourier transform infrared (FTIR) spectroscopy confirmed the successful nano-formulation process. The nanoformulated drugs demonstrated 30% greater efficacy than conventional oral doses in clearing *Plasmodium berghei* infection in Swiss albino mice.

**Conclusion:** This study successfully developed and evaluated a nanoformulated triple combination antimalarial therapy (DHA-LUM-PQ) using a solid lipid nanocarrier system. The formulation exhibited stable physicochemical properties, high drug encapsulation efficiencies, and controlled release over 7–68 hours. Stability studies confirmed its integrity under storage conditions, while in vivo efficacy tests showed a 30% improvement over conventional therapy. Toxicity studies demonstrated its safety with no adverse effects. These findings highlight the potential of nanoformulation for enhancing antimalarial drug performance and improving malaria treatment.

## 13. Interleukin-4/Interleukin-13-Mediated Susceptibility to Leishmania mexicana in BALB/c Mice is Independent of Macrophage/Neutrophil-IL-4Ra Signaling

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**Introduction:** Interleukin-4 and IL-13 signaling via the IL-4R $\alpha$  are disease-progressive during cutaneous leishmaniasis caused by L. mexicana in mice. Mechanistically, IL-4R $\alpha$  signaling promotes alternative activation of macrophages and limits neutrophil recruitment thereby permeating the survival of Leishmania parasites during infection. Despite this, earlier studies demonstrated that absence of IL-4/IL-13 on macrophages and neutrophils had minimal effect on the outcome of L. mexicana infection; however, this led to an acute host-protective response during L. major infection. Noteworthy, the L. mexicana model used amastigotes in a rump infection whilst the L. major study used promastigotes in a footpad infection model. Thus, the impact of IL-4 and IL-13 on cell-specific effector functions appears to be influenced by parasite species and the parasite stage and infection site used in experimental models. This study sought to investigate the role of IL-4 and IL-13 in macrophage/neutrophil cells in the cotrol of cutaneous leishmaniasis.

**Methodology:** BALB/c mice with a cell-specific deficiency of IL-4R $\alpha$  on macrophages and neutrophils (LysMcreIL-4R $\alpha$ -/lox) and control mice were exposed to L. mexicana promastigotes via footpad inoculation for 8 weeks after which humoral and cellular immune responses were evaluated using ELISA and flow cytometry.

**Results:** LysMcreIL-4R $\alpha$ -/lox exhibited fulminant disease, comparable to animals with IL-4R $\alpha$  sufficient macrophages and neutrophils, upon promastigote infection in the footpad, in accordance with studies using amastigote infection in the rump. Moreover, cytokine, immune cell phenotypes, and humoral immune responses were also unchanged in LysMcreIL-4R $\alpha$ -/lox compared to controls in the promastigote-based footpad infection model.

**Conclusion:** The results indicate that susceptibility to L. mexicana in mice occurs independently of IL-4R $\alpha$ + macrophages/ neutrophils irrespective of the parasite stage and site of infection used in experimental models.

### 14. A cost-effectiveness analysis: Pooling sputum testing to diagnose tuberculosis using xpert MTB/RIF ultra in public hospitals

#### Correspondent author: Silas Onyango Awuor

Affiliation: Microbiology Department, Jaramogi Oginga Odinga Teaching and Referral Hospital

**Background:** The World Health Organization (WHO) recommends diagnosing tuberculosis (TB) using molecular tests, such as Xpert MTB/RIF (MTB/RIF). These tests are expensive and resource-consuming, and cost-effective methods are needed for larger coverage.

**Methodology:** We evaluated the cost-effectiveness of pooling sputum samples for TB testing using a fixed amount of 300 MTB/RIF or Ultra cartridges in which four different samples were pooled in one cartridge. We used the number of people with TB detected as the indicator for cost-effectiveness. Cost-minimization analysis was conducted from the healthcare system perspective and included the costs to the healthcare system using pooled and individual testing.

**Results:** There was no significant difference in the overall performance of the pooled testing using MTB/RIF (sensitivity, 93.9% vs. 97.6%, specificity 98% vs. 97%, p-value > 0.1 for both). The total cost across all studies to test 300 samples singly was Ksh. 1.26M for the individual testing and Ksh. 315,000 for the pooled testing, resulting in a savings of Ksh.945000 in all the 300 sample tests performed (a 75% decrease). From the total 75 pools tested, 10 pools turned positive with 15 individual samples confirmed TB positive by individual testing. The mean unit cost per bacteriologically confirmed TB case was Ksh. 168,000 individual testing and Ksh. 42,000 for the pooled testing (25% decrease). Cost- minimization analysis indicates savings are directly associated with the proportion of positive samples. If the TB prevalence is  $\geq$  50%, pooled testing is not cost-effective.

**Conclusion:** Pooled sputum testing can be cost-effective for diagnosing TB, resulting in significant resource savings. This approach could increase testing capacity and affordability in resource-limited settings and support increased testing toward achieving the WHO End TB strategy.

#### **15. Active and Latent Tuberculosis Among Public Transportation Workers in Nairobi, Kenya Corresponding author:** Asiko Ongaya

**Co-authors:** Paul Mwangi, Fred Orina, Geoffrey Okallo, Evangeline Mathiu, Evans Amukoye, Videlis Nduba, Christine Mwachari

Affiliation: Kenya Medical Research Institute, Kenya

**Background:** Tuberculosis (TB) remains a major global health challenge, with approximately 10.6 million people worldwide currently living with active TB. Additionally, about 25% of the world's population is infected with TB, of whom 5% to 10% develop active TB. Kenya continues to be a high-burden country for TB. In 2019, an estimated 147,000 people contracted TB, but only 86,385 were diagnosed and treated, as reported by the Kenya National TB Program. Public transport has been associated with poor ventilation and high respiratory contact rates. Congregate settings, especially in poorly ventilated vehicles, may form an important pathway for TB transmission. This study therefore aims to investigate the prevalence of pulmonary TB and latent TB, along with associated risk factors, knowledge, and attitudes among drivers and conductors working in public transportation (locally referred to as matatus) in Nairobi County. Nairobi is the most populous city in Kenya and has the country's largest public transportation system.

**Methods:** This was a cross-sectional study that recruited 203 adult drivers and conductors within Nairobi. All participants were requested to provide a spot sputum specimen for testing using GeneXpert, Lowenstein-Jensen culture, and fluorescent microscopy, as well as a blood sample for HIV and QuantiFERON-TB Gold-Plus testing. Additional data were collected using a questionnaire.

**Results:** The study found that 1% of the participants had active TB, while 66.5% of participants (71.0% drivers and 64.5% conductors) tested positive for latent TB using QuantiFERON-TB Gold-Plus (p = 0.587). Additionally, 8.9% of participants (9.7% drivers and 8.6% conductors) were HIV-positive (p = 0.799).

**Conclusion:** Although the prevalence of active TB was low, latent TB was observed in a significant proportion of participants, highlighting the urgent need for targeted interventions to prevent reactivation and reduce the risk of active TB transmission.

Chest X- rays revealed some abnormalities despite negative TB bacteriological confirmation in certain cases. Public health interventions must focus on high-risk areas, such as public transportation, to effectively control TB transmission. These interventions could include improving ventilation in public vehicles, raising awareness about TB transmission, and establishing screening programs for high-risk groups.

## 16. Association of Human Cytomegalovirus (HCMV) exposure with tuberculosis disease susceptibility in TB presumptive South African adults

#### Corresponding author: Derrick Semugenze

**Affiliation:** 1. Department of Immunology and Molecular Biology, Makerere University, College of Health Sciences Kampala, Uganda. 2. Department of Global Health and Amsterdam Institute for Global Health and Development, Amsterdam University Medical Centers Location University of

**Background:** One of the most studied risk factors for TB is HIV. The effect of other viruses on TB disease remains less studied. Here we examined the association of Human Cytomegalovirus (HCMV) exposure with tuberculosis disease susceptibility in TB presumptive South African adults.

**Methods:** In a cross-sectional study, plasma and serum samples that were collected and stored by the BAR-TB Dx study in Cape Town, South Africa were analyzed. Tuberculosis presumptive participants were stratified into; TB cases living with HIV, non-HIV TB cases, controls living with HIV, and non-HIV controls. Ninety-eight (98) TB cases and 199 TB controls were selected. HCMV DNAemia was diagnosed from the stored plasma using artus CMV PCR kit (Qiagen, Hilden, Germany) on QuantStudio5 platform. Previous exposure to HCMV was determined by IgM and IgG avidity using commercial ELISA assays (Euroimmun, übeck, Germany). Association of HCMV exposure with TB disease was determined using multivariate analysis model while controlling for confounders.

**Results:** The median age of the participants was 37 years (IQR 29-47), 194 (65.3%) were of mixed-race ancestry, n (55.2%) were male, n (40.1%) were previously treated for TB. A total of 164 (7.1%). Had HCMV DNAemia, 19(6.4%) had positive HCMV IgM and 295(99.3%) had indication of high HCMV avidity. HCMV DNAemia was significantly associated with TB disease susceptibility (adjusted OR 3.69, 95% CI 1.19-12.51; p=0.028). Previous exposure to HCMV and HIV positivity were not significantly associated with TB disease. Other risk factors for TB disease included; anemia (aOR 2.6, 95% CI 1.40-4.79; P= 0.0026), leukocytosis (aOR 2.17, 95% CI 1.08-4.37; P=0.029), and underweight (non-significantly) (aOR 1.64, 95% CI 0.88-3.05; P= 0.12).

**Conclusion:** In our study population, active HCMV replication was strongly associated with TB disease irrespective of the HIV status. Future studies exploring role HCMV reactivation in TB disease progression are needed.

## 17. Cost-Effective and Efficient Tuberculosis Diagnosis: Evaluating Sputum Pooling with Xpert MTB/RIF Ultra in Rwanda

Corresponding author: Francois Hakizayezu

**Co-authors:** Jean Claude Ngabonziza Semuto

Affiliation: Rwanda Biomedical Centre, Rwanda

**Background:** The Xpert MTB/RIF Ultra has transformed the rapid diagnosis of tuberculosis (TB) and rifampicin resistance, yet its high cost restricts widespread implementation in low- and middle-income countries (LMICs). In these regions, traditional microscopy often serves as the primary diagnostic method despite its limited sensitivity. This study investigates the accuracy and reliability of a sputum pooling testing approach using Xpert MTB/RIF Ultra to enhance TB diagnosis in Rwanda, particularly in areas with low incidence.

**Methodology:** A cross-sectional study was conducted on sputum samples collected from individuals suspected of having TB. Initially, samples were tested individually at local health facilities using Xpert MTB/RIF Ultra, followed by retesting the pooled samples at the National Reference Laboratory in Kigali. Four sputum samples were pooled and tested per cartridge following a pre-established standard operating procedure (SOP). Data were analyzed with StataSE 13, and key metrics such as specificity, sensitivity, negative predictive value (NPV), positive predictive value (PPV), agreement, cost savings, and time savings were calculated.

**Results:** A study of 1,380 sputum samples in Rwanda showed that pooled testing for TB was effective, identifying 110 (7.9%) positive cases. The method had high accuracy with 97.5% agreement, 98% specificity, 90.4% sensitivity, 77.3% positive predictive value (PPV), and 99.3% negative predictive value (NPV). It also reduced costs by 41% (from 12,234 RwF to 5,013 RwF) and cut testing time by 42% (from 2.52 to 1.06 hours). A significant difference in CT values before and after pooling was found (p = 0.00704), though the effect size was small (Cohen's d = 0.307), indicating limited practical impact.

**Conclusion:** This study demonstrates that the sputum pooling approach using Xpert MTB/RIF Ultra significantly reduces both costs and testing time in Rwanda. The findings support the potential for broader access to molecular TB diagnostic services,

ultimately conserving resources for other essential primary healthcare needs. The relatively low prevalence of TB in Rwanda allows for an effective pooling strategy, minimizing the need for repeated testing of positive pools.

## 18. Assessment of Bacterial Contamination and their Antimicrobial Susceptibility of Public Buses at Musanze Park station in Rwanda

#### Corresponding author: Celestin Musabyumuremyi

#### Affiliation: University of Rwanda

**Introduction:** Public transportation systems, especially buses, are often exposed to various environmental and microbial contaminants due to the high volume of passengers and frequent contact with shared surfaces and most bacterial contamination are resistant to most common used antibiotics. In Musanze, Rwanda, the cleanliness and microbial safety of public buses remain largely unassessed. This study aimed to evaluate the level of bacterial contamination on public buses and to assess the susceptibility of isolated bacterial strains to various antibiotics in order to determine the potential public health risks.

**Methods:** The study was conducted over a period from 19th June till 13rd July 2024. Buses operating at Musanze Bus Park Station were randomly selected, and bacterial samples were collected from frequently touched surfaces, including handrails, seat backs, door handles, and window latches. Sterile swabs were used to collect samples, which were immediately transported to INES Ruhengeri microbiology laboratory. The samples were cultured on appropriate media, and bacterial isolation and identification were carried out using standard biochemical tests. Antibiotic susceptibility testing was performed using the disk diffusion method (Kirby-Bauer method), with antibiotics commonly used in treating bacterial infections, including penicillin, tetracycline, ciprofloxacin, and chloramphenicol.

**Results:** A total of 60 buses were sampled, with bacterial contamination found on all buses. The most commonly isolated bacteria included Escherichia coli (27%), Staphylococcus aureus (22%), Klebsiella pneumoniae (15%), and Salmonella spp. (10%). The other isolates included Enterococcus faecalis, Pseudomonas aeruginosa, and Proteus vulgaris. Antibiotic susceptibility testing revealed that the majority of E. coli and Klebsiella pneumoniae strains were resistant to common antibiotics such as penicillin and tetracycline. However, most bacterial strains showed susceptibility to ciprofloxacin and chloramphenicol. Interestingly, Staphylococcus aureus strains exhibited significant resistance to methicillin (MRSA) in 40% of the isolates.

**Conclusion:** The results of this study indicate high contamination rate with potentially pathogenic bacteria, which could pose a significant health risk to passengers. Antibiotic resistance was notably present in some of the isolated bacterial strains, which highlights the growing concern of antimicrobial resistance (AMR) in public spaces. Therefore, Bus operators at Musanze Bus Park implement regular and thorough cleaning and disinfection practices and promote good hygiene practices among passengers such a hand washing.

#### 19. Asymptomatic malaria: a hidden reservoir for the transmission and circulation of artemisinin partialresistant Plasmodium falciparum in Tanzania

#### Corresponding author: Ernest Mazigo

Co-authors: Winifrida Kidima

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**Abstract Background:** Asymptomatic malaria infections contribute significantly to the silent transmission of the disease. However, the prevalence of artemisinin resistance (ART-R) markers among asymptomatic individuals remains understudied and is given less attention in the National Malaria Control Programs (NMCPs).

**Methodologies:** This community-based cross-sectional study was conducted in Tanzania from December 2022 to July 2023, involving 3,489 participants from three regions: Geita (1,120 participants), Kigoma (1,145), both high malaria transmission areas, and Arusha (1,124), a low transmission area. Four villages were randomly selected from each region. Venous blood samples were collected and tested for Plasmodium falciparum infection using HRP2- based RDT, microscopy, and qPCR. P. falciparum mono-infection isolates, confirmed by qPCR, were sequenced to identify genetic markers associated with artemisinin resistance, focusing on the pfk13 gene. Further sequencing at the pfmdr1 gene locus investigated markers linked to reduced susceptibility to artemisinin partner drugs. The quality of chromatograms were confirmed by SnapGene software and identification of SNPs performed by the ClustalW algorithm in MEGA11 and Lasergene software. Mutations were calculated as a percentage, and differences were statistically analyzed using GraphPad Prism 8.0.2.

**Results:** Overall, 25.5% of samples were positive by RDT, 16.1% by LM, and 28.2% by qPCR. RDT and species-specific qPCR were used to confirm P. falciparum mono-infections, and 83 isolates with co-infections were excluded from the drug resistance marker sequencing analysis. Finally, 866 out of 2,265 (38.2%) isolates from high-transmission areas and 35 out of 1,124 (3.1%) from low-transmission areas were sequenced for drug resistance markers at the pfk13 and pfmdr1 genes. At the pfk13 gene, 23 out of 802 (2.9%) of isolates from high- transmission regions harbored validated markers for artemisinin partial

resistance, including Y493H (0.2%), R561H (1.8%), and A675V (0.7%), while all isolates from low- transmission areas had wild-type codons. Sequencing of the pfmdr1 gene revealed the N86 wild-type codon in all isolates. The PfMDR1-NFD haplo-type, which is associated with reduced susceptibility to artemisinin partner drugs, was detected in 385 out of 804 (47.9%) isolates across all villages.

**Conclusion:** We suggest intensification of ongoing molecular surveillance strategies to include asymptomatic populations, as these undetected individuals may serve as reservoirs for the continued circulation of artemisinin partial resistant parasites in Tanzania.

## 20. Carbapenemase-producing Enterobacterales recovered from Nairobi River, Kenya surface water and from nearby anthropogenic and zoonotic sources

#### Corresponding author: Rael J Too

Affiliation: University of Nairobi/KEMRI

**Background:** Carbapenem-resistant Enterobacterales (CRE) present a significant global public health concern. Sub-Saharan Africa has borne a heavy burden of CRE with several studies reporting a prevalence of up to 60% in some patient populations. Most studies in Africa focus on clinical CRE isolates, with limited data on their spread in the natural environment. Therefore, the purpose of this study was to report the recovery of CRE from Nairobi River surface waters and nearby anthropogenic and zoonotic sources in Nairobi County, Kenya.

**Methods:** This was a longitudinal study in which wastewater samples were filtered through membrane filters of 0.45µm to capture bacteria. Swiffer samples from animal contact areas were also collected from slaughterhouse. The membrane filters and swiffer samples were then placed on whirl-pak bags containing MacConkey (MAC) broth modified with 0.5 µg/mL meropenem and 70 µg/mL of ZnSO4 and incubated overnight at 37°C. Carbapenemase production was done using the Carba-NP test, and positive suspect organisms were identified using Matrix-assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometry (MS). The presence of carbapenemase-encoding genes was examined by conventional PCR.

**Results:** Three hundred and thirty-six CRE isolates were recovered from 336 (250 mL) wastewater and swiffer samples, with 230 of the samples (68.5%) producing one or more CRE isolates. CRE was most commonly recovered from nearby untreated sewage influent (100% of 36 samples; 79 total isolates), treated effluent (93% of 118 samples; 116 total isolates), Nairobi River surface waters upstream (100% of 36 samples; 57 total isolates), downstream (100% of 36 samples; 45 total isolates), and way downstream from the wastewater treatment plant (WWTP) (73% of 11 samples; 19 total isolates). CRE were also recovered from slaughterhouse effluent discharges at 1.5%, (5/336), animal contact areas like holding pens and killing floors at 0.9%, (3/336), and a manhole sewer from the affluent neighborhood of Karen at 2.7%, (9/336) respectively. The CRE included Escherichia coli (158, 47%), Klebsiella pneumonia (74, 22%), Enterobacter spp. (43, 13%), Aeromonas spp. (29, 9%), Acinetobacter baumannii (12, 3.6%), Citrobacter freundii (7, 2.1%), Pseudomonas aeruginosa (5, 1.5%) and other species (8, 2.4%). CRE genotypes included blaNDM (246,73.2%), blaKPC (40, 12%),) blaVIM (51, 15.2%, blaOXA-48-like (65, 19.3%) blaIMP (15,4.5%), and blaGES (7, 2.1%).

**Conclusion:** Our results indicate that clinically important CRE are common in Nairobi River surface water and from nearby wastewater and livestock sources. These pose an important public health threat that requires urgent intervention strategies and additional investigation.

## 21. Environmental Reservoirs and Transmission Pathway of Nontyphoidal Salmonella in an Urban Informal Settlement in Nairobi, Kenya

#### Corresponding author: Collins K. Kebenei

**Co-authors:** David Onyango, Kelvin Kering, Cecilia Mbae, Susan Kavai, Michael Muraya, Celestine Wairimu, Kristin Weber, Michael Pietsch, Tanja Pilz, Oliver Drechsel, Andrea Thürmer, Torsten Semmler, Stephan Fuchs, Sandra Simon, Antje Flieger, Lothar H Wieler, Samuel Kariuki

Affiliation: Kenya Medical Research Institute, Maseno University, Robert Koch Institute

**Introduction:** Non-typhoidal Salmonella (NTS) presents a considerable health threat to children in low- resource settings, where clean water, sanitation, and hygiene are often inadequate. However, the environmental factors influencing NTS persistence and spread remain poorly understood.

**Methods:** We employed a case-control design to identify environmental factors associated with NTS infection among children in Nairobi's informal settlements between August 2022 and July 2023. Fecal specimens were collected from febrile children, with or without diarrhea, attending healthcare facilities. The study included 42 laboratory-confirmed NTS- positive cases and 42 NTS-negative children from the same community. Environmental samples, including drinking water, open drains, soil, and household effluent, were collected from both case and control households, as well as raw sewage from main sewer-line

convergence points. Conventional microbiological culture and quantitative Polymerase Chain Reaction techniques were employed for NTS detection, with genomic sequencing conducted for strain characterization.

**Results:** Environmental samples from case households showed a higher NTS contamination rate of 33.3% (42/126) compared to control households of 7.2% (9/126). Among the case-household samples, effluent showed the highest NTS detection rate (45.2%, 19/42), followed by drinking water (33.3%, 14/42) and soil (21.4%, 9/42), with open drains ( $\chi^2$  (1) = 339.66, p < 0.001, OR = 5.10) and drinking water ( $\chi^2$  (1) = 191.24, p < 0.001, OR = 5.38) identified as potential transmission pathways. Genetic analysis revealed a common strain, Salmonella Enteritidis ST11, in clinical and environmental isolates.

**Conclusion:** The study's findings underscore the plausible role of household environments in sustaining NTS transmission cycles in the community. Addressing these risks requires a multi-faceted approach, including targeted improvements in sanitation infrastructure and comprehensive environmental and clinical NTS surveillance to mitigate infection and reinfection in high- risk populations.

### 22. Evaluation of the Efficacy of Artemether Lumefantrine in uncomplicated malaria patients in Kwale County Corresponding author: Kelvin Thiongó

Co-authors: Miriam Chelangat, Mary Ombati, Francis Kimani

Affiliation: Kenya Medical Research Institute

**Introduction:** Malaria remains a disease of public health concern, with over 247 million cases and 619,000 deaths reported globally in 2021, with Kenya reporting more than 3.5 million clinical cases and over 10,000 deaths.) Antimalarial drug resistance markers, especially on the *Plasmodium falciparum* Kelch propeller domain (Pfk13), have widely been reported in Southeast Asia (SEA) and have slowly found their way in SSA with cases of delayed parasite clearance being reported in Uganda Tanzania and Rwanda. . This project, therefore, aimed to conduct a therapeutic efficacy study in the border county of Kwale, which was a single- arm 42-day follow-up trial on patients with uncomplicated malaria.

**Methods:** This project recruited participants from September to December 2024 in Msambweni sub- county Hospital in Kwale County. It followed an inclusion criterion of patients with uncomplicated malaria, with plasmodium falciparum mono-infection, aged 6 months -14 years and a HB level of above 7g/dl. All the patients were treated with Artemether lumefantrine as per the malaria treatment guideline dosage in Kenya. Dihydroartemisinin piperaquine was used as the rescue treatment for participants who had episodes of malaria after the treatment period.

**Results:** A total of 1,189 patients who fulfilled the inclusion criteria were screened for recruitment into this clinical trial. 247 patients had a mono infection of Plasmodium falciparum which represented a 20.7% positivity rate. From this, a total of 166 participants were recruited into the TES and followed up for a total of 42 days. During this period, 21 patients were lost to follow up for various reasons, and a total of 145 participants completed the study. From this group a total of 107 patients had Adequate Clinical Parasitological Response (ACPR). 38 patients (22.9%) had an episode of malaria relapse after the treatment period on various follow-up days as follows: Day 3=2, Day 14=1, Day 21=10, Day 24=1, Day 26=2, Day 28=9, Day 33=1, Day 38=1, Day 40=1, Day 42=8. **Conclusion:** Evidence of malaria at Day 3 is a strong indicator of an Early Treatment Failure of Artemether lumefantrine. 22.9% of recurrent parasitemia cases also indicate that there could be either a problem with drug or vector control in the community. Molecular and genomic analysis of the samples is ongoing which will paint a true picture of the efficacy of AL in Kwale county and inform malaria treatment guidelines in the country.

### 23. Genomic Insights of Multi-drug resistant Non-typhoidal Salmonella among children in the Urban Slums of Nairobi, Kenya

Corresponding author: Kelvin Kering

Affiliation: Kenya Medical Research Institute

**Background:** Nontyphoidal Salmonella (NTS) infection is characterized by self-limiting enterocolitis but can become invasive resulting in bacteremia. Salmonella enterica serovars Typhimurium and Enteritidis (S. Typhimurium and S. Enteritidis) are the most common causes of NTS with the highest incidences reported among children  $\leq$  5 years and in sub- Saharan Africa. Asymptomatic carriers of NTS are hypothesized to be reservoirs of new infections in vulnerable individuals, consequently, this study aimed to investigate the antimicrobial resistance and genomic characteristics of NTS from children under five years of age during acute disease and carriage post-treatment.

**Methods:** NTS (S. Typhimurium and S. Enteritidis) isolates recovered from stool and blood of children under five years during acute disease (fever with/without diarrhoea) and carriage were subjected to antimicrobial susceptibility testing using Kirby-Bauer disk diffusion. Genomic DNA was subjected to whole genome sequencing using Illumina NextSeq 2000 platform and analysed to identify AMR and virulence genes and plasmid replicons. GraphPad Prism 8 was used to perform statistical analyses.

**Results:** A total of 44 isolates (26 S. Enteritidis and 18 S. Typhimurium) were recovered from 43 NTS positive children during acute disease. In addition, from 13 children found to be shedding NTS post-treatment, 25 isolates (19 S. Enteritidis and 6 S. Typhimurium) were recovered. All the 45 S. Enteritidis and 24 S. Typhimurium isolates were sequence type 11 and 19 respectively. Resistance to Azithromycin, the current antibiotic of choice for treatment of invasive NTS, was observed in 14.49% of all isolates with reduced susceptibility in 71%. Resistance to azithromycin was higher in S. Enteritidis (20%) compared to S. Typhimurium (4.2%). Multi-drug resistance was observed in 20.8% of S. Typhimurium isolates with three (12.5%) isolates being co-resistant to ceftriaxone, cefotaxime and cefpodoxime. Resistance profiles did not differ significantly between acute disease and shedding (p> 0.05). All isolates possessed at least one and up to ten AMR genes with extended spectrum  $\beta$ -lactamase genes (blaTEM and blaCTX-M) present in 23.1% of S. Typhimurium. Prediction of plasmid replicons detected six types with IncFIB(S)\_1 present in all isolates, while IncQ1\_1 was present in one isolate. All the isolates respectively.

**Conclusion:** Resistance to last-resort antibiotics and decreasing susceptibility to Azithromycin is concerning as it could result in therapy failure, consequently, these findings underscore the need for vaccine introduction.

## 24. Genomics Landscape of Quinolone Resistant and ESBL- producing *Klebsiella pneumoniae* in Tanzanian Referral Hospitals

#### Corresponding author: Boaz Wadugu

**Co-authors:** Happiness Kumburu, Melkiory Beti, Shabani Mziray, Patrick Kimu, Davis Kuchaka, Blandina Mmbaga, Stella Mpagama, Tolbert Sonda

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**Background:** Multidrug-resistant Gram-negative bacteria, particularly Extended Spectrum Beta-Lactamase (ESBL)-producing Klebsiella pneumoniae, pose a significant global public health challenge. The coexistence of quinolone and beta-lactam resistance limits low-cost treatment options, especially problematic in low and middle-income settings. We aimed to examine the genomic landscape of these resistant strains and their virulence factors in Tanzania.

**Methods:** We studied 38 K. pneumoniae clinical isolates from adults and children collected from four referral hospitals in Tanzania between September 2021 and December 2022. Classical microbiological procedures were used for bacterial isolation. Whole genome paired-end sequencing was performed on the Illumina Nextseq550 platform. The assembled genome was analyzed using the PathogenWatch tool to identify MLST, virulence genes, and resistance genes from each isolate.

**Results:** These isolates were mainly collected from adults (35/38), mostly originating from pus or wound swabs (13/38), sputum samples (11/38), and blood samples (5/38). These K. pneumoniae isolates were highly diverse, representing 27 different sequence types (STs), with the most prevalent being ST307, ST452 and ST35 (all 3/38); ST17, ST23, and ST 281 (all 2/38); all other isolates were singletons. Out of the isolates sharing sequence types, those of, ST452, ST17, ST281, and ST23 were isolated from the same hospital settings. Almost all (36/38) isolates were phenotypic ESBL-producers, and 18/38 of the isolates showed resistance to fluroquinolones. Genotypically, 18/38 carried genes conferring both forms of resistance to both. The most frequently detected resistance genes were blaCTX-M-15 (19/38) and blaTEM-1D (21/38), and qnrB1 (9/24%). Yersinibactin was the most common virulence factor, with hypervirulence gene determinants present in 18.4% of the isolates.

**Conclusion:** There is a high diversity of K. pneumoniae strains in these Tanzanian referral hospitals, with very little overlap of sequence types between hospitals. The ESBL-producing and quinolone resistance levels are high. There is a need for robust surveillance and intervention strategies to address antibiotic resistance as a significant public health concern.

## 25. High dominance of ctx-m and tem genes from the *enterobacteriaceae* family revealed for the first time in Burundi

#### Corresponding author: Armstrong Ndihokubwayo

**Affiliation:** National Reference Laboratory, National Institute of Public Health (INSP), Laboratory of Clinical Immunology, Inflammation and Allergy (LICIA), Hassan II University of Casablanca, Morocco

**Background:** Antimicrobial resistance, dominated by the ESBL-producing Enterobacteriaceae (ESBL-PE), is a silent pandemic and a central health challenge of the twenty first century. Although UTIs due ESBL-mediated bacterial resistance is recognized as a serious concern in the adult population and children and account for 25% of all infections. Limited data are currently available on ESBL-PE prevalence and molecular characteristics in Sub-Saharan Africa. To our knowledge, there is no study on the epidemiology and molecular detection of ESBL-PE isolates from UTIs patients in Burundian hospitals. The goal of this study is to suggest the prevention and treatment measures based on our findings in Burundi.

**Methods:** We conducted a laboratory-based cross-sectional study from 1st September 2023 to 30 May 2024. Enterobacteriaceae isolates were randomly collected from urinary samples from different hospitals (Gitega, Kayanza, Rumonge, HPCR, CHUK) and

INSP Laboratory. The isolates were identified by standard bacteriological techniques. Antimicrobial susceptibility testing and screening of ESBLs were undertaken by using standard disk diffusion and double disk synergy tests methods. A conventional PCR was used for genotypic detection of ESBLs genes according to the standard protocol.

**Results:** Out of 247 Enterobacteriaceae isolates; Escherichia coli predominated, accounting for 72.47% positive UTIs cases followed by Klebsiella spp (18.62%), and Proteus spp (4.85%). The isolates, were collected from the INSP National Reference Laboratory (n=50; 20.24%), Gitega regional Hospital (n=45; 18.21%), Rumonge hospital (n=32; 12.95%), Kayanza Hospital (n=35; 14.17%), Prince Regent Charles Hospital (n=42; 17%) and Kamenge Teaching Hospital (n=43; 17.40%). Among them, 45.34% were resistant to ceftriaxone and/or cefotaxime; and 28.74% were ESBL positive. The antimicrobial susceptibility testing showed that the isolates were most resistant to antibiotics including Tetracycline (96.76%), Ampicillin (85.02%), Amoxyclav (77.73%), Cotrimoxazole (65.99%), Doxycycline (63.15%), and Cefuroxime (55.46%). No resistance to both Meropenem and Imipenem was reported. The CTX-M genes (80.28%) were predominantly detected among ESBL positive isolates from UTIs patients. TEM and SHV accounted respectively 53.52% and 25.35%.

**Conclusion:** BlaCTX-M is a predominant gene conferring ESBL-E production. Carbapenems were the drug of choice for the treatment of ESBL-PE producers. IPC measures, antibiotic stewardship and routine surveillance of ESBL producers are needed, as well as further investigation to understand the transmission dynamics of CTX-M and TEM types of resistance due to ESBL in hospital settings.

# 26. Incorporating genomics in routine vector surveillance: *Anopheles coluzzii* detection, insecticide resistance profiles and population genetic structure in relation to conspecific populations in West and Central Africa **Corresponding author:** Luna Kamau

#### Affiliation: Kenya Medical Research Institute

**Background:** Genomics significantly enhances the capacity for timely, effective, and precision-based vector surveillance, leading to better disease management and control. The current study incorporated genomics in vector and insecticide resistance surveillance leading to the first detection of Anopheles coluzzii, a primary vector of malaria found in West and Central Africa, but hitherto never been documented in Kenya.

**Methods:** Mosquitoes were sampled as larvae from Busia, Kwale, Turkana, Kirinyaga and Kiambu counties, representing the range of malaria endemicities in Kenya, in 2019 and 2021 and emergent adults analysed using Whole Genome Sequencing (WGS) data processed in accordance with the Anopheles gambiae 1000 Genomes Project phase 3. Where available, historical samples from the same sites were included for WGS. Comparisons were made with An. coluzzii cohorts from West and Central Africa.

**Results:** The study reported the detection of An. coluzzii for the first time in Kenya. The species was detected in Turkana County across all three time points from which samples were analyzed and its presence confirmed through taxonomic analysis. Additionally, there was a lack of strong population genetic differentiation between An. coluzzii from Kenya and those from the more northerly regions of West and Central Africa, suggesting they represent a connected extension to the known species range. Mutations associated with target-site resistance to DDT and pyrethroids and metabolic resistance to DDT were found at high frequencies up to 64%. The profile and frequencies of the variants observed were similar to An. coluzzii from West and Central Africa but the ace-1 mutation linked to organophosphate and carbamate resistance present in An. coluzzii from coastal West Africa was absent in Kenya.

**Conclusions:** These findings emphasize the need for the incorporation of genomics in comprehensive and routine vector surveillance to inform on the range of malaria vector species, and their insecticide resistance status to inform the choice of effective vector control approaches.

## 27. Insecticide Resistance Status of *Anopheles arabiensis*, a Major Malaria Vector, in Rice Irrigation Schemes in Kenya

#### Corresponding author: Winfred Mutwiri

#### Affiliation: Chuka University/ICIPE

**Background:** Malaria control in Kenya relies on case management and vector control using long-lasting insecticidal nets and indoor residual spraying. However, the development of insecticide resistance can compromise the effectiveness of these insecticide-based vector control programs. This study aimed to assess the current status of insecticide resistance in *Anopheles arabiensis*, a major malaria vector, in the rice-irrigated areas of Mwea and Ahero in Kenya.

**Methods:** The study was conducted between June and December 2024 in the Mwea and Ahero rice irrigation schemes. Bloodfed and half-gravid female Anopheles mosquitoes were collected indoors and used to establish a first filial generation (F1). Adults aged 3-5 days (F1) were tested for susceptibility levels to various insecticides using the Centre for Disease Control (CDC) bottle bioassay. Synergist assays with the P450 inhibitor piperonyl-butoxide (PBO) were performed, and polymerase chain reaction (PCR) amplification was used to identify sibling species and genotype for the presence of resistance knockdown (kdr) mutations.

**Results:** The results showed that *Anopheles arabiensis* was the predominant species in both regions. Resistance to permethrin, alphacypermethrin, and deltamethrin was observed in all sites, with possible resistance to dichlorodiphenyltrichloroethane (DDT) in Ahero. All assayed vector populations were fully susceptible to malathion and bendiocarb. In Mwea, susceptibility to permethrin and deltamethrin was restored after pre-exposure to the synergist PBO, suggesting the involvement of metabolic resistance mechanisms. In Ahero, susceptibility to alphacypermethrin and deltamethrin was restored after pre-exposure to the synergist PBO with remarkable increase in mortality to PBO+ permethrin (4.67% to 86.7%).

**Conclusion:** The findings indicate a significant level of phenotypic resistance to permethrin, deltamethrin, and alphacypermethrin, which could severely impact the effectiveness of current vector control tools reliant on pyrethroids. However, the malaria vector's susceptibility to malathion, bendiocarb, and the use of PBO synergists in pyrethroids provides a promising outlook for indoor residual spraying (IRS) and insecticide-treated net- based interventions. These results highlight the urgent need for integrated vector control strategies, particularly in irrigated areas where agricultural pesticide use is poorly regulated.

#### 28. Integrating One Health Approaches for the Management of Communicable and Non-Communicable Diseases Corresponding author: Marthe Uwamariya

#### Affiliation: University of Rwanda

**Background:** The global burden of communicable diseases (e.g., HIV, tuberculosis, malaria) and non- communicable diseases (NCDs, e.g., cardiovascular diseases, cancer) has been increasing, with NCDs projected to account for 70% of all deaths by 2030. Antimicrobial resistance (AMR) further exacerbates these challenges, particularly in low- and middle-income countries. The One Health framework, which integrates human, animal, and environmental health, offers a comprehensive approach to managing these interconnected health concerns. However, despite progress in communicable disease management, AMR and the growing burden of NCDs remain urgent global health issues. This study aims to evaluate the effectiveness of the One Health framework in managing both infectious and non- communicable diseases, focusing on reducing AMR, improving occupational and environmental health, and addressing nutrition security.

**Methodology:** A mixed-methods approach will be utilized, combining quantitative, qualitative, and policy analysis techniques. Statistical models will assess the impact of One Health initiatives on health outcomes, specifically regarding communicable diseases and AMR. A review of health policies will be conducted to examine the integration of One Health principles in disease control efforts. Case studies from high-burden regions and interviews with key stakeholders will identify challenges and best practices for implementing One Health strategies in resource-limited settings.

**Results:** Preliminary findings suggest that One Health implementation could result in a 10% reduction in communicable infections in regions that adopt the framework. However, non- communicable diseases continue to rise globally, and AMR remains a significant threat, with projections estimating 10 million deaths annually by 2050. The study emphasizes the need for integrated strategies to address both communicable and non-communicable diseases and the rising challenge of AMR.

**Conclusion:** The study emphasizes the importance of cross-sectoral cooperation in tackling the dual burden of communicable and non-communicable diseases. Recommendations will focus on strengthening the One Health framework to improve environmental health, enhance healthcare access in low-resource settings, and address AMR control, thereby guiding future public health policies and interventions.

#### 29. Malaria molecular surveillance in Western Equatoria State, South Sudan

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**Co-authors:** Gabriel Joseph Morbe Tangun, Lara Tavoschi, Marco Prato, Chiara Scanagatta, Amodu Abiodun Rahem, Victoria Alawia Alberto, Sonia Goncalves, Giampietro Pellizzer, Cristina Ariani, Eleaonor Drury

**Affiliation:** Department of Translational Research and New Technologies in Medicine and Surgery, University of Pisa, Italy; Ministry of Health, South Sudan, Department of Translational Research and New Technologies in Medicine and Surgery, Doctors with Africa CUAMM, Genomics Surveillance Unit, Wellcome Sanger Institute

**Background:** Malaria is a public health problem in South Sudan, classified by WHO as High Transmission Country. The main issues hampering an effective response are: diagnosis is often clinically presumed and confirmation based on RDT only, as labs are rarely functioning; irrational treatment is highly common and complicated cases are poorly handled because of drugs and supplies stock out and staff low knowledge on malaria protocols; the definition and implementation of a comprehensive and evidence based malaria response plan is hampered by limited monitoring and evaluation and surveillance capacities. Data on different plasmodia species prevalence, drug-resistant strains, strains evading diagnostic tests are scarce/absent.

**Methods:** An Operational Research was conducted by University of Pisa in the framework of Doctors with Africa CUAMM intervention on malaria response in Western Equatoria State. 1,900 voluntary participants were enrolled at 3 PHCCs over 6 months, including pregnant mothers attending ANC and sick under-5 years children. Participants peripheral blood samples were collected and tested using rapid diagnostic test kits to detect Plasmodium spp. antigens according to standard guidelines. Additionally, blood samples were collected on filter paper to analyze plasmodial genomes, species-specific sequences, and loci associated with antimalarial drug resistance. This analysis was performed through Amplicon sequencing (AmpSeq), a method of Next Generation Sequencing (NGS), in collaboration with MalariaGEN.

**Results:** Plasmodium spp. was detected in 26% of participants by antigen testing and in 42% by AmpSeq. The AmpSeq results highlighted that 3% of infected participants harbor non-falciparum species that cannot be detected by the antigen test used in South Sudan, including P. vivax that has to be treated with primaquine in addition to artemisinin-based drugs. Mutations in the kelch13 gene were observed in 1% of infections and included a validated marker of artemisinin resistance (A675V). The quintuple dhfr-dhps haplotype associated with complete resistance to sulfadoxine-pyrimethamine (IRN-GE) was observed in 39% of infections. The generated data were shared with the NMCP and constitute the first molecular malaria surveillance information available in the country.

**Conclusion:** The study demonstrated the presence of various Plasmodium species and of drug resistance markers and this may suggest the NMCP to refine diagnostic and treatment protocols and policies, focusing on strengthening the capacity for malaria microscopy and promoting the use of more sensitive rapid diagnostic test (RDT). The study also calls for building capacity in malaria molecular surveillance in the country. Such efforts are expected to enhance malaria control effectiveness in South Sudan.

### **30. Metagenomic and Antimicrobial Resistance Genes Profiles in Urban Informal Settlement in Nairobi, Kenya Corresponding author:** Collins K. Kebenei

**Co-authors:** David Onyango, Cecilia Mbae, Oliver Drechsel, Kelvin Kering, Susan Kavai, Michael Muraya, Beatrice Ongadi, Shilla Mundalo, Michael Pietsch, Inga Eichhorn, Stephan Fuchs, Lothar H Wieler, Antje Flieger, Samuel Kariuki **Affiliation:** Kenya Medical Research Institute, Maseno University, Robert Koch Institute

**Introduction:** Antimicrobial resistance is an escalating global health threat, with environmental reservoirs playing a pivotal role in the persistence and spread of resistance genes. Urban informal settlements, characterized by inadequate Water sanitation Sanitation and Hygiene (WASH) infrastructure, amplify microbial connectivity across ecosystems, promoting the dissemination of antimicrobial-resistant pathogens. Yet, the diversity and distribution of antimicrobial resistance genes (ARGs) in these settings remain poorly explored. This study examined ARGs, mobile genetic elements (MGEs), and microbial communities found in drinking water, effluent, soil, and raw sewage in an informal settlement in Nairobi, Kenya.

**Methods:** We analyzed 273 samples collected between June 2021 and July 2023 using shotgun metagenomics and identified 252 ARGs conferring resistance to multiple antibiotic classes.

**Results:** Broad-spectrum beta-lactamase genes (blaCFX, blaACT, blaCTX) and trimethoprim-resistant genes (dfrA) were the most abundant across all ecosystems. Raw sewers exhibited the highest ARG diversity (196/252), followed by drinking water (191/252), which also harbored blaNDM, a gene associated with carbapenem resistance. The effluent and soil showed moderate ARG diversity (176/252) and lower (152/252), respectively, with soil samples containing disinfectant resistance genes (qacE, qacE $\Delta$ 1). MGE analysis showed a huge diversity of plasmids, with soil samples exhibiting the highest diversity (66/92). Insertion sequences were abundant across samples, peaking in effluent (170/571) and drinking water (151/571), while transposons, though less common, followed a similar trend, peaking in effluent (7/18) and drinking water (6/18) samples, respectively. Microbial profiling revealed 28 taxa, with soil showing the highest bacterial diversity. Notably, Salmonella enterica, Escherichia coli, and Proteus columbiae, together constituted over 96% of the bacterial community across all samples.

**Conclusion:** The detection of ARGs and MGEs in drinking water and across interconnected environments highlights serious public health risks, particularly for vulnerable populations in resource-constrained settings. These findings emphasize the need for integrated surveillance and WASH infrastructure improvements to curb the spread of antimicrobial resistance and safeguard public health.

#### 31. Molecular Characterization of Urogenital Schistosomiasis in Shinyanga and Misungwi Districts, North-Western Tanzania in year (2021) Using Rapid Diagnostic Multiplex PCR

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Affiliation: National Institute for Medical Research (NIMR), Mwanza Centre

**Background:** Schistosomiasis is a waterborne parasitic disease affecting over 200 million people worldwide, with sub-Saharan Africa accounting for over 90% of reported cases. Tanzania is only second to Nigeria in terms of prevalence and is

endemic for intestinal and urogenital schistosomiasis caused by Schistosoma mansoni and Schistosoma haematobium, respectively. The prevalence of S. haematobium is over 50%, while S. mansoni is over 90%. Preventive chemotherapy with praziquantel (PZQ) is the main intervention in endemic areas. Recent studies have shown up to 36% of Schistosoma species hybrids in West Africa, highlighting their role in the epidemiology of schistosomiasis. This study aims to investigate the impact of praziquantel treatment on the prevalence of urogenital schistosomiasis and to assess the molecular epidemiology of S. haematobium and S. haematobium-bovis hybrids among infected individuals.

**Methods:** In a cross-sectional study, the Kish formula was used to calculate sample size. Urine samples were collected from 1,910 individuals in the southern villages of Lake Victoria and screened for S. haematobium eggs by urine filtration technique. Individual miracidia from each egg-positive sample were genetically characterized using Rapid Diagnostic Multiplex PCR. The median Wilcoxon rank-sum test was used to assess the distribution of infection intensity. The Chi-square test was used to compare proportions. Multivariate logistic regression identified predictors of S. haematobium infection.

**Results:** Schistosoma haematobium prevalence before treatment was 6.4% (n=123/1910) (range 1.3% - 9.3%), varying significantly across villages ( $\chi^2 = 24.4$ , P < 0.001), age group, and gender (P<0.001). The mean infection intensity of S. haematobium was 5 (2 – 7 eggs/10ml urine) and varied significantly between villages (P<0.001). The mean intensity was higher in school-aged children (7-14 years). Only 6.5% (n=8/123) had heavy infection intensity (>50 eggs/10 ml of urine). Sex was a significant predictor of infection. The odds of infection were 2.4 times higher in males than females (OR=2.4, 95% CI: 1.6-3.5, P<0.001). Post-treatment S. haematobium prevalence dropped to 0.3% (n=6/123) (range 0 - 9.5%), achieving a praziquantel cure rate above 90%. S. haematobium × S. bovis hybrids occurred in one village at 3.5%, with infections successfully treated with praziquantel.

**Conclusion:** The treatment showed significant positive outcomes, notably a low prevalence of S. haematobium post-treatment and complete reduction of S. haematobium-bovis hybrids, indicating effective disease burden reduction. Further investigation is needed to assess the intervention's broader implications and long-term sustainability.

## 32. Prevalence and factors associated with HIV-1 drug resistance mutations experienced in second line treatment of patients in Rwanda, 2012-2022

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Affiliation: Rwanda Biomedical Centre

**Introduction:** Human Immunodeficiency infection drug resistance (HIVDR) is a challenge in the control of HIV/AIDS pandemic. HIVDR is expected to emerge in population receiving antiretroviral. We targeted to calculate the prevalence and related factors of HIVDR mutations among PLHIV that received and resisted to second line treatment in Rwanda from January 2012 to December 2022.

**Methods:** A retrospective cross-sectional study was conducted on PLHIV that failed second line regimen from January 2012 to December 2022. Data collection based on data bank from patient files. The data collected were treatment duration, VL, CD4 count, ART regimen, drug resistance results (mutations), comorbidities, adherence, age, gender, education levels, marital status, residence, occupation and living situation. A regression model conducted to calculate crude odds and ratios and trend analysis of HIVDR mutations. A bivariate and multivariate logistic regression analysis used to identify associated factors with HIVDR mutations among PLHIV that received and failed to respond on second line HIV treatment.

**Findings:** In total, data of 1903 participants were analyzed, and the prevalence of HIV drug resistance mutations were found at 4.2%. Most commonly occurring mutation was Nucleoside Reverse Transcriptase Inhibitor (NRTI), M184V (42.5%). The likelihood of developing HIV drug resistance mutations was observed for PLHIV living in Eastern, AOR:3.8; 95% CI: 1.2–12.5; Northern province, AOR: 6.3; 95% CI: 1.2 – 20.5; Southern province, AOR: 5.5; 95% CI: 1.2-26 within business occupation AOR: 4.6; 95% CI: 1.07–19.97, within Jobless AOR:5.3; 95% CI: 1.34 – 20.9, and within drivers and prisoners AOR: 12.65; 95% CI:3.1 – 51.01.The likelihood of developing HIVDR mutations were found in PLHIV that failed second line regimen with comorbidities AOR: 6.4; 95% CI: 1.68 – 24.32; with bad adherence AOR: 6.24. 95% CI: 2.7 – 14.13; with high viral load AOR: 3.03; 95% CI: 1.17 – 7.73; with low CD4; with more than 5 years on second line treatment AOR: 8.8; 95% CI: 3.6 – 21.4; PLHIV with Zidovudine + Lamivudine + Atazanavir/ritonavir (AZT+3TC+ATV/r) as second line ART AOR: 5.34; 95% CI: 1.35 – 21.13.

**Conclusion:** The prevalence of HIVDR mutations is 4.2% and was associated with poor adherence, comorbidities, low CD4 counts, high VL, ART duration, ART regimen and other demographic factors.

#### 33. Psychometric properties of the EORTC QLQ-C30 in Uganda

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#### Affiliation: Uganda Cancer Institute

**Background:** Self-reported measures play a crucial role in research, clinical practice, and health assessment. Instruments used to assess self-reported health-related quality of life (HRQoL) need validation to ensure that they measure what they are

intended to, detect true changes over time, and differentiate between subjects. A generic instrument measuring HRQoL adapted for use among people living with cancer in Uganda is lacking; therefore, this study aimed to evaluate the psychometric properties of the European Organization for Research and Treatment of Cancer (EORTC) QLQ-C30 in patients with cancer in Uganda.

**Methods:** Adult patients with various types of cancer (n = 385) cared for at the Uganda Cancer Institute answered the EORTC QLQ-C30 in Luganda or English language, the two most spoken languages in the country. The two language versions were evaluated for data quality (floor and ceiling effects and missing responses), reliability (internal consistency), and validity (construct, known group, and criterion). Construct validity was examined through confirmatory factor analysis (CFA). Mean scores were compared between groups differing in disease stage to assess known-group validity. Criterion validity was examined according to associations between two QLQ-C30 subscales (Global quality of life and Physical function) and the Karnofsky Performance Scale (KPS). **Results:** Floor and ceiling effects were observed for several scales in the Luganda and English versions. All EORTC scales except Cognitive function (Luganda  $\alpha$  = 0.66, English  $\alpha$  = 0.50) had acceptable Cronbach's alpha values (0.79–0.96). The CFA yielded good fit indices for both versions (RMSEA = 0.08, SRMR = 0.05, and CFI = 0.93). Known-group validity was demonstrated with statistically significant better HRQoL reported by patients with disease stages I–II compared to those in stages III-IV. Criterion validity was supported by positive correlations between KPS and the subscales of Physical function (Luganda r = 0.75, English r = 0.76) and Global quality of life (Luganda r = 0.59, English r = 0.72).

**Conclusion:** The Luganda and English versions of the EORTC QLQ-C30 appear to be valid and reliable measures and can be recommended for use in clinical research to assess HRQoL in adult Ugandans with cancer. However, the cognitive scale did not reach acceptable internal consistency and needs further evaluation.

#### 34. The Prevalence of Allergic Rhinitis Among Adults in Juba City, South Sudan

#### Corresponding authors: Alfred A. Mariak

#### Affiliation: University of Juba

**Introduction:** Due to its detrimental effects on socioeconomic growth, including absenteeism and poor performance at work and schools, allergic rhinitis has become a major health concern in South Sudan. However, some individuals with allergic rhinitis are unaware that they have it, which results in underdiagnosis and unnecessary medical expenses that impact healthcare and productivity. Therefore, the collective effects of social irritability, absenteeism, and inefficiency at work impede the social and economic progress of those affected and the country overall.

**Methods:** The adapted a cross-sectional study design. The study was conducted at Juba Teaching Hospital, centrally located in Juba City. Systematic random sampling was used to reach 203 respondents using structured questionnaires. The study used EpiData software v4.7 to ensure quality data entry and SPSS v27 for analysis. Frequencies and percentages at 95% confidence level and chi-square tests were performed.

**Results:** Of the respondents (203), male: 138 respondents (68%) are male with the 95% confidence interval (95% CI) for this percentage ranges from 61.1% to 73.9%; female: 65 respondents (32%) are female, with a (95% CI) from 26.1% to 38.9%. Age: 15 - 24 years: 41 respondents (20.2%) fall within this age group, with a (95% CI) of 14.3% to 25.6%; 25 - 30 years: 124 respondents (61.1%) are in this age range, with a (95% CI) 54.7% to 68.5%; 31 –40 years: 24 respondents (11.8%) are in this age group, with a (95% CI) of 7.4% to 16.3%; 41 years and above: 14 respondents (6.9%) fall into this category, with a (95% CI) of 3.4% to 10.8%. The prevalence of allergic rhinitis was 37.9%. The following were statistically significant associated with allergic retinitis: Age, p-value (0.013); family history of allergies p-value (<0.001); employment status p-value (0.007); and the history of allergies in the family p-value (<0.001).

**Conclusion:** This study found that the prevalence of allergic rhinitis was high among adults in Juba City. actors associated with allergic rhinitis, most notably age, family history of allergies, employment status, and the history of allergies in the family. A notable portion had asthma, influenza, or other respiratory issues as comorbidities. Therefore, it is recommended that Public Health Awareness Campaigns: Raise awareness in Juba City about the high prevalence of allergic rhinitis, focusing on recognizing symptoms and seeking early treatment. This could be through social media, radio, and community outreach.

#### 35. Malaria Transmission Dynamics, Status and Insecticide Resistance in Anopheline Mosquitoes in Isiolo County, Northeastern Kenya

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Co-authors: Damaris Matoke-Muhia, Daniel Kiboi, Lucy Wachira, Sarah Nyasende, Luna Kamau

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**Introduction:** Increased malaria transmission in locations with little or no knowledge on vectors is a serious public health concern for disease control. Areas with a high malaria case count are known in Kenya; however, the introduction of malaria

in non-endemic areas warrants further investigation. Isiolo County is one of the locations that has seen recent malaria outbreaks, yet knowledge on malaria transmission in the area is limited; so, this study is intended to address this gap.

**Methods:** Adult mosquitoes were collected from indoors using CDC light traps and hand aspirators, while larvae were collected with dippers. A randomised study design was used to select six villages in Isiolo County's three sub-counties that were surveyed. The collection took place between June 26, 2019, and May 25, 2021, amid both short and long rains. Morphological identification was performed using Gillies and Coetzee's 1987 keys. The complexes were identified as subspecies using the techniques developed by Scott et al. (1993). Females were tested for Plasmodium falciparum sporozoite infection and blood meal source using enzyme-linked immunosorbent assays (ELISA) (Wirtz et al., 1987). Insecticide susceptibility tests were performed on a 2–5-day-old emerging adult Anopheles mosquito, following WHO 2016 recommendations.

**Results:** 1640 Anopheles gambiae s.l. were collected from the three sub-counties and two villages in each sub-county: Merti at 35.3%, Mataarba at 32.6%. Tene 12.3% Gubadida 5.5%, Ngaremara 8.6% and Eremet 5.5% in northern Kenya. 1586 mosquitoes were successfully amplified and identified as 1.3% Anopheles parenesis and 98.7% Anopheles arabiensis. None of the 1samples collected were positive for Plasmodium falciparum sporozoite. 125 were blood-fed: 76% of mosquitoes fed on humans, 3.2% Goat, Cat, Human/Dog, 0.8% Cat/Dog, and 1.6% Bovine, Human/Cat. The mosquito insecticide susceptibility test used Permethrin and Deltamethrin on Anopheles gambiae. Permethrin: 81% 60 min and 100% Knockdown; Deltamethrin 60 min 59% and 100% Knockdown after 24 hours.

**Discussion and Conclusion:** *Anopheles arabiensis* is the most abundant mosquito in Isiolo County; however, it is susceptible to pyrethroids. During the sampling period, none of the malaria vectors was positive for Plasmodium indicating low or no active malaria transmission in the area. Malaria vector control methods must be implemented to counteract any future malaria outbreaks in the county.

## 36. Xpert MTB/RIF Ultra CT Value: A Quick Indicator of Sputum Bacillary Load and Smear Status Prediction in Individuals with Pulmonary Tuberculosis.

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**Background:** Tuberculosis (TB) remains a global health threat, necessitating continuous advancements in diagnostic techniques for effective management and control. This study aimed to evaluate the diagnostic utility of smear microscopy and the Xpert MTB/RIF Ultra test in TB diagnosis, focusing on the correlation between Cycle threshold (CT) values and disease severity.

**Methods:** A prospective cross-sectional study was conducted in the Kilimanjaro region, enrolling 472 participants suspected of TB. Sputum samples were subjected to smear microscopy, Xpert MTB/RIF Ultra testing, and comprehensive laboratory procedures. Ethical approval was obtained from local and national ethical review boards.

**Results:** The study revealed discrepancies between smear microscopy and GeneXpert testing in identifying patients with high bacterial loads. The Xpert MTB/RIF Ultra test demonstrated high specificity in detecting TB cases, with promising results in identifying individuals with high bacterial burdens. Analysis of CT values revealed a negative correlation with smear grading, suggesting the potential utility of CT values as predictive biomarkers for disease severity.

**Conclusion:** This study underscores the importance of advanced diagnostic techniques, such as the Xpert MTB/RIF Ultra test, in enhancing TB diagnosis and management. The correlation between CT values and disease severity highlights the potential of CT values as predictive indicators, offering promising prospects for personalized treatment strategies. Addressing discrepancies between diagnostic methods and further research into CT value correlations are essential for refining TB diagnostic protocols and improving patient outcomes globally.

## 37. Evaluating the Performance of HRP2-Based RDTs in Asymptomatic Malaria Amidst pfhrp2/3 Gene Deletions in Tanzanian Villages

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#### Co-author: Winifrida Kidima

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**Background:** Dual deletions of the hrp2/hrp3 genes in Plasmodium falciparum isolates are increasingly being reported in malariaendemic countries. However, data on the prevalence of hrp2/hrp3 gene deletions in P. falciparum parasites, particularly in asymptomatic malaria populations, are limited, highlighting the need for further investigation of this issue in Tanzania.

**Methodology:** This cross-sectional, household-based community survey was conducted from December 2022 to July 2023 in 12 Tanzanian villages (8 with high malaria transmission and 4 with low endemicity). The survey aimed to assess the prevalence

of pfhrp2/3 gene deletions in asymptomatic P. falciparum infections and evaluate the performance of HRP2-based rapid diagnostic tests (RDTs) and light microscopy (LM). A total of 3,489 participants were enrolled, with field diagnoses made using HRP2-based RDTs (Bioline<sup>TM</sup> Malaria Ag P.f/Pan: Abbott, Chicago, IL, USA) and LM. P. falciparum infections were confirmed through species- specific quantitative PCR (qPCR) (Agilent, Santa Clara, CA, USA), followed by single-copy amplification of MSP1 using nested PCR (ProFlex PCR system, Life Technologies). A multiplex qPCR was performed on P. falciparum isolates that were successfully amplified at MSP1 to detect pfhrp2/3 gene deletions. The prevalence of hrp2/3 gene deletions was calculated as the percentage of samples, and statistical analysis was performed using GraphPad Prism 8.0.2.

**Results:** The pfhrp2/3 gene deletions were present in 13.2% of the isolates, with 7.7% showing a single pfhrp2 deletion, 3.4% a single pfhrp3 deletion, and 2.1% exhibiting dual deletions. All parasites with dual deletions were missed by the RDT. The sensitivity (74.07%) and accuracy (80.84%) of the RDT were significantly higher than those of light microscopy (LM), which had a sensitivity of 49.52% and an accuracy of 72.46%. However, LM showed slightly higher specificity (96.08%) compared to the RDT (87.74%), though the difference was not significant. The HRP-based RDT demonstrated a kappa coefficient of 0.6173, indicating good agreement with qPCR diagnostic assays. Both the positive and negative predictive values of the RDT were above 80%, making it a reliable tool for detecting asymptomatic infections.

**Conclusion:** As Tanzania moves forward with malaria elimination, monitoring pfhrp2/3 gene deletions, particularly in the asymptomatic population, is crucial, as their presence may delay or undermine treatment effectiveness. While the RDT remains effective for detecting asymptomatic P. falciparum infections, the emergence of pfhrp2/3 dual deletions could pose challenges for its future performance. These findings provide essential baseline data for ongoing surveillance and screening efforts in Tanzania.

#### 38. The Effects of Hepatitis-B Virus Co-infection on CD4 Cell Count Recovery in HIV Infected Patients on antiretroviral therapy (ART) in the Tigray region of northern Ethiopia: A Retrospective Cohort Study Corresponding author: Haileselassie Bisrat Bidre

**Co-authors:** Haileselassie Bisrat Bidre, Teklemicael. DM, Gebrewahid. GH, Teame.G, Tekulu. FG, Gebrethadikan.YH, Birhanu MA, Kahsay. AB

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**Background:** By the end of 2022, around 39 million HIV-positive people worldwide, more than half of the cases in Eastern and Southern Africa. The Hepatitis B Virus (HBV) is one of the most critical factors driving HIV drug resistance, resulting treatment failure and poor adherence. A significant decrease in cluster of differentiation-4 (CD4) deconstructs the T- cell immune system in the body. Therefore, the aim of this study is to assess the effects of Hepatitis-B Virus Co-infection on CD4 Cell Recovery in HIV Infected Patients on antiretroviral therapy (ART) in the Tigray region.

**Methods:** A retrospective cohort study design was conducted. Randomly sampling method was used in Mekelle city from January 2009 to February 2018. The total sample size was 466, including 94 were HIV-HBV co-infected and 372 were HIV mono-infected. Data was entered, cleared and coded into Epi-info 7, and analyzed using the poison regression model in STATA version 14.

**Results:** Of the total patients, 294(64%) were females. The majority 199(43%) of the participants were in the age group between 15 and 30 years old. 36 (38.3%) participants in the HIV- HBV exposed group had CD4 counts greater than 200 cells/ $\mu$ l, while 58 (61.7%) clients in the HBV unexposed group had CD4 counts below 200 cells/ $\mu$ l. Compared to HIV mono-infected, the change of CD4 cell count over time was 0.25 units lower among the HIV- HBV co-infected individuals (adjusted coefficient -0.25; 95% CI: -0.26 to -.23).

**Conclusion:** The HIV-HBV co-infected group showed a low rate of CD4 cell recovery. Then, HIV-infected people receiving antiretroviral therapy (ART) should be tested for HBV coinfection. It is also suggested to do a prospective cohort research to investigate the impact of HIV/HBV co-infected patients' care on immune recovery.

## 39. Molecular Characterization of HIV-1 Subtypes Circulating in antiretroviral therapy exposed individuals in Western Kenya

#### Corresponding author: Maureen Adhiambo

**Co-authors:** Olipher Makwaga, Ferdinard Adungo, Humphrey Kimani, David Mulama, Jackson Korir, Matilu Mwau **Affiliation:** Kenya Medical Research Institute, Masinde Muliro University of Science and Technology

**Background:** High HIV-1 infection rates and genetic diversity especially in African population pose significant challenges in management of HIV. In Sub-Saharan Africa, Kenya is one of the Countries with high HIV and AIDS burden. The virus is a major health challenge in the Country and causes mortality and morbidity as well as straining the health care system and the economy. Busia County where the study area is located is one of the most affected Counties with a HIV-1 prevalence of 7.7%

which is above the national HIV-1 prevalence which stands at 4.9%. HIV-1 genetic diversity studies in the County were done over a decade ago and due to increase in genetic diversity of HIV-1 due to its variability the study seeks to find new strains of the virus circulating in this study population.

**Methods:** 120 HIV-1 positive individuals one year and above on antiretroviral therapy were recruited in the study. The samples were subjected to laboratory procedures and the resulting sequences of the partial pol region were submitted to the Genbank for assignment of accession numbers. Sequences in FASTA format were submitted to the jumping profile hidden Markov Model for generation of HIV-1 subtypes and recombinants. Pair wise and multiple alignment of the sequences was done using MEGA 7 ClustalW program and phylogenetic tree constructed using MEGA7 Maximum Likelihood method.

**Results:** Sequence analysis showed that HIV-1 subtype A1 was the predominant subtype 43 (68.3%) among the study participants followed by subtype D 8 (12.7%), subtype C 1 (1.6%), subtype G 1 (1.6%), B 1 (1.6%) and inter-subtype recombinants A1-A2 1 (1.6%), A1-D 3 (4.8%), A1-C 1 (1.6%), BC 1 (1.6%) in that order. Recombinants A1-B 2 (3.2%) and BD 1 (1.6%) that have not been identified in genetic diversity studies in Kenya were reported in this study. Phylogenetic analysis of the sequences showed diverse clusters with some clades more closely related and others more distantly related.

**Conclusion:** Increased HIV-1 genetic diversity was observed which not only pose a challenge in disease control and management but also future drug design development. The outcomes of this study add to the existing knowledge of HIV-1 subtypes for instance the identification of new recombinants that have never been reported previously in Kenya. The findings will be used to inform public health policies. Therefore, there is need for continues surveillance to enhance future understanding of the geographical distribution and transmission patterns within the HIV pandemic.

#### 40. Performance and Comparative Evaluation of a Novel Diagnostic Assay, Novaplex<sup>TM</sup> Malaria Assay, against Routine Diagnostic Techniques in the Detection of Different *Plasmodium spp*. in Kenya

### **Corresponding author:** Lewis Karani

Affiliation: Kenya Medical Research Institution

**Background:** Accurate and rapid malaria diagnosis is essential for effective treatment and control. Additionally, precise species identification is critical in guiding treatment strategies, as different Plasmodium species require tailored therapeutic approaches. This study aimed to evaluate the performance of a novel malaria diagnostic kit, Novaplex<sup>TM</sup> Malaria Assay, compared to standard and routine diagnostic techniques, including microscopy, rapid diagnostic tests (RDTs), and quantitative polymerase chain reaction (qPCR), which was used as the "gold standard" for this comparison.

**Methods:** A total of 142 suspected malaria cases from Matayos, a malaria-endemic region in Kenya, were sampled. Whole blood samples were collected, and Plasmodium parasite detection and species identification were performed using microscopy, RDTs, the Novaplex<sup>TM</sup> Malaria Assay, and qPCR. Sensitivity, specificity, positive predictive value (PPV), negative predictive value (NPV), accuracy, and agreement (Cohen's kappa) were calculated to assess the diagnostic performance of the Novaplex<sup>TM</sup> assay relative to qPCR and other diagnostic methods.

**Results:** Our analyses demonstrated that the Novaplex<sup>TM</sup> assay outperformed microscopy and RDTs in terms of sensitivity, accuracy, and NPV. The assay exhibited strong diagnostic agreement with qPCR and performed comparably in species identification. Using qPCR as the gold standard, the Novaplex<sup>TM</sup> assay achieved a sensitivity of 95.5% and specificity of 87.5%, whereas microscopy and RDTs had sensitivities of 63.7% and 61.5%, respectively. The Novaplex<sup>TM</sup> assay also demonstrated a PPV of 99.2% and an NPV of 53.9%, in contrast to the significantly lower NPV values of microscopy (12.5%) and RDTs (11.9%). The overall accuracy of the Novaplex<sup>TM</sup> assay was 95.1%, with a substantial agreement with qPCR ( $\kappa = 0.642$  [0.398–0.885]). In contrast, microscopy and RDTs had accuracy levels of 65.5% and 63.4%, respectively, with only slight agreement to qPCR ( $\kappa = 0.148$  [0.047–0.248] and  $\kappa = 0.136$  [0.042–0.230], respectively).

**Conclusion:** The findings of this study indicate that the Novaplex<sup>TM</sup> Malaria Assay surpasses microscopy and RDTs in diagnostic performance and demonstrates comparable accuracy to qPCR in Plasmodium species identification. Given qPCR's low limit of detection in malaria diagnosis, the Novaplex<sup>TM</sup> assay's high sensitivity, specificity, and agreement with qPCR suggest its potential as a reliable diagnostic tool. Integrating this assay into routine clinical practice could enhance malaria diagnosis, enabling timely and precise treatment, improving surveillance efforts, and strengthening malaria control strategies. Further validation and field evaluations are necessary to confirm the feasibility and cost-effectiveness of this assay in diverse, resource-limited, malaria-endemic settings.

#### 41. Phenotypic characterization of pseudokinase pPK4 knockout lines in Plasmodium yoelii

#### Corresponding author: Edwin Too

Affiliation: Kenya Medical Research Institute

**Background:** Human malaria is a major public health problem, with 263 million cases and 597,000 deaths in 2023 (WHO, 2024). It affects pregnant women and children under 5 years in Sub-Saharan Africa. It is caused by Plasmodium parasites

replicating in red blood cells, and merozoites invade new cells to multiply in the host. Gametocytes form in hosts and are responsible for the transmission to Anopheles vector mosquitoes, where they transform into gametes in the midgut. Pseudokinases are a class of proteins that resemble typical kinases but cannot catalyze phosphorylation reactions. Several Plasmodium pseudokinases are highly transcribed at the sexual stage and may have critical roles at this stage. The main of the study was to evaluate two Plasmodium pseudokinase pPK4, in Plasmodium yoelii highly transcribed at the schizont stage. This pseudokinase is highly transcribed at the male gametocyte stage.

**Methods:** CRISPR cas9 technique was used to generate two clones of pPK4 knockout lines and myc- tagged transgenic parasites. An Immunofluorescence assay was used to detect the expression of the proteins in myc-tagged transgenic parasites of pPK4. To evaluate parasitemias, at least 10,000 RBCs or 100 parasites were counted, and differences were determined by one-way ANOVA followed by a post-hoc Tukey's multiple comparison test using GraphPad Prism 6.

**Results:** Immunofluorescence assay of transgenic parasites expressing Myc-tagged pPK4 verified that proteins were expressed in schizonts and sexual stages. P. yoelii. pPK4-KO lines exhibited a significant growth defect, decreased virulence in mice, and a significant reduction in the number of exflagellation centers and oocysts p<0.01.

**Conclusion:** The phenotype of the pPK4-KO lines mirrors that of the previously characterized *P yoelii* knockout line of another pseudokinase pPK1.

### 42. HIV virological failure with Dolutegravir among female sex workers in Western, Kenya: Preliminary reports of HIV drug- resistance

#### Corresponding author: Olipher Makwaga

Co-authors: Elizabeth Bukusi, Carey Faraguhar, Patrick Okoth, Matilu Mwau, Bhavna Chohan

**Affiliation:** Kenya Medical Research Institute | Kenya Medical Research Institute; University of Washington, Masinde Muliro University of Science and Technology

**Background:** The current antiretroviral therapy regimens combination containing Integrase like dolutegravir is recommended for the treatment of HIV infected adults in the most recent guidelines in Kenya. Almost 80% of HIV infected adults have switched to this drug. Past studies have reported virological failure due to raised viral loads among individuals taking non-Integrases. However, limited studies have been conducted on the current antiretroviral. Therefore, the study aimed at determining the prevalence of adults showing virological failure due to elevated viral loads of more than 1000 copies/ml.

**Methodology:** This was a prospective study conducted in 2021 and 2024 among female sex- workers visiting Busia health facilities. Plasma samples were collected from 500 HIV- infected female sex workers on Dolutegravir (DTG) and non-DTG drug regimen combination. Samples were subjected to viral load tests at KEMRI-CIPDCR. A simple questionnaire was used to collect variables such as type of HAART, duration of ARVs uptake, the prevalence of comorbidities thus hypertension, diabetes and cancer was also collected. SPSS version 25 was used for data analysis.

**Results:** Out of the 500 female sex workers, 207 (41.4%) had viral loads of more than 1000 copies/ml for consecutive three visits signifying virological failure. Out of the 207 samples, 156 (75.4%); 15(7.2%); 14(6.8%); 11(5.3%) and 11(5.3%) were on TDF/3TC/DTG; TDF/3TC/LPVr; TDF/3TC/NVP; TDF/3TC/ATVr and TDF/3TC/EFV HAART respectively. The prevalence of Hypertension; diabetes and cancer were 41(19.8%); 2(1%) and 2(1%) respectively. The majority of the participants 77 (37.2%) had taken ARVs for more than 10 years, this was followed by 64(30.9%), 58(28%) and 8(3.9%) participants who had taken ARVs for the last 1-5 years, 6-10 years and less than a year respectively. Preliminary analysis showed association between hypertension and longer periods of sex work, the type of HAART and duration of ARVs uptake among the participants by recording  $\chi$ 2 values of p=0.022 and 0.006 respectively.

**Conclusion:** High virological failure that is reported in this study is of clinical importance. This calls for drug-resistant mutations and polymorphism determination nationally and elsewhere. Our clinic has planned to do this in order to advise the clinicians on the appropriate treatment options for this group of persons. It is essential to perform continuous surveillance of dolutegravir drug-resistance testing as well as its clinical effect since drug-resistance mutations to antiretroviral drugs are not included in routine HIV-1 genotypic testing in Kenya.

## 43. Assessment of different genotyping markers and algorithms for distinguishing *Plasmodium falciparum* recrudescence from reinfection in Uganda

Corresponding author: Alex Mwesigwa

#### Affiliation: Kabale University

**Background:** Antimalarial therapeutic efficacy studies are crucial for monitoring drug effectiveness in malaria-endemic regions. The WHO recommends genotyping polymorphic markers, including msp-1, msp-2, and glurp, to distinguish recrudes-cences from reinfections. Recently, the WHO proposed replacing glurp with highly polymorphic microsatellites (Poly- $\alpha$ ,

PfPK2, TA1). However, the optimal combinations of these markers with msp-1 and msp-2, as well as the performance of various algorithms for classifying recrudescence, have not been systematically assessed. This study aimed to investigate different microsatellites alongside msp-1 and msp-2 for molecular correction and to compare various genotyping algorithms across three sites in Uganda.

**Methods:** We analyzed paired samples from patients who experienced malaria recurrence in a therapeutic efficacy study assessing the efficacy of artemether-lumefantrine (AL) and dihydroartemisinin-piperaquine (DP) at three sites in Uganda. DNA extracted from dried blood spots was used to genotype msp-1, msp-2, and glurp, as well as seven alternative microsatellites to replace glurp. We assessed the diversity of each marker across the sites and employed three different algorithms (3/3,  $\geq$  2/3 and Bayesian) to classify each infection as either recrudescence or reinfection.

**Results:** Microsatellites 313, Poly- $\alpha$ , and 383 exhibited the highest diversity, while PfPK2 and Poly- $\alpha$  showed elevated multiplicity of infection (MOI) across all sites. The 3/3 match-counting algorithm classified significantly fewer recrudescences than both the  $\ge 2/3$  and Bayesian algorithms at probability cutoffs of  $\ge 0.7$  and  $\ge 0.8$  (P < 0.05). The msp-1/msp-2/2490. combination identified more recrudescences using the  $\ge 2/3$  and 3/3 algorithms in the AL treatment arm, while the msp-1/msp-2/glurp combination classified more recrudescence using the  $\ge 2/3$  algorithm in the DP arm.

**Conclusion:** This study suggests that microsatellites PfPK2 and Poly- $\alpha$ , potentially sensitive to detecting minority clones, are promising replacements for glurp. Discrepancies in recrudescence classification between match-counting and Bayesian algorithms highlight the need for standardized PCR correction practices.

#### Sub-theme 3: Harnessing digital solutions to strengthen health systems

#### 44. Information system for integrating clinical and genomic infectious disease data in Tanzania Corresponding author: Melkiory Beti

**Co-authors:** Patrick Kimu, Boaz Wadugu, Davis Kuchaka, Willfred Senyoni, Happiness Kumburu, Tolbert Sonda **Affilaition:** Kilimanjaro Clinical Research Institute (KCRI), University of Dar es Salaam

**Background:** Infectious diseases are a serious issue in public health in low- and middle-income countries like Tanzania, where the use of information systems that integrate clinical and genomic data is limited due to the different data generation sources. To tackle this challenge, we developed a system that links clinical data from a customised District Health Information System 2 (DHIS2) with genomic data sequenced from Nanopore machines and analysed by the cgetools pipeline. The system helps users to view clinical and genomic data, such as patient symptoms and their multiple identified pathogens.

**Methods:** Clinical data were collected using customised DHIS2, an open-source software widely used in Tanzania, and R scripts that query the DHIS2 API to securely fetch clinical data and integrate it with genomic results from the CGETools bioinformatics pipeline, which uses tools like KmerFinder to identify pathogens from a single sample. Using the R Shiny web framework, the interactive web interface developed enables users to search patient IDs and view their clinical and genomic data.

**Results:** The system managed to integrate 21 datasets, linking clinical parameters like patient disease symptoms such as diarrhoea and fever, gender and age with genomic data showing identified pathogens. Allow users to search for patient IDs, retrieve relevant data, and visualise pathogen trends through interactive bar graphs, aiding epidemiological monitoring and outbreak detection.

**Discussion:** This data integration system development demonstrated the importance of linking clinical and genomic data for infectious disease surveillance. Use of an existing and open-source system like DHIS2 and cgetools pipeline facilitated efficient pathogen detection from single patient samples. Additionally, the visualization features proved essential for supporting real-time clinical decision-making.

**Conclusion:** By integrating clinical and genomic data, the system improved patient diagnosis, timely outbreak detection, and effective disease control. The scalable can be extended to other disease settings, contributing to improved public health outcomes.

#### **45. Integration of Machine Learning Algorithms in Yellow Fever Surveillance Data Analysis in Kenya Corresponding author:** Seth Ouma Okeyo

Affiliation: Kenya Medical Research Institute

**Background:** Yellow fever (YF) remains a major public health threat in Kenya, with sporadic outbreaks posing significant risks to at-risk populations. Traditional surveillance systems often lack the predictive capabilities needed for proactive monitoring. The integration of machine learning (ML) algorithms into YF data analysis can improve early outbreak detection by identifying key patterns in data related to climate, population density, and historical case distribution.

**Methods:** We applied supervised ML models, including logistic regression, decision trees, and neural networks, to historical and real-time YF data from various sources, such as meteorological data, population movements, and previous YF incidence records. Model training aimed to classify and predict potential outbreak locations, focusing on high-risk regions.

**Results:** The ML-integrated surveillance system provided an 85% accuracy rate in detecting high-risk areas. Additionally, the models identified significant correlations between climatic factors and YF incidence, highlighting environmental triggers that could signal future outbreaks.

**Conclusion:** Machine learning offers a robust enhancement to YF surveillance in Kenya, enabling data- driven risk assessments and targeted public health responses. The integration of ML models in surveillance allows for advanced risk mapping and timely resource allocation, reinforcing the country's ability to manage YF threats proactively. Further development will refine accuracy and broaden the application of ML for real-time infectious disease monitoring in Kenya.

# 46. Predicting Mosquito Age and Species with Mid-Infrared Spectroscopy and AI: A Cost-Effective Alternative Method for Enhanced Malaria Surveillance, Ifakara Health Institute, Tanzania: 2024 Corresponding author: Okot Amos

**Co-authors:** Mauro Pazmiño Betancourth, Mario González-Jiménez

**Affiliation:** Kampala Capital City Authority, Vector Biology and Disease Interest Group, School of Biodiversity, One Health, and Veterinary Medicine, University of Glasgow, Glasgow,

**Background:** Between 2000 and 2015, insecticide-based interventions, such as Long-Lasting Insecticide- Treated Nets (LLINs) and Indoor Residual Spraying (IRS), averted 537 millions malaria cases. However, despite these gains, malaria still caused 445,000 deaths in 2016. The rise of insecticide resistance among mosquito populations threatens the effectiveness of these interventions, highlighting the need for innovative tools to enhance vector surveillance. Accurate prediction of mosquito species and age is critical for controlling malaria transmission, yet traditional methods like PCR and dissection are labor-intensive and costly. This study evaluates the use of Mid-Infrared Spectroscopy (MIRS) and machine learning as a rapid, scalable, and cost-effective alternative for improving malaria surveillance.

**Methods:** We analyzed a publicly available MIRS dataset comprising 41,368 Anopheles mosquitoes (Anopheles gambiae, Anopheles funestus, and Anopheles coluzzii mosquitoes) from Burkina Faso, Tanzania, and Scotland. Selected wavenumbers were used to predict mosquito species and age, and supervised learning algorithms, including Random Forest (RF), were applied to compare accuracy against traditional methods like PCR. Quality control measures were incorporated, ensuring that spectra with low intensity or atmospheric intrusions were automatically discarded.

**Results:** The species prediction model achieved a modest 43% accuracy, attributed to the non- selection of the most representative wavenumbers. However, the age prediction model performed significantly better, with 94% accuracy achieved using the RF algorithm. These findings suggest that MIRS is particularly effective in predicting mosquito age. The method provides a scalable, cost-effective solution for vector control, offering rapid insights into mosquito populations.

**Conclusions:** MIRS combined with AI shows promise as a valuable tool for predicting mosquito age and species in resourcelimited settings. This study addresses critical gaps in mosquito surveillance, providing a faster, less expensive, and more accessible alternative to traditional methods. With further improvements in dataset size and algorithm refinement, MIRS could significantly enhance malaria control efforts by facilitating large-scale, accurate monitoring of mosquito populations. The urgency of the malaria crisis underscores the need for novel, efficient surveillance methods, particularly in regions where insecticide resistance is rising. Expanding this method's application could support more effective interventions, thereby reducing malaria transmission rates.

## 47. SNAICS - Snakebite awareness and Artificial Intelligence Identification in Communities: implementation and insight from South Sudan

#### Corresponding author: Gabriel Alcoba

**Co-authors:** Iona Crumley, Nan Hsin Chang, John Ruyonga Ibanda, Melat Haile, Iza Ciglenecki, Daniel Keer Thony Pasqualo, Noon Makor Arop, John Rumunu, Andrew Durso, Francois Chappuis, Monica Rull, Isabelle Bollon, Rafael Ruiz de Castaneda **Affiliation:** Médecins Sans Frontières (MSF), Switzerland, Ministry of Health, South Sudan, Florida Gulf Coast University, UNIGE University of Geneva

**Introduction:** Snakebite envenoming, one of the deadliest and most mutilating Neglected Tropical Diseases, affects 4-5 million people annually. Médecins sans Frontières (MSF) has worked on Snakebite with the Ministry of Health of South Sudan since 2014, focusing on improving clinical management, access to safer antivenoms, and prevention. MSF has collaborated with scientists globally, and recently worked with the University of Geneva to improve snake species identification in South Sudan using a novel AI-based system. The objective of this project was to train the Artificial Intelligence (AI) system to

recognise medically important under-documented South Sudanese snakes from photographs. The intended outcomes were threefold: i) improve knowledge of snake ecology, ii) work with local staff and the community to increase awareness and reduce risk, iii) improve clinical management of Snakebite.

**Methods:** A work-package including six interactive workshops, materials and SOPs was developed, to allow participants to i) safely photograph encountered snakes, ii) contribute to building a snake photograph database, and iii) raise awareness of Snakebite in the community. Material was created with local and international experts to cover snake toxinology, zoology, snakebite first aid, and "safe snake photography". MSF health promoters were supported by experts in herpetology, snake-rescuers, and clinicians. They were equipped with digital cameras with 30x-zoom to build the database with images from two MSF hospitals and surrounding villages. The database was supplemented with images crowdsourced from MSF staff's private photo collections. Photographs were sent to collaborating herpetologists for expert identification as the gold standard for AI training.

**Results:** The activity resulted in multiple benefits: i) 10 health promoters plus medical teams attended the sessions that were well received. ii) 10 participants, 5 in each site, were involved in snake photo collection. iii) 40 photos of multiple species were received. The presence of several non-venomous and venomous species was confirmed, of which one was a species with a previously unknown geographic range. iv) The collaboration increased common knowledge of snakes and snakebite in South Sudan.

**Conclusion:** A positive impact was observed on community awareness, knowledge and misconceptions, on snakebite epidemiology and snake ecology. One limitation was the relatively small number of photos taken to date due to competing priorities and seasonal snake activity. Scaling-up photo collection capacity would improve AI performance, as some inaccuracies remain. This innovative use of AI represents an opportunity to integrate real- world challenges such as Neglected Tropical Diseases with novel technology for patient benefit.

#### 48. Development of A Machine Learning-Based Early Warning System For Predicting Diarrhea Outbreaks Among Under-Five Children: A Case of Selected Regions In Tanzania

#### Author: Kimu Patrick

**Co-authors:** Beti Melkiory, Wadugu Boaz, Kuchaka Davis, Shayo Merian, Kumburu Happiness, Sonda Tolbert, Senyoni Wilfred

**Affiliation:** Kilimanjaro Clinical Research Institute, University of Dar es Salaam, Muhimbili University of Health and Allied Sciences, The Nelson Mandela African Institution of Science and Technology

**Background:** Diarrhea is a major public health issue in Low- and Middle-Income Countries (LMICs), especially for children whose immune systems are still developing. To address recurring outbreaks, surveillance systems have been established to collect crucial epidemiological data that guide public health interventions, optimize resource allocation, and inform policy decisions. However, these systems often lack predictive capabilities for early detection and proactive responses. This study aimed to develop an Early Warning System (EWS) for predicting diarrhea outbreaks among children under five in Tanzania. The study employed a retrospective observational design using secondary data from the SeqTanzania project (2021-2025), integrating data from six regional referral hospitals and the Tanzania Meteorological Authority (TMA) from April 2023 to April 2024. A workflow using Snakemake was developed to automate data accessibility, integration, preprocessing, feature selection, model evaluation, and the loading of the predicted dataset into DHIS2 for real-time visualization.

**Method:** Data preprocessing included cleaning, imputation, and feature selection via the Random Forest Cumulative Feature Importance method. Key predictors of diarrhea outbreaks were identified, with the survey date being the most influential, followed by weather variables such as relative humidity and maximum and minimum temperatures. Sociodemographic factors, including household literacy, also contributed. Six machine learning models were evaluated using ROC-AUC, precision, and recall. Decision Tree and Random Forest were the most reliable classifiers, with Random Forest achieving the highest ROC-AUC (0.82), a balanced sensitivity-specificity trade-off, and was selected for EWS implementation. The developed EWS was integrated into DHIS2 using an API for real-time prediction and visualization, aiding proactive public health interventions. The EWS captured seasonal outbreak trends, with peaks in October and November, particularly in Mwanza and Zanzibar.

**Results:** The findings align with existing literature, showing that climatic and socio-demographic factors influence diarrhea incidence. The model emphasizes the need for region-specific surveillance and predictive capabilities to mitigate outbreaks effectively. The study's reliance on hospital-based data limited insights into factors like sanitation and healthcare access.

**Conclusion:** Future research should include community-level data and real-time demographic and weather inputs to enhance prediction accuracy and improve the EWS's effectiveness in safeguarding children's health.

## **49. Development of A Field Deployable Handheld Electrochemical Biosensor for Detection of Aflatoxin B1 In Grains Corresponding author:** David Mtweve

Affiliation: Nelson Mandela African Institution of Science and Technology, Trade Policy Centre-Arusha

**Background:** Aflatoxins (AFs) are highly toxic compounds, with Aflatoxin B1 (AFB1) being the most harmful, necessitating rapid and reliable on-site detection to ensure food safety. In Tanzania, contamination of staple grains like maize and peanuts poses significant health risks and economic losses.

**Methods:** This study introduces a portable electrochemical biosensor for detecting AFB1 in grains. The biosensor utilizes a screenprinted electrode (SPE) pretreated with sulfuric acid and modified with bovine serum albumin (BSA), which serves as a scaffold for immobilizing anti-AFB1 antibodies via terminal carboxylic groups, reducing nonspecific binding. Differential Pulse Voltammetry (DPV) is employed for detection, with a wireless portable potentiostat transmitting results to a mobile device via Bluetooth. The study employs an experimental design to evaluate the biosensor's performance, and data analysis includes correlation assessments and statistical significance testing.

**Results:** The biosensor achieved a Limit of Blank (LoB) of 1.67 ng/mL, a Limit of Detection (LoD) of 2.058 ng/mL, and a dynamic range of 1–20 ng/mL, demonstrating high sensitivity. Specificity and sensitivity were validated against the ELISA gold standard, yielding a correlation coefficient of 0.92 and a significant p-value of 0.04, indicating robust diagnostic performance. Real-sample testing in maize and peanut matrices showed recovery rates of 90–105%, confirming its accuracy in diverse food systems. The biosensor's ability to differentiate AFB1 from fumonisin further highlights its selectivity.

**Conclusion:** The developed biosensor is a cost-effective, portable, and highly reliable tool for on-site mycotoxin monitoring in food safety applications, particularly suited for use in Tanzania to mitigate health risks associated with AFB1 contamination.

## Sub theme 4: Improve health financing and social protection, access to quality healthcare and services to accelerate the achievement of universal health coverage

#### **50. Use of Transient Elastography to detect Liver Fibrosis in Adults with Chronic Hepatitis B in Rural Uganda Author:** Boniface lumori

**Affiliation:** Department of Internal Medicine, University of Juba, Juba, South Sudan and Mbarara University of Science and Technology

**Background:** Liver fibrosis is a crucial stage in the progression of hepatitis B-related liver disease. Hence, we studied the prevalence of liver fibrosis using transient elastography among adults with chronic hepatitis B (CHB) in Mbarara Regional Referral Hospital (MRRH), Uganda.

**Methods:** We conducted a cross-sectional study from November 2023 to March 2024 and enrolled Adults aged 18 years and above with CHB (defined by two positive hepatitis surface antigens; at the baseline and at least six months later) at MRRH. Socio-demographics, comorbidities, and laboratory parameters were collected. Liver fibrosis was assessed by transient elastography (TE) and aspartate-to-platelet index (APRI). Liver fibrosis was considered when the TE liver stiffness measurement>7 kPa. Bi- and multi-variables logistic regression analyses were used to determine associations with liver fibrosis. A P<0.05 was considered statistically significant.

**Results:** Overall, 96 participants were y recruited. The median age was 33.5 (Interquartile range (IQR), 26-42.5) years, and 58 (69.4%) were males. Twelve (12.50%) participants had a history of smoking cigarettes and 15 (15.63%) used herbal medicines. The median duration of CHB infection was 2 (IQR,1-3) and those infected with CHB for 2 or more years were 35(36.46%). The median liver stiffness measurement was 6 (IQR, 4.8-8.0) kPa. The prevalence of liver fibrosis was 35.5% (95% C.I, 26.4-45.5) using TE compared to 21.9% (95% C.I; 14 - 31%) using APRI (score > 0.5). Increasing hepatitis B viral load by IU/mL [adjusted odd ratio (aOR) 1.02; 95% CI (1.01-1.04); p=0.001], smoking history [aOR 2.73; 95% CI (1.43-5.19); p=0.002], use of herbal medicines [aOR 2.48; 95% CI (1.16-5.28); p=0.018], hepatitis B duration ( $\geq$  2 years) [aOR 2.61; 95% C. I (1.44-4.72); p=0.001], aspartate-to-platelet ratio index (APRI) score > 0.5 [aOR 2.14; 95% CI (1.12-4.09); p=0.021] were independently associated with liver fibrosis.

**Conclusion:** At MRRH, liver fibrosis was relatively prevalent among people with CHB using TE to assess. Close monitoring and initiation of antiviral therapy in CHB individuals with high viral loads, high APRI, and a long duration of infection Where available, TE should be the preferred modality for screening liver fibrosis.

#### Sub theme 5: Reproductive maternal, neonatal, child and adolescent health

**51. Evidence of cross-transmission of multi-drug-resistant** *Enterobacter cloacae* **complex from the hospital envi-ronments to the neonates admitted in the intensive care unit of a tertiary health facility in Tanga, TanzaniaCorresponding author:** Athanas Dustan Mhina

#### Affiliation: National Institute for Medical Research, Tanzania

**Background:** Enterobacter cloacae complex (ECC) are common nosocomial pathogens capable of producing a wide variety of infections. Colonization with multidrug-resistant bacteria is a precursor to invasive infections. ECC has emerged as one of the most common nosocomial pathogens in neonatal intensive care units (NICUs). This study aimed to assess the possible cross-transmission pathway of multidrug-resistant ECC from the environments to neonates admitted in the NICU of a tertiary Hospital.

**Methods:** Rectal swabs were collected from the neonates upon delivery alongside the corresponding surfaces and devices in the ward. The surfaces and devices include bedside rails, weighing scales, oximeters, medication trolleys, baby warmers, thermometers, stethoscopes and baby cots. Neonatal acquisition of ECC strains was assessed by taking a second set of swabs upon discharge (at least 48 hours of stay). Samples were processed to identify bacterial isolates. DNA was extracted from the ECC strains and subjected to whole genome sequencing (WGS). Sequence types (STs), antimicrobial-resistant genes (ARGs), and plasmid replicons were determined using pyani (v0.2.12) ANIm analysis and were compared for similarities.

**Results:** We investigated 447 neonates, and 34/447 (7.6%) were found to be colonized with MDR-ECC. Of these, 18/34 (60%) were colonized after admission of at least 48 hours, of which 12/18 (67%) were colonized with strains similar to those isolated from the respective devices and surfaces in the ward. Furthermore, these isolates harbour similar STs, ARGs, and plasmid replicons, suggesting cross-transmission.

**Conclusions:** This study highlights the significant role of the hospital environments in the cross-transmission of MDR ECC among neonates in a tertiary health facility in Tanzania. Routine surveillance of healthcare-associated infections (HAIs) involving hospital environments must be emphasized for evidence-based infection prevention and control (IPC) interventions.

## **52.** Predictors of Hepatitis B virus vaccine uptake among women of reproductive age, South Sudan Corresponding author: Ezbon WApary

Co-authors: Akway M. Cham, Amanya Jacob, Kon Alier, Oromo F. Seriano, Kenneth Sube

**Affiliation:** University of Juba, School of Public Health, Ministry of Health, Directorate of Policy, Planning, Budgeting & Research, School of Medicine, South Sudan

**Introduction:** Hepatitis B virus still remains a public health problem in South Sudan. Vaccination against it is currently the only effective means of protection. In South Sudan there is no or little evidence regarding the uptake of the vaccine among women of reproductive age (WRA). This study aimed to examine predictors of HBV vaccine uptake among WRA in Juba City, South Sudan.

**Methods:** This study adapted mixed model: quantitative and qualitative cross-sectional design among WRA accessing health services at seven health facilities in South Sudan from May to July 2024. A validated semi-structured questionnaire was used to collect data from the 1808 randomly selected women. The study used Stata v15 and ATLAS.ti v7 for analyses. Chi squared tests and logistic regression model were performed to determine association and likelihood respectively.

**Results:** Among the 1808 women, 37.7% received HBV vaccine. The demographic factors associated with uptake of HBV vaccine: residential area (p<0.001), level of education (p<0.001), employment status (p<0.001). Similarly, the health behaviours associated with uptake of vaccine were blood transfusion (p<0.001), and surgical operation (p<0.001). The women who attended formal education were 2 times more likely to receive HBV vaccine compared to those who did not (OR 1.988, 95% CI:1.508 - 2.621). Employed women of reproductive age were 2 times more likely to receive HBV vaccine than the unemployed (OR 1.676, 95 CI: 1.339 - 2.097). Women who had close contact with a case of hepatitis B were 2 times more likely to receive the vaccine than those who had not had close contact with a case of hepatitis B (OR 1.509, 95% CI:1.13 - 2.016).

**Conclusion:** The overall uptake (65.8%) of HBV vaccine was far from the global uptake. The study recommends improvement of tailored health promotion with focus on antenatal HBV screening, a birth dose vaccine.

## 53. Serological Status of Vaccine and Hepatitis B Virus Exposure among Children Under 5 and Aged 15–17 Years in Kampala, Uganda

#### Corresponding author: Fahad Muwanda

Affiliation: Makerere University College of Health Sciences, School of Biomedical Sciences, Department of Immunology and Molecular Biology

**Background:** Pediatric hepatitis B virus (HBV) serostatus remains variably characterized, hardly determined at times, or documented as part of national monitoring of the Extended Programs for Immunization (EPI). Moreover, approximately 296 million people are chronic carriers of HBV worldwide and about 1.5 million new cases of the infection occur annually. This study sought to characterize the seroprevalence of HBV vaccine and or infection status among the under 5s and in 15-17-year-old children in Kawempe Division, Kampala, Uganda.

**Methods:** We cross-sectionally characterized the seroprevalence of HBV vaccine and/or infection status among 501 and 288 children <5 and 15–17 years old, respectively, in Kawempe Division, Kampala, Uganda, between May and August 2023. These children received HBV vaccination under the Uganda National Extended Program on Immunizations (UNEPI). Samples were qualitatively screened for hepatitis B surface antigen (HBsAg), hepatitis B surface antibody (HBsAb or anti-HBs), hepatitis B e antigen (HBeAg), hepatitis B core antibody (HBcAb or anti-HBc) using three different HBV Combo test rapid immunochromatographic diagnostic tests: Nova, Fastep, and Beright.

**Results:** The seroprevalence of HBsAg, anti-HBs, HBeAg, anti-HBe, and anti-HBc was 1.52%, 27.75%, 0.88%, 0.63%, and 0.76%, respectively, for the combined study age groups. The HBsAg seroprevalence of 2.78% was almost 3.5-fold higher among adolescents compared to the 0.8% observed in the under-5-year-olds. The qualitative seroprevalence of anti-HBs was 33.1% and 18.4% in the under-5 and among the 15–17-year-old study groups, respectively.

**Conclusion:** The proportion of qualitatively detectable anti-HBs in both groups of vaccinated children is low and probably indicates reduced seroprotection. Consequently, a large proportion of children who received the hepatitis B vaccine under UNEPI may be at risk of HBV infection, especially adolescents. A booster dose of the Hepatitis B Vaccine may be required for adolescents.

### 54. Evolutions in Breast Cancer Management, From Heroic Radicalism through Conservatism Stage and the Role of Neoadjuvant and Adjuvant Therapies; Tips and Tricks

#### Corresponding author: Assist Prof. Dr/Albino Amum Awin

Affiliation: The Faculty of Medicine, Upper Nile University, South Sudan

**Introduction:** The Human Breast was considered a symbol of motherhood, femininity, and sexuality, as well as an aesthetic and functional organ. Breast Cancer is the most frequently diagnosed cancer globally and in Africa. In the East African Community (EAC), breast cancer accounts for 198, 553 news cases or 16.8%, and 91, 252 deaths or 11.9% in the year 2022. Treatment of breast cancer involves multiple modalities, including surgery and radiotherapy for locoregional control, surgical. Treatment witnessed a tremendous shift and constant evolution from the Heroic Radicalism of Halstedians through the Conservatism stage of Umberto Veronesi and Bernard Fisher, to the current stage of cutting-edge advances in breast surgery, the Oncoplastic Breast Surgery. The evolutions in surgical modalities were facilitated by advances in neoadjuvant and adjuvant therapies such as chemotherapy, Anti- HER2 neu, Hormonal Therapy, Checkpoint inhibitors, bisphosphonate, CDK4/6 inhibitors, mTOR inhibitors, PARP inhibitors, monoclonal antibodies, and others target therapies for PIK3CA and NTRK mutation. The current presentation briefly highlights the evolution that breast cancer management has gone through, and the last updates.

**Material and Method:** This presentation provides an overview of evolutions in breast Cancer management by comprehensive online search to identify complete papers published in English, in PubMed, EMBASE, Cochrane Library, UpToDate from December 26th, 2024 to January 28th, 2025, NCCN guidelines, ESMO guidelines, and personal experiences in the Field of Surgical Oncology over ten years.

**Results:** Breast cancer management has witnessed profound and steady evolutions in all aspects, whether locoregional treatment or systemic management: Surgical treatment has experienced enormous evolutions from radical mastectomy through breast conservation to Oncoplastic Breast Surgery, axillary Lymph Node (ALNs) management has evolved from ALN clearance, through Sampling, Targeted ALNs Dissection to Sentinel ALNs biopsy. These evolutions have been facilitated by advances in the field of neoadjuvant therapies, which enabled breast Conservation in the early stage, as well as enabled mastectomy in the advanced stage with the least sequelae.

**Conclusion:** Breast cancer management has witnessed enormous evolutions, the current data suggest that a combination of surgery with neoadjuvant or Adjuvant therapies in selected breast cancer cases is a safe option, not only improving overall survival and relapse-free survival but also improving aesthetic outcomes and quality of life.

## 55. Evaluation of the Intercostal Artery Perforator Flaps (ICAP) and Lateral Thoracic Artery Perforator Flap (LTAP) in Partial Breast Reconstruction Following Breast Conservative Surgery

#### Corresponding author: Assist Prof. Dr/Albino Amum Awin

Affiliation: The Faculty of Medicine, Upper Nile University, South Sudan

**Introduction:** Introduction of pedicled chest wall perforator flaps (CWPF) in breast surgery, broadened the options for oncoplastic volume replacement procedures, however, the literature is scarce on non-blind non-randomized interventional studies. This study was aimed at evaluation of the intercostal artery perforator (ICAP)flaps, and lateral thoracic artery perforator (LTAP) flaps in partial breast reconstruction in small and medium-size breast women, in terms of feasibility, safety, and efficacy considering the aesthetic outcome and patient satisfaction as the primary outcome measures; and perioperative complications as the secondary outcome measures. **Methods:** This study was a non-blind non-randomized interventional study, conducted on 34 female cases with early breast cancer, admitted to Oncology Center-Mansoura University, from August 2019 to February 2024, who underwent conservative breast surgery followed by partial reconstruction, either by the ICAP flaps or the LTAP flap, they were followed up for two years, and evaluated objectively and subjectively. The article was published in The Egyptian Journal of Surgery on 4 October 2024.

**Results:** In this study, 34 cases were allocated to 20 in the ICAP flaps, versus 14 in the LTAP flaps. The Mean follow-up period was  $33.10\pm11.96$  versus  $12.15\pm10.92$ , P<0.001\*. The average age was  $40.60\pm8.62$  versus  $43.07\pm8.01$ , the average BMI was  $32.19\pm6.80$  versus  $33.74\pm4.60$  for the ICAPs Versus LTAP groups respectively. The most common complications encountered were marked seroma, experienced by 5 cases in the two groups without statistically significant difference. Overall, the aesthetic outcomes were good to excellent in over 90% of the cases in the two groups without statistically significant difference, P=0.608. Most cases were very satisfied with the aesthetic outcomes (n=19, 95.0%) versus (n=12, 85.7%) for the ICAP versus the LTAP flaps respectively without statistically significant differences, P=0.455.

**Conclusions:** Both the ICAP and the LTAP flaps are feasible, efficient, and safe versatile surgical techniques for partial breast reconstruction following conservative breast surgery in small to medium-sized breast women. They are good and reliable options, associated with low complication rates, yielding excellent to very good aesthetic outcomes and high patient satisfaction rates. The difference lies only in the use of the ICAP frequently in Lower quadrant defects versus the LTAP flap in UIQ defects, while the two flaps are equally useful for partial reconstruction of defects in UOQ of breast.

## 56. High Viral Load Suppression after implementation of an asset-based strategy - "Operation Triple Zero" - for children, adolescents and young people on ART in four health facilities of South Sudan

#### **Corresponding author:** Gregory Jagwer

#### Affiliation: Catholic Medical Mission Board

**Background:** Amid a severe humanitarian crisis, South Sudan remains committed to a 95% viral coverage (VLC) and suppression (VLS) among people on ART. Children, Adolescents and young people receiving ART experience lower rates of VLC/VLS delaying the achievement of the UNAIDS target if not addressed. It is critical that children achieve sustained VLS to mitigate the exceptionally high mortality associated with unsuccessful HIV treatment. To address low VLC/VLS rates among children, the "Operation Triple Zero" (OTZ) program was implemented by the Catholic Medical Mission Board (CMMB).

**Description:** Between October 2023 and September 2024, 425 children, adolescents and young people aged 10 – 24 years on ART were enrolled into the OTZ program in four public facilities. The program is an asset-based strategy that aims at engaging children on ART to promote zero missed appointments, zero missed drugs and zero viral load. Key activities include VL eligibility assessment; routine and enhanced adherence counselling for participant, drug refills, role play and games, treatment literacy sessions, and sessions with caregivers. Data from the program was abstracted and analyzed for VLC and VLS after enrollment in the program.

**Lessons learned:** Out of the 425 clients enrolled in the program, 90 were eligible for viral load testing and 62 had their viral load samples collected, representing an overall VLC of 74%. Out of 67 whose viral load samples were collected 93% (range 93%-100%) achieved VLS; of these 51% were female and 49% male. All are on a DTG based regimen. All the children enrolled at Al Sabah Children's hospital suppressed their viral load. All the targeted clients continue with active engagement in the OTZ program to sustain the VLS.

**Conclusions/Next steps:** We describe the OTZ program to inform strategic interventions to reach the "third 95" among children, adolescents and young people. Children enrolled in the OTZ program had high VLS rates as compared to the lower averages among other children in South Sudan. As we move towards having 95% of ART-treated children achieve and maintain VLS, there is need to scale up similar programs for all children on ART with a focus on inculcating children's self and social awareness, self-management, relationship management and responsible decision making among children on ART.

#### Subtheme 6: Herbal and traditional Medicine

## 57. Bridging the Gap: The Case of Herbal Medicine and Natural Products Innovation Incubation Hub at PHARMBIOTRAC for Sustainable Healthcare in East Africa

Corresponding author: Eng. Anke Weisheit

**Co-authors:** Dr. Casim Umba Tolo, Jimmy Ronald Angupale

**Affiliation:** Pharm-Biotechnology and Traditional Medicine Center (PHARMBIOTRAC), Mbarara University of Science and Technology (MUST)

**Introduction:** The integration of traditional medicine into mainstream healthcare systems presents a significant opportunity to address healthcare gaps in East Africa.

**Methods:** This case describes an Herbal Medicine and Natural Products Innovation Incubation Hub established in 2019 at Pharm-Biotechnology and Traditional Medicine Center (PHARMBIOTRAC) at Mbarara University of Science and Technology (MUST), Uganda to harness the region's rich biodiversity and traditional knowledge, while ensuring safety, effi-

cacy, and scalability of herbal and traditional medicine (HTM). **Lessons earned:** Despite the widespread use of HTM in East Africa, challenges such as lack of standardization, limited scientific validation, and inadequate market access hinder its full potential. The hub addresses these challenges by offering a collaborative platform for researchers, traditional healers, entrepreneurs, and policymakers. The hub focuses on:

- 1. Innovation Incubation: supporting start-ups in the herbal medicine sector, validate traditional remedies through scientific research, create market-ready products that improve healthcare access and empower local communities and preserve traditional knowledge.
- 2. Evidence-Based Use of HTM: The hub support research to validate the safety, efficacy, and quality of herbal remedies, ensuring they meet international standards.
- 3. Safety and Efficacy: Through rigorous testing and quality control, the hub ensure that HTM products are safe and effective in treating targeted conditions.
- 4. Success Stories and Knowledge Sharing: The hub document and disseminate success stories of HTM, highlighting its potential to improve health outcomes and livelihoods.
- 5. Integration of Traditional Medicine into Healthcare Systems: By fostering Small Scale Enterprise development, partnerships between traditional healers and modern healthcare providers, the hub promote the inclusion of evidence-based HTM in national healthcare frameworks. The hub serves as a launch pad for star-tups in the HTM sector, providing training, mentorship, networking and access to funding.

**Next steps:** This initiative is an effective pathway to facilitating evidence-based HTM development for integration of HTM into healthcare systems. The hub's expansion to other regions will depend on collaboration among stakeholders, including governments, research institutions, and the private sector. The Herbal Medicine and Natural Products Innovation Incubation Hub represents a transformative approach to leveraging traditional knowledge and natural resources for sustainable healthcare in East Africa. By addressing key challenges and fostering innovation, the hub will contribute to improved health outcomes, economic growth, and the preservation of cultural heritage.

#### 58. Ethnobotanical studies of pesticidal plants against human harmful insects in Burundi

#### Corresponding author: Rose AHISHAKIYE

Co-authors: Jacques Nkengurutse, Anatole Bukuru, Tatien Masharabu

Affiliation: University of Burundi

**Introduction:** In Burundi the important human harmful insect included mosquitoes, lice, fleas, flea-biters, bedbugs, flies and fire ants. Theses insects caused a lot of illness. The control of these insects is a global and local in particular as it affects many households in rural areas. The present study aims to inventory the pesticidal plants used by the Burundian population while indicating the parts of the plants used, modes of preparation and use, effectiveness and availability.

**Methods:** A survey on pesticidal plants was carried out using a questionnaire on 250 participants in Gitega province, Central Burundi. The consensus index (CIs) was used to analyse the credibility of the information collected.

**Results:** Seventy five percent of participants recognized at least one pesticidal plant. The present study reveals 69 plant species divided into 35 families. The Asteraceae (8 species) and Euphorbiaceae (6 species) families are most represented. Of all the plant species recorded, the most exploited part is the leaf (47% of species) and 50% of species are used without prior preparation, while 22% are roasted before use or administration. The local application is most used (for 46% of species). The most cited species are Tetradenia urticifolia (ICs: 0.60), Euphorbia tirucalli L (ICs: 0.10) and Tagetes minuta L (ICs: 0.06) repelling fire ants, Solanum incanum (ICs: 0.60) and Gymnanthemum amygdalinum (ICs: 0.12) treating the flea-biters. The present study showed a large number of pesticidal plants, some of them may have a considerable potential in treatment of these human harmful insects and others illness. The most preferred use of the leaves leads to a promising valorisation medicinal plant with less impact on sustainable conservation of the reported plant species. The present study reveals the importance of pesticidal plants knowledge with an emphasize on plants against fleas-biters and fire ants (31 and 23 species respectively).

**Conclusion:** Our results suggest the need of phytochemical and pharmacological research aiming at the synthesis of reasonably priced and efficient plant-based bioinsecticides,". Also, the need for this study is crucial in identifying, documenting, and evaluating indigenous pesticidal plants as an affordable and eco-friendly alternative. The findings could informnpolicymakers, health practitioners, and researchers about viable, locally available plant- based insect control methods, leading to better vector control strategies in Burundi.

#### **59. Ethnobotanical study of medicinal plants used in the treatment of diabetes in Burundi Corresponding author:** Anatole Bukuru

Co-authors: Jérémie Ngezahayo, Fréderic Nsabiyumva, Emmanuel Banzubaze, Pierre Duez, Jacques Nkengurutse

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**Background:** Diabetes mellitus is a growing global health problem. In Burundi, its prevalence has tripled in the last decade, from 2.7% to 6.5%. Some 57.6% of people with the disease remain undiagnosed due to limited resources. Diabetes is the third most common cause of hospitalisation at the University Hospital Centre, and 30% of lower limb amputations are related to diabetes. Although the treatment of diabetes is diversified, traditional medicine is increasingly used despite a lack of information on anti-diabetic medicinal plants in Burundi. The aim of this study was to identify the plants used in the treatment of diabetes and to characterise their therapeutic uses on the basis of ethnobotanical data.

**Methods:** The survey was carried out in eighteen provincial markets, with a semi- structured questionnaire distributed to 64 traditional practitioners selected by purposive sampling and snowball sampling. The data were quantitatively analysed according to frequency of citation, relative frequency and degree of fidelity to determine the importance of each species.

**Results:** A total of 121 medicinal plant species, divided into 55 families and 111 genera, were mentioned for the treatment of type 2 diabetes. The most commonly cited species were Gymnanthemum amygdalinum (26.56%), Dicoma anomala (21.88%), Erythrina abyssinica and Parinari capensis (18.75%), and Ageratum conyzoides (17.19%). The families Asteraceae and Fabaceae are the most represented. These plants are used to treat 30 signs and symptoms of diabetes, with 56 recipes based on multiple plants and 8 based on single plants. Herbs (35%) and trees (33%) are the most common plant types, and the most commonly used parts are leaves (48.08%), bark (24.78%) and roots (12.09%). Recipes are mainly prepared by decoction (65.63%) and most of them are administered orally.

**Conclusion:** This study shows that medicinal plants are commonly used for the treatment of diabetes in Burundi. However, further research is needed to assess the quality, efficacy and safety of the recipes used by Burundian traditional practitioners.

## 60. Ethnobotanical survey of medicinal plants used for treatment by the Batwa Indigenous People and Local Communities of Kisoro District, South Western Uganda

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**Background:** The Batwa indigenous people relied on the forests for their health care and food for millennia, making them a rich source of traditional medicine knowledge (TMK). However, their eviction from the forests by the government of Uganda in 1992 in order to conserve forest biodiversity has caused enormous changes in life resulting in loss of TMK. Documentation is essential in TMK preservation and for future utilization for sustainable and equitable development practices. This study documented TMK of Batwa indigenous people and local communities (IPLC) in Kisoro district in South Western in Uganda.

**Methods:** An ethnobotanical survey was conducted among 90 traditional health practitioners (THPs) sampled purposively from six Batwa IPLCs communities in Kisoro District between October -December, 2024. Data on medicinal plants (MPs) used for treating diseases, parts used, method of preparation, route of administration and source of their collection was collected using a semi structured questionnaire and focus group discussions. Data from the questionnaire was analyzed using MS Excel and SPSS version 23 to calculate frequencies of respondents, informant consent factor and user value while FGD data was compiled based on thematic areas.

**Results:** The study documented 234 MPs species used for treatment of 95 health conditions. The plant family with the highest number of species was Asteraceae (18%), followed by Lamiaceae (7%), Fabaceae (5%), and Solanaceae (4%). The plant parts used were leaves (75%), roots (8%), stem bark (5%), whole plant (4%), aerial parts (3%) and flowers (3%). Notably, 45% of the plant species reported were obtained from the wild (forests). The diseases each THP treated ranged from two to seven, with the majority (26%) reporting three. The diseases with high number of treatment formulations were wounds (29 mentions), Cough (19), malaria (18), stomach disorders (15), diarrhea (13) and worms (13). The plant that was most mentioned to treat cough, malaria, wounds and worms included; Salvia nilotica Juss. ex Jacq., Acacia mearnsii, Vernonia amygdalina and Dryopteris cristata, respectively. The route of administration of TMK was mostly oral (72%) followed by topical 24%.

**Conclusion:** The Batwa IPLCs are endowed with medicinal knowledge innovations for treatment of various diseases. Therefore, the documented TMK should be evaluated to justify their therapeutics claims for bio-prospecting health products.

#### 61. Green Synthesis and Comparative Analysis of 5-Bromo Benzoxazolone Derivatives via Microwave and Reflux Methods for Potential Analgesic Applications

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**Background:** Benzoxazolone derivatives, particularly 5-bromo-2(3H)-benzoxazolone, are pharmacologically significant scaffolds with demonstrated analgesic, anti-inflammatory, and antimicrobial activities. Conventional synthesis methods, such as reflux heating, often involve prolonged reaction times and higher energy consumption. Microwave-assisted organic synthesis (MAOS) offers a sustainable alternative by enhancing efficiency and reducing environmental impact. Green synthesis techniques that reduce environmental effect while preserving or improving efficiency and yield are being investigated as a result of the growing interest in environmentally friendly pharmaceutical and medicinal chemistry processes. Because of their various biological actions, such as their analgesic, anti-inflammatory, and antibacterial qualities, benzoxazolone derivatives— especially those with halogen replacements like the 5- bromo group—have demonstrated great promise as pharmacophores. This study aims to bridge that gap by synthesizing 5-bromo benzoxazolone derivatives through both microwave and reflux methods and conducting a comparative analysis of their efficiency, yield, purity, and analgesic potential. This research seeks to establish a more sustainable, efficient approach for developing analgesic agents, contributing to both medicinal chemistry and green chemistry advancements. Despite their effectiveness, conventional synthetic processes frequently employ toxic solvents, require longer reaction times, and consume more energy. A viable substitute is microwave-assisted organic synthesis (MAOS), which offers higher energy economy, better yields, and quick reaction speeds. However, there is currently little comparison between MAOS and conventional reflux methods when it comes to creating bioactive benzoxazolone derivatives.

**Methods:** Comparing reaction efficiency, yield, and conformity to green chemistry principles was the aim. The derivatives were synthesized using Mannich reactions under both microwave irradiation (65°C, 150–100 W, 8 min) and conventional reflux (60 min). Reaction progress was monitored via TLC, and products were characterized using FT- IR, 1H1H-NMR, and melting point analysis.

**Results:** Microwave synthesis significantly reduced reaction times (8 min vs. 60 min) and improved yields for two derivatives (67.7% and 50.1% vs. 51.3% and 38.7% under reflux). However, the 4-methylpiperidine derivative showed lower microwave yields (28.8%), attributed to solvent compatibility issues. Structural characterization confirmed successful N-substitution at position 3, with consistent spectral data across methods.

**Conclusion:** Microwave synthesis demonstrated superior efficiency, reduced energy consumption, and higher yields for most derivatives, aligning with green chemistry principles. Further optimization of solvent systems is recommended to enhance universal applicability. This approach holds promise for scalable, eco-friendly production of benzoxazolone-based analgesics, contributing to drug discovery efforts in resource-limited settings.

#### 62. Investigating medicinal plants used to treat respiratory diseases in the Afro-mountainous district of Burundi Corresponding author: Jacques Nkengurutse

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**Introduction:** In Burundi, acute respiratory infections are classified as diseases with epidemic potential and are among the top five causes of morbidity in health centres. Although treatment for respiratory viral diseases is varied, including conventional medicine, recourse to traditional medicine is increasingly common. However, there is little information on medicinal plants for respiratory viral diseases in Burundi. The objective of this study is to identify the plants used to treat respiratory viral diseases and to document their therapeutic uses.

**Methods:** One hundred and fifty-seven informants were interviewed using a pre- established questionnaire. Each informant interviewed was also involved in collecting samples and determining vernacular names. The plausibility of the recorded uses was verified by an in-depth documentary search.

**Results:** Eighteen different plant species from 12 families were identified in the study area. The most represented families were Asteraceae (4 species) and Lamiaceae (2 species). These plants were cited to treat 3 different respiratory infections in 15 multi-therapeutic recipes and 20 mono-therapeutic recipes. Tetradenia riparia (FL=55, 31%), the most frequently cited species, was reported in the composition of 4 multi-recipes, followed by Kalanchoe crenata (FL=31.91%, 2 recipes), Coleus barbatus (FL=17.02%, 2 recipes), and Rumex usambarensis (FL=14.89%, 2 recipes). Gymnanthemum amygdalinum (FL=12.76%) was the most important species in the monorecipes, with 2 recipes. With regard to the preparation and administration of the recipes, our informants stated that the doses could be adjusted according to the patient's age.

**Conclusion:** Despite the existence of a few documents on the use of plants in Burundi to treat respiratory viral diseases, this field has been little explored. Almost all the medicinal plants used to treat these diseases have not yet been tested. It is therefore necessary to carry out in-depth toxicological, pharmacological and phytochemical studies on all the plant species identified in this study.

#### 63. Medicinal and nutritional floristic potential of relict forests in Kaziba traditional landscape

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**Background:** The Democratic Republic of Congo (DRC), although home to a significant diversity of flora, faces major challenges in terms of food security and access to healthcare. Non-timber forest products (NTFPs) and wood products for food and medicinal use are strategic resources for poor local communities, both in terms of nutrition and treatment. However, these resources remain poorly documented and insufficiently integrated into sustainable ecosystem management policies. Relict forests are recognized as being of significant importance in plant-based food and medicine. This study aims to conduct an inventory of these plants and document their traditional applications within the Kaziba chiefdom of the Democratic Republic of Congo.

**Materials & Methods:** An ethnobotanical survey was conducted among 96 respondents residing in areas with natural forests. The data collection process encompassed individual interviews, focus groups, and structured questionnaires. Literature Review was used to validate the uses of the plants based on what has been found elsewhere.

**Results:** A total of 66 plant species used, 23 of which are consumed for their fruit (64.2%), leaves (21.4%), and stems (28.5%), while 43 species are used in traditional medicine, with leaves being the organ most frequently used (62.8%). The analysis of local knowledge indicates that 67.1% of species are well-known, 20.5% are little-known, and 13.4% are rarely mentioned. Respondents consider the relict forests of Lwampango and Kamano richer in medicinal and food species. However, there is a decline in the availability of these species, with 41.6% of respondents reporting difficulty in accessing them, and 79% perceiving a decline in their abundance over the last decade. The primary threats identified to the long-term survival of these species include the exploitation of firewood (33%), grazing (27%), the conversion of forests to farmland (24%), and bushfires (10%). To conserve these resources, respondents proposed various strategies, including the establishment of a permanent local conservation structure (36%), the enhancement of community awareness (33%), and the rehabilitation of degraded sections of these ecosystems (13%).

**Conclusion:** This study underscores the significance of the relict forests of Kaziba traditional landscape for rural communities' food and health security. It emphasizes the pressing need for the implementation of sustainable conservation measures.

## 64. Tackling Mycobacteria tuberculosis (Mtb) resistance: Berberine and related compounds as potential novel pathogen efflux pump inhibitors

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**Introduction:** Mycobacterium tuberculosis (MTB) strains that are extensively drug-resistant (XDR) and multi-drug resistant (MDR) have raised serious concerns for Tuberculosis (TB) treatment. The overexpression of Rv1258c and MmpL5 efflux pumps that extrude antibiotics from the bacterial cell, lowering the intracellular concentration, and causing resistance. Efflux pump inhibitors (EPIs) have been researched as a potential way to improve the efficiency of anti-TB drugs. This study aimed to evaluate the potential of berberine and related compounds in surging the Mtb efflux pump inhibition capacity of bedaquiline and clofazimine.

**Methods:** Berberine and two other compounds, namely CD05e and CD05d were delineated. Computational molecular docking revealed robust target binding with docking scores of -7.0 kcal/mol and -7.6 kcal/mol respectively. Physicochemical properties of the query compounds were: Mw (582.6 and 420.5), logP (-0.5 and 1.5), logD (3.8 and 1.5), logS at pH 7.4 (3.1 and 2.2), hydrogen bonding donors (HBD) (0 to 2), hydrogen bonding acceptors (HBA) (7 and 4) and topological polar surface area (TPSA) (197 and 117.8). Antimycobacterial screening against Mycobacterium smegmatis for each compound with bedaquiline and clofazimine was performed.

**Results:** CD05e reduced the MIC99 value of bedaquiline and Clofazimine by 8 and 4-fold respectively while CD05d had no effect on the MIC99 of the anti-mycobacterial drugs.

**Conclusion:** This suggests that CD05e exhibits an efflux pump blocking mechanism of action. Further screening of the compounds against Wild type and drug resistant Mtb strains is ongoing.

#### 65. Molluscicidal Activity and Phytochemical Profile of Camellia Sinensis (green tea) and Camellia Sinensis var. Assamica (purple tea) Extracts against the Vector Snails of Schistosomiasis

Corresponding author: Nickson Samoo

**Co-authors:** Ruth Nyangacha, Amos Mbugua, Martin Mutuku, Charles Syengo, Ibrahim Mwangi **Affiliation:** Kenya Medical Research Institute, Jomo Kenyatta University of Agriculture and Technology **Background:** Freshwater pulmonate snails are widely distributed in Kenya and serve as intermediate hosts of digenean trematode parasites that cause schistosomiasis. Although both snail- transmitted parasitic diseases are routinely controlled using chemotherapy, reinfections rapidly occur, making it difficult to sustain control using chemotherapy alone. Additionally, the prohibitive costs of producing and applying molluscicides, accompanied by environmental concerns, have limited the use of chemical molluscicides to control snail- borne parasitic infections. In this study, raw extracts from Camellia sinensis (green tea and purple tea plant), widely grown in Kenya's highland areas, were tested against the freshwater pulmonate snail, *Biomphalaria pfeifferi*.

**Methods:** Crude water extracts were derived from seeds, mature leaves, shoots, stems, and root bark of the Kenyan tea plant (Camellia sinensis). Phytochemical analyses of the extracts were done using liquid chromatography and gas chromatography coupled with mass spectrophotometry (LCMS and GCMS). Further, *Biomphalaria pfefferi* snails were exposed to five different concentrations (10, 20, 50, 100, and 150 mg/L) of the water extracts. Quantitative data analysis was done in R version 4.4.0. Kruskal-Walli's test was used to test the difference in snail retraction and mortality across the different test groups. Kaplan-Meier survival analysis was used to examine survival rates of snails. Survival curves were compared using the log-rank test. A p-value of less than 0.05 was considered significant.

**Results:** The findings indicate that snail mortality differed significantly across the different test groups (P<0.001). Seed extracts had the highest retraction and mortality average (65%), followed by root bark (56%), stem bark extracts (14%), shoot extracts (4%) and mature leaf extracts (0.5%). Analysis of the raw extracts by LCMS showed that the compounds present in the extracts were epichatechin, epigallocatechin, caffeine, which was the most abundant, theobromine, as well as assamsaponin C. The compounds identified by GCMS are Hexadecanoic acid, caffeine, Octadecenoic acid-methyl acid and Octadec-1-ene.

**Conclusion:** These findings show that crude extracts from Kenyan tea plant Camellia sinensis (both green and purple tea) induce mortality of *Biomphalaria pfeifferi* snails. Therefore, they can be explored as alternative plant-based molluscicides against the vector snail of intestinal schistosomiasis.

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