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70 YEARS

70TH ANNIVERSARY & 5TH IFAKARA ANNUAL SCIENTIFIC CONFERENCE

NOVEMBER 10 – 12, 2026
(Nov. 13 - Bagamoyo Open House)

APC HOTEL & CONFERENCE CENTER
Mbweni-Bunju, Dar es Salaam

70 YEARS OF IMPACT: ROOTS, REACH, AND WHAT'S NEXT

From a field station in rural Tanzania to a continent-shaping institute, and we're only getting started

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Programme overview

Overview of the scientific programme and plenary sessions, 10–13 November 2026. Scientific parallel sessions are shown in bold; the abstracts in this book are organised according to those sessions.

Day 1 · Tuesday 10 November 2026

Foundations: Building the science base from the field laboratory to the institute (1956–2000s)

07:00–08:00	Registration
08:30–09:50	Opening Ceremony: Roots, Reach, and What's Next
09:50–10:20	Institutional Legacy Lecture: 70 Years of Ifakara Health Institute Science (How did it start?)
10:20–10:45	Legacy Awards Ceremony and Group Photos: Celebrating Partnerships That Shaped Our Science
10:45–11:30	Tea Break
11:30–12:30	From the Director's Office: Lessons Learned – Reflections Panel Discussion 1
12:30–13:00	Plenary Lecture: Ifakara at 70: What have seven decades of African science meant for Global Health?
13:00–14:00	Lunch Break
14:00–15:00	High-level conversation: The partnerships that built Ifakara and the partnerships it needs next
15:00–15:35	Keynote 1: From Evidence to Policy: What It Actually Takes
15:35–16:40	Fireside Chat: Growing Scientists. Growing Science: Stories, Lessons and a Legacy for the Next Generation
17:00–17:45	Coffee and Booths
18:00–22:00	70th Anniversary Gala Dinner (Theme: Swahili Night)

Day 2 · Wednesday 11 November 2026

Translations: Evidence into Policy and Practice (2000s–Present)

07:00–08:20	Registration
08:15–08:20	Special Tribute: Dr. Mohamed Y. Janabi, Regional Director, WHO AFRO
08:20–09:15	Keynote 2: Beyond Efficacy: What It Takes for Vaccines to Deliver Health Impact, and What Ifakara's Experience Teaches Us
09:15–10:15	Panel Discussion 2: Women Shaping the Future of Ifakara Science
10:15–10:40	Tea Break
10:40–12:10	Reflection from IHI Management: "Where does IHI stand, and what must we strengthen to deliver the next 70 years of impact?"
12:10–13:40	**SCIENTIFIC PARALLEL SESSIONS I: Emerging Challenges and the Future of Health Research** Rhino Hall: Changing infectious disease landscapes Antelope A: From scientific discovery to health impact Antelope B: Vector Biology, Behaviour and Control I
13:40–14:25	Lunch Break
14:25–15:00	Flagship Session: Community Voices – From Evidence to Policy and Practice
15:00–17:00	**PARALLEL SYMPOSIA** Rhino Hall: Advancing Malaria Research, Policy, and Building Analytics Capacity in Africa through Geospatial Modelling Antelope A: Maternal and Child Health Symposium Antelope B: Advancing Vector Control for the Next Generation (Vector Control Product Testing Unit – VCPTU)

17:00–18:00	Entertainment (games; stand-up comedy)

Day 3 · Thursday 12 November 2026

Frontiers: The Next 70 Years

07:00–08:00	Registration
08:30–09:15	Visionary Talk: "What should the next 70 years of African Global Health Science look like?"
09:15–10:15	Panel Discussion 3: The Voice of Scientists for the Next 70 Years
10:15–10:40	Tea/Coffee Break
10:45–11:15	Masterclass Lecture: From Algorithms to Action, AI Across Africa's Disease Burden
11:15–12:30	Panel Discussion 4: Responsible use of AI, Data and Biomedical Innovation for Africa's Disease Burden
12:30–13:25	Lunch Break
13:30–15:00	**SCIENTIFIC PARALLEL SESSIONS II: Next-Generation Science, Technology and Health Systems** Rhino Hall: Emerging and re-emerging diseases, genomics, and outbreak preparedness Antelope A: AI, Digital Science, and Intelligent Disease Surveillance & Response Antelope B: Vector Biology, Behaviour and Control II
15:00–15:30	Future Direction Talk: What Can IHI Become? Building the Next Generation African Centre of Excellence for Health Research
15:35–15:40	Memorial: Many stories Within a Larger Legacy
15:50–17:00	Awards Ceremony: Best Oral Presentation (Days 2–3), Turbo talks by the top 5 presenters (3 minutes presentation + 2 minutes Q&A each)
17:00–17:30	Closing Remarks

Day 4 · Friday 13 November 2026

Bagamoyo Open House: Site visit

07:00–09:30	Registration and Departure to Bagamoyo
09:30–10:30	Clinical Trial / Laboratory
10:30–11:00	Tea/Coffee Break
11:00–13:00	Transmission Zero / VCPTU / Training unit
13:00–14:30	Lunch Break and Departure to Dar es Salaam

Organising information

Event	70th Anniversary & 5th Ifakara Annual Scientific Conference: 70 Years of Impact: Roots, Reach, and What's Next
Organiser	Ifakara Health Institute
Dates	10–12 November 2026 (Bagamoyo Open House: 13 November 2026)
Venue	APC Hotel & Conference Center, Mbweni-Bunju, Dar es Salaam, Tanzania
Guest of Honour	H.E Dr. Jakaya Mrisho Kikwete, Former President of the United Republic of Tanzania
Day themes	Day 1 Foundations · Day 2 Translations · Day 3 Frontiers · Day 4 Bagamoyo Open House
Masters of ceremonies	Day 1: Sheikha Salum & Yeromin Mlacha · Day 2: Kyeba Swai & Hania Msami · Day 3: Robert Ndege & Farida Katunzi · Day 4: Kyeba Swai & Sarah Mswata
Scientific parallel sessions	Moderators – Sessions I (11 November): Grace Mwangoka (Rhino Hall), Grace Mhalu (Antelope A), Brian Tarimo (Antelope B). Sessions II (12 November): Brian Tarimo (Rhino Hall), Naomi Masanja (Antelope A), Aneth Tumbo (Antelope B).
Award	Best Oral Presentation (Days 2–3): turbo talks by the top five presenters at the Awards Ceremony on 12 November.
About the abstracts	Abstracts are reproduced as submitted by the authors, with consistent formatting. Reference numbers (IHI70-01 to IHI70-45) run in the order of the sessions in this book. Scientific content is the responsibility of the authors.

SESSION 1 OF 6

Scientific Parallel Sessions I · Rhino Hall

Changing infectious disease landscapes

Wednesday 11 November 2026 · 12:10–13:40

Moderator: Grace Mwangoka

Format: 10 minutes per presentation; combined Q&A of 15 minutes at the end of the session.

Ref.	Title	Presenting author
IHI70-01	Undernutrition and Mycobacterial burden predict disease severity at diagnosis among TB patient in Dar-es Salaam	Omary Ngome
IHI70-02	Biological Determinants and Epidemiological Consequences of Subclinical Tuberculosis	Jacqueline Nkouabi
IHI70-03	Hospital Post-Discharge Outcomes of People Living with HIV in Rural Tanzania- a Prospective Observational Study.	Edgar Enzigard
IHI70-04	The unaddressed burden of elevated blood pressure among adult people living with HIV in rural Tanzania: A longitudinal study	Franzisca Alfred
IHI70-05	Methodology and baseline characteristics of the Ifakara Heart and Lung Clinic Cohort	Evance Mahundi
IHI70-06	Awareness and care-seeking behaviour towards non-communicable diseases of people living in the rural Kilombero valley	Evance Mahundi
IHI70-07	Etiological detection of sexually transmitted infections through integrated community-based cervical cancer screening outreach among women in rural Tanzania.	Dorcas Mnzava

IHI70-01 Undernutrition and Mycobacterial burden predict disease severity at diagnosis among

TB patient in Dar-es Salaam

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Department of Biomedical Research and Clinical Trial, Ifakara Health Institute
Department of Parasitology and Medical Entomology, School of Public Health and Social Sciences, Muhimbili University of Health and Allied Sciences, Dar es Salaam, Tanzania

Background: Tuberculosis (TB) remains a leading cause of morbidity and mortality globally and in Tanzania. Treatment outcomes are routinely monitored, but disease severity at diagnosis and its determinants have received less attention. Characterizing severity at diagnosis could guide early risk stratification, clinical management and resource allocation.

Objective: To determine factors that are associated with disease severity at diagnosis among adults with pulmonary TB in Dar es Salaam, Tanzania.

Materials and Methods: We analysed baseline data from the TB-DAR prospective cohort in Temeke, Dar es Salaam (2013–2023). Adults aged ≥18 years with GeneXpert-confirmed pulmonary TB were included; those with extrapulmonary TB or missing GeneXpert results were excluded. TB severity was classified using a modified Bandim TBScore as mild (SC I), moderate (SC II), or severe (SC III). Crude and adjusted odds ratios (CORs and AORs) were estimated using ordinal logistic regression. Variables with p < 0.20 in bivariable analyses, alongside a priori confounders identified using directed acyclic graphs, were included in final multivariable model. Multicollinearity was assessed, and the proportional-odds assumption was tested using the Brant test. Analyses were performed in R version 4.5.2. All tests were two-sided, with p < 0.05 considered statistically significant.

Results: Data was retrieved from 1,475 adults TB patients, 1,079 (73.1%) were male and 245 (16.6%) were HIV-positive with median age of 32.5 years (IQR: 25–41). 1,029 (69.8%) had mild disease, 327 (22.2%) moderate disease and 119 (8.1%) severe disease. Undernutrition, assessed clinically at enrolment and classified as present or absent based on signs of wasting, fat or muscle loss, and generalized weakness was most strongly associated with higher severity (AOR 5.19; 95% CI 3.65–7.41), followed by bacillary load (high: AOR 2.66; 95% CI 1.54–4.83; medium AOR 2.16; 95% CI 1.27–3.87, versus low) and recurrent TB (AOR 1.90;95% CI 1.04–3.41).

Conclusion and Recommendations: TB severity at presentation was associated with nutritional status, mycobacterial burden, and previous TB treatment, with undernutrition showing the strongest association. Routine nutritional assessment, incorporation of GeneXpert semi-quantitative results into risk stratification, and closer monitoring of patients with recurrent TB may facilitate early identification and targeted management of patients at risk of severe disease. Prospective studies are needed to evaluate the impact of nutritional interventions on TB severity.

IHI70-02 Biological Determinants and Epidemiological Consequences of Subclinical Tuberculosis

Mbeya B, Portevin D, Sasamalo M, Signorell A, Kurscheid J, Mhalu G, Brites D, **Nkouabi J**, Reither K, Gagneux S.

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Background:

Tuberculosis (TB) is increasingly understood as a dynamic spectrum from Mycobacterium tuberculosis infection through subclinical TB (asymptomatic TB) to clinical TB, along which individuals may progress, regress, or self-cure. National prevalence surveys show that around 50% of individuals with bacteriologically confirmed TB report no TB specific symptoms.

Modelling further suggests that subclinical TB may contribute substantially to transmission. However, the biological, immunological, and epidemiological characteristics of subclinical TB remain poorly understood. This study aims to characterize the host and pathogen determinants of subclinical TB and to quantify its contribution to household transmission.

Methods: Sub-TB is a prospective cohort study conducted in Temeke, Dar es Salaam. Adults (≥18 years) with bacteriologically confirmed pulmonary TB are enrolled as index cases, and their household contacts (≥18 years), are screened for TB. Households in which at least one additional TB case is identified are enrolled and followed up. Subclinical TB cases identified among household contacts undergo a range of biological and epidemiological investigations that include epidemiological data collection, host and pathogen genotyping, bacterial genomics and proteomics, immune response investigations, hosttranscriptome investigation including single-cell transcriptomics and bacterial burden measurement. Patient-based infection models and phylodynamic modelling are also applied. A nested mixed-methods sub-study addresses the treatment of subclinical TB.

Recruitment status:

As of 13 Oct 2026, 509 index cases have been enrolled and 1012 household contacts screened. Additional TB was identified in 36 households, yielding 10 co-prevalent cases, 4 of which were subclinical.

Conclusion: Systematic screening detects TB among household contacts who report no TB specific symptoms and would therefore be missed by routine case finding. Sub-TB links pathogen and host characteristics with transmission dynamics. This will characterize the biological basis epidemiological contribution of subclinical TB and inform how it should be detected and managed. Participants also receive earlier diagnosis and linkage to care.

IHI70-03 Hospital Post-Discharge Outcomes of People Living with HIV in Rural Tanzania- a Prospective Observational Study.

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Background: People with HIV (PLHIV) hospitalized with advanced disease are at high risk of dying during hospitalization and after discharge. Evidence on post-discharge mortality and its associated factors in rural Tanzania is limited. We assessed in-hospital and 90-days post-discharge mortality and associated factors among PLHIV enrolled in the Kilombero and Ulanga Antiretroviral Cohort (KIULARCO).

Methods: We conducted a prospective observational study nested in the KIULARCO cohort at Saint Francis Regional Referral Hospital, rural Tanzania. Adults living with HIV admitted between February 2024 and November 2025 were consecutively included. Clinical data came from routine records, and vital status after discharge was ascertained at 90 days by clinic visit, record review or telephone contact. The primary outcome was death within 90 days of discharge. Associated factors were assessed using logistic regression, and survival using Kaplan–Meier and Cox models. Best-case and worst-case sensitivity analyses addressed loss to follow-up.

Results: Among 394 hospitalized participants**, 82 (20.8%)** died during hospitalization and **312 (79.2%)** were discharged alive. Median age at admission was **48** years (interquartile range [IQR] 38–56); **259 (66%)** had advanced HIV disease (WHO stage III/IV). Among discharged participants, 71 of 274 with information available at 90-days, had died within the follow-up, corresponding to a mortality of **25.9%** (95% confidence interval [CI] 20.8–31.5%), an additional 38 participants **(12.2%)** were lost to follow-up. In adjusted analyses, WHO stage III/IV or advanced HIV (adjusted odds ratio [aOR] 1.99, 95% CI 1.12–3.56) and ART naive and those who had treatment interruption at point of admission (aOR 2.06, 95% CI 1.24–3.43), were associated with in hospital mortality. Participants who were female (aOR 2.65, 95% CI 1.33–5.25), had advanced HIV disease (WHO stage III/IV; aOR 4.49, 95% CI 2.06–9.78), were referred to another facility (aOR 10.94, 95% CI 3.00–39.92), or were discharged against medical advice (aOR 3.33, 95% CI 1.42–7.85) had higher odds of dying within 90 days after discharge.

Conclusion: Mortality was substantial during hospitalization and within 90 days after discharge. Advanced HIV disease was associated with mortality at both stages. Strengthening inpatient care, particularly for females and people with advanced HIV disease, together with discharge counseling, improved referral systems and post discharge follow-up, may improve outcomes for PLHIV in rural settings.

Keywords: HIV; mortality; hospitalization; post-discharge care; Tanzania.

IHI70-04 The unaddressed burden of elevated blood pressure among adult people living with HIV in rural Tanzania: A longitudinal study

IHI70-05 Methodology and baseline characteristics of the Ifakara Heart and Lung Clinic Cohort

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Background

In rural areas of sub-Saharan Africa, data on care of non-communicable diseases remains scarce. This study aimed to describe the setting, methodology and baseline characteristics of a patient cohort with chronic heart or lung conditions from the rural Kilombero valley in Tanzania.

Methods

Since August 26th 2021 adults and children presenting with chronic heart and lung diseases diagnosed at the rural St Francis Regional Referral Hospital in Ifakara, Tanzania are offered participation in the Ifakara Heart and Lung Clinic Cohort. Clinical, echocardiographic, and spirometric data are entered directly in a RedCap Database.

Results

From August 26th, 2021, to June 20th, 2025, 925 participants were enrolled. Of these, 874 (94%) were adults, and 523 (57%) were female; the median age was 57 years (interquartile range [IQR] 40-70). At enrollment, diagnoses included hypertension in 409 (45%) participants, chronic heart disease in 771 (83%), chronic lung disease in 124 (13%), and both heart and lung disease in 30 (3%). The most common heart conditions were hypertensive heart disease (340/801; 42%), dilated cardiomyopathy (293/801; 37%), peripartum cardiomyopathy (40/801; 5%), and rheumatic heart disease (35/801; 4%). Of 680 patients with heart disease who underwent comprehensive echocardiography, 374 (55%) had reduced left ventricular ejection fraction (LVEF), of whom 147 (22%) had an LVEF <30%, 67 (10%) had mildly reduced LVEF, and 239 (35%) had a preserved LVEF. The most common lung diseases were asthma

(46/154, 30%), post-tuberculosis sequelae (45/154, 29%), and chronic obstructive pulmonary disease (40/154, 25%). At enrollment, 490 (53%) participants were taking medication regularly. The most frequently prescribed medications were angiotensin-converting enzyme inhibitors (n=663), beta-blockers (n=604), and furosemide (n=530).

Conclusion: A specialized heart and lung clinic could be implemented successfully in rural Tanzania. Hypertensive heart disease and dilated cardiomyopathy was the most common cause for a heart disease in this cohort of patients.

IHI70-06 Awareness and care-seeking behaviour towards non-communicable diseases of people living in the rural Kilombero valley

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Background:

Non-communicable diseases (NCDs) cause a substantial burden of disease in sub-Saharan Africa. Information about awareness and health seeking behaviour towards NCDs of people living in rural areas in Tanzania are scarce. The objective of this study was to explore the awareness of NCDs, to identify parameters influencing health seeking behaviour, and to identify adherence to NCD care of community members, and to identify health system barriers in the rural Kilombero valley in Tanzania.

Methods:

This was an observational cross-sectional study using a mixed method evaluation design, incorporating both quantitative and qualitative approaches for data collection and analysis using in-depth interviews and focus group discussions (FGDs). Participants were patients suffering from NCDs, community members, health workers, and district health managers of Kilombero, Ulanga, Malinyi, and Mlimba districts. Here, only the qualitative part is reported.

Results:

From June 16th 2025 to July 14th 2025, a total of 8 facilities and 130 participants were included: 23 patients suffering from an NCD, 8 health workers, and 3 district health officials participated in In-depth interviews; 96 community members participated in FGDs.

Awareness of NCDs: The community awareness of NCDs was on a low level. Many patients recognized their NCD in late stages when they became symptomatic due to end organ dammage. NCD conditions were connected to traditional beliefs and superstitions, which are supposed to be treated by traditional healers and witch doctors. Few people in the communities received health education related to NCD from various sources, such as radio broadcasts, from healthcare workers, and peer-to-peer discussions, and few read flyers.

Influence of health seeking behaviour: The study revealed that the main causes of delayed detection and treatment of chronic diseases included a lack of knowledge about the importance of early medical intervention and poor perception about modern medical care, and limited access to early screening and health education. Some patients and their families believed that NCDs were caused by witchcraft, so they prefer to seek care from traditional healers and use local medicines. Worries of sexual performance after medication intake and financial challenges limited individuals with NCDs from seeking early diagnosis and treatment. Treatment- and transport costs were found to be barriers. Interviewed patients and community members revealed that many patients' treatment contributions come from family contributions.

NCD care adherence: Factors contributing to patients' retention in medical care were perceived quality of care, support from healthcare workers, influence from family members to remain in medical care, and the availability of health insurance. Patients asserted that primarily they are motivated by the quality of services that include the availability of medicines, testing, timely care and treatment, and the availability of healthcare workers. Patients with health insurance reported being motivated to seek care because health insurance provides them access to care and treatment. Factors that made registered patients drop from NCD clinics were perceived ineffectiveness of formal healthcare, financial barriers, geographic factors and seasonal barriers, preference for traditional or spiritual healing, and slow recovery from medical care.

District capacity and health system barriers in providing NCD services: Screening for NCDs was reported as a routine triage process in all the health facilities visited. However, inadequate space and infrastructure, shortage and low capacity of health care workers to manage NCDs, and shortage of NCD diagostic equipment and supplies was reported. Essential NCD drugs were basically available, but stock outs were commonly reported. All healthcare workers and health managers interviewed affirmed that economic barriers remain a major challenge in accessing care for NCDs. Although community health workers play a vital role in community sensitization for various health interventions such as HIV and maternal and child health, their involvement in NCD prevention and control remains minimal. Health workers and managers expressed concerns over the absence of structured data systems and dedicated reporting record-keeping systems for NCD patients, in comparison to more established programs such as maternal and child health and HIV. All visited health facilities reported challenges in conducting outreach services due to limited budgets and a lack of internal resources, despite acknowledging the critical importance of such efforts. A major gap identified was the lack of a structured referral and feedback system for NCDs.

Areas of improvement: Community members emphasized the urgent need for NCD education at the community level, enhanced collaboration between health workers and professional NCD providers, strengthened health workers participation in community meetings, increased access to NCD information, to introcude exercise programs, and to make NCD screening mandatory. Health care workers and district health managers across the study districts put forward the provision of essential NCD equipment, capacity building, empowering primary health care facilities, outreach activities, and community sensitization.

Conclusion

NCD services in rural districts require substantial improvements in infrastructure, diagnostics, training of health care workers, service delivery, data systems, and community outreach for awareness to effectively address the growing burden of NCDs.

IHI70-07 Etiological detection of sexually transmitted infections through integrated community-based cervical cancer screening outreach among women in rural Tanzania

Dorcas Mnzava

Background

Sexually transmitted infections (STIs) remain a major global public health problem, particularly due to high proportions of asymptomatic infections that sustain transmission causing serious reproductive health complications. In Tanzania, there is limited STIs screening, and integration with cervical cancer screening program may improve STIs etiological detection in underserved rural populations.

Objectives

1. To evaluate the feasibility of integrating STI screening into community-based cervical cancer screening outreach using self-sampling among women in rural Tanzania.

2. To identify the etiological agents of sexually transmitted infections using molecular diagnostic methods.

3. To determine the prevalence of sexually transmitted infections among women attending community-based cervical cancer screening outreach activities.

Methods

This cross-sectional community-based study enrolled participants aged 21-65 years attending cervical cancer screening outreach in rural eastern-central Tanzania between 2023 and 2026. Cervical-vaginal self-sampling using Evalyn® Brushes was performed and analyzed using Allplex™ STI Essential Assay to detect STIs pathogens and genital mycoplasmas. HIV and syphilis were tested using rapid diagnostic tests. Data was analyzed using STATA version 18.

Results

Among 1183 participants (median age 40 years), prevalence of STI pathogens was 44.89%, with *Trichomonas vaginalis* being most common. 220 (18.6%) participants reported at least one symptom. The HIV prevalence was 8.71% (Figure 1). Of 531 participants with genital detection of STI pathogens, 41 (7.72%) received on-site antibiotic treatment during invasive treatment for cervical lesions, 321 (60.45%) received an antibiotic prescription, while 169 (31.83%) were lost to follow-up (Figure 2). No treatment was given for genital mycoplasmas colonization alone. Co-infection was low, with only 35 (2.96%) having ≥2 pathogens. *C. trachomatis* positivity was 7.41 times higher among women with detection of *Mycoplasma genitalis* (aPR=7.41, 95% CI: 1.03–53.52; p<0.047), while *M. hominis* colonization was more frequent in women living with HIV compared to HIV-negative participants (aPR=1.38, 95% CI: 1.19–1.61; p<0.001).

Conclusions

Integration of STIs screening into cervical cancer outreach represents a feasible strategy for addressing reproductive health priorities. These findings reveal a burden of predominantly asymptomatic STIs in the community, supporting etiological-based screening to improve treatment and antimicrobial stewardship while leveraging health outreach platforms to expand access to STIs screening in rural communities. However, 31.83% did not return for STIs treatment, highlighting the need for same-visit screening and treatment strategies in future programs to ensure timely diagnosis and treatment.

Recommendations

1. Integrate STI and cervical cancer screening: Consider offering other STIs screening alongside HPV self-sampling to improve access to testing in the communities.

2. Consider same-visit management: Evaluate the feasibility of same-visit treatment for eligible infections to minimize delays and loss to follow-up.

3. Expand access to molecular diagnostics: Explore sustainable approaches to molecular STI testing in resource-limited settings.

4. Improve clinical management: Distinguish pathogenic infections from colonization to support appropriate treatment and antimicrobial stewardship

SESSION 2 OF 6

Scientific Parallel Sessions I · Antelope A

From scientific discovery to health impact

Wednesday 11 November 2026 · 12:10–13:40

Moderator: Grace Mhalu

Format: 10 minutes per presentation; combined Q&A of 15 minutes at the end of the session.

Ref.	Title	Presenting author
IHI70-08	Safety and Age-Related Performance of the Direct Skin Feeding Assay in Children: A Community-Based Study in Chalinze, Tanzania	Rafael Lubida
IHI70-09	Detection and treatment of low-density malaria infection and child health: Findings from CHILD malaria, a three-arm individually randomized open-label controlled trial in coastal Tanzania	Deborah Sumari
IHI70-10	Anti-Schizont Immune Responses and Malaria Exposure among Children with Low-Density Malaria Infections in a Randomized Controlled Trial in Bagamoyo, Tanzania	Reward G. Lyimo
IHI70-11	Transitioning to Dolutegravir-Based ART in Children Living with HIV: A Retrospective Cohort Study from the Kilombero and Ulanga Antiretroviral Cohort in Tanzania.	Bernard Kivuma
IHI70-12	Impact of dolutegravir on body weight changes in children and adolescents living with HIV in rural Tanzania: A prospective cohort study	Lilian Moshi
IHI70-13	Strengthening the health system to establish a chain of care and referral for management of non-communicable diseases (NCDs) in rural areas of Tanzania (CARECHAIN - NCD).	Samuel Salvatory
IHI70-14	Policy-practice gaps and barriers to the effective management of insecticide resistance in Tanzania	Hamenyimana Gervas

IHI70-08 Safety and Age-Related Performance of the Direct Skin Feeding Assay in Children: A Community-Based Study in Chalinze, Tanzania

Rafael Lubida[1], Salum Hassan[1], Isack Ruta[1], Mgeni Tambwe[1], Nicolaus Gutapaka[1], Muanuzi Mutabuzi[1], Renatha Nindi[1], Silvester Simando[1] and Ally Olotu[1]

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Background: In the era of malaria elimination, vaccine-based strategies to reduce parasite transmission are receiving increased attention. Evaluating transmission-blocking vaccines requires reliable, safe, and standardized xenodiagnostic tools to measure human-to-mosquito transmission in endemic field settings. While direct skin feeding (DSF) assays closely mimic natural parasite uptake by vectors, field assessments of their safety, acceptability, and performance remain essential.

Methods: This four-month (March–July) longitudinal observational study was conducted at the Miono site in Chalinze. Of 223 participants aged 5–18 years screened, 210 (111 male, 99 female) were enrolled, balanced across age and sex. Participants underwent monthly follow-ups where standardized DSF assays were performed to assess safety and acceptability. Each assay involved allowing laboratory-reared female *Anopheles gambiae* s.s. (30 mosquitoes per cup per arm) to feed for 15 minutes. Safety was actively monitored post-procedure. Monthly, mosquito feeding rates and parasite transmission dynamics were quantified, with the DSF determined by midgut oocyst dissection 7–9 days post-feeding.

Results: High study retention was achieved, with 207 of 210 enrolled participants (98.6%) completing follow-up. The DSF procedure was found to be safe and well-tolerated. All reported adverse events were mild local skin reactions that resolved spontaneously within 48 hours; no serious adverse events occurred. Mosquito feeding performance improved over time, with an overall feeding rate of 91.9%, increasing from 88.8% in Month 1 to 94.5% in Month 4. Blood-smear parasite positivity ranged between 8% and 22%, peaking at Month 3. Sixteen out of 807 participant visits demonstrated infectivity to mosquitoes, indicating a persistent low-level infectivity of 1.98%. The overall mosquito infection rate was 62/36,929 (0.02%).

Conclusions: The DSF bioassay proved to be a safe, highly acceptable, and reproducible method for measuring malaria parasite transmission dynamics in Chalinze. Despite low individual infectivity rates, the assay consistently generated quantifiable transmission endpoints, supporting its utility as a primary tool for evaluating transmission-blocking vaccines.

IHI70-09 Detection and treatment of low-density malaria infection and child health: Findings from CHILD malaria, a three-arm individually randomized open-label controlled trial in coastal Tanzania

Deborah Sumari[1], Ally Olotu[1], Sylvia Jebiwott[2,3], Nicolaus Gutapaka[1], Sylvester Simando[1], Thabit Athumani[1], Xue Wu[2], Reward Lyimo[1], Nasoro Lilolime[1], Lewis Batao[1], Omary Juma[1], Georg Loss[4,5], Pamela Gangar[6,7], Sarah Mswata[1], Bryan Greenhouse[2], Grant Dorsey[2], Jade Benjamin-Chung[8], Günther Fink[4,5], Michelle S. Hsiang[2,3,7]

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Untreated low-density, subpatent malaria infections can persist for months. There are limited data on whether testing and treatment of these infections improves child health. We conducted an open-label randomized controlled trial in Kiwangwa and Fukaysosi, coastal Tanzania. Six hundred children aged 6 months–10 years were randomized 1:1:1 to receive interventions for 2 years: **ACDm**: intermittent (3x/year) active case detection with rapid diagnostic testing (RDT) and molecular testing (qPCR) plus standard passive case detection using RDT only with fevers (PCD); **PCDm**, standard PCD with RDT plus molecular testing (qPCR) with fevers; or **Control**: standard PCD. Artemether-lumefantrine (AL) was given by directly observed therapy for all RDT or qPCR(+) tests. The primary outcome was all-cause sick visits and secondary outcomes included clinical malaria, parasitemia, anemia, and growth faltering. 86% completed 2-year follow-up. In PCD, 38.0%, 27.5%, and 41.5% received AL at least once for RDT(+) fevers in the ACDm, PCDm, and Control arms, respectively. In ACDm, 16.1% and an additional 25.1% received AL at least once for RDT(+) and RDT(-)/qPCR(+) infections, respectively. In PCDm, 6.0 % received AL for RDT(-)/qPCR(+) fevers. For all-cause sick visits, overall incidence was 1 per child-year; compared to control, Incidence Rate Ratios (IRRs, 95% CI) for ACDm and PCDm were 0.91 [0.76–1.09] and 1.05 [0.88–1.24], respectively. For clinical malaria, overall incidence was 0.43 (0.37–0.5); compared control, IRRs for ACDm and PCDm were 0.73 [0.51–1.05] and 0.96 [0.71–1.30], respectively. In Kiwanga, clinical malaria incidence was higher (0.59, 0.49–0.69 *vs.* 0.22, 0.15 – 0.30 in Fukayosi). IRR for ACDm against control was 0.67, 0.44–0.996. No impacts on anemia or growth faltering were observed. Lower than expected rates of subpatent infection in PCDm and all-cause sick visits limited statistical power for some outcomes. However, ACDm reduced the incidence of clinical malaria in higher incidence sites, where it can be considered an alternative strategy to chemoprevention, particularly as molecular testing approaches the point of care.

IHI70-10 Anti-Schizont Immune Responses and Malaria Exposure among Children with Low-Density Malaria Infections in a Randomized Controlled Trial in Bagamoyo, Tanzania

Lyimo R[1*], Sumari D[1*], Gutapaka N[1], Lyatuu A[1], Mpina M[1], Lazaro Linda O[1], Athuman T[1], Simando S[1], Jebiwott S[2], Wu X[2], Hsiang MS[2], Olotu A[1]

[1]Ifakara Health Institute, Tanzania; [2]University of California, San Francisco, USA

Background

Malaria exposure during childhood is crucial for developing immunity against *Plasmodium falciparum.* However, low-density malaria infections (LMI) that remain undetected by rapid diagnostic tests (RDTs), can significantly impact cumulative

exposure and immune development. Understanding how malaria exposure relates to antibody development is essential for characterizing natural immunity and identifying immune responses that may be relevant to malaria vaccine development and evaluation.

Objective

To assess malaria exposure and anti-schizont immune responses among children participating in the CHILD (Child Health Infected Malaria randomized controlled trial using an enzyme-linked immunosorbent assay (ELISA) based on *P. falciparum* schizont-stage parasite lysate and to compare antibody responses among children in the Active Case Detection by qPCR (ACDm), Passive Case Detection by qPCR (PCDm) and Control arms (Control).

Methodology

The CHILD Malaria study is a randomized controlled trial conducted in Bagamoyo, Tanzania, involving 599 children of less than 6 months to 10 years. The interventions used qPCR to identify and quantify low-density infections and assess malaria exposure against *P. falciparum* schizont-stage antigens using ELISA.

Results

Preliminary results indicated that LMI in children detected by qPCR was 64% in children who had low malaria exposure, as shown by low antibody titers (P<0.05), while 23% had high antibody production. The results show that the presence of low parasitemia, as indicated by the qPCR detection, may contribute to the presence of high antibody titers but may not be directly correlated to recent exposure.

Conclusion

The results indicate that malaria immunity usually controls the infection rather than preventing, hence, detecting and treating LMI in children has a chance to enhance vaccine efficacy once administered in this population.

IHI70-11 Transitioning to Dolutegravir-Based ART in Children Living with HIV: A Retrospective Cohort Study from the Kilombero and Ulanga Antiretroviral Cohort in Tanzania.

Bernard Kivuma [1,2,3], Ezekiel Luoga [1,2,7] , Mgolegrace Smart Mabusi [4], Kalisha Bheemraj [3], Yashna Singh [5] , Dvora Joseph Davey [3,5,6], Fiona Vanobberghen [7,8], Maja Weisser [1,2,7,8], Robert Christopher Ndege [1,2,7], on behalf of the KIULARCO Study Group.

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Background: Dolutegravir (DTG) is the WHO-recommended first-line antiretroviral therapy (ART) for children living with HIV, yet most evidence on its virological and retention outcomes comes from clinical trials or adolescent populations. Few studies describe how DTG-based regimens perform in younger children treated in routine programmes in sub-Saharan Africa. Tanzania introduced DTG 50mg into paediatric care for children ≥30 kg from 2019), followed by DTG 10 mg paediatric formulation in 2021/22. We compared 12-month viral suppression and retention in care among children initiating DTG-based versus non-DTG-based ART in a rural Tanzanian cohort.

Methods: We conducted a retrospective analysis of prospectively collected data from the Kilombero and Ulanga Antiretroviral Cohort (KIULARCO) in Ifakara, Morogoro, Tanzania. We included children aged 0-14 years who initiated ART between January 2017 and December 2024 and followed them until June 2025. The exposure was DTG-based versus non-DTG (PI- or NNRTI-based) ART at initiation. Outcomes assessed at 12-months were viral suppression (<50 copies/mL) and attrition (death or loss to follow-up [LTFU; no contact ≥60 days from scheduled visit]). We used Fisher's exact tests and multivariable logistic regression (adjusted for age, sex, baseline immune severity, caregiver education and calendar period for suppression; age, sex and WHO stage for attrition).

Results: Of 222 children included, 50 (22.5%) initiated DTG and 172 (77.5%) non-DTG regimens. DTG initiators were older (median 8.7 vs 2.6 years) and a higher proportion initiated ART in 2022-2024 compared with non-DTG initiators (58.0% vs 3.5%). Among the 125 (56.3%) children with a viral load at 12-months, 79.3% (23/29) on DTG were suppressed versus 62.5% (60/96) on non-DTG regimens (aOR 2.68; 95% CI 0.70-10.30; p=0.152). Attrition occurred in 1/42 (2.4%) children on DTG versus 22/154 (14.3%) in non-DTG initiators (aOR 0.21; 95% CI 0.01-1.11; p=0.139).

Conclusion: In routine care, children initiating DTG-based ART had numerically higher 12-month viral suppression and lower attrition than those on non-DTG regimens, but neither difference was significant. Small sample size, few attrition events, residual confounding, and missing viral load data limit interpretation. Larger studies with complete viral load data are needed.

Keywords: dolutegravir; paediatric HIV; viral suppression; attrition; Tanzania.

IHI70-12 Impact of dolutegravir on body weight changes in children and adolescents living with HIV in rural Tanzania: A prospective cohort study

IHI70-13 Strengthening the health system to establish a chain of care and referral for management of non-communicable diseases(NCDs) in rural areas of Tanzania (CARECHAIN - NCD).

S. M. Salvatory* [1,2] A. Katende[1,2], V.Z. Urio [2], E. Mahundi [1,2], V. Myovela [1], C. Mlula[1], C. Chitimbwa[1], L. Wilson [1,2], M. K. Kapalaunga[1,2], M. Emanuel[1,2], F. Faustine [1], R. Ngulukila[1], G. Mbunda[1,2], J.K. Kitila[1], I. Mwasongwe[1], C. Bucher[1,3,4], M. Mwambashi[1,2], B. Kasuga[1,2], J. Okuma[3,4], M. Weisser[1,2,4,7], T. Zoller[6], M. Rohacek[1,2,3,]

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Switzerland; [4]*University of Basel, Basel, Switzerland*; [5]*Department of Cardiology, University Hospital Basel, Basel, Switzerland*; [6]*Charité – Universitätsmedizin Berlin, corporate member of Freie Universität Berlin and Humboldt-Universität zu Berlin, Department of Infectious Diseases and Respiratory Medicine*; [7]*Division of Infectious Diseases and Hospital Epidemiology, University Hospital Basel, Basel, Switzerland.*

Introduction.

In sub-Saharan Africa, Understanding and implementation of a function and effective long-term care models for NCDs in rural areas for diagnosis and treatment are scarce.

Objectives

To improve NCD care to populations in the Kilombero valley and in Bagamoyo in the central and coastal regions of Tanzania, respectively, by establishing an integrated protocol-based care and referral system for patients with NCD´s across all levels of the local healthcare system, complemented by a training program for healthcare workers and public education on NCD`s, aiming at improving NCD prevention.

Methods

CARECHAIN-NCD addresses hypertension, heart failure, diabetes, obstructive lung disease, and cancer. NCD clinics are implemented at participating health facilities in Kilombero valley on the level of health center and village dispensaries, with clinical management standardized using standard operating procedures. Healthcare is further supported by consultation and clinical decision support system, allowing for expert advice and informed referral decisions. An IT system supports data collection, monitoring, and patient referral. Training of health care workers, basing on the Train the Trainer concept offers clinical diagnosis-making, point of care ultrasound, lung ultrasound, and echocardiography courses. Community health education is provided through clinicians and NCD counselors at the central referral center, radio casting, and community health care workers. Community outreach programs offer NCDs screening by clinical assessment and if indicated by focused echocardiography, lung sonography, electrocardiography, blood sugar measurement, spirometry, and cervical cancer self-screening tests.

Expected Outcomes

We expect project implementation to improve NCD prevention through early detection, risk factor avoidance, and healthy lifestyles in the community. It will improve NCD care and access for rural population to high-level facilities, depending on disease severity. An educated and trained healthcare workforce will be available at all healthcare levels, and knowledge will eventually be disseminated beyond the project areas. The project will serve as a clinical and public health research platform to inform policy.

Conclusion

The chain of care model, which extends the expertise of referral institutions to rural settings, using a highly cost-effective and sustainable approach is crucial in reducing the burden of non-communicable diseases and potentially expanding NCD services across rural areas of Tanzania.

Keyword; Non-communicable disease, care chain, rural Tanzania

IHI70-14 Policy-practice gaps and barriers to the effective management of insecticide resistance in Tanzania

Hamenyimana Gervas

Background

Malaria control gains are stagnating or reversing, in part due to widespread insecticide and drug resistance, as well as increasing financial and implementation challenges. This study assessed the national strategies for insecticide resistance monitoring and management in Tanzania to identify key barriers and misalignments between policy and actual practice.

Objectives

The study aimed to critically assess the national strategies for insecticide resistance monitoring and management in Tanzania, with the objective of identifying key barriers and misalignments between policy and actual practice

Methods

We initially reviewed technical documents from Tanzania's National Malaria Control Programme (NMCP) produced between 2014 and 2024, along with World Health Organization (WHO) guidelines and reports on insecticide resistance monitoring and management. This was followed by in-depth interviews with key informants in Tanzania, including policymakers, representatives from funding agencies, technical experts, scientists, and vector control implementers at district and regional levels. The qualitative data was analyzed thematically using NVivo software.

Results

The document review revealed strong policy alignments of the NMCP strategies for monitoring and management of insecticide resistance with international practice as recommended by WHO. However, implementation of the policy intentions remained limited, with resistance monitoring being conducted in only 22 of Tanzania's 184 district councils. Interviews with 24 stakeholders highlighted significant gaps between the stated policies and guidelines and the actual practice. These gaps were driven by inadequate financing, donor dependence, insufficient coordination and dissemination of guidelines, limited technical capacity, and weak engagement of communities and district-level operators. Participants emphasized that without strengthened surveillance systems, sustainable local financing, and greater community and intersectoral collaboration, achieving the current strategic goal of malaria elimination by 2030 remains unlikely.

Conclusions

Despite strong policy alignment and strategic planning, Tanzania's capacity to implement insecticide-resistance management initiatives remains constrained by several policy-practice gaps, particularly in funding, staffing and coordination. Addressing these persistent challenges will be essential for more effective malaria vector control and will require sustained financing, stronger coordination, improved vector monitoring, and greater community and intersectoral engagement.

Recommendations

Summary of recommendations to strengthen insecticide resistance management and malaria elimination efforts in Tanzania:

Challenge: Funding and resource constraints, and donor dependence

Recommendations: Increase domestic funding and resource mobilization through public-private partnerships, improved taxation, health levies, innovative financing mechanisms (including diaspora bonds), and efficient use of natural resource revenues. In particular, diaspora bonds can provide an additional source of financing by enabling Tanzanians living abroad to invest in national health and development priorities, including malaria control and insecticide resistance management.

Enhance governance, transparency, and accountability, while reducing corruption

Challenge: Poor coordination and shortage of trained personnel

Recommendations: Establish a well-defined coordination unity for insecticide resistance monitoring and management (IRM) with a clear mandate and dedicated budget

Disseminate guidelines and provide context-specific training to local implementers

Establish adequate and equitable remuneration structures for vector control personnel to enhance motivation, retention, and workforce capacity

Challenge: Inadequate community malaria education and engagement

Recommendations: Strengthen community engagement and culturally tailored behavior change communication by involving community, religious, traditional, and political leaders, leveraging social and mass media platforms, and integrating malaria education into school curricula.

SESSION 3 OF 6

Scientific Parallel Sessions I · Antelope B

Vector Biology, Behaviour and Control I

Wednesday 11 November 2026 · 12:10–13:40

Moderator: Brian Tarimo

Format: 10 minutes per presentation; combined Q&A of 15 minutes at the end of the session.

Ref.	Title	Presenting author
IHI70-15	Contrasting environmental drivers of *Anopheles funestus* and *Anopheles gambiae* larval abundance in Kilombero valley, Tanzania	Yohana A. Mwalugelo
IHI70-16	Indoor microclimate shapes resting patterns of *Anopheles funestus* in south-eastern Tanzania	Polius G. Pinda
IHI70-17	Climate Variability and Malaria Trends in Rural Tanzania: Insights from Health Data, Environmental Records, and Community Narratives	Winifrida P. Mponzi
IHI70-18	An Inventory of Mosquitoes (Diptera: Culicidae) in the Kilombero Valley, Southern-Eastern Tanzania.	Joel D. Nkya
IHI70-19	How reliable is the Polovodova mosquito age-grading method? A blinded multi-rater validation in *Anopheles* mosquitoes	Doreen Josen Siria
IHI70-20	Indoor Microclimate and Mosquito Collections in Huts with Sliding Aluminium versus Fully Screened Windows: A Semi-Field Study in Tanzania	Jesca James Mawala

IHI70-15 Contrasting environmental drivers of *Anopheles funestus* and *Anopheles gambiae* larval abundance in Kilombero valley, Tanzania

Yohana A. Mwalugelo[1], Dickson S. Msaky[1], Herieth H. Mahenge[1], Polius G. Pinda[1], Joel D. Nkya[1], Mohamed Jumanne[1], Paul C. Mrosso[1,2], Reuben E. Mmweteni[1], Ismail H. Nambunga[1], Amos J. Ngonzi[1], Abdallah R. Kipekepeke[1], Khamis S. Kifungo[1], Hamis Bwanaly[1], Letus L. Muyaga[1,2], Douglas E. Norris[3], Michael Reddy[4], Isaiah Hoyer[4], Halfan S. Ngowo[1], Issa H. Mshani[1], Fredros O. Okumu[1,2] & Emmanuel W. Kaindoa[1]

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Background

Understanding larval ecology of malaria vectors is essential for optimizing larval source management. However, species-specific environmental drivers of larval abundance remain poorly understood, particularly for *Anopheles funestus* and *Anopheles gambiae*, which occupy distinct ecological niches but are rarely compared under natural field conditions. This study quantified habitat characteristics and environmental predictors of larval abundance of both species in the Kilombero Valley, Tanzania.

Methods

A longitudinal grid-based surveillance system covering 62 grids (15×15 km) was implemented, with up to 600 aquatic habitats characterized and sampled monthly from March 2024 to April 2026. Larvae were collected using standard dippers or 10L buckets and morphologically identified using standard taxonomic keys; *Anopheles funestus* sensu lato and *Anopheles gambiae* sensu lato were included in analysis. Habitat characteristics were recorded, including physicochemical variables and physical features. Associations between environmental factors and larval abundance were analyzed using negative binomial generalized linear mixed-effects models.

Results

For *An. funestus* s.l., abundance increased with higher pH (RR=1.14, $p < 0.001$), vegetation (RR=1.60, $p < 0.001$), algae (RR=1.39, $p < 0.001$), shade (RR=1.24, $p < 0.001$), and slow-moving water (RR=1.73, $p < 0.001$), but decreased with increasing temperature (RR=0.89, $p < 0.001$) and turbidity (RR = 0.32, $p < 0.001$). In contrast, *An. gambiae* s.l. abundance increased with temperature (RR=1.16, $p < 0.001$), temporary habitats (RR=1.24, $p < 0.001$), and turbidity (RR=1.67, $p < 0.001$), but decreased in shaded, vegetated, and algae-rich habitats (RR=0.53–0.85, $p < 0.001$).

Conclusion

These findings demonstrate clear ecological divergence between *Anopheles funestus* s.l. and *Anopheles gambiae* s.l. with distinct environmental conditions associated with larval abundance. The identified habitat characteristics highlight opportunities to refine larval source management by prioritizing habitat types that disproportionately contribute to each species without increasing operational complexity.

Keywords: Larval ecology, malaria vectors and environmental drivers

IHI70-16 Indoor microclimate shapes resting patterns of *Anopheles funestus* in south-eastern Tanzania

Polius G. Pinda[1,2,3*], Dickson S. Msaky[1,4], Gustav Mkandawile[1], Samwel Makayula[1], Douglas E. Norris[5], Michael R. Reddy[6], Isaiah Hoyer[6], Antoine Cribellier[3], Constantianus J.M. Koenraadt[7], Florian T. Muijres[3], Fredros O. Okumu[1,2,4,8], Emmanuel W. Kaindoa[1,2,4]

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Background: Indoor resting patterns of malaria vectors are changing, potentially driven by housing design including roofing materials, wall construction and associated indoor thermal and humidity-steered microclimates. This study quantifies how microclimatic gradients shape the resting choices of *Anopheles funestus* in southeastern Tanzania, testing whether different indoor zones create distinct thermal and humidity niches that influence mosquito microhabitat selection.

Methods: Between November 2024 and January 2026, thirteen sentinel houses, representing variation in house materials, roofing (metal or grass thatched), and wall material (bricks or mud) were sampled three times a week. In each house, mosquitoes were collected from indoor bottom, mid and top section using Prokopack aspirators. Sampling occurred in the morning (6:00-9:00h) or afternoon (12:00-15:00h). Indoor temperature and relative humidity were recorded at 30-minute intervals. Associations between house materials and zone, microclimate and resting behaviour were analysed using mixed-effect models.

Results: Across 153 sampling days, 1,910 *An. funestus* were collected. Most of these rested near the bottom house-section (40%), while the top-section had the smallest proportion (27%) ($p = 0.012$). Brick-walled houses had 80% higher abundance than mud-walled houses ($p < 0.001$), and grass-thatched houses had a 52% higher mosquito abundance than metal-roofed houses ($p = 0.002$). Indoor thermal microhabitats matched mosquito resting patterns, as both temperature and humidity varied between house materials and zones. The strong negative correlation between temperature and relative humidity ($r = -0.738$) limited the explanatory value of relative humidity, whereas the weaker correlation between temperature and absolute humidity enabled separation of temperature and humidity effects on resting behaviour. Abundance of resting *An. funestus* was associated with the joint interaction of mean

temperature ($\bar{T}$), temperature fluctuations (T_{range}), and absolute humidity ($\overline{AH}$), with highest abundance near $\bar{T}$=32.7°C and $\overline{AH}$=16.4 g/m³, and for minimal temperature fluctuations (T_{range}≈0°C).

Conclusion: The joint interaction between mosquito abundance, resting stratification and environmental variables (temperature and humidity) explains indoor resting patterns of *An. funestus*. These highlight the importance of incorporating indoor microclimatic heterogeneity into vector control strategies where housing improvements could alter indoor suitability for mosquito resting, survival, and malaria transmission.

Keywords: Indoor, Microclimate, Microhabitat, *Anopheles funestus*, Resting behaviour, House structure, House zones, and Vector control.

IHI70-17 Climate Variability and Malaria Trends in Rural Tanzania: Insights from Health Data, Environmental Records, and Community Narratives

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Background: Tanzania is experiencing increasing climate variability, including changing rainfall patterns and rising temperatures, which may influence malaria transmission. However, evidence linking climate variability to malaria trends at local scales remains inconsistent, particularly in areas with ongoing control interventions. This study examines whether recent malaria trends in Ifakara can be explained by climate factors alone or by a broader set of environmental and socioeconomic drivers.

Methods: A mixed-methods design combined retrospective malaria data from three health facilities (2018–2024) with rainfall and temperature records from nearby meteorological stations. Quantitative data were analyzed to assess temporal trends and associations between climate variables and malaria cases. Qualitative data were collected from community members and analyzed thematically to explore perceptions of malaria trends and climate variability.

Results: A total of 114,460 patient records were analyzed, with a malaria test positivity rate of 9%. Malaria burden fluctuated between 2018 and 2020, declined sharply in 2021, and remained relatively low from 2022 to 2024 with minor seasonal peaks. Rainfall was highly variable and showed a weak and inconsistent temporal relationship with malaria incidence, with occasional increases following periods of higher rainfall, suggesting that rainfall alone does not fully explain the observed trends. Temperature followed typical seasonal patterns but showed no clear association with malaria incidence. Qualitative findings indicated a perceived decline in malaria, attributed to improved awareness, increased uptake of preventive measures, and environmental changes, alongside persistent socioeconomic and ecological factors, including poverty and local habitat conditions.

Conclusion: Malaria trends in Ifakara cannot be explained by climate variability alone but reflect a complex interplay of climatic, environmental, and socioeconomic drivers. These findings underscore the need for integrated surveillance approaches that combine environmental, epidemiological, and community-level data to inform adaptive and targeted malaria control strategies.

Key words: Climate change, Malaria cases, Climate variability, Malaria transmission

IHI70-18 An Inventory of Mosquitoes (Diptera: Culicidae) in the Kilombero Valley, Southern-Eastern Tanzania.

Joel D. Nkya, Mohammed Jumanne, Polius G. Pinda, Abdallah R. Kipekepeke, Dickson S. Msaky, Herieth H. Mahenge, Paul C. Mrosso, Ismail Nambunga, Amosi Ngonzi, Yohana Mwalugelo, Reuben Mmweteni, Winifrida Mponzi, Rukiyah M. Njalambaha, Halfan S. Ngowo, Fredros O. Okumu, Issa Mshani, Emmanuel W. Kaindoa

Background

Despite decades of malaria vector research, the wider mosquito fauna of Tanzania's Kilombero Valley remains poorly characterised, as previous surveys have been generally limited in duration, geographical coverage and taxonomic scope. Beyond malaria vectors, the local fauna includes species from other genera such as Culicidae species capable of transmitting arboviruses and lymphatic filariasis. We therefore assessed mosquito richness, diversity and community composition across four District councils in the Kilombero Valley.

Methods

From March 2024 to June 2026, adult mosquitoes were sampled monthly at 615 households in 159 villages over 23 monthly rounds (47,467 trap-nights). Multiple traps were used to sample host seeking and resting mosquitoes both indoors and outdoors. All mosquitoes were identified morphologically. Richness and sampling completeness were estimated from incidence data, councils compared at common sample coverage and assemblage composition and turnover tested among councils and collection methods.

Results

We collected 1,025,561 mosquitoes (76.5% female), representing 76 taxa (15 Anophelinae species, 61 Culicinae species) in 10 genera. The *Culex pipiens* complex (72.7%), *Anopheles gambiae* complex (9.1%) and *Anopheles funestus* group (8.8%) comprised over 90% of specimens; 70 of the remaining 73 taxa each contributed under 1%, and seven were singletons. *Aedes* was the most speciose genus (22 taxa) but comprised 0.17% of the catch. Observed richness was 36 - 61 taxa per council and 35.8 - 48.9 after coverage standardisation; estimated completeness of species inventory was 70–80%. Hill diversity (q = 1) was 1.3–4.4 effective taxa per council. CDC light traps detected 73 taxa, yet three were recorded only by other methods and 17 by a single method. Turnover accounted for 95% of Sørensen dissimilarity among villages. Composition

differed among councils (PERMANOVA $R^2 = 0.26$) and collection methods ($R^2 = 0.09$; both $P < 0.001$).

Conclusion

The Kilombero Valley mosquito fauna is far richer than vector focused work implies, yet remains incompletely sampled. Because villages share few species, no single site or trap type represents the valley: documenting regional diversity requires complementary methods applied across many locations.

IHI70-19 How reliable is the Polovodova mosquito age-grading method? A blinded multi-rater validation in *Anopheles* mosquitoes

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Accurate estimation of mosquito age is critical for malaria surveillance, as only older female *Anopheles* mosquitoes can transmit the parasite. Traditional age-grading methods include the Polovodova technique in which dilatations on the ovarian pedicel to tally completed gonotrophic cycles (GC) are counted. Despite their widespread use, these techniques remain poorly validated under realistic operational conditions, with limited evidence on their precision and accuracy across different parity rates, GC, and species. In this study, the accuracy and precision of the Polovodova method were evaluated across multiple age-graders and species under both laboratory and field conditions. A blinded validation study was conducted using laboratory-reared *Anopheles arabiensis* and *Anopheles funestus* (N>3,600) spanning 4 GC and field-collected mosquitoes from Ulanga district, Tanzania (N=600). Three blinded researchers performed dissections and readings, while a fourth unblinded researcher served as the reference reader (R0) to obtain ground truth (for parity) or assumed truth (for GC) for laboratory mosquitoes. Accuracy and precision for parity and GC classification were assessed using pairwise inter-rater comparisons, percent agreement, Fleiss' kappa, and Cohen's kappa (κ) statistics. For field mosquitoes, which had no age-referenced group, only precision was assessed. The Polovodova method accurately classified parity in both species, correctly identifying 98% to 100% of nulliparous and 94% to 96% of parous mosquitoes compared with the reference dataset. Inter-rater reliability for parity was almost perfect in *An. arabiensis* and *An. funestus* (κ=0.81 to 0.83), with 82% to 96% pairwise agreement. GC classification was highly accurate for early stages (GC0 to GC2: 85% to 100%) but declined at later stages GC4 (34% to 46%), reflecting systematic underestimation of mosquito age. Overall GC reliability was moderate (κ=0.56 to 0.59). Field classifications showed almost perfect agreement (κ=0.87 to 0.88), supporting operational applicability. The Polovodova method provides robust estimates of parity and early gonotrophic-cycle status in *Anopheles* mosquitoes, but late-cycle classifications are more prone to reader disagreement and systematic underestimation. Operational use should therefore rely on trained multiple-reader workflows, including adjudication of discordant or late-cycle specimens, rather than single-reader classification. These findings provide empirical benchmarks for quality-assured Polovodova age-grading in malaria vector surveillance and intervention evaluation.

IHI70-20 Indoor Microclimate and Mosquito Collections in Huts with Sliding Aluminium versus Fully Screened Windows: A Semi-Field Study in Tanzania

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Background: Housing improvements may complement malaria control, but can also alter indoor ventilation and thermal conditions. Evidence on sliding aluminium windows, which provide a smaller openable area for natural ventilation, is limited. This study compared indoor microclimate and *Anopheles arabiensis* collections in semi-field huts fitted with sliding aluminium versus fully screened windows in Tanzania.

Methods: Four huts represented two house-size categories, with one hut per window design within each category. Both designs incorporated insect mesh, and mosquitoes could enter only through standardised door openings. Female *An. arabiensis* were released nightly, mosquito collections were measured using CDC light traps, and temperature, relative humidity and carbon dioxide (CO_2) were monitored at 30-minute intervals. Outcomes were analysed using linear and negative-binomial mixed-effects models.

Results: Across 96 hut-nights, mosquito collections were higher in the small- than large-house category (incidence rate ratio [IRR] 1.44, 95% confidence interval [CI] 1.18–1.76). Collections did not differ significantly between window designs in the large-house (IRR 1.19, 95% CI 0.98–1.43) or small-house comparison (IRR 0.99, 95% CI 0.82–1.19). During daytime, sliding-aluminium huts were cooler than screened-window huts (large: −0.41 °C, 95% CI −0.77 to −0.05; small: −0.64 °C, 95% CI −1.01 to −0.27). At night, the large sliding-aluminium hut was warmer (+0.40 °C, 95% CI 0.04–0.76). Daytime relative humidity was higher in the small sliding-aluminium hut (+1.86 percentage points, 95% CI 0.21–3.52). CO_2 was lower during daytime in the large sliding-aluminium hut (geometric mean ratio 0.97, 95% CI 0.94–1.00) and higher at night in the small sliding-aluminium hut (1.11, 95% CI 1.06–1.15), although differential missingness limits interpretation.

Conclusion: Indoor microclimate differed between studied window-design huts, but mosquito collections did not differ

significantly within house-size comparisons. Because each design was fixed to one hut per size category, findings cannot establish independently replicated window-design effects. Further replicated field studies are needed before recommending specific window designs for malaria-endemic housing.

Keywords: *Anopheles arabiensis*; housing; indoor microclimate; malaria; mosquito collections; semi-field system; sliding aluminium windows; ventilation.

SESSION 4 OF 6

Scientific Parallel Sessions II · Rhino Hall

Emerging and re-emerging diseases, genomics, and outbreak preparedness

Thursday 12 November 2026 · 13:30–15:00

Moderator: Brian Tarimo

Format: 10 minutes per presentation; combined Q&A of 15 minutes at the end of the session.

Ref.	Title	Presenting author
IHI70-21	A Cross-Sectional Analysis of CCHFV-Specific IgG Levels and Exposure Profiles in Pastoralist Populations of Tanzania	J. A. Jumaa
IHI70-22	Genomic Epidemiology of Antimicrobial Resistance in *Klebsiella pneumoniae* in Sub-Saharan Africa; Insights from Publicly Available Genomes, 1994–2024.	Alfred Boniphace Lazaro
IHI70-23	From Isolates to Insights: Integrating Whole-Genome Sequencing and Bioinformatics for Tuberculosis Drug-Resistance Analysis.	Veronica Misana
IHI70-24	Tackling Antimicrobial Resistance in Prevention of Surgical Site Infections in rural sub–Saharan Africa - An observational study - TARSI	Franzisca Mmbando
IHI70-25	Using VectorGrid Africa to Build a Rapid Workforce and Surge Capacity for Climate Sensitive Outbreaks	Ninael Jonas
IHI70-26	Biogeographic zoning and establishment of sampling nodes for VectorGrid Africa's network of long-term observatories of mosquitoes and mosquito-borne diseases in Africa	Mohamed Jumanne
IHI70-27	Mapping the spread of Sulfadoxine-pyrimethamine resistance in Mainland Tanzania and its potential impact on malaria chemoprevention: A Bayesian geostatistical spatiotemporal analysis	Nicholaus Mziray

IHI70-21 A Cross-Sectional Analysis of CCHFV-Specific IgG Levels and Exposure Profiles in Pastoralist Populations of Tanzania

[1]Jumaa, J.A., [1]Sayale, H.M., [1]Orotta, J.T., [1]Nkilosubi, D.M., [1]Lyatuu, A., [1]Nyaulingo, G., [1]Mwanzalila, M.I., [1]Mtambo, M., [1]Mbusule, M.A., [1]Julius, G.L., [1]Temu, S.,[1]Tumbo, A.M., [1]Mpina, M., [1]Mwangoka, G.

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Introduction: Crimean-Congo hemorrhagic fever (CCHF) is a tick-borne zoonotic disease that poses a significant public health threat and socioeconomic burden on livestock value chain actors. While CCHF is endemic across parts of Africa, data regarding long-term Immunoglobulin G (IgG) profiles post-exposure remain limited. This study evaluated quantitative CCHF virus (CCHFV)-specific IgG profiles among seropositive and seronegative individuals within pastoralist communities in the Morogoro, Iringa, and Pwani regions of Tanzania.

Methods: A cross-sectional sub-study was conducted between May and July 2025. From a primary study population (n=362), a subset of 40 participants was randomly selected for detailed IgG quantitative analysis. Serum samples were screened using the ID Screen CCHF Double-Antigen Multispecies ELISA Kit. Relative units (RU) equivalent to antibody units were calculated using the sample-to-positive control net optical density ratio. Statistical analyses were performed using Excel and R software.

Results: Seropositive individuals exhibited a markedly higher average relative unit (ARU) profile than seronegative individuals (peak: 251.64 RU vs. 14.66 RU). Among the seropositive individuals, Males demonstrated a higher seroprevalence (n=17) and a higher peak antibody profile (251.64 RU) compared to females (n=1, and 120.50 RU). Further antibody stratification based on different age categories revealed a downward trend in peak IgG levels with advancing age where youth (n=3) aged 15–24 years showed the highest peak value (251.64 RU), followed by young adults (n=6) aged 25–44 (184.76 RU), middle-aged adults (n=7) aged 45–59 (169.51 RU), and older adults (n=2) aged 60+ (136.91 RU) across the study sites.

Conclusion: CCHFV-specific IgG levels varied significantly across serostatus, sex, and age. The lower peak antibody levels observed in older age groups may indicate age-related variations in exposure history or age-associated humoral immunity decline. These findings highlight the need for prospective longitudinal studies and IgG avidity testing to better characterize long-term immunity against emerging zoonotic pathogens in Tanzania.

IHI70-22 Genomic Epidemiology of Antimicrobial Resistance in *Klebsiella pneumoniae* in Sub-Saharan Africa; Insights from Publicly Available Genomes, 1994–2024.

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Background: *Klebsiella pneumoniae* is an important cause of healthcare-associated infections, and the spread of antimicrobial-resistant strains, particularly carbapenem-resistant isolates, poses a major public health challenge. However, genomic data remain unevenly distributed across sub-Saharan Africa, limiting understanding of the geographical distribution and diversity of resistant lineages. This study aimed to characterise the genomic diversity and distribution of antimicrobial resistance determinants in *K. pneumoniae* across the region.

Methods: A retrospective analysis of publicly available *K. pneumoniae* genomic data collected between 1994 and 2024 was conducted. Genome metadata were used to describe geographical and temporal distributions, while multilocus sequence typing and acquired antimicrobial resistance gene profiles were examined to characterise circulating lineages and resistance determinants. Descriptive analyses were performed using R.

Results: The analysis included 3,679 genomes. South Africa contributed the largest number (1,390), followed by Malawi (443), Nigeria (335), Zambia (267) and Tanzania (263), demonstrating an uneven geographical distribution of available genomic data. Multiple sequence types were identified, including ST39, ST307, ST17, ST2621 and ST14. Resistance determinants spanning several antimicrobial classes were detected, including the carbapenemase genes OXA-181 and NDM-1. Carbapenem-resistant genomes were identified across multiple countries and collection years, highlighting the importance of sustained genomic surveillance.

Conclusions: Publicly available genomic data demonstrate substantial diversity among *K. pneumoniae* lineages and antimicrobial resistance determinants across sub-Saharan Africa. Uneven geographical representation limits comprehensive regional comparisons, underscoring the need to strengthen genomic surveillance, improve data sharing and support collaborative approaches to antimicrobial resistance monitoring and control.

Keywords: *Klebsiella pneumoniae*; antimicrobial resistance; genomic epidemiology; carbapenem resistance; sub-Saharan Africa.

IHI70-23 From Isolates to Insights: Integrating Whole-Genome Sequencing and Bioinformatics for Tuberculosis Drug-Resistance Analysis

Veronica Misana, Mahmud Mahmud, Hellen Hiza, Mohamed Sasamalo, Jacqueline Nkoabi, Sharifa Athumani, Tatu Matuzya, Thomas Maroa, Lujeko Kamwela, Lilian Tina Minja, Damien Portevin, Klaus Reither, Daniel Paris, Sebastien Gagneux, Daniela Brites.

Introduction: Bacterial antimicrobial resistance (AMR) is associated with 4.7 million deaths annually, with Mycobacterium tuberculosis complex (MTBC) the cause of Tuberculosis (TB),

accounting for 29% of deaths. Despite advances in molecular diagnostics, detecting the full spectrum of MTBC drug resistance remains challenging. Assays such as Xpert® MTB RIF and XDR, targeting predefined resistance-associated mutations, potentially missing novel mutations. Advanced molecular techniques such as Whole genome sequencing (WGS) enable comprehensive MTBC genomics characterization and detection of drug resistance mutations. Therefore, this sub-study utilizes WGS to characterize MTBC cultures isolates from TB patients in Dar es Salaam to identify their genetic diversity and drug-resistance profiles.

Objectives: To establish and optimize a WGS and a bioinformatics workflow for comprehensive genomic analysis of cultured MTBC isolates.

Methods: This sub-study was embedded within the TB-DAR cohort, 34 samples were collected from consented TB patients at the Temeke district hospital TB clinic and transported to Bagamoyo Laboratory for laboratory analysis. Positive liquid cultures were then analyzed to confirm MTBC species using smear microscopy and Mycobacterium protein 64 (MPT64) to confirm MTBC species. Genomic DNA was extracted from the confirmed cultures and sequenced by illumina Miseq. All genomes were then analyzed using GOMA pipeline.

Results: Xpert® MTB RIF detected MTBC in 29(85.3%) of all the collected samples while 23 (67.6%) were culture confirmed MTBC. Non-Tuberculosis Mycobacterium (NTM) was reported in one sample and 10 (29.4%) were contaminated. 20 genomes had over 97% of genomic coverage, with 73.88× [IQR: 46.02–84.30×] mean sequencing depth and a median of 966 MTBC variants were identified across the sequenced isolates. Lineage 3 was predominant accounting for 45% of the isolates, Lineage 4[30%], Lineage 1 [20%] and Lineage 2 [5%]. All sequenced isolates were pan-susceptible.

Significance: A standardized WGS and bioinformatics workflow is essential for comprehensive characterization of MTBC genetic diversity and drug-resistance profiles, with important implications for public health surveillance and understanding the transmission of circulating strains strengthening the TB control initiatives.

IHI70-24 Tackling Antimicrobial Resistance in Prevention of Surgical Site Infections in rural sub–Saharan Africa - An observational study – TARSI

Franzisca Mmbando[1,2], Michele Müller[3], **Jamali Siru[1]**, Deogratius Desderius[2], Mohamed Mbaruku[1], Jenifa Tarimo[1], Elizabeth Dotto[1],Lulu Wilson[1], Christamonica Chitimbwa[2], Peter Mang'ara[2], Josephine Mhina[1], Ezekiel Luoga Yoram[1], Andrew Katende[1], Martin Rohacek[4], Fassil Gebreegziabher[2], Winfrid Gingo[2], Maja Weisser[1,3,4]

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Background: Surgical site infections (SSIs) are the most common healthcare-associated infections (HAIs) in sub-Saharan Africa ranging from 7% to 41%, and substantially contribute to morbidity and mortality. High levels of antimicrobial resistance complicate the management. Preliminary evidence points at a possible association of gut colonization with multidrug-resistant Gram-negative bacteria (MDR-GNB) and SSI development, however evidence from rural sub-Saharan Africa on causative pathogens, resistance patterns in SSI and colonization rates remain scarce. Another challenge is that infection prevention and control (IPC) practices to prevent SSI are often not fully implemented in LMIC.

The objectives of this study are therefore to determine the rate of SSI, causative pathogens, resistance patterns, to determine the impact of colonization with multidrug-resistant gram-negative bacteria (MDR-GNB) in SSI development and to explore challenges in implementation of IPC measures

Methodology: This is an ongoing prospective, single-site observational study conducted at St. Francis Regional Referral Hospital in Ifakara, Tanzania, started October 1, 2025, through to March 31, 2027. In part 1 (surveillance) we prospectively enroll patients aged ≥15 years undergoing major elective or emergency abdominal surgery. After consenting, participants undergo a rectal swab before operation and are followed up clinically until discharge and by phone call at day 30. Clinical specimens from surgical sites, blood cultures when indicated, and intraoperative swabs are collected and analyzed using standardized microbiological methods to identify causative bacteria and assess antimicrobial resistance profiles. Rectal swabs are plated on selective agar plates (CHROMagar™ ESBL and CHROMagar™ SuperCARBA™) followed by identification using API20E (Biomerieux®). For the second part (IPC assessement), monthly monitorings are performed by using pre-specified checklist according to the WHO *Global Guidelines for the Prevention of Surgical Site Infection* focussing on four components: 1) hand hygiene, 2) use of personal protective equipment (PPE), 3) safe handling of wounds and 4) perioperative antibiotic prophylaxis. Feedback after every monitoring is given to the team and changes over time are recorded. Data from both parts are entered into a secure REDCap database and analyzed using descriptive statistics to determine SSI prevalence, pathogen and resistance distribution as well as IPC practice adherence, cox regression to analyse risk factors associated with occurrence of SSI.

Preliminary results: As of September 2026, 137 patients undergoing abdominal surgery were enrolled, 99 (72%) of these underwent emergency procedures. Overall, 22 (16%) participants developed an SSI. Of these, 7 (32%) were superficial incisional, 12 (55%) deep incisional, and 3 (13%) organ/space infections. The predominant pathogen identified in intraoperative samples from SSI was *Klebsiella spp*, with almost all being ESBL-carrying isolates. Pre-operatively, 80% of patients

were colonized with ESBL-producing gram-negative pathogens and 19.6% with carbapenemase-carrying bacteria. Within the IPC assessment, the average adherence to the four assessed components were 75% for hand hygiene, 69% for use of personal protective equipment, 59.3% for safe handling of wounds and 23% for correct perioperative antibiotics prophylaxis.

Preliminary conclusion: These preliminary findings show a relevant burden of SSIs with predominantly MDR-GNB among the causative pathogens. The high colonization rate of MDR-GNB in rectal screenings highlights the need to reassess surgical antibiotic prophylaxis in patients undergoing major abdominal surgery in this setting. Within IPC gaps, particularly the perioperative antibiotic prophylaxis showed room for improvement, emphasizing the need for targeted interventions to strengthen IPC practices.

Key words
Surgical site infection (SSI), Infection prevention and control (IPC), Antimicrobial resistance (AMR), Multidrug-resistant Gram-negative bacteria (MDR-GNB).

IHI70-25 Using VectorGrid Africa to Build a Rapid Workforce and Surge Capacity for Climate Sensitive Outbreaks

Presenter: Ninael Jonas

Climate variability and extreme weather events are increasing the risk of mosquito-borne disease outbreaks across Africa, highlighting the need for rapid, coordinated responses. Emerging arboviral threats, the spread of *Anopheles stephensi*, and shifting malaria transmission patterns underscore the importance of strengthening surveillance and workforce preparedness. VectorGrid-Africa, is establishing standardised permanent mosquito observatories and laboratory capacity across five African countries. However, translating surveillance intelligence into timely operational responses remains a challenge.

This project aims to develop and evaluate a competency-based, gender responsive Rapid Vector Response (RVR) workforce model in Tanzania, Kenya, and Mozambique, leveraging VectorGrid-Africa and existing national surveillance systems. In collaboration with Ministries of Health and subnational authorities, the project will establish activation thresholds integrating climate early warnings, health facility alerts, and entomological surveillance signals. The RVR package will include a competency-based training and certification framework, ministry-endorsed deployment protocols, and pre-positioned equipment at one surge hub per country to support mobilisation within 72 hours.

Each country will undertake one national training cycle and at least one live or simulated activation, followed by structured after-action reviews. Performance will be assessed through mobilisation times, laboratory turnaround, data completeness, and gender-disaggregated participation. Over 18 months, the project is expected to deliver a certified, surge-ready workforce comprising approximately 50% women, operational deployment mechanisms, tested activation pathways, and policy recommendations for sustainable financing and integration into existing health systems.

By linking climate, epidemiological, and entomological intelligence to operational response, the RVR model aims to strengthen climate-resilient health systems and support a shift from reactive outbreak containment towards anticipatory preparedness.

IHI70-26 Biogeographic zoning and establishment of sampling nodes for VectorGrid Africa's network of long-term observatories of mosquitoes and mosquito-borne diseases in Africa

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Introduction: Mosquito-borne diseases impose a major public health burden across Africa and are increasingly intensified by climate and land-use change, yet most of the continent lacks the long-term, standardized surveillance needed to track their evolving patterns. To address these gaps, we have recently established VectorGrid-Africa, a network of permanent observatories of mosquitoes and mosquito-borne diseases in the continent. The network is initially active in Kenya, Tanzania, Mozambique, South Africa, and Madagascar, with plans for continent-wide expansion. The goal of the platform is to enable tracking across spatial and temporal scales of key trends, including effects of climatic and land-use changes, spread of emerging pathogens, vector invasions, genomic shifts and novel mutations, and impacts of vector control interventions. To ensure our sampling sites represent prevailing environmental, epidemiological and landscape-level variations in mosquito communities and disease patterns, we used a two-stage framework combining multilayer biogeographic zoning with structured consultations of in-country partners.

Methods: First, we characterized second-level administrative units in each country using publicly available data on six key environmental and climatic variables: elevation, population density, urban extent, transport-network density, Köppen-Geiger climate classification, and Sentinel-2 land cover. We then applied principal component analysis, retaining components that explained at least 90% of the variance, and used spatially constrained SKATER clustering to divide each country into a minimum of six bioregions. In the second stage, in-country teams identified candidate nodes within each bioregion and resolved them to a set of national priority sites for vector borne disease surveillance through iterative consultations, considering additional factors, including historical surveillance records, security, accessibility, and local expertise. The teams also provided additional country-specific data on mosquito-borne diseases (if available) to further refine the bioregions; and documented the rationale for their final selections using structured consultation forms.

Results and conclusion: This framework enabled identification of 23 permanent sentinel nodes, being districts or district-equivalents, for continuous long-term sampling across diverse biogeographic settings in the five founding VectorGrid-Africa countries. By integrating reproducible ecological stratification based on publicly available data with contextual operational knowledge, this two-stage approach provides a transparent, scalable, and adaptable method for designing long-term mosquito surveillance networks even in data-limited regions.

IHI70-27 Mapping the spread of Sulfadoxine-pyrimethamine resistance in Mainland Tanzania and its potential impact on malaria chemoprevention: A Bayesian geostatistical spatiotemporal analysis

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Background

Sulfadoxine-pyrimethamine remains widely used for malaria chemoprevention despite increasing resistance driven by mutations in Plasmodium falciparum dihydrofolate reductase (dhfr) and dihydropteroate synthase (dhps) genes. Different mutations, including A437G, K540E, and A581G in the dhps gene and N51I, C59R, S108N, and I164L in the dhfr gene are associated with high resistance to SP. SP resistance markers are more prevalent in Eastern Africa, including Tanzania, and pose a growing threat to the effectiveness of SP-based interventions. However, recent evidence on the spatial and temporal distribution of these mutations remains limited. This study modelled spatiotemporal trends of these resistance markers across mainland Tanzania from 2021 to 2025, providing evidence to support malaria control and SP chemoprevention policy.

Methods

We analysed point-referenced molecular surveillance data collected between 2021 and 2025 using a spatiotemporal geostatistical model. The model was used to predict pixel-level

prevalence and associated uncertainty for K540E, A581G, and I164L across Mainland Tanzania. Prediction uncertainty was quantified using posterior standard deviation surfaces.

Results

Distinct spatial patterns were observed across mainland Tanzania. The K540E mutation

exhibited the broadest geographic distribution and remained highly prevalent throughout thestudy period, indicating widespread establishment of this marker. In contrast, A581G showed a persistent hotspot in northeastern Tanzania and a localised focus in northwestern Tanzania, with substantially lower prevalence elsewhere. An additional hotspot emerged in central Tanzania, where predicted prevalence increased from 12.5% (95% CrI: 6.2-21.5) in 2021 to 20.8% (95% CrI: 10.5-34.9) in 2025. The I164L remained rare and geographically restricted, occurring primarily in localised foci in the northwestern region of Kagera, where predicted prevalence

increased from 8.9% (95% CrI: 6.1-12.1) in 2021 to 11.0% (95% CrI: 9.0-13.5) in 2025.

Conclusion

The widespread establishment of K540E alongside localised hotspots of A581G and I164L demonstrates substantial spatial heterogeneity in SP resistance across mainland Tanzania. These findings suggest that parasite populations associated with the highest levels of SP resistance remain geographically clustered rather than uniformly distributed. Strengthened subnational molecular surveillance is therefore needed to monitor the persistence and spread of resistance markers, particularly in identified hotspot areas. Geostatistical modelling provides a valuable framework for identifying emerging resistance foci and generating evidence to support malaria chemoprevention policies and resistance surveillance strategies in mainland Tanzania and other malaria-endemic settings.

SESSION 5 OF 6

Scientific Parallel Sessions II · Antelope A

AI, Digital Science, and Intelligent Disease Surveillance & Response

Thursday 12 November 2026 · 13:30–15:00

Moderator: Naomi Masanja

Format: 10 minutes per presentation; combined Q&A of 15 minutes at the end of the session.

Ref.	Title	Presenting author
IHI70-28	High-throughput identification of mosquito species using flatbed scanner imaging	Dickson S. Msaky
IHI70-29	Geospatial-based surveillance of malaria risk in Dar es Salaam using a hybrid 3DCNN + LSTM and CA model	Edmund Steven Kanjagaile
IHI70-30	HealthScope: An open web-based platform of service-level health facility data revealing gaps in access to care in sub-Saharan Africa	Kasim Chambulilo
IHI70-31	Strengthening national health facility registry data for planning: an automated validation and monitoring pipeline applied to Tanzania's Health Facility Registry	Samuel Mbano
IHI70-32	Subnational Malaria Response Gaps: An Interactive Dashboard for Priority Setting in Eastern Africa	E. Saria
IHI70-33	Spatiotemporal mapping of insecticide resistance mechanisms in malaria vectors in Africa	Sylviane Miharisoa
IHI70-34	Routine malaria entomological surveillance in mainland Tanzania shows strong gains in data quality but requires greater integration to improve data use and ensure sustainability	Rosemary F. Nguruwe

IHI70-28 High-throughput identification of mosquito species using flatbed scanner imaging

Presenter: Dickson S. Msaky

Background: Accurate mosquito species identification is central to vector surveillance, but traditional morphological methods are slow and depend on specialized expertise. This study evaluated consumer-grade flatbed scanner imaging combined with deep learning for accurate, high-throughput mosquito identification, benchmarked across six neural network architectures on specimens from south-eastern Tanzania.

Methods: Mosquito specimens (n = 6,288), representing 13 species from five genera, were obtained from field collections and laboratory-reared colonies and imaged using a flatbed scanner. Six neural network architectures, five convolutional networks (MobileNetV2, ResNet-50, Inception-v3, DenseNet-121, and EfficientNetV2-S) and one vision transformer (DINOv2-ViT-B/14), were fine-tuned by transfer learning from ImageNet and self-supervised pretraining, then evaluated separately for species and sex classification using accuracy and macro-averaged F1-score, both on a stratified holdout test set and by stratified 5-fold cross-validation, with Cohen's kappa additionally reported for the cross-validated species classification. Grad-CAM++ and self-attention analysis were used to visualize model attention.

Results: All six architectures achieved high species classification accuracy. In stratified 5-fold cross-validation, species accuracy ranged from 98.53% to 98.81%, with macro-averaged F1-scores of 0.985 to 0.988 and Cohen's kappa of 0.983 to 0.986. On the holdout test set (n = 965), species accuracy was 98.34% to 99.17% and sex classification accuracy 98.55% to 99.69%. Grad-CAM++ and self-attention analyses indicated that model attention was concentrated on relevant features on the specimen.

Conclusion: Flatbed scanner imaging provided sufficient morphological detail for both convolutional and transformer models to achieve consistently high species and sex classification accuracy across architectures of different design. High throughput and standardized imaging make this approach suitable for mosquito identification in settings where specialized taxonomic capacity is limited.

Keywords: mosquito identification; deep learning; flatbed scanner imaging; species and sex classification; vector surveillance; malaria

IHI70-29 Geospatial-based surveillance of malaria risk in Dar es Salaam using a hybrid 3DCNN + LSTM and CA model

Edmund Steven Kanjagaile[1*] , Dorothea Deus[2] and Anastazia Daniel Msusa[2]

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Introduction Malaria remains a significant public health burden in tropical and subtropical regions, where the efficient identification and prediction of risk areas remain challenging. Conventional field surveys used to map *Anopheles* breeding sites are costly, time consuming and often incomplete. Therefore, there is a pressing need for a geospatially integrated surveillance framework that can accurately map malaria risk and forecast future risk dynamics to support targeted control efforts.

Methods A geospatial hybrid modelling framework was developed by integrating multi-source remote sensing (LULC, NDVI and NDWI), malaria, and climate datasets. A Random Forest model was employed to determine the relative importance of the input variables, which were then weighted and selected for inclusion in a deep-learning architecture. The predictive model combines a 3D Convolutional Neural Network (3DCNN) to capture spatial patterns with a Long Short-Term Memory (LSTM) network to learn temporal dynamics. The model was trained against a baseline mean squared error (MSE) of 0.1 representing a naïve mean predictor. To improve spatial realism of the final risk maps, a Cellular Automata (CA) model was incorporated using a 3×3 Moore neighborhood structure, with parameters calibrated at $\gamma = 0.293$ and $\beta = 43.9$ to enhance the spatial propagation of risk across neighboring cells.

Results The framework successfully mapped malaria risk in Dar es Salaam with a Spearman rank correlation of 0.92, identifying Kigamboni South, Tundwi, and Msongola as high-risk areas. The hybrid 3DCNN-LSTM model reduced the training by 97.3% and validation losses by 90.2% respectively from the baseline. Projections to 2060 indicate a steady spatial increase in malaria risk, with a cumulative slope of 0.077 risk units over the 35-year horizon (an annual slope of 0.002), demonstrating the model's ability to estimate future risk.

Conclusion: The integrated 3DCNN-LSTM-CA framework accurately maps current malaria risk and estimates its future spatial dynamics, offering a cost-effective alternative to conventional field surveys and a practical tool for guiding targeted malaria control in Dar es Salaam.

IHI70-30 HealthScope: An open web-based platform of service-level health facility data revealing gaps in access to care in sub-Saharan Africa

K. Chambulilo[1], C. Myalla[1,2], S. Ketende[1,2], P. Amratia[1,2], S. Rumisha[1,2]

[1]Malaria Atlas Project, Dar Node, Ifakara Health Institute, Dar es Salaam, Tanzania; [2]The Kids Research Institute Australia, Perth, Western Australia

Background: Planning for universal health coverage requires knowing where facilities are, what services they offer, and who can reach them. Regional datasets such as the WHO AFRO public facility list and OpenStreetMap-based sources on HDX mainly record facility location and type, with little service information. Ministry of Health registries that do hold service data are fragmented and inconsistently formatted. As a result, access is usually measured to any facility, regardless of the services it offers. We developed HealthScope to provide harmonized, service-level facility data and to show how it can be used to measure access.

Methods: We collected facility and service data from Ministry of Health registries in eight countries: Botswana, Ethiopia, Kenya, Malawi, Nigeria, Tanzania, Uganda and Zambia. A reproducible pipeline harmonized these data into a common schema and a standardized service taxonomy. It also validated coordinates against national boundaries, removed duplicates and assigned stable facility identifiers. As a proof of concept in Tanzania, we combined facility locations with WorldPop 2026 population estimates (100 m) and a modelled travel-time surface. This gave us the population within 30, 60 and 90 minutes of the nearest facility, nationally and by district. We included a tool that finds the nearest facilities offering a chosen service and estimates road distance and travel time by driving, walking or cycling (OpenRouteService).

Results: We managed to have an open web portal with four modules which are registry explorer, service gap analysis, population access maps, and a facility finder. The registry holds over 136,000 facility records from eight countries, 97% with valid coordinates. Of these, over 59,000 facilities in six countries have recorded services. In Tanzania, 82.4% of the 69.9 million people modelled lived within 30 minutes of a health facility and 90.0% within 60 minutes. About 7.0 million people 10.0% lived more than an hour away, including 4.7 million 6.8% more than 90 minutes away. In 21 of 183 districts, more than a quarter of residents lived over an hour from care, reaching 54.9% in Kaliua and 38.7% in Ikungi.

Conclusions: National averages hide large differences in access between districts. Harmonized service-level data make it possible to measure access to specific services rather than to any facility, and to extend the analysis to other countries. HealthScope gives ministries, council health teams and the public a shared, open evidence base for planning facility upgrades, referrals and emergency response.

IHI70-31 Strengthening national health facility registry data for planning: an automated validation and monitoring pipeline applied to Tanzania's Health Facility Registry

Samuel Mbano[1,2], Christina Myalla[1,2], S. Ketende[1,2], S. Rumisha[1,2]

[1]Malaria Atlas Project, Ifakara Health Institute, Dar es Salaam, Tanzania; [2]The Kids Research Institute Australia, Perth, Western Australia

Background: Accurate facility locations underpin access modeling, referral planning, outbreak response and resource allocation. Tanzania's Health Facility Registry (HFR), maintained by the Ministry of Health, is the authoritative national source of facility information. However, the public portal presents only a current listing, with no visible history of changes, no check on whether coordinates are plausible, and no route for data users to propose corrections. We developed an automated pipeline that complements the HFR by adding these quality-assurance and monitoring steps while keeping the original records intact.

Methods: The pipeline extracts publicly available HFR records into a versioned PostgreSQL/PostGIS database and is designed to compare each sweep with earlier versions to identify new, changed and closed facilities. Each facility's location passes through up to six validation layers: plausibility checks, ward and council boundary tests, OpenStreetMap name matching, Google Places matching, multi-source geocoding and, as a last resort, ward centroids, with free sources run before paid ones. Each location receives a high, medium or low confidence grade. Proposed corrections are stored alongside the original coordinates, which are never overwritten, and applied only after human review; approved decisions are locked against later automated runs. A scheduled AI-assisted report summarizes changes, with every reported figure automatically checked against the underlying data.

Results: These preliminary results come from an early version of the pipeline that is still being refined. In an initial extract of 2,000 of the 14,386 HFR facility records from five regions (Mara, Kagera, Iringa, Lindi and Katavi), 87.2% had complete coordinates that passed all plausibility checks; 5.8% had missing coordinates, 5.8% were placed by geocoders in a different ward from the one recorded, and 1.9% shared an identical point with another facility. After validation, 2.1% of facilities had high-confidence locations, 67.8% medium and 30.2% low, and 69.8% were corroborated by an OpenStreetMap or Google Places name match. Reviewers approved 42 corrections, all for facilities with missing coordinates, and 74 facilities (3.7%) still lack a usable location. Every record carried its recorded ward and council, which were compared with the geocoded location, but ward boundary polygons were not yet available to the point-in-ward test; this kept most name-matched facilities at medium confidence, and the high-confidence share is expected to rise once boundary data are loaded. All facilities were listed as operating, and 64 had opened during 2026.

Conclusions: Early results suggest that automated validation with human review can turn national registry data into a more reliable, current, analysis-ready resource that complements, rather than replaces, the official system. The pipeline feeds the HealthScope platform, and its outputs could support the Ministry of Health's own registry maintenance. The approach is transferable to other national facility registries.

IHI70-32 Subnational Malaria Response Gaps: An Interactive Dashboard for Priority Setting in Eastern Africa

E. Saria[1,2], K. Ilomo[1,2], S. Ketende[1,2], S. Rumisha[1,2]

[1]Malaria Atlas Project, Ifakara Health Institute, Dar es Salaam, Tanzania; [2]The Kids Research Institute Australia, Perth, Western Australia

Introduction: Malaria control remains undermined by a persistent mismatch between disease burden and intervention coverage. National surveillance can identify which countries lag but mask within-country heterogeneity, leaving program managers unable to see where inside a country the response is failing to match the disease and the very scale at which resources are actually deployed. ----

Methodology: Malaria incidence, *P. falciparum* prevalence ($PfPR_{2-10}$), ITN use, and effective treatment were drawn from Malaria Atlas Project modelled surfaces for eight countries (Tanzania, Kenya, Uganda, Ethiopia, Eritrea, Rwanda, South Sudan, Madagascar), 2015–2024, and aggregated to first-level administrative units (Uganda to districts) yielding over 150 subnational areas. A Malaria Response Gap Index defined the

gap as burden left uncovered: burden (mean of scaled incidence and prevalence) × (1 − response), response being the mean of ITN use and treatment. Units were tiered into four priority classes and visualized in an interactive R Shiny dashboard with choropleth drill-down and trends.

Results: Unmet need was concentrated, not uniform. South Sudan's Equatoria states ranked highest; Western Equatorial sustained incidence above 320 per 1,000 and prevalence above 30% against coverage near 50%. The subnational lens exposed hotspots masked by national adequacy, notably western Kenya's Lake Victoria basin (Siaya, Busia). Coverage rose across most regions over the period, narrowing gaps overall, yet a subset of high-burden regions retained substantial unmet need through 2024.

Conclusion: A sub-national Response Gap Index turns routine modelled surveillance into region-specific intelligence, pinpointing which provinces and districts not just which countries warrant investment, giving programs a practical, scalable subnational priority-setting tool.

IHI70-33 Spatiotemporal mapping of insecticide resistance mechanisms in malaria vectors in Africa

Sylviane Miharisoa[1,2,5], David Duncan[1,2,3,5], Gerry Ryan[1,3,4,5], Emmanuel Mpolya[2], Susan Rumisha[6], Nick Golding[1,3,4,5]

[1]The Kids Research Institute Australia; [2]The Nelson Mandela African Institution of Science and Technology, Arusha, Tanzania; [3]University of Melbourne; [4]University of Western Australia; [5]Vector Atlas; [6]Ifakara Health Institute

Background: Insecticide resistance in malaria vectors threatens the effectiveness of vector control across Africa. Previous work has used phenotypic bioassay data to produce maps of the spatial pattern in mortality response in African malaria vectors. However, resistance arises through multiple biological mechanisms, including target-site mutations and metabolic detoxification, so knowledge of the mechanism responsible for resistance in a given location are needed to better target interventions such as insecticide-treated nets.

Methods: We developed a mechanistic multi-locus population genetic model in a Bayesian framework that integrates the phenotypic response of resistance (bioassay mortality) with genotype frequencies signaling target site and metabolic resistance mechanisms. The model infers the genotype frequencies and population-level susceptibility to insecticide across space and time. Insecticide exposure covariates modulate locus-specific selection coefficients and dominance.

Results: Model performance was validated through a simulation estimation study in which synthetic data for 2 loci were generated for 100 mosquitoes through 2 generations in each of 2 villages. The model successfully recovered (identified) the jointly estimated parameters using 4 MCMC chains; results were consistent regardless of the prior distributions used, except for dominance, which was more sensitive to prior choice.

Conclusion: The model can already estimate multilocus genotype frequencies across space and time. Future work will increase the simulated complexity, inferring phenotypic mortality and allele frequency. Finally empirical bioassay and genotype data from across Africa will be modelled to produce mechanism-specific spatiotemporal resistance maps for targeted intervention planning.

IHI70-34 Routine malaria entomological surveillance in mainland Tanzania shows strong gains in data quality but requires greater integration to improve data use and ensure sustainability

Presenter: Rosemary F. Nguruwe

Background: Routine entomological surveillance is essential for evidence-based malaria control, but its effectiveness depends on geographical reach and data quality. This study assessed the quality, utilization, and sustainability of the nationwide Malaria Vector Entomological Surveillance System (MVES) in mainland Tanzania.

Methods: Routine MVES data from 34 sentinel districts collected between 2017 and 2025 were assessed on three quality dimensions: completeness (extent to which expected data was submitted); reliability (consistency of reporting across districts and periods); and validity (degree of agreement between field-reported and laboratory-confirmed results). Timeliness was not assessed as submission dates were largely unavailable. A structured survey was conducted among 62 Community-Owned Resource Persons (CORPs) involved in data collection, 34 District Malaria and Vector Surveillance Officers (DMVSOs), 59 Council Health Management Team (CHMT) members, and 11 National Institute for Medical Research (NIMR) staff involved in MVES. Additionally, key informant interviews were conducted with 6 National Malaria Control Programme (NMCP) officers and 3 NIMR laboratory staff. All data were integrated to assess MVES data quality, utilization, operational challenges, and sustainability.

Results: The completeness of MVES data increased from low and variable levels in 2017-2018 to near-complete reporting (>95% completeness) by 2024-2025. Reliability also improved from inconsistent early reporting to stable performance. Agreement between field-reported and laboratory-confirmed mosquito identification exceeded 80% in most districts, although year-on-year validity was 73% in 2023. MVES data were used mainly to support deployment of vector control measures (IRS, ITNs, and larviciding), monitor trends, and target health education. Major constraints included limited transportation (reported by 77.4% of CORPs); weak feedback (only 24.2% of CORPs received feedback after sample submission); staff turnover, uneven training; and limited integration of MVES into district planning. The introduction of a digital mosquito database improved completeness and reduced data entry errors. However, concerns regarding sustainability persisted due to high dependence on donor funding and weak integration into routine district health systems.

Conclusion: MVES improved data quality and capacity for evidence-based vector control, but weak feedback and limited integration hinder effectiveness. Sustained improvement requires stronger district capacity, supportive supervision, adequate financing, better use of data, and institutionalized entomological surveillance within district systems.

Keywords: Entomological surveillance, Malaria vectors, Data quality, Surveillance system, Vector control, Mainland Tanzania

SESSION 6 OF 6

Scientific Parallel Sessions II · Antelope B

Vector Biology, Behaviour and Control II

Thursday 12 November 2026 · 13:30–15:00

Moderator: Aneth Tumbo

Format: 10 minutes per presentation; combined Q&A of 10 minutes at the end of the session.

Ref.	Title	Presenting author
IHI70-35	Molecular Characterization of *Anopheles* Species Diversity and Associated *Plasmodium* Parasites in the Kilombero Valley, Tanzania	Ismail Nambunga
IHI70-36	Establishing the VectorGrid-Africa network of permanent mosquito observatories	Joel O. Odero
IHI70-37	Entomological surveillance of onchocerciasis transmission in the residual hotspots of Southeastern Tanzania	Idrisa S. Mchola
IHI70-38	The role of nuisance biting in sustaining bed net adherence in south-eastern Tanzania	Winnie A. Lema
IHI70-39	Evidence of limited mitochondrial differentiation but pronounced nuclear haplotype structuring between eastern and western populations of *Anopheles funestus* in Tanzania	Emmanuel E. Hape
IHI70-40	The role of neglected species within the *An. funestus* group and *An. gambiae* complex in malaria transmission across Africa	Frank M. Jackson
IHI70-41	Semi-field evaluation of the effect of cow and chicken dung on life history traits of *Anopheles funestus* in rural south-eastern Tanzania	Mary David Matovolwa
IHI70-42	Development and optimization of the modified-arm in cage method for evaluation of spatial emanators	Honesta K. Costa

IHI70-35 Molecular Characterization of *Anopheles* Species Diversity and Associated *Plasmodium* Parasites in the Kilombero Valley, Tanzania

Ismail Nambunga, Paul Mrosso, Herieth Mahenge, Mohammed Jumanne, Reuben Mmweteni, Dickson Msaky, Letus Muyaga, Yohana Mwalugelo, Abdallah Kipekepeke, Joel Nkya, Pinda Polius, Amos Ngonzi, Issa Mshani, Fredros Okumu, Emmanuel Kaindoa

Background: Although PCR-based mosquito identification and ELISA-based parasite detection are established in the Kilombero Valley, the added value of integrating broad molecular taxonomic characterization with morphological identification and *Plasmodium* detection in the same surveillance dataset remains to be established. This study combined these approaches to characterize *Anopheles* species diversity across larval and adult specimens, assess the performance of morphological identification across taxa, and describe *Plasmodium* species detections in molecularly classified mosquitoes.

Methods: Larval and adult *Anopheles* specimens collected from the Kilombero Valley, Tanzania, were submitted to the Wellcome Sanger Institute for molecular characterization using the ANOSPP (ANOpheles Species and *Plasmodium*) targeted amplicon sequencing. The resulting sequence data were used to identify mosquito taxa and detect *Plasmodium* parasites. Molecular identifications were compared with morphological classifications to assess the performance of morphological identification.

Results: Of 6,270 specimens submitted, 5,839 (93.1%) received successful molecular classifications, identifying 24 *Anopheles* taxa. Among adults, *Anopheles arabiensis* (49.9%) and *An. funestus* subgroup clade 1 (34.0%) predominated. Additionally, one *Anopheles gambiae* s.s was identified, a species that has reportedly remained undetected in most parts of the valley for some time. Larvae showed a broader distribution, with *An. arabiensis* (41.0%), *An. squamosus* (13.2%), and *An. funestus* subgroup clade 1 (12.1%) being most common. Morphological identification showed high sensitivity for the *An. gambiae* complex and *An. funestus* group among adults (97.0% and 97.5%, respectively), but lower performance for several other taxa. *Plasmodium spp* was detected in 32 specimens: 26 (23 *P. falciparum*, 3 *P. malariae*) in *An. funestus* subgroup clade 1 and six (5 *P. falciparum*, 1 mixed *P. falciparum–P. ovale wallikeri*) in *An. arabiensis*.

Conclusion: Molecular characterization identified 24 *Anopheles* taxa, revealed limitations in morphological identification for several taxa, and linked *Plasmodium* detections to molecularly classified mosquitoes. These findings demonstrate the added value of molecular methods for resolving taxonomic diversity beyond the major vector groups and characterizing parasite detections where morphological identification alone may be insufficient.

IHI70-36 Establishing the VectorGrid-Africa network of permanent mosquito observatories

Joel O. Odero[1,2], Mohamed Jumanne[1,2], Yeromin Mlacha[1], Emmanuel Mwanga[1], Ninael Jonas[1], Emmanuel Kaindoa[1], Halfan Ngowo[1], and Fredros O. Okumu[1,2], on behalf of the VectorGrid-Africa Consortium

[1]Ifakara Health Institute, Tanzania; *[2]University of Glasgow, United Kingdom*

Background: Long-term mosquito surveillance is essential for understanding changing disease risks, but data across much of Africa remain fragmented and often focus on individual diseases or short research projects. VectorGrid-Africa is establishing a locally owned network of permanent mosquito observatories to support research, vector control and outbreak preparedness.

Approach: With scientific leadership from Ifakara Health Institute and coordination by the University of Glasgow, the network spans Tanzania, Kenya, Mozambique, South Africa and Madagascar. Standardised monthly sampling and seasonal surveys are designed to link mosquito abundance, species composition, pathogen detection and genetic variation with climate, land use, vector-control interventions and human and animal health information. Biogeographic zoning and consultations with national teams guide site selection, while laboratory workflows and specimen archives will support molecular and genomic analyses.

Progress: We have identified 23 sentinel nodes across the five countries using environmental stratification and consultations with national teams. Work is progressing on harmonised sampling and specimen-processing protocols, data governance and coordination between field and laboratory teams. In Tanzania, an inception meeting in Morogoro brought government departments and research partners together to align implementation with national surveillance priorities. Complementary activities are strengthening country ownership and preparing rapid vector response in Tanzania, Kenya and Mozambique, where pilot areas and priority disease threats have been identified and reviews of existing response systems are under way.

Conclusion: VectorGrid-Africa offers Ifakara a shared platform connecting entomology, genomics, environmental research and One Health. Sustained sampling and links to national decision-making will be essential to translate these investments into better surveillance and outbreak preparedness.

Keywords: VectorGrid-Africa; mosquito surveillance; permanent observatories; One Health; outbreak preparedness; Africa

IHI70-37 Entomological surveillance of onchocerciasis transmission in the residual hotspots of Southeastern Tanzania

Idrisa S. Mchola[1,2], Sophia H. Mwinyi[1,3], Neema Zephania[1], Robert D. Sumaye[1], Godian Selemani[1], Martha A. Ndaikeje[1], Francesco Baldini[1,3], Mario Gonzalez Jiminez[4], Benjamin Makepeace[5], Issa H. Mshani[1,2,3], Fredros O. Okumu[1,2,3,4], Lizette Koekemoer[2], Simon A. Babayan[3], Emmanuel P. Mwanga[1,2,3].

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Life Science and Bioengineering, The Nelson Mandela African Institution of Science and Technology, P. O. Box 447, Arusha, Tanzania.

Background: Onchocerciasis remains a public health concern in the local communities of southeastern Tanzania, particularly in the Mahenge focus of Ulanga District, despite ongoing ivermectin-based mass drug administration (MDA). It is caused by the *Onchocerca volvulus* nematode and transmitted by blackflies of genus *Simulium.* Verification of elimination requires continued entomological surveillance to determine whether *Onchocerca volvulus* infection persist in vector populations. Human Landing Catch (HLC) is the standard method for collecting host-seeking blackflies, but it exposes collectors to potentially infectious bites. Alternative trapping methods are therefore needed to collect epidemiologically relevant blackflies while reducing direct human exposure. Information is also limited on the diversity of local *Simulium damnosum* complex and their potential roles in sustaining transmission. This study compared the performance of alternative blackfly trapping methods, characterised the diversity of blackfly cytoforms present, and assessed *O. volvulus* infection in blackflies collected from the Mahenge focus in southeastern Tanzania**.**

Methodology: A longitudinal entomological study was conducted in eight villages in Ulanga District between 2023 and 2024. Blackflies were collected using HLC, Miniaturized Double Net Traps (DN-mini), and Esperanza Window Traps (EWTs). Trap performance of the three collection methods was compared in four villages using a Latin square design. Blackfly cytoforms were characterized using PCR assay targeting internal transcribed spacer 1 and 2 (ITS1 and ITS2). Real-time PCR targeting the mitochondrial ND5 gene was used to detect *O. volvulus* DNA in the collected blackflies.

Results: A total of 17,000 blackflies were collected during the study period, including 10,211 collected during the trap comparison experiment. HLC collected nearly 12 times as many blackflies as DN-mini (rate ratio [RR] = 11.86, 95% CI: 7.01 - 20.06; $P < 0.001$), whereas EWT collected fewer blackflies than DN-mini (RR = 0.45, 95% CI: 0.26-0.78; $P = 0.004$). Trap performance also varied between villages. Year-round surveillance across eight villages showed that blackflies were present throughout the 12-month study period, although their abundance varied by village and month. Compared with Chikuti, estimated blackfly abundance was approximately four times higher in Makanga (RR = 4.02, 95% CI: 2.81-5.75) and more than three times higher in Ketaketa (RR = 3.42, 95% CI: 2.38-4.91) and Uponera (RR = 3.39, 95% CI: 2.36-4.87). Blackfly abundance was also significantly higher in Msogezi, Lyandu and Mdindo ($P \leq 0.05$). Molecular analysis identified Nkusi J as the predominant cytoform profile (72.3%), followed by *Simulium kilibanum* (17.6%), Nkusi J variant (1.9%), *S. kilibanum* variant (1.2%) and unknown profiles (7.0%). Of the 5,000 blackflies screened by PCR, 119 (2.4%) tested positive for *O. volvulus* infection, demonstrating the presence of parasite DNA in blackflies collected from the study area.

Conclusion: HLC produced substantially higher catches than the tested-alternative collection methods. However, DN-mini consistently outperformed EWT and may provide a safer alternative method for blackfly surveillance by reducing direct human exposure. The predominance of Nkusi J, together with the detection of *S. kilibanum* and other cytoforms, demonstrates the diversity of the *S. damnosum* complex in the study area, and highlight the need to determine their relative contributions to local transmission. The detection of *O. volvulus* DNA in the collected blackflies indicates parasite-vector contact. Continued entomological and molecular surveillance, is therefore required to determine spatial distribution and drivers of residual transmission and to inform targeted control and elimination decisions.

IHI70-38 The role of nuisance biting in sustaining bed net adherence in south-eastern Tanzania

Winnie A. Lema[1,2], Naomi H. Urio[1,4], Dickson S. Msaky[1], Emmanuel E. Hape[1,3], Frank M. Jackson[1,3], Yeromin P. Mlacha[1,2], Esther G. Kimaro[2], Fredros O. Okumu[1,4] and Halfan S. Ngowo[1,5].

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Background: Consistent use of insecticide-treated nets (ITNs) is a core malaria vector-control intervention, yet adherence depends not only on perceived transmission risk but also on other factors such as thermal comfort (indoor temperature) and biting intensity (including nuisance bites from non-vector mosquitoes) but also access to and condition of the ITNs. In rural south-eastern Tanzania, ITN use remains high even in seasons of low malaria transmission, and similarly high use is reported in low-transmission urban settings, a pattern that risk-perception models cannot fully explain. Here, we tested whether nuisance mosquito biting is associated with this sustained adherence during low-transmission periods in the Kilombero valley, South-eastern, Tanzania.

Methods: Using data from 21 months of entomological surveillance and repeated household observations of ITN use, a Bayesian autoregressive logistic model and applied counterfactual attribution analysis were fitted to estimate the contribution of nuisance biting to sustained net use. This quantitative analysis was complemented by 20 in-depth interviews with community members and district health officials.

Results: Culicine mosquitoes, predominantly *Culex* and *Mansonia* species, outnumbered *Anopheles* 2.4- to 63.8-fold. Although *Anopheles* densities fell by over 98% in the 2025 dry season, ITN use remained high (83-99%) among net-owning households. Culicine densities were modestly associated with persistent ITN use in dry season (β=0.59, 95% CrI 0.26, 0.92), but no such association was observed for *Anopheles* densities (β=0.12, -0.27, 0.51). Entrenched household habits (evidenced by previous use of ITNs) also predicted current use (β=0.35, 0.01–0.90). Unexpectedly, the culicine-by-dry-season interaction was negative (β = -0.20, 95% CrI -0.36 to -0.04), indicating that the association was attenuated, not amplified, in the dry season. Counterfactual removal of culicines reduced predicted mean dry season use from 89% to 79%, a maximum attributable fraction of 11% (95% Crl 0, 25%). The interviews

confirmed that nuisance avoidance, sleep comfort, and adherence to nightly household routines motivated ITN use in both seasons, whereas inability to replace damaged nets was the leading barrier.

Conclusion: Sustained ITN use in the Kilombero Valley is not explained by malaria risk alone. Use remained high after *Anopheles* densities collapsed and was modestly associated with culicine nuisance biting, nightly household routines, and sleep comfort but not densities of *Anopheles* vectors. Messaging to sustain adherence should therefore consider both comfort and nuisance relief alongside disease prevention outcomes, and should address the cost of replacing worn nets.

Keywords: Habit, nuisance, culicine, *Anopheles*, *Culex, mansonia,* Bayesian model, Insecticide treated nets, south-eastern and Tanzania.

Ethics approval and consent to participate: Approvals for this study was obtained from the Ifakara Health Institute Institutional Review Board (IHI/IRB)-IHI/IRB/EXT/No:36-2025 and the National Institute for Medical Research of Tanzania (NIMR)-(NIMR/HQ/R.8c/Vol, l/2844) prior to data collection. Written informed consent was obtained from all participants before their involvement in the study, and all methods were carried out in accordance with the Declaration of Helsinki. Confidentiality was maintained by assigning unique identifiers to all participants (both community members and district officials) in place of names across all transcripts and outputs. For the quantitative component, household-level consent was obtained from designated representatives. No biological samples were collected from human participants, as mosquito surveillance relied exclusively on CDC light traps.

IHI70-39 Evidence of limited mitochondrial differentiation but pronounced nuclear haplotype structuring between eastern and western populations of *Anopheles funestus* in Tanzania

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Background: *Anopheles funestus sensu stricto* is one of the most important malaria vectors in sub-Saharan Africa. Its population genetic structure may be shaped by major ecological gradients and topographic barriers, with key implications for vector evolution and control. This study used mitochondrial and nuclear molecular markers to compare *An. funestus* populations from eastern Tanzania (coastal and southeastern zones) and western Tanzania (inland and Lake Zone), and to evaluate whether gene flow is restricted between these regions.

Methods: Indoor-resting *An. funestus* mosquitoes were collected using CDC light traps from six sites: three in eastern Tanzania (Morogoro, Tanga, and Ruvuma areas; total n = 179) and three in western Tanzania (Mara near Lake Victoria, Shinyanga, and Katavi areas; total n = 166). Species identity was confirmed by PCR, and only *An. funestus sensu stricto* specimens were included. Mitochondrial *clades* (*I* and *II*) were identified using a *Taq*Man probe assay targeting mitochondrial single-nucleotide polymorphisms. The D3 region (domain 3) of the 28S ribosomal DNA (rDNA) variation (~400 bp) was assessed by PCR amplification followed by *Hpa*II restriction digestion; haplotypes (M, W, MW, Y, Z, and including a putative novel H-Type at Mara) were assigned based on agarose gel banding patterns.

Results: Analysis of 241 *An. funestus s.s.* specimens from five sites revealed limited mitochondrial differentiation but pronounced nuclear haplotype structuring. Mitochondrial *Clade I* predominated across all sites (73.3-100.0%), with moderate geographic variation (χ^2 = 23.084, p < 0.001, Cramér's V = 0.309) but low east-west differentiation (Jost's D = 0.085). In contrast, D3-RFLP haplotypes showed extremely strong geographic structure (χ^2 = 514.762, p < 0.001, V = 0.731) with near-complete east-west differentiation (χ^2 = 225.659, p < 0.001, V = 0.968; Jost's D = 0.744). Eastern populations were dominated by Y-type (90.1% at Morogoro) and M-type (68.9% at Ruvuma) haplotypes, while western populations were characterized by MW-type (97.6-100.0% at Shinyanga and Katavi). A novel H-type haplotype was identified at Mara (68.3%), exclusive to the Lake Victoria basin population.

Conclusion: These findings reveal limited mitochondrial differentiation but pronounced nuclear haplotype structuring between eastern and western *Anopheles funestus* populations in Tanzania, suggesting restricted gene flow between the regions. This pattern likely reflects topographic and ecological barriers, including the Great Rift Valley and climatic zonation. The observed population structure has important implications for region-specific malaria vector control, insecticide resistance management, and understanding the evolutionary dynamics of *An. funestus* in eastern Africa.

Key words: Main African malaria vector, Clades, D3-RFLP, rDNA, and ecological barrier

IHI70-40 The role of neglected species within the *An. funestus* group and *An. gambiae* complex in malaria transmission across Africa

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Background: Malaria vector control and research in Africa have primarily focused on the major malaria vectors, including *Anopheles funestus s.s.*, *An. coluzzii*, and *An. gambiae s.s.*, because of their established roles in malaria transmission. However, other members of the *An. funestus* group and *An. gambiae* complex have received comparatively less research attention, and their potential contributions to malaria transmission and insecticide susceptibility profiles remain poorly characterised. This systematic review aimed to evaluate the available evidence on the distribution, human blood-feeding, *Plasmodium* infection, biting rates, entomological inoculation rates (EIR), and insecticide susceptibility of neglected species within the *An. funestus* group and *An. gambiae* complex across Africa, to assess their potential roles in malaria transmission and identify key knowledge gaps.

Methods: A systematic review was conducted in accordance with PRISMA 2020 guidelines. PubMed, Web of Science, Scopus, and Google Scholar were used to search for studies reporting blood-feeding patterns, sporozoite infection, biting patterns, EIR, and insecticide susceptibility of neglected species within the *An. funestus* group and *An. gambiae* complex vector across Africa. Findings were synthesised descriptively because of heterogeneity in study designs, sampling methods, parasite detection and reporting methods.

Results: Seventy-three articles were included. Evidence was concentrated in Eastern and Southern Africa, with *An. rivulorum*, *An. leesoni*, and *An. parensis* frequently reported. Sporozoite rates varied widely, although most reported estimates were below 2%, and *Plasmodium falciparum* was the predominant parasite identified. Median human blood indices varied across species, reaching 81.1% in *An. melas*. The highest reported human biting rates included 6 b/p/n for *An. quadriannulatus* and 4.8 b/p/n for *An. rivulorum*. Reported EIR were 17.52 ib/p/y for *An. rivulorum*, 41.6 for *An. melas*, and 18.3 for *An. merus*. Most species were susceptible to the insecticides tested, although pyrethroid resistance was reported in four species (*An. amharicus*, *An. parensis*, *An. quadriannulatus,* and *An. rivulorum*).

Conclusion: Neglected *Anopheles* species may contribute to malaria transmission in some African settings, as evidenced by reported *Plasmodium* infections, measurable entomological inoculation rates, and human blood-feeding behaviour. Further species-specific investigations are needed to clarify their epidemiological importance and inform malaria surveillance and vector control strategies.

IHI70-41 Semi-field evaluation of the effect of cow and chicken dung on life history traits of *Anopheles funestus* in rural south-eastern Tanzania

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Background: *Anopheles funestus* is a major malaria vector in south-eastern rural Tanzania. Larval development and survival are influenced by environmental conditions, including livestock manure present in breeding habitats. While previous studies on *An. arabiensis* and *An. gambiae* have documented that nutrient-rich substrates like manure can affect mosquito life history traits, the impact of substrates on *An. funestus* remains poorly understood. Therefore, this study assessed the effect of cow and chicken dung on selected life history traits of *An. funestus* under semi-field system.

Methods: First-instar *An. funestus* larvae were exposed to cow or chicken dung leachate at four concentrations (0.25, 0.5, 0.75 and 1.0 g/100mL) and compared with clean-water controls under semi-field conditions. For each dung type, 20 larvae were introduced per concentration per replicate across five replicate rounds. Larval survival, adult emergence, development rate, and wing length were recorded.

Results: Chicken dung caused concentration-dependent reductions in larval survival and adult emergence ($p < 0.001$), increased larval development rate ($p = 0.004$), and reduced adult body size, while cow dung produced weaker effects. Physicochemical parameters, including pH, electrical conductivity, temperature and algae presence, varied with dung concentration for both dung types and were associated with larval mortality. However, these associations should be interpreted cautiously because they were correlated with dung concentration; ammonia and nitrate also increased progressively with concentration for both dung types.

Conclusions: Under the semi-field conditions and concentrations tested, livestock manure differentially affected *Anopheles funestus* life-history traits. Chicken dung showed strong concentration-dependent negative effects, whereas cow dung produced comparatively milder effects. Field validation is required before drawing operational conclusions about manure management and malaria vector control.

Keywords Malaria, *Anopheles funestus*, cow dung, chicken dung, Semi-field system, Life history traits, Ifakara Health Institute

IHI70-42 Development and optimization of the modified-arm in cage method for evaluation of spatial emanators

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Introduction: Spatial emanators (SE) are emerging as a complementary vector control tool following their endorsement by WHO in 2025. As second-generation SE products enter the market, there is a need for standardized and reproducible laboratory methods to screen new active ingredient. Developing a lab-scale screen would increase throughput and reduce costs when shortlisting candidates for further evaluation in the semi-field system. This study aimed to develop and optimize a customized glass sealed chamber (CGSC), modified from the arm-in-cage (AIC) method, for laboratory evaluation of spatial emanators.

Methods: Experiments were conducted in a 70x70x70 cm cage inside a climate-controlled laboratory to optimize transfluthrin concentration, mosquito density, and exposure duration. Following optimization, experiments investigated the influence of mosquitoes' circadian rhythms, anthropophilic behavior, and insecticide resistance on the protective efficacy (feeding inhibition and 24-hour mortality) of a transfluthrin emanator. Transfluthrin-treated filter paper was placed inside the chamber for 15 minutes before mosquitoes release. Three minutes after mosquito release, volunteers inserted their clean arms into the chamber, allowing mosquitoes to feed for 12 minutes. To assess circadian rhythms, 50 susceptible *Anopheles gambiae* sensu stricto and 50 susceptible *Aedes aegypti* mosquitoes were tested separately in the morning (0800hrs) and evening (1800hrs). To investigate anthropophilic behaviour and insecticide resistance, 50 mosquitoes from each of three groups resistant *Anopheles arabiensis*, susceptible *An. arabiensis*, and susceptible *An. gambiae* s.s. were tested in the evening (1800hrs). Blood-feeding success was recorded and mosquito mortality was assessed after 24 hours.

Results: Transfluthrin at 0.000001 g/ml was selected as a suitable concentration in the CGSC, giving 46.0% blood-feeding inhibition (BFI) with (95% CI: 39.5–52.5) in *An. gambiae* and 66.5% (95% CI: 60.1–72.9) in *Ae. aegypti*, with 24-hour mortality below 10% in both species. In treated chambers, morning versus evening testing did not significantly affect blood feeding odds in *Aedes aegypti* or *Anopheles gambiae* mosquitoes. *An. arabiensis* had lower feeding odds than *An. gambiae* (OR: 0.70, 95% CI: 0.60–0.80; P<0.001), while resistant *An. arabiensis* had lower feeding odds than the susceptible strain (OR: 0.30, 95% CI: 0.20–0.40; P<0.001).

Conclusion: The modified arm in cage method demonstrated potential for the laboratory evaluation of spatial emanators. However, differences in feeding responses between susceptible *An. gambiae*, susceptible and resistant *An. arabiensis* highlight the importance of standardizing test conditions and accounting for mosquito characteristics when interpreting efficacy estimates. Under controlled environment mosquitoes' circadian rhythm could have no influence in SE evaluation. Further assessment of the repeatability and reproducibility of the modified arm in cage method is required before it can be considered a validated method.

Keywords: Spatial emanator, anthropophily, circadian rhythm, mosquito resistance, entomological efficacy, laboratory evaluation, arm in the cage

Symposium topics

Parallel symposia · Wednesday 11 November 2026 · 15:00–17:00

Rhino Hall

Advancing Malaria Research, Policy, and Building Analytics Capacity in Africa through Geospatial Modelling

Moderator: Victoria Githu

Theme: Malaria Atlas Project (MAP): Advancing Geospatial Modelling for Malaria Research, and Decision-Making in Africa.

Overall objective: To showcase geospatial data processing and modelling approaches, employed by the Malaria Atlas Project (MAP) Dar Node, to generate malaria risk maps that inform policy, guide strategic planning and support evidence-based decisions making for malaria control and elimination.

Background and rationale

Generating reliable, high-resolution estimates of malaria burden requires the integration of diverse data sources, robust data processing approaches, and appropriate statistical and geospatial modelling techniques. Routine data from health facilities and traditional surveys provide important information for understanding malaria burden and its spatial distribution. However, limitations in data completeness, quality, geographical referencing and representativeness can affect the accuracy of resulting estimates. Addressing these challenges requires a systematic analytical approach encompassing data processing, quality assessment, and spatial referencing (geocoding). Geostatistical modelling provides a framework for integrating information from multiple sources to characterize spatial variation, generate predictions in areas with limited observations and quantify uncertainty in resulting estimates.

The Malaria Atlas Project (MAP) Dar Node, based at the Ifakara Health Institute in Tanzania, in collaboration with The Kids Research Institute Australia, applies geospatial analytics and statistical modelling approaches to generate evidence supporting malaria research and control. The team develops and applies analytical methods that integrate routine surveillance data and household survey information to produce estimates of malaria burden.

This symposium will showcase these approaches and explore the future of African-led geospatial and infectious disease modelling for malaria control and elimination. Discussions will focus on integrating transmission models, geospatial risk mapping, vector ecology and climate information to generate actionable evidence for policy and support sustainable, evidence-informed interventions.

Symposium programme

Time	Activity	Presenter / Responsible
15:00–15:10	Welcoming Remarks	Dr. Susan Rumisha
15:10–15:20	Presentation 1: Malaria routine data processing	Yasini Kokoda
15:20–15:30	Presentation 2: Geocoding for Geospatial Modelling in Public Health: A Multi-API Approach	Kaiza Ilomo
15:30–15:40	Presentation 3: Geostatistical Modelling of Care Seeking Behavior for Malaria Incidence Adjustment in Democratic Republic of Congo (DRC)	Dr. Ousmane Diao
15:40–15:50	Q&A session on Presentations 1–3	Moderator: Victoria Githu
15:50–16:20	Panel discussion: What does African-led geospatial modelling need in the next decade?	Panelists: Dr. Susan Rumisha, Dr. Sam Kiware, Ernest Moyo, Dr. Lembris Njotto, Sylviane Miharisoa, NMCP Representative

Time	Activity	Presenter / Responsible
16:20–16:50	Solution Demo: An interactive tool that aims to improve health care accessibility by providing individuals with key information to support with decision-making as they navigate through their health care journeys.	MAP DET Team
16:50–17:00	Closing Remarks	NMCP Representative

IHI70-45 Malaria Routine Data Processing

Presenter: Yasini Kokoda

Electronic health information systems like DHIS2 and the Master Facility List (MFL) are increasingly used for malaria modelling, subnational tailoring (SNT), and risk stratification. These data were not built for analysis, though, and need heavy pre-processing before they can be used. Standardized, reproducible processing workflows are rarely documented. This study describes the workflow used to prepare malaria surveillance data for SNT in Tanzania.

Methods: The team extracted facility-level malaria indicators for 2017–2024 from DHIS2, split by age (under 5 and 5 and over). They linked these to the MFL using facility identifiers and harmonized council names to match the administrative shapefile. They then cleaned the data in four ways:

1. **Excluded facilities:** facilities that do not provide malaria services, and facilities that never reported malaria data, were removed.

2. **Missing values:** DHIS2 does not distinguish zeros from missing values. Blanks were treated as zeros in very low- and low-risk areas, and as truly missing in moderate- and high-risk areas.

3. **Implausible records:** records where confirmed cases exceeded tests were set to missing.

4. **Outliers:** extreme values were flagged using both Median Absolute Deviation (MAD) and interquartile range (IQR) methods, then set to missing.

Key findings:

1. Facility and council details often did not match across DHIS2, the MFL, and the shapefiles, leaving facility attributes missing after linkage.

2. Very low- and low-risk strata had more ambiguity between zeros and missing values than moderate- and high-risk strata.

3. Some outliers were extreme. One facility reported about 160,000 tests in one month for people aged 5 and over, when typical monthly values are in the hundreds.

Conclusion: Working reliably with routine malaria data requires three things: keeping the different data systems synchronized, checking quality at several stages, and interpreting values in their local context. The study offers a transparent, reproducible framework for turning DHIS2 malaria data into analysis-ready inputs for evidence-based decisions.

IHI70-43 Geocoding for Geospatial Modelling in Public Health: A Multi-API Approach

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Introduction: Geocoding is the process of converting textual descriptions of locations such as addresses or place names into geographic coordinates (latitude, longitude) or other explicit spatial representations. Accurate geocoding of public health entities of interest such as health facilities, study locations, etc is a foundational step in geospatial modelling for public health. It underpins disease surveillance, healthcare accessibility analysis, and spatial disease risk prediction. Yet reliance on a single geocoding service (an API - Application Programming Interface) often introduces systematic gaps in spatial coverage and positional accuracy, particularly in regions with incomplete or non-standardised address systems.

Methodology: This study presents a multi-API approach that integrates several geocoding providers to improve the completeness, reliability, and spatial accuracy. We developed a reproducible R programming workflow that queries multiple geocoding APIs including commercial (Google and ESRI) and open-source services(OSM, Photon), harmonises their outputs, and applies a consensus and confidence-scoring strategy to select the most plausible coordinates for each record. The approach was evaluated against a reference dataset using metrics for match rate, positional error, and geographic coverage, and benchmarked against single-API baselines.

Results: The multi-API method achieved a higher overall match rate and reduced positional error relative to any individual provider, with the largest gains observed for ambiguous, sparsely documented, or informally described locations. Complementary strengths across providers allowed successful geocoding of records that single services failed to resolve, while the confidence-scoring step flagged low-quality matches for review before downstream modelling.

Conclusion: These findings suggest that combining multiple geocoding APIs offers a practical, scalable strategy for strengthening the quality of spatial data inputs to public health models, especially in resource-constrained or data-sparse settings.

IHI70-44 Geostatistical Modelling of Care Seeking Behaviour for Malaria Incidence Adjustment in Democratic Republic of Congo (DRC)

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Introduction: Estimating the malaria incidence in the community directly using routine surveillance data from DHIS2 can result in biased estimation because the routine surveillance system only captures populations who seek care from health facilities. As a result, WHO recommends adjusting the routine data before estimating the incidence, often using care seeking rates obtained from most recent DHS/MIS surveys. However, the careseeking rates from the surveys are aggregated at regional level and assumed to be the same across operational units of each region which does not reflect the reality. In this work, we applied a geostatistical model on the cluster level data from EDS-RDC III 2023–2024 survey to estimate care seeking rates at pixel level and aggregated at operational units in DRC.

Methodology: From the survey, we extracted the responses to the questions whether care was sought for children with fever in the last two weeks and where it was sought. For each cluster, we partitioned the febrile survey respondents into three categories. Sought care from DHIS2 sources for all sources of cares that report to DHIS2, non-DHIS2 sources for any source that provides effective treatment but does not report to DHIS2, and did not seek care for those who did not seek care as well as those sought care from sources considered to provide ineffective treatments.

Using the three categories formed and covariates known to drive careseeking behaviour, the Bayesian geostatistical model with multinomial likelihood, and Gaussian Markov Random Field (GMRF) was fitted via Template Model Builder (TMB). This produced 1kmx1km resolution surfaces for the probability of seeking care from DHIS2, and non DHIS2 sources. The obtained surfaces were then aggregated to operational units for incidence adjustment.

Results: At the pixel level, care-seeking estimates ranged from 8.0% (95% CrI: 2.1–16.6%) to 56.1% (37.1–76.8%) for DHIS2 sources and from 5.4% (1.7–10.4%) to 71.3% (54.7–86.2%) for non-DHIS2 sources. At the operational unit level, DHIS2 estimates ranged from 11.3% (5.6-20.3%) in Mwana Health Zone, South Kivu, in eastern DRC, to 49.4% (29.2-70.1%) in Kimputu Health Zone in the southwest. Non-DHIS2 estimates ranged from 8.1% (2.9-16.0%) in Butumba Health Zone in the southeast to 55.6% (30.8-73.9%) in Goma, North Kivu, in eastern DRC.

Conclusion: Geostatistical modelling revealed substantial spatial heterogeneity in care-seeking behaviour across the DRC, both within and between operational units. The resulting high-resolution estimates provide a more geographically refined alternative to region-level survey estimates and can support more accurate adjustment of routine DHIS2 malaria data for estimating community-level malaria incidence.

Antelope A

Maternal and Child Health Symposium

Moderator: Walter Msilikale

Theme: Strengthening Maternal & Newborn Care in Tanzania: Innovations, Quality Improvement and Lessons from Health Facilities

Overall objective: To facilitate knowledge exchange, critical reflection, and strategic dialogue on research evidence, innovations, partnerships, and implementation experiences that can strengthen the quality, integration, and sustainability of maternal and newborn healthcare services in Tanzania.

Background and rationale

Tanzania has made considerable progress in improving maternal and newborn health through sustained government commitment, research, health systems strengthening, and strategic partnerships. Nevertheless, preventable maternal and newborn deaths, stillbirths, and complications related to pregnancy and childbirth remain important public health challenges. Addressing these challenges requires integrated approaches that go beyond expanding access to health services to ensuring that every woman and newborn receives timely, safe, respectful, and high-quality care.

The Ifakara Health Institute, working closely with the Ministry of Health, the Prime Minister's Office, Regional Administration and Local Government (PMO-RALG), health facilities, academic institutions, and development partners, has contributed to advancing maternal, newborn and child health through implementation research, clinical innovations, capacity strengthening, infrastructure improvements and evidence-informed policymaking. These efforts have generated valuable evidence and practical lessons on how to strengthen health systems, improve clinical practices, and enhance maternal and newborn outcomes in Tanzania.

This scientific symposium will provide a platform to share research findings, implementation experiences, innovations, and lessons learned from maternal and newborn health initiatives in Tanzania. Through a keynote address and seven scientific presentations, the symposium will examine the effectiveness of clinical interventions, the contribution of infrastructure and equipment management to quality care, and opportunities to strengthen integrated maternal and newborn services. Attention will be given to translating research findings and implementation experiences into practical recommendations for policy, programming, and sustainable health systems strengthening.

The symposium will also highlight the importance of collaboration among government institutions, research organisations, healthcare providers, and development partners in accelerating progress towards national and global commitments to end preventable maternal and newborn deaths and stillbirths.

Symposium programme

Time	Activity	Presenter / Responsible
15:00–15:10	Welcoming Remarks	TBI
15:10–15:25	Keynote: Advancing Maternal Health in Tanzania: A Journey of Programmes, Partnerships and Lessons from (IHI)	Dr. Fatuma Manzi – IHI
15:25–15:35	Presentation 1: Effectiveness of Low-Dose Calcium Supplementation on Maternal and Pregnancy Outcomes	Calcium Project Team
15:35–15:45	Presentation 2: Beyond the Bricks: Impact of the Opening of Mary Machemba Ward on Neonatal Care at Amana Regional Referral Hospital, Tanzania	Sr. Mary Machemba – Amana RRH
15:45–15:55	Presentation 3: The Role of Training and Proper Equipment Management in Improving Quality of Clinical Care	Eng. Hope Peter – NEST360
15:55–16:05	Presentation 4: Enhancing High-Quality Neonatal Care Services through Improving Infrastructure in Low-Resource Settings: Lessons Learned from Hai District Hospital	Dr. Castro Tematema – Hai DH
16:05–16:15	Presentation 5: Rooming-In in Tanzanian Hospitals: Health Systems Barriers and Opportunities for Implementation	Jacqueline Minja – NEST360

Time	Activity	Presenter / Responsible
16:15–16:25	Presentation 6: One Team, One Warm Chain: Reducing Hypothermia Among Inborn Newborns through Labour Ward and NICU Collaboration at Sekou Toure Regional Referral Hospital	Dr. Lilian Majengo – Sekou Toure RRH
16:25–16:35	Presentation 7: Beyond Coverage: Kangaroo Mother Care Coverage and Timeliness of Initiation among Preterm and Low-Birth-Weight Newborns in Three Facilities, Mwanza, Tanzania	Magdalena Maikambo – NEST360
16:35–16:55	Discussions: Towards Zero preventable maternal and newborn deaths: national progress, priorities and strategic directions in Tanzania	MoH, PMO-RALGH, IHI
16:55–17:00	Closing Remarks	Moderator

Antelope B

Advancing Vector Control for the Next Generation (Vector Control Product Testing Unit – VCPTU)

Moderator: Betwel Msugupakulya

Theme: Advancing the testing methodologies and guidelines for the next generation of vector control products

Overall objective: To raise awareness of the Vector Control Product Testing Unit at IHI, share experience and findings on work done on spatial emanators, vector control in urban settings with focus on *Aedes* and evaluating the next generation of insecticide treated bed nets from laboratory to community durability assessment and generating evidence for policy makers.

Background and rationale

Vector control interventions, particularly insecticide-treated nets (ITNs) remain the cornerstone of malaria prevention in Africa. However, their effectiveness is increasingly undermined by widespread insecticide resistance and suboptimal product durability, underscoring the need for new insecticide classes, improved product quality, and a diversified vector control innovation strategy that includes technologies beyond ITNs to address malaria and other mosquito-borne diseases such as dengue. Vector control technologies cannot enter the market without rigorous independent evaluation demonstrating safety, efficacy, and operational performance under realistic use conditions. Testing platforms that meet global standards while remaining embedded in malaria-endemic settings remain limited.

The Ifakara Health Institute's Vector Control Product Testing Unit (VCPTU) was established in 2017 and the obtained Good Laboratory Practice (GLP) certification in 2021 The unit is advancing tools and evidence to address evolving challenges in vector control. Bringing together product innovation, evaluation methods and operational relevance, the session considers how African research leadership can improve protection against malaria and emerging urban vector threats.

Symposium programme

Duration	Activity	Presenter / Responsible
5 mins	Where we began: building the foundations of the VCPTU	Emmanuel Mbuba
10 mins	Advancing spatial emanators	Kyeba Swai
10 mins	New mosquitoes, changing cities: vector control in urban Africa	Janeth Machange
10 mins	Better nets, stronger evidence: evaluating the next generation of ITNs	Olukayode Odufuwa
10 mins	Beyond distribution: how long do nets protect?	Emmanuel Mbuba
30 mins	Panel discussion: Future priorities for vector control	Sarah Moore
10 mins	Q&A, Closing Remarks	Facilitator

