



PAMCA - Kenya Chapter **Annual Meeting 2026**

Abstract Book

*Reconnect and Reimagine Mosquito
Control in Africa*



September 1-3, 2026



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Welcome Address

Message from PAMCA Founder

Prof. Charles Mbogo, PhD; Retired



Distinguished guests, scientists and researchers, policymakers, development partners, industry leaders, colleagues, ladies and gentlemen, Good morning, and welcome to the PAMCA- Kenya 2026 Annual Conference and Exhibition. It is my great pleasure to welcome you to Nairobi for this important gathering from 1–3 September 2026. We are especially delighted to welcome you back to Kenya, where the first PAMCA Conference was held in 2014 following the launch of our Association in Durban, South Africa, in 2013. It is wonderful to host colleagues and friends from across Africa and around the world as we reconnect, share knowledge, and renew our collective commitment to protecting our communities from vector-borne diseases.

The theme of this conference, "Reconnect and Reimagine Mosquito Control in Africa," is equally timely and meaningful. It reflects our recent journey and our vision for the future.

The past two years have been challenging for PAMCA. The cancellation of our conferences in 2024 and 2025 allowed us to assess our governance, financial sustainability, and institutional structures. While these trials challenged us, they also reminded us that strong institutions are built through transparency, accountability, and a desire to improve. Today, we begin a new chapter. Our commitment must be to strengthen PAMCA through good governance, sound financial management, ethical leadership, and purposeful engagement with our members and partners.

An important priority will be reviewing and strengthening our Constitution and By-Laws to ensure they provide a solid governance framework that protects the Association, promotes accountability, and lowers the risk of future governance challenges.

Above all, I wish to convey my heartfelt appreciation to all our country chapters. You are the engine of PAMCA. You are where research is undertaken, innovation is translated into action, young scientists are mentored, and communities are served. If the engine stops, the organization cannot move. If the country chapters are weak, PAMCA is weak.

I am therefore immensely encouraged that throughout the recent obstacles, our country chapters remained strong, resilient, and united. They continued to serve their communities, advance science, and sustain the vision of PAMCA. Because the engine remained alive, PAMCA remained alive.

As we look ahead, let us continue to strengthen our country chapters, invest in the next generation of African scientists, deepen collaboration, and build an Association that is respected for its scientific excellence, integrity, and service to Africa.

Mosquitoes do not recognize borders, and neither should our obligation to control the diseases they transmit. Let us therefore unite for the good of our continent, work together in solidarity, continue serving our communities with zeal and excellence, and create lasting impact.

Finally, I thank every participant, partner, sponsor, and organizer for making this conference possible.

I wish you fruitful discussions, new partnerships, and inspiring scientific exchanges.

Enjoy the renowned Kenyan hospitality, enjoy your stay in Nairobi, and above all, enjoy the conference.

Thank you, and may God bless PAMCA, our nations, and the people of Africa.



Message from PAMCA – Kenya Chapter Chairman

Elijah Juma, PhD



Dear Colleagues, friends, partners, sponsors, ladies and gentlemen. It is a moment of great pride and exceptional honour for me and the entire leadership of PAMCA – Kenya Chapter, to welcome all of you to Nairobi, Kenya, the city under the sun and indeed the birthplace of the Pan-African Mosquito Control Association (PAMCA). It has been exactly three years now since such a congregation of the PAMCA community was constituted.

Undoubtedly, a lot of water went under the bridge during that period. Friends, colleagues, and partners have missed the connections that we were accustomed to every year during the PAMCA Annual Conference & Exhibition. This meeting is, therefore, truly monumental in its nature. Over the next three days, we will have an unparalleled opportunity to interact, share knowledge, bounce ideas across each other, learn, and have fun as we seek to reinvigorate PAMCA's pan-African solidarity spirit encapsulated in our vision of An Africa free of vector borne diseases.

On behalf of the PAMCA – Kenya Chapter Leadership, and Conference Organizing Committee that planned and organized this meeting, I hope that you do have a wonderful and memorable conference experience while you are here in Nairobi. Besides the conference, I hope you also have the chance to experience Nairobi and Kenya, its natural beauty, warm hospitality and wonderful weather. Welcome to PAMCA – Kenya Chapter Annual Conference 2026, welcome to Nairobi, karibuni sana!

Message from the Immediate Former Executive Director of PAMCA

El Hadji Amadou Niang, PhD

The Rebirth of PAMCA: A New Chapter for Africa



Dear PAMCA family, it is with immense pride, hope, and gratitude that I welcome you to this historic conference. More than another scientific meeting, this gathering represents the rebirth of the Pan-African Mosquito Control Association. Every great institution faces defining moments. The past few years have tested our resilience as a community. We experienced the painful loss of our visionary Executive Director and friend, Dr. Prosper Pius Chaki, whose unwavering commitment transformed PAMCA into the continent's leading professional network for vector control. His legacy reminds us that leadership is measured not only by achievements, but by the people inspired and the institutions strengthened. Today, as we reunite in Nairobi the birthplace of PAMCA we honour that legacy not through remembrance alone, but through renewal.

Africa stands at a pivotal moment. Emerging vector-borne diseases, insecticide resistance, invasive species, climate change, urbanization, and shrinking global health resources demand a different way of thinking. Yet these challenges also present an unprecedented opportunity for African scientists, practitioners, policymakers, entrepreneurs, and communities to lead the next generation of vector control innovation. PAMCA has never been merely an association. It is a movement built on collaboration across countries, disciplines, generations, and sectors.

It exists to strengthen African leadership, champion scientific excellence, build capacity, and translate research into impact for the communities we serve. As someone privileged to have served as Executive Director during an important chapter of our journey, I have witnessed firsthand the extraordinary talent, passion, and generosity within this community. I am confident that PAMCA's brightest days lie ahead not because of any one individual, but because of the collective strength of its members. This conference marks the beginning of a new era. Let us reconnect as colleagues, reimagine what African vector control can become, and recommit ourselves to building an organization that is stronger, more inclusive, more innovative, and more influential than ever before.

To our young scientists: you are not the future of PAMCA you are already shaping its future today. To our partners: thank you for believing in African leadership and walking this journey with us. To every member: this Association belongs to you. Its future will be defined by your ideas, your commitment, and your willingness to work together across borders for a healthier Africa.

May this conference inspire new partnerships, bold ideas, lifelong friendships, and renewed determination to achieve our shared vision of an Africa free from vector-borne diseases.

Welcome to the rebirth of PAMCA. Together, we reconnect. Together, we reimagine. Together, we lead.



Keynote Speaker

Topic: Disruption, Invasion and Opportunity: A Decisive Moment for African Vector Control

Dr. Eric Ochomo: Deputy Director, Centre for Global Health Research, Kenya Medical Research Institute (KEMRI), Kisumu, Kenya and Founding Member, PAMCA



Dr. Ochomo is a Senior Entomologist and the Deputy Director of the Kenya Medical Research Institute's Centre for Global Health Research in Kisumu, Kenya the region where his lifelong commitment to defeating malaria began. Raised in western Kenya, where the disease claimed lives around him throughout childhood, Dr. Ochomo has spent two decades translating that lived urgency into rigorous science that shapes national and continental policy. His research spans malaria vector surveillance, *Anopheles* genomics, insecticide resistance characterization, and the evaluation of novel vector control tools from laboratory and semi-field studies through to large-scale randomized controlled trials measuring real-world impact on malaria transmission. He led the team that first detected *Anopheles stephensi* in Kenya in 2023, adding a critical chapter to Africa's understanding of this rapidly spreading invasive vector.

He has served as Principal Investigator on landmark trials including the AEGIS spatial repellent study – leading to WHO recommendation in 2025 and evaluations of next-generation IRS compounds and has been instrumental in developing Kenya's national Insecticide Resistance Management Plan and Mosquito Surveillance Guidelines among other tools that directly inform which interventions reach over 20 million Kenyan households. With more than 100 publications and over 3,300 citations, Dr. Ochomo is among the most influential vector biologists on the continent. He is a member of Kenya's National Malaria Control Programme Vector Control Committee of Experts, a collaborator on multiple vector control and surveillance initiatives, and a mentor who has shaped over 40 postgraduate careers in vector biology. He is also a founding member of PAMCA which makes this keynote not merely a professional address, but a personal reckoning with the state of the institution and the continent he has devoted his career to defending.

Abstract: Growing up in malaria-endemic western Kenya, I watched this disease take children who never had a fighting chance. That memory has driven two decades of work on surveillance, insecticide resistance, and vector control trials and it is what makes this moment, and this Association's survival, deeply personal to me. Our field is being reshaped by forces that demand a fundamentally new response. The spread of *Anopheles stephensi* to more than 8 African countries is the clearest signal that our surveillance systems are lagging behind our vectors. This invasive species crosses borders as freely as commerce and climate allow. Tracking it, and understanding the shifting bionomics of all our vectors, requires real-time, cross-border surveillance networks with shared data platforms, harmonised protocols, and genuine political will across governments. No country can monitor or contain this threat alone.

Our intervention toolkit must also evolve. Waning insecticide efficacy demands we prioritise sustainable, durable solutions. Structural house modifications including screening, eave closure, improved construction offer protection that outlasts any spray campaign and puts control in the hands of communities permanently. We must champion these approaches more boldly. Equally, larval source management remains the most upstream and cost-effective investment we consistently underfund. Our community health systems are at our disposal and can make vector control and surveillance so much cheaper!

We cannot keep depending on imported tools built for other contexts. Africa must manufacture its own vector control solutions. This includes embracing 3D printing for affordable, locally produced surveillance equipment, and deploying AI-powered tools for vector identification, behavioural monitoring, and early-warning systems technologies that can leapfrog decades of infrastructure gaps if we invest in them deliberately. None of this is possible without sustainable financing. With over 36% of USAID malaria funding cut and the Global Fund under strain, donor dependency is no longer a tenable strategy. African governments must ring-fence revenues from extractive industries, agriculture, and universal health funds specifically for vector control and PAMCA must make that economic and political case relentlessly, through empowered country chapters that sit at national policy tables. PAMCA must be more than a conference. It must be the continent's vector control conscience, standard-setter, and champion. That is the Association we built. That is the Association we owe this generation. As a PAMCA founding member, I refuse to accept that a three-year gap in our convening is anything other than a warning. We must reconnect and we must reimagine.

The Late Dr. Prosper Chaki Inaugural Memorial Lecture

Prof. Nicodemus Govella, Public Health Scientist/Medical Entomologist, Ifakara Health Institute, Tanzania

Prof. Nicodemus Govella, Public Health Scientist/Medical Entomologist, Ifakara Health Institute, Tanzania



Prof. Govella, is an extraordinary independent public health researcher who has made remarkable contributions to the field of vector biology and malaria control. He holds a PhD in Infectious Diseases from the Liverpool School of Tropical Medicine (University of Liverpool) and currently serves as Chief Research Scientist at Ifakara Health Institute and an Honorary staff at the University of Glasgow. He has over 20 years of experience in Infectious diseases research, and his work bridges research, engagement with national malaria control priorities, policy-relevant surveillance, operational studies, technical leaderships and capacity strengthening of early-scientists and strategic organization development.

Because of his established scientific leadership, he holds multiple prestigious international recognition Awards including, UKRI-MRC African Research Leaders Award, awarded by UK-Medical Research Council and DFID, 2019, International Knowledge Exchange Award, awarded by the University of Glasgow, 2016, and The Wellcome Trust International Training Fellowship Award, awarded by the Wellcome Trust, 2013. He sits on various Advisory committee both nationally and internationally. He is a member of NMCP Tanzania Vector Control Technical Working Group, Zanzibar Malaria Elimination Technical Working Group, and a member of Vector Control Technical Working Group of the WHO-Roll Back Malaria. These Technical Groups are responsible for policy recommendation of all disease-vector control tools nationally and at a global level. Prof Govella has published over 80 peer-reviewed articles and two book chapters; some influenced global health practice and informed policy. For example, his joint work with the late Dr. Chaki, in collaboration with the Dar es Salaam City Medical Office of Health, spearheaded the development and evaluation of new malaria and filariasis mosquito surveillance tool and system which make, for the first time, community-based routine programmatic surveillance of malaria transmission affordable, practical and scalable.

This community-based mosquito trapping system which was first piloted in Urban Dar es Salaam to support the first largest larval control programme in Africa, is now already being adapted at the National level with the Ministry of Health in Tanzania through National Malaria Control Programme (NMCP) and National Malaria Elimination in Zambia. Beyond his scientific excellence, he has extensive expertise in Personal, People, and Organizational leadership.

Dr. Prosper Pius Chaki Memorial Lecture: Honouring His Life and Legacy

Environmental Health and Ecological Sciences Department, Ifakara Health Institute, Dar es Salaam, Tanzania

This memorial lecture honors the life and works of Dr. Prosper Pius Chaki, the past Executive Director (2014 – 2024) of the Pan-African Mosquito Control Association (PAMCA) and a long serving Chief Research Scientist at Ifakara Health Institute (IHI), Tanzania. He was a renowned independent public health researcher who made remarkable contributions to the field of disease-vector ecology and control, with particular focus on malaria disease that is spread by the most dangerous animal on Earth, the mosquito. His scientific credibility bridged research, policy-relevant surveillance, technical leadership, community engagement systems, and capacity strengthening of early career scientists and national-diseases control programmes. He strongly believed and promoted that elimination of disease vectors could only be achieved through strong partnerships, meaningful engagement with policymakers, and without downplaying community engagement. This philosophy was shaped following his first professional appointment with the Dar es Salaam City Medical office of Health under the Urban Malaria Control Programme and, reinforced by his prior one-year experience of living and working in hard-to reach communities in northern Tanzania, immediately after his undergraduate degree. He realized the power of local knowledge and ability of community to drive big initiatives when genuinely engaged.

Dr. Chaki's leadership style was characterized by inclusivity, humility, and not claiming to "know it all." He never claimed to know everything and consistently sought diverse perspectives from the team before making decisions. He demonstrated great ability to balance institutional rules with human realities in decision-making processes. Born and raised in Tanzania, he came from humble beginning. During his childhood, he enjoyed swimming and hunting wildlife before moving from a rural setting to urban Dar es Salaam to pursue his higher secondary education and, later, university studies. While attending school, he also ran small businesses to support himself financially.

This demonstrates his resilience and determination of attitudes. Beyond his professional achievements, his impact was felt far beyond his area of expertise. He was a devoted family man, married to his wife Doreen Ndosi, and together they were blessed with four children. All who knew him were impressed by his compassion, generosity, and willingness to create opportunities for others. He inspired colleagues, students, and partners not only through his scientific intelligence but also through kindness and commitment to serving humanity. His legacy lives through countless lives he touched and impacted his work on global health.



Plenary Talks

Plenary Talk 1

Title: Reimagining Malaria Control through Community-Based Efforts Akin to Mosquito Abatement Programs in the US

Joseph Wakoli Wekesa, PhD, District Manager, East Side Mosquito Abatement District, USA



Dr. Wakoli Wekesa is a highly distinguished Kenyan-born medical entomologist and vector ecologist who has fundamentally shaped public health practices in the United States and globally. Over a career spanning more than three decades, he has transitioned from a dedicated field researcher into a prominent administrative leader, specializing in the suppression of vector-borne illnesses. Wekesa's academic foundation began at the University of Nairobi, where he completed his

Bachelor of Science in Biology and Chemistry in 1987, followed closely by a Master of Science in Medical and Veterinary Entomology in 1990. Recognizing his profound professional potential, he moved to the United States to pursue doctoral studies, culminating in a Ph.D. in Medical Entomology from the University of California, Davis, in 1995. His professional life highlights a steady rise through the ranks of American public health administration. Wekesa spent nearly twenty years serving as a Vector Ecologist for the San Bernardino County Department of Public Health, alongside a vital stint as an Associate Public Health Biologist for the State of California.

In this leadership role, Wekesa achieved widespread acclaim by pioneering a comprehensive digital transformation. He completely overhauled the district's legacy, paper-based tracking methods, replacing them with high-tech software networks.

This allowed field technicians to utilize advanced digital mapping to deploy precise larval and adult mosquito control via specialized backpack sprayers, fleet trucks, and aircraft. Beyond North America, Wekesa serves as a key global health advocate. Collaborating frequently with organizations like the Pan-African Mosquito Control Association, he passionately champions utilizing California's localized vector-control framework to eradicate malaria across Africa, effectively bridging scientific technology and community safety.

Abstract: Effective mosquito control leads to reduction in biting nuisance and mosquito-borne diseases and focus of such effort has been attacking mosquitoes at their source of reproduction. Organized mosquito control in the United States led the way in achieving dramatic outcomes in improving people's quality of life and reducing disease. The strategy evolved from local communities organizing themselves with a common goal of reducing mosquito bites and disease transmission. This model is technically supported by local universities and strategically by departments of public health. The replication of this model across the United States brought significant changes to distribution and prevalence of mosquito-borne disease throughout the country, national and regional planning but locally operated with the focus on controlling the mosquito vector and tangentially controlling the pathogen. How can we re-imaging malaria control in Africa by focusing on controlling the mosquito vector, and empowering local communities to play a central role in such a structure. I discuss this approach to malaria control in the context of special district establishments anchoring mosquito control, and eventually mosquito-borne diseases. Adopting some of these approaches by PAMCA affiliated member nations may help create centers of excellence; the models emulated thereafter by many parts of the continent. We must encourage country chapters to focus on areas that may achieve greatest impact and replicate the results to more communities.

Such positive outcomes may encourage other chapters to adopt similar efforts to improve the malaria condition over time. A sustained effort among PAMCA and affiliated entities like AMCA towards this goal shall yield significant results. I offer some experiences and perspectives gained across several special districts in the US and my own background on malaria research in Africa.

Plenary Talk 2

Title: The future of Vector control: Tackling challenges and embracing innovation

Charles Wondji, PhD, Executive Director of the Centre for Research in Infectious Diseases (CRID, Cameroon)



Prof. Charles Wondji is Professor of genetics and vector biology at LSTM (UK). He is Executive Director of the Centre for Research in Infectious Diseases (CRID, Cameroon), heading the LSTM Research Unit at CRID (LRUC). For nearly 25 years, his research has focused on understanding the biology and genetics of mosquitoes, vectors of tropical diseases including malaria and arboviral diseases. Through several Wellcome Trust Fellowships, his group has made significant breakthroughs in elucidating the genetics basis of metabolic resistance to insecticide in malaria vectors with the detection of key genes and genetic markers allowing the design of simple DNA-based tools to easily detect resistance by national control programs to inform resistance

management strategies. His grant portfolio includes funding from diverse funders such as BMGF, NIH, CDC, MRC/BBSRC, global funds, and UNITAID. He is strongly committed to creating a positive research environment in his team and has contributed to the careers of many helping them secure grants to start their path to independence.

He has supervised 19 PhD students (UK/Africa) and sponsored 14 African scientists to secure Wellcome fellowships (Master, training, intermediate and senior levels) a work for which he was awarded the Chalmers medal by the UK Royal Society of Tropical Medicine and Hygiene in 2021. He is a member of several international bodies including the WHO Guideline Development Group for Vector Control, the external scientific advisory committee (ESAC) of IVCC and several research consortiums. He sits on several international funding review committees (e.g. Wellcome Early Career Award committee).

Abstract: Vector control remains one of the most effective strategies for reducing the burden of vector-borne diseases, particularly malaria, dengue, and other emerging infections. However, its future is increasingly challenged by insecticide resistance, changing vector behaviours, climate change, and operational constraints that threaten the sustainability of current interventions. This plenary will explore the evolving landscape of vector control and the need to move beyond single-tool approaches toward integrated, evidence-based strategies, highlighting both the challenges and opportunities that lie ahead. It will examine recent advances in vector surveillance, molecular monitoring, genomics, data-driven decision-making, and next-generation control tools. The talk will also discuss the importance of strengthening local research capacity, fostering cross-sectoral collaboration, and ensuring equitable access to new technologies. By embracing innovation while addressing existing limitations, the global health community can develop more resilient, adaptive, and sustainable vector control programs capable of meeting future public health challenges and accelerating progress toward disease elimination goals.

Plenary Talk 3

Title: Biorational Larvicides, Larviciding and Resistance Management for Mosquito Control – Then, Now and the Future

Tianyun Steven Su, Ph.D., Doctor of Medicine



Dr. Tianyun Steven Su, is a Chinese-born American Doctor of Medicine, Vector Biologist and Ecologist, and Epidemiologist, who has a broad education in preventive medicine and infection diseases (1979-1984), human parasitology and medical entomology (1984-1987), and vector biology and control (1991-1994). Throughout his career in academia (1987-2002), governments (2002-2021) and industries (2002-present),

Steven has been on a productive, achieving and rewarding track for the following areas: outstanding teaching and mentorship for undergraduate and graduate students in parasitology and medical entomology, theoretical and practical research in biorational and sustainable vector and pest control, organization, quality analysis and quality control of vector and pest control entities, research, development and regulation in vector and pest control products, pesticide resistance management in vector and pest control operations, as well as other collaborations among academia, governments and industries at local, domestic and global scales.

Since 1987, Steven has functioned as principal investigators for over 50 research projects in vector and pest management from academia and industries, authored over 125 peer-reviewed, 35 non-peer reviewed publications in national and international journals, 290 research reports on product evaluation for industries, 8 book chapters, and other publications, organized and chaired over 30 symposia and workshops, and delivered over 200 presentations at various national and international events.

To serve the scientific community, Steven volunteers as a member of editorial board or reviewer for numerous international scientific journals, as well as review committee member of various research funding sources. Steven holds membership or fellowship of numerous prestige professional associations in the USA, Europe, and China, and is recognized by these organizations for his significant contributions. After he retired from US government in 2021, Steven continues to run his business as Founder, CEO and Chief Medical Entomologist, as well as serves as a member of Board of Trustees, Northwest Mosquito and Vector Control District in California.

Abstract: Mosquito larvicides derived from microbials and insect growth regulators have been increasingly used to control mosquito larvae. Their relative target specificity, non-target safety, and environmentally friendly profile have been well documented. There is an urgent need to promote biorational larvicides for mosquito control in Africa, while facing the bottleneck of adult control. Various formulations have been made available; application techniques, efficacy evaluation procedures, and resistance management tactics have been developed in the USA and elsewhere. *Bacillus thuringiensis* subsp. *israelensis* (B.t.i.) is highly target-specific against mosquitoes and blackflies, resistance toward intact B.t.i. was rare. *Bacillus sphaericus* is another highly active larvicide against mosquitoes, toward which resistance have occurred in both laboratory and field mosquito populations. The Cyt1A toxin from B.t.i. and Mtx toxin from *B. sphaericus* are the key components in resistance management to B.t.i. and *B. sphaericus*. The resistance management strategies have been well developed and implemented in the laboratory, field, and industrial development. Spinosad derived from *Saccharopolyspora spinosa* has been recently used for mosquito control; high levels of resistance have occurred in laboratory populations, as well as in some local wild populations; no management tactics have ever been developed.

Methoprene has been used to control mosquitoes for over 40 years; resistance has been reported in both laboratory and field mosquito populations. Development of S-methobutene with enhanced stability and activity may bring future promise for resistance management. Very little attention has been paid to the resistance management in mosquitoes to other insect growth regulators. In nature, multiple resistance and cross resistance make resistance management more challenging. Efficacy validation, prevention of resistance and restoration of susceptibility in mosquitoes to the biorational larvicides are crucial to the success of sustainable mosquito management, particularly while adult control is failing.

Plenary Talk 4

Title: Integrated Mosquito Management in the USA: Structure, Surveillance, Research, and Control

Ary Faraji, PhD, Salt Lake City Mosquito Abatement District



Dr. Ary Faraji has been passionate about entomology since a very young age and has collected insects from all over the globe during the past 35 years. His professional career in entomology started when he first applied for a position as a Seasonal Vector Ecologist at a Southern California mosquito and vector control district in 1998. This position exposed him

to not only entomology, but wildlife biology, parasitology, arbovirology, molecular techniques, and most importantly, learning about Integrated Pest Management by working directly with mosquito

surveillance and control techniques. He has pursued these interests in his academic and professional careers and has tried to combine applied research into real-world scenarios to better understand the biology and ecology of disease vectors, and to determine improved techniques for surveillance and control of mosquitoes and mosquito-borne diseases.

He received his master's degree from Rutgers University in 2005 and his PhD in 2014. He has published over 115 peer-reviewed manuscripts, in addition to best management practices and book chapters; delivered over 350 presentations at professional meetings and extension events; mentored dozens of students; and garnered over \$15 mil USD in external grant funding throughout his career. He has been the past president of many local associations in addition to the American Mosquito Control Association and is the immediate past-president of the Medical, Urban, and Veterinary Entomology section of the Entomological Society of America. His current employment with the Salt Lake City Mosquito Abatement District provides him the flexibility to pursue applied and academic research, in addition to mentoring students, and remaining active on a domestic and international level. He is most proud of utilizing the latest technologies in mosquito/vector control and providing reduced-cost alternatives to help enhance and improve the field of mosquito surveillance and control globally.

Abstract: This presentation will cover the financial and operational structure of a publicly funded mosquito control program in the United States. Mosquito control services are generally provided by local governmental districts that are funded by property taxes. Operations incorporate a holistic Integrated Mosquito Management approach which relies on surveillance of both larval and adult mosquito stages to better direct abatement efforts. The vast majority of actual abatement efforts rely on larval source management (laicising), followed by adult control (adulticiding) only if absolutely deemed necessary. Operational research, insecticide resistance, and non-target monitoring are also integral components of many operations. All aspects of a modern mosquito control program will be presented to the audience.

Plenary Talk 5

Title: Reality check: Africa is not prepared to tackle mosquito borne diseases. Can PAMCA re-engineer a new paradigm?

Silas Majambere, PhD, Business Manager – Africa, Europe & Middle East, Valent Health LLC



Dr. Silas Majambere is a medical entomologist. His PhD focused on mosquito ecology and the role of larval source management for malaria control in Africa. He has more than 15 years of field experience in mosquito ecology and control. He spent his academic career working in The Gambia, Tanzania, Zanzibar and Burundi and providing technical assistance to dozens of National Malaria Control Programs in Africa. He later worked for the Innovative Vector Control Consortium (IVCC) which is a leading portfolio on new vector control tools addressing residual and outdoor malaria transmission. After that, he joined The Pan-African Mosquito Control Association (PAMCA) as the Director of Scientific operations supporting mosquito surveillance in PAMCA member institutions. He currently works for Sumitomo Biorational Company, Valent Health, overseeing the company's public health and forest health portfolio in Africa, Middle East and Europe.

Abstract: Africa remains inadequately prepared to tackle mosquito borne diseases despite bearing the world's highest malaria burden and increasing threats from dengue and other arboviruses. Current mosquito control approaches rely heavily on externally funded commodities and promises for technological interventions, while neglecting sustainable environmental management and the social and economic conditions that drive disease transmission. Local communities often lack the knowledge, agency, and ownership needed for long-term control efforts.

Africa continues to follow externally driven and colonial-era priorities, where research often serves publications for careers and donor agendas more than locally relevant solutions. The Pan-African Mosquito Control Association platform offers an opportunity to reverse this trend through a new generation of dynamic African scientists and practitioners committed to locally driven, contextually relevant, and sustainable mosquito abatement strategies for malaria, dengue, and other vector-borne diseases.

Plenary Talk 6

Title: Countering the scramble for African faces and voices: Objective criteria for distinguishing friend from foe and managing those distinct relationships accordingly

Gerald Killeen, PhD, *AXA Research Chair in Applied Pathogen Ecology; School of Biological, Earth, and Environmental Sciences; University College Cork, Ireland.*



Prof. Gerald Killeen Prior to joining UCC as the AXA Research Chair in Applied Pathogen Ecology, he was based at the Ifakara Health Institute (IHI) in Tanzania for almost 17 years, during which time he established what is now known as its Environmental Health and Ecological Sciences Department. During his time in Tanzania, he worked for the Liverpool School of Tropical Medicine, Durham University and the Swiss Tropical and Public Health Institute. Before that he worked at the International Centre of Insect Physiology and Ecology in Kenya and at Tulane University in the USA. Over the years, he worked on a variety of basic and applied aspects of malaria transmission control, especially vector control, with a strong emphasis upon quantitative ecology and mathematical modelling, as well as capacity strengthening at individual, systems, institutional, national, and regional levels.

He supported several national malaria control programmes and established the locally managed Dar es Salaam City Council Urban Malaria Control Programme, which has since been used as a model system for government scale up of environmentally friendly, pro-active larval source management for malaria vector mosquitoes more broadly across Tanzania. Some of his work on adult mosquito control with insecticidal bednets has shaped global policies regarding universal coverage targets for this life-saving technology, as well as investment in innovations to address limitations and vulnerabilities of this key front line vector control measure. More recently, he worked on applying some of these new vector control approaches to combat malaria, Zika, Dengue and Chikungunya in both Africa and the Caribbean.

Also, some of his postgraduate research training collaborations with the Zambian Malaria Elimination Centre have since resulted in nationally led initiatives to mobilize tens of thousands of Community Health Workers to serve the basic healthcare needs of isolated rural populations. Since joining UCC, he has continued to develop his interests in malaria epidemiology, control, and vector ecology, as well as relevant capacity strengthening initiatives. Returning to Ireland at the outset of the ongoing SARS-CoV-2 pandemic, he also wrote several simple arithmetic models to inform pandemic response policy and practice and played an active role in evidence-based advocacy for elimination of the virus while that was still feasible. He has also really enjoyed branching out a little by developing new interests

in the behaviour and ecology of large mammals of the tropics, as well as sustainable conservation of the high biodiversity ecosystems they live in, his particular favourites being lions and community-run protected areas in the moist miombo woodland zone of southern Tanzania.

Abstract: Here I present a conceptual framework for distinguishing between strategic system strengthening investments that enable the sustainable development of African institutional capacity over the long term and tactically expedient system support expenditures that undermine it. I also outline specific criteria for objectively distinguishing south-friendly collaborative models that facilitate authentic capacity building from the alternative pseudo-capacity building or outright incapacity building business models commonly practiced by de facto competitors headquartered in high-income countries (HICs). Authentic capacity building practices not only cover the full direct and indirect costs of participation by LMIC recipients, they also either embed carefully crafted benefit sharing plans into associated collaborative agreements or offset the opportunity costs or commitments to service provider contracts with correspondingly increased overhead rates. In contrast, the outright incapacity building business models practiced by many HIC-headquartered primary recipients aim to either exclude local institutions entirely from funding opportunities or confine them indefinitely to trivial token roles. While more nuanced, pseudo-capacity building business models do support the development of LMIC organizations and investigators to levels of technical competence, they also insidiously undermine their progress towards excellence and independent competitiveness. They achieve this by subtly promoting mediocrity within African subrecipients, thus enabling HIC-headquartered primary recipients to sustain their leadership roles indefinitely. Beyond approaches to productive engagement with genuine allies at HIC institutions, I also explain specific tactics that de facto competitors commonly deploy to seed division within and between local institutions in African LMICs and then outline effective approaches for countering them.

Plenary Talk 7

Title: Re-centering Malaria Financing on Vector Control: Correcting Strategic Drift in the Fight Against Transmission

Manuel Lluberas, PhD, IDHA



Prof. Manuel Lluberas is a public health entomologist recognized globally for nearly four decades of expertise shaping all components of the business architecture of public and private mosquito population management initiatives in four continents. Among his most notable achievements, he played a pivotal role in mobilizing key stakeholders and partners to design the malaria vector control business architecture framework of the US President's Malaria Initiative and those of several private corporations and mineral extraction companies in Africa. He designed and directed disaster preparedness workshops and conducted post-event emergency mosquito control operations in the aftermath of the Indonesian and Haitian earthquake of 2004 and 2010, respectively, and several other major events in two continents. His contributions extend beyond the academic and institutional realms, highlighted by his pivotal role in crafting the World Health Organization's Operational Manual for Indoor Residual Spraying, a cornerstone resource in global malaria vector control strategies. He has written two books on vector control, has delivered keynote addresses in Africa, South America, the Caribbean Basin, Canada, and the United States in English and Spanish, has published extensively about mosquito control matters, and has conducted simultaneous interpretation from Spanish to English or vice versa for the American Mosquito Control Association for two decades.

His many contributions have been recognized with the Global Trade Award from the Global Trade Chamber, the Meritorious Service Award of the American Mosquito Control Association, and as finalist for the Rear Admiral Charles S. Stevenson Award for excellence in US Navy Preventive Medicine.

Abstract: Despite decades of progress, malaria elimination efforts across Africa are losing momentum. The prevailing explanation, insufficient funding, fails to fully account for the stagnation. Evidence from the 2025 Africa Malaria Progress Report suggests a more consequential issue: a structural drift in how malaria financing is allocated. While total resources have fluctuated, a growing share of investments has shifted away from interventions that directly suppress mosquito populations, the very engine of malaria transmission.

We examine how and why malaria financing has diverged from its most epidemiologically impactful interventions of the 20th Century, challenging the dominant scarcity narrative by demonstrating that misalignment, not merely insufficiency of funding is a central barrier to progress. The consequences of this shift are visible in resurgent transmission, fragile program continuity, and increased vulnerability to external shocks such as climate variability and funding instability.

Plenary Talk 8

Title: Building on successes from malaria vector control to enhance progress on Neglected Tropical Diseases – A call for solidarity

Heather Ferguson, PhD. *Infectious Disease Ecology at the University of Glasgow*



Prof. Heather Ferguson teaches Infectious Disease Ecology at the University of Glasgow. She is a vector-borne disease specialist whose research encompasses the study of ecology, behaviour and control of mosquitoes that transmit malaria and Neglected Tropical Diseases. She is involved in the development of new tools for vector surveillance and control with partners from endemic countries

in Africa, South America and Asia, and studies on the emergence of vector-borne diseases in Europe from a One Health perspective. Professor Ferguson has a long-term research and training collaboration with the Ifakara Health Institute in Tanzania where she holds a visiting scientist position. She is a former member (2017-2022) and Co-Chair (2018-2022) of the World Health Organization's Vector Control Advisory Group, and current Chair of the Strategic Technical Advisory Group on Neglected Tropical Diseases.

Abstract: The World Health Organization (WHO) estimates that 2.3 billion malaria cases and 14 million deaths have been averted since 2000, with most of this impact attributed to vector control. Although current tools remain insufficient for elimination, this represents a major public health success and demonstrates what can be achieved through well-coordinated, adequately funded, and evidence-based vector control at scale. In contrast, progress in controlling vector-borne neglected tropical diseases (NTDs) has lagged and, in some cases reversed. Examples include the global expansion of Aedes-borne viruses and resurgence of visceral leishmaniasis in East Africa. These disparities between malaria and NTDs reflect complex, multifactorial challenges, including entrenched hierarchies in prioritisation across health systems, research and funding structures. Over the past decade, several new vector control interventions for malaria have been developed, rigorously evaluated, and incorporated into WHO guidelines. In contrast, research and investment on NTD vector control – particularly for those not spread by Aedes mosquitoes – has been extremely limited.

This has hindered the development of evidence-based policy, with WHO guidelines on vector control for many NTDs either not available or outdated. Integrating research, surveillance and control across these disease areas offers major but under-used opportunities for progress.

The recent merging of malaria and NTD programmes at WHO provides a unique opportunity to accelerate progress on policy development for NTD vector control by building on the successes of malaria; with the planned integration of guidelines on vector control being a positive step in this direction. Further gains will depend on strengthening integrated surveillance and evaluating interventions in settings where malaria and vector-borne NTDs co-occur. By fostering collaboration rather than competition, integrated vector control can deliver mutual benefits, strengthen health systems, and ensure that populations affected by all vector-borne diseases are not left behind.

Plenary Talk 9

Title: The unfortunate neglect of *Anopheles funestus* in east and southern Africa

Fredros Okumu, PhD, MBA; Professor of Vector Biology (Infectious Disease Ecology); School of Biodiversity, One Health & Veterinary Medicine, University of Glasgow, Glasgow, G12 8QQ



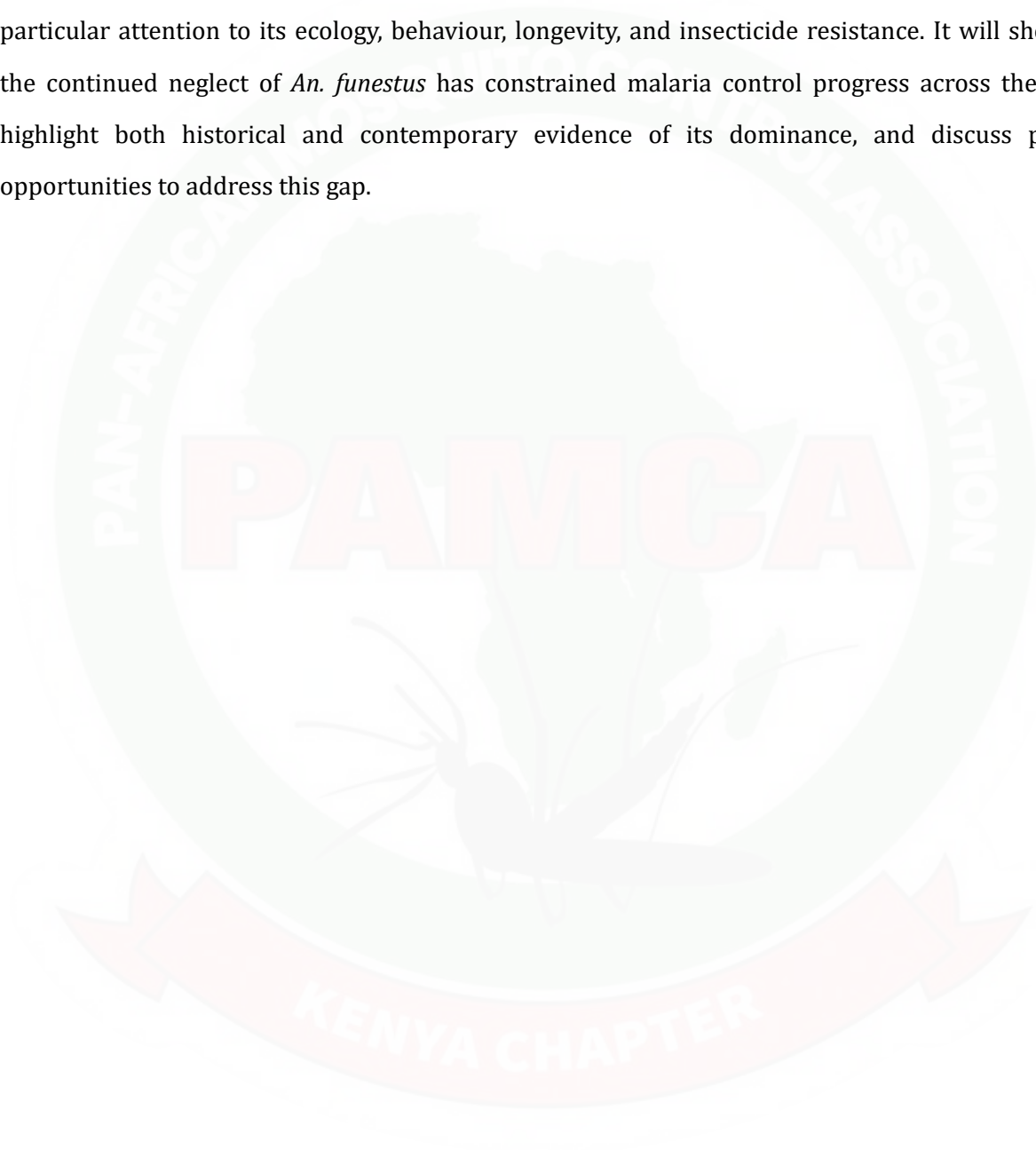
Prof. Fredros Okumu is a public health researcher and mosquito biologist, with interests in surveillance and control of vector-borne diseases. He is a former Director of Science at Ifakara Health Institute, where he maintained an active research program with several partners and students. He also served in various advisory groups, including WHO Malaria Policy Advisory Group (MPAG) and the Gates Foundation's Malaria Strategic Advisory Panel (MSAP). He began his education in Kenya, studying Public Health at Moi

University College of Health Sciences (2001-2005) and subsequently a master's degree in applied Parasitology at the University of Nairobi and also obtained a second master's degree in Geo-Information Sciences, Earth Observation and Environmental Modelling at Lund University, Sweden. In 2012, he was awarded a PhD in Infectious Diseases from the London School of Hygiene and Tropical Medicine, followed in 2019 by an MBA in International Health Management from the University of Basel & Swiss Tropical and Public Health Institute in Switzerland. Previously, he held the 2021 Heath Clark Lectureship at the London School of Hygiene & Tropical Medicine, a Howard Hughes Medical Institute –Gates International Research Scholars Award (2017-2023) and a Wellcome Trust Intermediate Fellowship for Public Health & Tropical Medicine (2014-2019).

His research is centered on biology, control, and elimination of mosquito-borne diseases, notably malaria and currently have a large portfolio of work covering the field and lab studies on dominant

vector species, new systems for monitoring disease transmission, and strategies for integrating new technologies such as genetically modified mosquitoes into disease control programs. Moreover, he is passionate about improving ecosystems for young researchers in Africa.

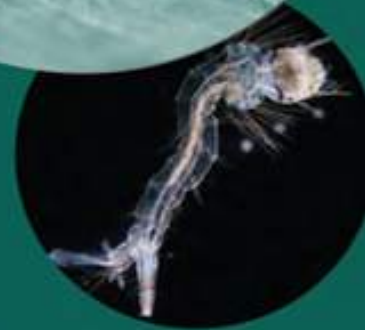
Abstract: *Anopheles funestus* now accounts for most malaria transmission in many parts of East and Southern Africa, yet it remains insufficiently recognized in research, surveillance, and control strategies. This talk will examine why this species has become so epidemiologically important, with particular attention to its ecology, behaviour, longevity, and insecticide resistance. It will show how the continued neglect of *An. funestus* has constrained malaria control progress across the region, highlight both historical and contemporary evidence of its dominance, and discuss practical opportunities to address this gap.



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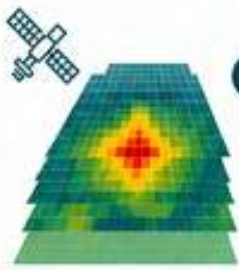
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02

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03

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04

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ABOUT CRID

Established in 2018, the Centre for Research in Infectious Diseases (CRID) is a non-profit research centre working on the main tropical vector borne diseases.

CRID's mission is to contribute to the fight against infectious diseases in Africa by advancing knowledge and strengthening research capacity on infectious diseases in an endemic environment and thanks to its state-of-the-art laboratory.



OUR CORE ACTIVITIES

 VECTOR BIOLOGY & CONTROL Studying mosquito biology, behavior and insecticide resistance to develop effective control strategies.	 MOLECULAR ENTOMOLOGY & EPIDEMIOLOGY Using advanced molecular tools to study resistance mechanisms in vectors and understand humans/vectors/pathogens interactions.	 INNOVATIVE TECHNOLOGIES Integrating cutting-edge technologies (GIS, bCUBE, eDNA & RNA, Bioinformatics) for surveillance and decision-making.	 ONE HEALTH & ENVIRONMENT Investigating environmental determinants and promoting One Health approaches for sustainable solutions.	 TRAINING & CAPACITY BUILDING Building skills through training, mentorship and knowledge exchange programs.	 COMMUNITY ENGAGEMENT Working with communities to promote prevention, health education and behavior change.
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MAIN PROJECTS

African Consortium in Modelling for Effective Vector Control (ACoMVeC) 	African Centre for Vector Genomics (AVeGen) 	Epidemiology Research through Genomics and Translational Systems biology (EMERGENTS) ICIMR 	Next generation vector surveillance: Development and deployment of bCUBE and VectorCAM surveillance system 	International Centre for Antimicrobial Resistance Solutions (ICARS) 	CANVeCT Catalyzing the Adoption of a Novel Vector Control Toolbox (ConveCT)
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MAIN PARTNERS








IFAKARA AT 70: PIONEERING SCIENCE AGAINST MALARIA AND MOSQUITO-BORNE DISEASES

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Vector Control

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Summary of the Keynote Address, Plenary Talks, and Panel Discussions

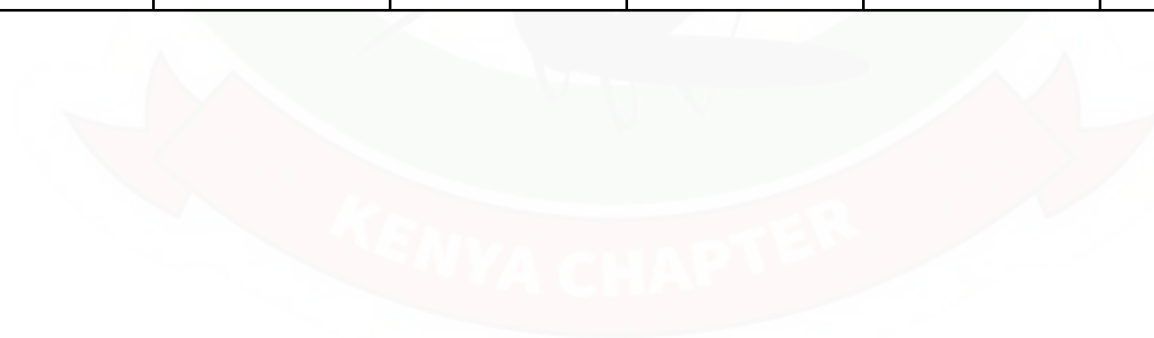
Name	Presentation Title	Presentation Type	Dates
Dr. Eric Ochomo	Disruption, Invasion and Opportunity: A Decisive Moment for African Vector Control	Keynote Address	Day 01: September 01, 2026
Prof. Nicodem Govella	The Dr. Prosper Pius Chaki Memorial Lecture: Honouring His Life and Legacy.	Inaugural Dr. Prosper Chaki Memorial Lecture	Day 01: September 01, 2026
PAMCA Secretariat and Board members	The Dr. Prosper Pius Chaki Memorial Lecture: Honouring His Life and Legacy.	Panel Discussion	Day 01: September 01, 2026
Dr. Joseph Wakoli Wekesa	Reimagining Malaria Control through Community-Based Efforts Akin to Mosquito Abatement Programs in the US	Plenary presentation 1 & panel discussion 1:	Day 02: September 02, 2026
Prof. Charles Wondji	The future of Vector control: Tackling challenges and embracing innovation	Plenary presentation 2 & panel discussion 1:	Day 02: September 02, 2026
Dr. Tianyun Steven Su	Biorational Larvicides, Larviciding and Resistance Management for Mosquito Control – Then, Now and the Future	Plenary presentation 3 & panel discussion 2:	Day 02: September 02, 2026

Dr. Ary Faraji	Integrated Mosquito Management in the USA: Structure, Surveillance, Research, and Control	Plenary presentation 4 & panel discussion 2:	Day 02: September 02, 2026
Dr. Silas Majambere	Reality check: Africa is not prepared to tackle mosquito borne diseases. Can PAMCA re-engineer a new paradigm?	Plenary presentation 5 & panel discussion 3	Day 03: September 03, 2026
Prof. Gerard Killeen	Countering the scramble for African faces and voices: Objective criteria for distinguishing friend from foe and managing those distinct relationships accordingly	Plenary presentation 6 & panel discussion 3:	Day 03: September 03, 2026
Prof. Manuel F. Lluberas	Re-centering Malaria Financing on Vector Control: Correcting Strategic Drift in the Fight Against Transmission	Plenary presentation 7 & panel discussion 3:	Day 03: September 03, 2026
Prof. Heather Ferguson	Building on successes from malaria vector control to enhance progress on Neglected Tropical Diseases – A call for solidarity.	Plenary presentation 8 & panel discussion 4	Day 03: September 03, 2026
Prof. Fredros Okumu	The unfortunate neglect of <i>Anopheles funestus</i> in east and southern Africa	Plenary presentation 9 & panel discussion 4	Day 03: September 03, 2026

Summary of Symposia

No	Symposium title	Thematic area	Organizer	Dates	Time
1	The Stephensi Shift: Current Evidence, Knowledge Gaps, and the path to elimination.	Vector surveillance, vector biology, emerging vectors, insecticide resistance management, data information systems, modelling	Samson Kiware	Day 01: September 01, 2026	16:00 - 18:00
2	The African Vector Genomics Hub (AVECGen): Building integrated genomic expertise to accelerate the fight against vector-Borne Diseases	Emerging technologies and interventions , IVM	Estelle Mewamba Mezajou	Day 01: September 01, 2026	16:00 - 18:00

3	Assessing effects of housing modification on indoor thermal comfort and malaria vector densities in hot and humid zones of western and coastal Kenya	Emerging technologies and interventions, IVM	Bernard Abong'o	Day 02: September 02, 2026	16:00 - 18:00
4	Rethinking the population dynamics and control targets for malaria vector guilds in east Africa	Emerging technologies and interventions, IVM	Gerry Killeen	Day 02: September 02, 2026	16:00 - 18:00
5	Building a Sustainable Modelling Capacity in Malaria-Endemic Countries	Data information systems, modelling and IVM	Samson Kiware	Day 02: September 02, 2026	16:00 – 18:00



Conference Program

Day One: Tuesday September 01, 2026

Time	Activity		Speaker
07:00am – 08:00	Breakfast and Registration		
08:00 – 09:00	Opening Ceremony Room: Main Auditorium Chair: Dr. Elijah Juma; Co-Chair: Dr. Jessy Goupeyou-Youmsi		
	Welcoming of dignitaries		Dr. Jessy Goupeyou-Youmsi
	Sponsors Appreciation		
	Welcome Remarks	PAMCA -Kenya Chapter Chair & Head of Conference Planning Committee	Dr. Elijah Juma
		PAMCA Chapters' Leadership	Prof. Delenasaw Yewhalaw
		Former PAMCA Executive	Prof. El Hadji Amadou Niang
		PAMCA Founder	Prof. Charles Mbogo
Guest of Honour & official opening of		Dr. Eric Muok - Director of	
09:00 -10.00	Keynote Address Topic: Disruption, invasion, and Opportunity: A Decisive Moment for African Vector Control Speaker: Dr. Eric Ochomo Room: Main Auditorium Chair: Prof. Marta Maia, Co-Chair: Dr. Antonio Nkondjio		

10:00-10:30	Coffee Break/Exhibition Hall open/ Poster session 1 - Posters #1 – 36	
10:30 -11:30	Inaugural Memorial Lecture for the Late Dr. Prosper Chaki Room: Main Auditorium Chair: Dr. Samson Kiware, Co- chair: Rosalia Joseph	Prof. Nicodem Govella
11:30 -13:00	PAMCA Panel Discussion PAMCA in the past three years: Retracting the events of the past three years and re- imagining and redefining a new future for the organization Room: Main Auditorium Chair: Dr. Silas Majambere, Co- Chair: Prof. El Hadji Amadou Niang	PAMCA Secretariat and Board of Directors

13:00 - 14:00	Lunch Break/Exhibition Hall open/Poster session 1 - Posters #1-36
14:00 - 15:30	Parallel Scientific Session 1 - 4
	Scientific Session 1: Surveillance Data Systems & Digital Platforms Room: Main Auditorium Chair: Dr. Joseph Mwangangi Co-Chair: Dr. Adedapo Adeogun
	Scientific Session 2: Insecticide Resistance monitoring and Management Room: Tsavo Hall Chair: Dr. Samson Kiware Co-Chair: Dr. Magellan Tchouakui
	Scientific Session 3: Novel Vector Control Tools & Product Innovation Room: Mavuno Hall Chair: Dr. Silas Majambere Co-Chair: Dr. Fatoumata Seck
	Scientific Session 4: Indoor environment and control tools Room: Maasai Mara Hall Chair: Dr. Eric Ochomo Co-Chair: Dr. Damaris Matoke-Muhia

15:30 - 16:00	Coffee Break/Exhibition Hall open/ Poster session 1 - Posters #1-36	
16:00 - 18:00	Parallel Symposia sessions 1 - 2	
	Symposium session 1: The Stephensi Shift: Current Evidence, Knowledge Gaps and the path to elimination Organizer: Dr. Samson Kiware Speakers: Drs. Eric Ochomo, Samson Kiware, Fitsuma Girma, Heather Ferguson, Adedapo Adeogun Room: Maasai Mara Hall	
	Symposium session 2: The African Vector Genomics Hub (AVECGen): Building integrated genomic expertise to accelerate the fight against vector-Borne Diseases Organizer: Dr. Estelle Mewambe Mezajou Speakers: Profs. Charles Wodji, Isabella Oyier, Estelle Mewamba Mezajou Room: Mavuno Hall	
18:00 - 19:00	SORA Technology Workshop on Drone Technology in LSM	Lenana Hall
Day One Ends		

Day Two: Wednesday September 02, 2026

Time	Activity
07:00 – 08:00	Breakfast & Registration
08:00 – 09:30	Plenary Session 1 & 2 and Panel discussion 1 Chair: Ghislaine Ametchie Co-chair: Dr. Antonio Nkondjio Room: Main Auditorium
	Plenary 1: Reimagining Malaria Control through Community-Based Efforts Akin to Mosquito Abatement Programs in the US Speaker: Dr. Wakoli Wekesa
	Plenary 2: Indoor mosquito management (LLINs/IRS). The state of indoor interventions, funding landscape, policy priorities, ongoing and emerging challenges, PAMCA's role. Speaker: Prof. Charles Wondji Panelists: Wakoli Wekesa, Charles Wondji
09:30 - 11:00	Parallel scientific session 5 - 8
	Scientific session 5: Larval Source Management Room: Mavuno Hall Chair: Dr. Onyango Sangoro Co-Chair: Dr. Oumou Kalsom Gueye
	Scientific session 6: Outdoor vector control & IVM Room: Tsavo Hall Chair: Prof. Marta Maia Co-Chair: Dr. Joel Odero
	Scientific session 7: Vector Surveillance & Bionomics Room: Maasai Mara Hall Chair: Dr. David Tchouassi Co-Chair: Dr. Mercy Opiyo

	Scientific session 8: Parasite tracking and Genomics Room: Main Auditorium Chair: Kelvin Thiong'o Co-Chair: Dr. Yaw Akuamoah
11:00 - 11:30	Coffee Break/Exhibition Hall open/ Poster session 2 - Poster #37-76
11:30 - 13:00pm	Plenary presentations 3 & 4 and Panel discussion 2 Room: Main Auditorium Chair: Dr. Elijah Juma Co-chair: Dr. Mercy Opiyo
	Plenary 3: Biorational Larvicides, Larviciding and Resistance Management for Mosquito Control – Then, Now and the Future Speaker: Dr. Tianyun Steven Su Room: Main Auditorium
	Plenary 4: Integrated Mosquito Management in the USA: Structure, Surveillance, Research, and Control Speaker: Dr. Ary Faraj Panellists: Tianyun Steven, Ary Faraj
13:00 - 14:00	Lunch Break/Exhibition Hall open/ Poster session 2 - Poster #37-76
14:00 - 15:30	Parallel scientific session 9 - 13
	Scientific Session 9: Emerging & Invasive Vectors Room: Mavuno Hall Chair: Dr. Christophe Antonio Nkomdijo Co-Chair: Dr. Francis Mutuku
	Scientific Session 10: Climate, Environment & Vector Ecology (9 Abstracts) Room: Tsavo Hall Chair: Dr. Luna Kamau Co-Chair: Dr. Joseph Chabi

	Scientific Session 11: Social & Behavioural Science for Vector Control Room: Maasai Mara Hall Chair: Ghislaine Ametchie Co-Chair: Christina Sudi
	Scientific Session 12: Gender & Community Engagement Room: Main Auditorium Chair: Dr. Lydia Kibe Co-Chair: Dr. Oumou Kalsom Gueye
	Scientific Session 13: Vector Surveillance & Bionomics Room: Lenana hall Chair: Dr. Onyango Sangoro Co-Chair: Dr. Magellan Tchouakui
15:30 - 16:00	Coffee Break/Exhibition Hall open/ Poster session 2 - Poster #37-76
16:00 - 18:00	Parallel symposium session 3 -5
	Symposium session 3: Assessing effects of housing modification on indoor thermal comfort and malaria vector densities in hot and humid zones of western and coastal Kenya Speakers: Benard Abongo; Duncan Abala; Teresa Bange; Eric Ochomo; Daniel Kwaro; George Ndege; Kennedy Matheka; Eileen Mokaya; Kibor Keitany. Room: Main Auditorium Chair: Benard Abongo
	Symposium session 4: Rethinking the population dynamics and control targets for malaria vector guilds in East Africa Speakers: Fredros Okumu; Gerry Killeen; Deo Kavishe; Nicodemus Govella; Laizer Tajiri; Maneno Baravuga Room: Tsavo Hall Chair: Gerry Killeen

	Symposium session 5: Building a Sustainable Modelling Capacity in Malaria-Endemic Countries Speakers: Samson Kiware, James Michael, Gloria Shirima, Nicholas Mziray, Charles Dismas, ZamZam Pandu Room: Lenana Hall Chair: Samson Kiware; Co-Chair: Gloria Shirima
19:00 - 21:00	PAMCA Gala Dinner - African Night Cultural Experience Place: Gala Dinner Tent MC: TBD
Day two Ends	

Day Three: Thursday, September 03, 2026

Time	Activity
07:00 - 08:00	Breakfast & Registration
08:00 - 09:30	Plenary presentations 5, 6 & 7 and Panel discussion 3 Moderator: Dr. Silas Majambere Co-Moderator: Dr. Damaris Matoke-Muhia Room: Main Auditorium

	Plenary 5: Reality check: Africa is not prepared to tackle mosquito borne diseases. Can PAMCA re-engineer a new paradigm? Speaker: Dr. Silas Majambere Plenary 6: Countering the scramble for African faces and voices: Objective criteria for distinguishing friend from foe and managing those distinct relationships accordingly Speaker: Prof. Gerry Killeen Plenary 7: Re-centering Malaria Financing on Vector Control: Correcting Strategic Drift in the Fight Against Transmission Speaker: Prof. Manuel Lluberas Panelists: Gerry Killeen, Manuel Lluberas, El Hadji Niang, Evelyn Olanga
09:30 - 10:00	Coffee Break/Exhibition Hall open/ Poster session 3 - Poster #77– 98
10:00 - 11:30	Plenary presentations 8 & 9 and Panel discussion 4 Chair: Prof. El Hadji Niang, Co-chair: Dr. Sheila Ogoma Room: Main Auditorium
	Plenary 8: Building on successes from malaria vector control to enhance progress on Neglected Tropical Diseases – A call for solidarity Speaker Prof: Heather Ferguson: Plenary 9: The unfortunate neglect of <i>Anopheles funestus</i> in east and southern Africa Speaker: Prof. Fredros Okumu Panellists: Fredros Okumu; Heather Ferguson, Eric Ochomo

11:30 - 12:40	Sponsors session: Sponsors presentation Room: Main Auditorium Speaker: Sponsors Chair: Dr. Damaris Matoke-Muhia
12:40 - 13:00	Poster lightning talks Room: Main Auditorium Chair: Dr. Zawadi Mageni
13:00 - 14:00	Lunch Break/Exhibition Hall open/ Poster session 3 - Poster #77– 98
14:00 - 15:30	Parallel scientific session 14 - 18
	Scientific Session 14: Parasite tracking and Genomics Room: Maasai Mara Hall Chair: Dr. Fitsum Girma Co-Chair: Jacinta Muli
	Scientific Session 15: Novel Vector Control Tools & Product Innovation Room: Mavuno Hall Chair: Dr. Joseph Mwangangi Co-Chair: Dr. Zawadi Mageni
	Scientific Session 16: Insecticide Resistance monitoring and Management Room: Tsavo Hall Chair: Dr. Jessy Goupeyou Co-Chair: Dr. Magellan Tchouakui
	Scientific Session 17: Spatial Epidemiology & Modelling Room: Main Auditorium Chair: Dr. Onyango Sangoro, Co-Chair: Rosalia Joseph
	Scientific Session 18: Vector Surveillance & Bionomics Room: Lenana hall Chair: Dr. Evelyn Olanga Co-Chair: Lucy Abel

15:30 - 16:00	Closing ceremony and announcement of 2027 PAMCA Chapter Conference Host Room: Main Auditorium Chair: Dr. Elijah Juma, Co-Chair: Dr. Christian Obeng
16:00 -17:00	PAMCA Annual Business Meeting Moderators: Prof. Delenasaw, Dr. Emmanuel Hakizimana Room: Main Auditorium
End of 2026 PAMCA Conference	



List of Posters

Day 1 Posters

Indoor Residual Spraying and Insecticide Resistance			
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2	167	Nzira Lukwa	Sovrenta 15WP: potential game changer in malaria vector control against <i>Anopheles arabiensis</i> in Chiredzi, Zimbabwe
3	257	Riccardo Feudjio	Impact of metabolic pyrethroid-resistance genes (CYP6P4a and CYP6P4b) in <i>Anopheles funestus</i> on the efficacy of chlorfenapyr-based bed nets (Interceptor G2 and PermaNet Dual)
4	155	Olukayode Odufuwa	Are new insecticide-treated nets consistent in killing resistant mosquitoes?

5	160	Olukayode Odufuwa	The before and after method (BAM): a chemical approach to determining insecticide regeneration time in pyrethroid-chlorfenapyr ITNs
6	198	Umami Kibondo	The Ifakara Ambient Chamber Test (I-ACT) for Evaluation of Indoor Residual Sprays: A Non-Inferiority Test of Sylando® 240SC and SumiShield® 50WG
7	174	Love Opoggen	Spatial Colocation Analysis of Mosquito Species across selected Communities from Isoko, Delta State, Nigeria.
8	180	Souro Millogo	Molecular characterization, transgenerational transmission and sexual auto-dissemination within Anopheles Mosquitoes of the Malaria Parasite Transmission Blocking Microsporidia Sp MB in Burkina Faso
9	165	Jilly Mseti	The invisible factor behind insecticide loss in Olyset® nets

10	8	Judith Banda	The effect of repeated washing of the Royal Guard, Interceptor G1 and G2 nets on survival of anopheles mosquitoes in Chikwawa district; Malawi
11	261	Nadège Sonhafouo	High insecticide resistance and loss of net physical integrity: A big challenge for vector control in Cameroon
12	46	Seline Omondi	The evaluation of the sumione spatial emanators in experimental huts in Siaya, western Kenya.
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13	234	Antoine Sanou	Site-specific bio-efficacy of Interceptor G2 and Royal Guard against highly pyrethroid-resistant <i>Anopheles gambiae</i> s.l. in experimental hut trials in southwestern Burkina Faso.
14	143	Kemi Adetunji	Cytochrome P450-mediated pyrethroid resistance in <i>Anopheles</i> mosquitoes: A review of diversity and regional distribution in Africa

15	159	Khadidiatou Cissé-Niambélé	Effects of the diet of the mosquito <i>Anopheles gambiae</i> on its resistance to deltamethrin
16	157	Idrissa Yero Sarr	Susceptibility profile of <i>Anopheles arabiensis</i> populations in urban areas of Keur Massar and Rufisque in Dakar, Senegal
17	13	Lateef Busari	Kdr mutations and pyrethroid resistance undermine control of <i>Anopheles gambiae</i> s.l in Osun state, Nigeria
18	106	Hyacinthe Ki	Identification of novel gene cluster potentially associated with insecticide resistance in <i>Anopheles gambiae</i> s.l.
19	104	Darus Tagne	Identification of novel gene cluster potentially associated with insecticide resistance in <i>Anopheles gambiae</i> s.l.
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21	196	Murielle Wondji	Investigating the contribution of ATP-Binding Cassette (ABC) transporters to insecticide resistance in a major African malaria vector: <i>Anopheles funestus</i> s.s.
22	186	Chi Fru	Larvicidal activity and molecular interactions of furoquinoline alkaloids from <i>Araliopsis soyauxii</i> with wild-type and G119S mutant acetylcholinesterase of the malaria vector <i>Anopheles gambiae</i>
23	200	Charles Nignan	Nationwide surveillance of insecticide resistance in <i>Anopheles gambiae</i> s.l. across Burkina Faso: uniform pyrethroid failure, high-intensity resistance, and widespread CYP450-mediated metabolic mechanisms
24	130	Mohamed Haidy	Status of insecticide resistance in adult and larval <i>Aedes aegypti</i> in Nouakchott, Mauritania.

25	30	Jacklin Mosha	A survey of Aedes mosquito bionomics, insecticide susceptibility and sero-epidemiology of dengue in the lake zone, Tanzania
26	245	Bebert Fotso Kongne	The I236M-CYP6P4 mutation confers high fitness costs and increase susceptibility to chlorfenapyr-based nets in the malaria vector Anopheles gambiae from Uganda
27	263	Nadège Sonhafouo-Chiana	Rapid evolution of insecticide resistance and patterns of pesticides usage in agriculture in the city of Yaoundé, Cameroon
28	77	Chadrac Tshiakuisha	Spread of pyrethroid resistance and its impact on malaria burden in the Democratic Republic of the Congo using mathematical modelling
29	225	Paul Marie Ange	Effects of an artificial blood-based diet on the adaptive value and susceptibility to Plasmodium falciparum in Anopheles mosquitoes from Burkina Faso

30	109	Christopher Mfum Owusu-Asenso	Environmental contaminants drive insecticide resistance in <i>Anopheles</i> Mosquitoes in Ghana
31	169	Watson Ntabaliba	One-year efficacy of SC Johnson guardian™ spatial repellent against wild pyrethroid-resistant <i>Anopheles arabiensis</i> in Tanzania
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34	205	Armél Lingani	Larvicidal activity of green silver Nanoparticles from <i>Moringa oleifera</i> on insecticide-resistant <i>Anopheles coluzzii</i> , in Burkina Faso
35	72	Vincent Ntui-Njock	Temporal and Geo-ecological Patterns of Malaria and <i>Plasmodium falciparum</i> Antimalarial Drug Resistance in Cameroon, 2019-2021 and 2025

36	75	NZUNGIZE Lambert	Pyrethroid Resistance Patterns in Anopheles gambiae and Implications for Vector Control in Rwanda
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Day 2 Posters

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39	210	Aïcha Fatimata Sodre	Fungal microbiota of vector mosquitoes: synthesis of current knowledge and perspectives for biocontrol.
40	212	Odette Zongo	Spatial distribution and biodiversity of Anopheles mosquito species across climatic zones in Burkina Faso: Implications for malaria vector control
41	226	Martha Muturi	Adaptative dependence on saline water in An. gambiae s.s mosquitoes from coastal Kenya
42	208	Carine Traore	Characterization of the microbiota of Anopheles coluzzii infected with Microsporidia MB

43	133	Jane Machange	Comparison of trapping efficacy of modified Ovillanta, modified Gravid Aedes Trap (GAT), Biogent GAT and BG Sentinel for Monitoring Aedes aegypti in Tanzania
44	96	Issouf Iria	Effect of Guiera senegalensis leaf extracts on the gut bacterial flora of Anopheles gambiae complex mosquitoes.
45	146	Mgeni Tambwe	Impact of artemether-lumefantrine treatment, circadian rhythm, and serum replacement on the infectiousness of wild Plasmodium falciparum gametocytes to Anopheles gambiae sensu stricto mosquitoes
46	139	Deogratius Kavishe	Persistence of residual Anopheles gambiae populations associated with frontier human settlements and nocturnal livelihood-related activities at the fringes of a large conservation area in southern Tanzania

47	136	Denis Djegbe	Exploring near-infrared spectroscopy ability to determine the species of <i>Anopheles gambiae</i> sensu lato from different environmental conditions in Burkina Faso
48	170	Victoire Nsabatien	Mapping of malaria vectors in Kasai-Central Province, Democratic Republic of Congo to support subnational tailoring of vector control
49	124	Mara Maquina	Entomological Drivers of Malaria Transmission in Northern Mozambique: Evidence from a High-Burden Mining Setting
50	223	Maureen Otinga	Performance and comparative evaluation of a novel diagnostic assay, Novaplex™ Malaria Assay kit.
51	87	Damaris Kimonge	Individual-level and geospatial factors influencing malaria risk in Kwale County, Kenya

52	211	Issiaka Sare	Density-dependent inhibition of <i>Plasmodium falciparum</i> sporogonic development by <i>Microsporidia</i> MB in <i>Anopheles</i> mosquitoes from Burkina Faso
53	85	Naomi Amon	Assessing the abundance distribution of schistosome vector snails across Henga valley, Mzimba, Malawi
54	91	Zedekiah Ombogo	Integrating MALDI-TOF MS and Molecular Detection of <i>Plasmodium</i> Sporozoites into Routine National Malaria Vector Surveillance in Kenya
55	70	Zamzam Pandu	Species Composition and Distribution of <i>Anopheles</i> Mosquito Vectors in Zanzibar, Insights from Routine Entomological Surveillance (2015–2025)
56	204	Aïcha Fatimata SODRE	<i>Wickerhamomyces</i> spp. in <i>Anopheles gambiae</i> s.l. mosquitoes: a symbiotic yeast for malaria control in Burkina Faso.

57	209	John Michael	Molecular diversity of parasites and bacteria with profiling of pathogen derived metabolites in tsetse preferred hosts
58	202	Abdoulaye DERA	Mosquito biodiversity based on different trapping methods for mosquito surveillance in Burkina Faso
59	38	Bertille Djapoum	Assessment of the larval ecology of Aedes mosquitoes and arbovirus transmission risk in four mid-sized cities of southern Cameroon
60	39	Pascal Ngoy	Mathematical modelling as a decision-support tool for infectious disease control
61	44	Christiane Donkeu	PfTIP Secretion and immune modulation in Plasmodium falciparum.
62	254	Franck Yao	Mapping the distribution of invertebrate non-target organism in three villages in western Burkina Faso prior the implementation of genetic control tool against malaria vectors

63	252	Eric Nalianya	Mosquito population and dynamics in Webuye, Western Kenya
64	18	Gabriel Chindidi	Characterizing Anopheles species and their host preferences in Nkhotakota, Malawi
65	14	Kaghou Mbifung	High prevalence and risk factors associated with asymptomatic malaria among children (5-14) years in Nkwen village northwest region Cameroon
66	241	Wellington Nkweto	Malaria vector biting patterns and human nocturnal behaviour: risk assessment in Manchene village, Nchelenge district, Zambia
67	246	Rose Kitoyi	Choosing mosquito pool sizes: How many mosquitoes make a good pool?
68	36	Celestine Wekesa	Influence of different host blood-meal sources on the reproductive outcomes in Anopheles gambiae: enhancing fecundity in a mass rearing environment
69	240	Mgadjou Gorestine	Investigating the natural presence of Wolbachia and Microsporidia in An. gambiae in four Cameroonian villages

70	7	Judith Banda	Distribution of adult Anopheles mosquitoes in low and high malaria transmission areas in Malawi (Chikwawa and Balaka districts)
71	177	Limonty Simubali	Understudied vectors with outdoor-biting behaviour evade indoor-based interventions with potential to sustain residual malaria transmission in a pre-elimination setting of Choma District, Southern Zambia.
72	188	Dingani Chinula	Indoor residual spraying of distinct insecticide formulations in a household-scale micro-mosaic format: Feasibility and effectiveness for malaria vector control in rural Zambia
73	12	Moussa Sylla	Mosquito feeding assays according to standardized procedure in children from the sub-prefectures of Mafèrinyah and Baback, Guinea

74	21	Francis Chisakala	Estimating the entomological inoculation rate of <i>Plasmodium falciparum</i> transmitted by <i>Anopheles funestus</i> and <i>Anopheles gambiae</i> in Cholokoto and Chilungo villages in Salima district.
75	183	Mohamed Haidy	Physicochemical characterization of <i>Aedes aegypti</i> larval habitats in Nouakchott, Mauritania
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Day 3 Posters

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78	62	Fekadu Massebo	Molecular xenomonitoring for assessing malaria parasite prevalence as a proxy to human cases and vector blood-feeding patterns in South Ethiopia
79	51	Kwi Nkineh	Genome-wide sequence analysis of malaria vectors reveals genetically isolated <i>Anopheles coluzzi</i> populations along the slopes of Mount Cameroon
80	120	Mercy Tebamifor	Metabolomic Profiling of Insecticide Resistance in <i>Anopheles</i> Mosquitoes
81	118	Mahamadi Kientega	Genomic insights into the spread and evolution of insecticide resistance variants in <i>Anopheles gambiae</i> s.l. from Burkina Faso

82	214	Hilliar Okata	Prevalence of hrp2 and hrp3 gene deletions and characterization of their flanking regions in Plasmodium falciparum isolates from human blood and malaria vectors from Busia County.
83	221	Westone Hamwata	Genomic surveillance of insecticide resistance in Zambia among malaria vectors.
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84	251	Ange Gatien Bouly	Efficacy of permethrin/chrysanthemum- and icaridin-impregnated textiles in preventing Chrysops silacea and Chrysops dimidiata bites in a Loiasis-endemic region: A single-blind randomized controlled trial
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85	6	Trust Nyakunu	Emergent Anopheles arabiensis in Hwedza District, Zimbabwe 2023: A threat to malaria elimination

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86	34	Mwatima Ali	Determinants of household investigation coverage among malaria cases reported in Zanzibar's malaria surveillance system
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88	125	Sylvere Kezeta-Bondja	Optimizing insecticide deployment strategies to delay quantitative resistance in mosquito populations
89	168	Amos Langat	Reimagining mosquito control in Africa through climate data and bayesian spatio temporal modelling
90	64	Wezzie Banda	Do modelling approaches matter more than data in estimating public health impact? A malaria transmission dynamic modelling study.

91	243	Nilani Chandradeva	Modelling the influence of the duration of effectiveness and time taken to implement vector control interventions for vector-borne diseases.
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92	88	Gideon Laibon	Attractive resting and feeding lure (ATREFEEL) as a potential complementary tool against malaria transmission
93	179	Magdany Fru	The current status of Plasmodium falciparum chloroquine resistance transporter gene (K76T) and Plasmodium falciparum multi-drug resistance gene 1 (N86Y) in Cameroon
94	203	Bali jean Bazie	Contribution to the understanding of the supplementation of a probiotic candidate on the biology of Anopheles gambiae s.l: Case of Akkermancia Muciniphila

95	158	George Mlay	External validation of the Ifakara ambient chamber test for evaluating the bioefficacy of chlorfenapyr and pyrethroid insecticide-treated nets in varied settings: A comparative study in Bagamoyo and Kilimanjaro.
96	19	Wycliff Odude	Field evaluation of the efficacy, residual activity and acceptability of Sovrenta® 15WP against malaria vectors in Adjumani district, west Nile, Uganda
97	73	Tobias Odongo	Toxicity of ivermectin to bed bugs (<i>Cimex hemipterus</i>) and risk factors associated with infestation in Kwale county, coastal Kenya.

List of Symposia Abstracts

Symposium 1

Organizer: Janice Maige

Email: jmaige@ihi.ortz

Title: The Stephensi Shift: Current Evidence, Knowledge Gaps, and the path to elimination.

Symposium Chair: Ms. Janice Maige

Symposium Speakers: Dr. Samson Kiware, Ph.D. - Comprehensive assessment of the biology and public health importance of An. Stephensi (AnoSTEP Afrika)

• Dr. Luigi Sedda, Ph.D., and Dr. Heather Ferguson, Ph.D. - Spatial adaptive surveillance model and the Latin square methods for the emerging malaria vector *Anopheles stephensi*

- Mr. Gerald Kiwelu - Managing data within the AnoSTEP project Mr. Mohamed Ibrahim - The VBDs360 platform for data collection, storage and management: Experience from Djibouti
- Mr. Brian Polo-Kenya; Mr. Mohammed Ibrahim-Djibouti; Dr. Assalif Demissew, Ph.D. -Ethiopia; Dr Adedapo Adeogun, Ph.D. - Nigeria - AnoSTEP Afrika: Progress, Emerging Findings from the countries and their Implications for Malaria in Africa
- Panelists: Dr. Samson Kiware, Ph.D., Dr. Fitsum Girma, Ph.D., Dr. Eric Ochomo, Ph.D., Dr. Ghislaine Ouedraogo-Ametchie, Ph.D., Dr. Heather Ferguson, Ph.D., Edith Ramaita -
- Panel Moderator: Dr. Seth Irish, Ph.D.

Symposium Text: This symposium is designed to address the growing threat of *Anopheles stephensi*. This invasive malaria vector challenges the traditional rural-focused paradigms of malaria transmission in Africa. Despite its expanding presence, knowledge of the vector's behavior, ecology, and epidemiological impact in Africa remains limited. During this symposium, representatives from the AnoSTEP project will share new evidence generated from four African countries currently experiencing invasion.

Submission ID: 0e9c8023-0281-4ffc-bf06-51aff653f259

Symposium 2

Organizer: Estelle Mewamba Mezajou Email: estelle.mewamba@crid-cam.net

Title: The African Vector Genomics Hub (AVECGen): Building integrated genomic expertise to accelerate the fight against vector-Borne Diseases

Symposium Chair: Prof. Charles Wondji

Symposium Speakers:

Speaker 1: Charles Wondji, Professor, Centre or Research in Infectious Diseases (CRID), Cameroon

Talk 1: Genetic and molecular mechanisms of insecticide resistance in *Anopheles* spp. (15 min) Brief

biography 1: Prof. Charles Wondji is an internationally recognized leader in malaria vector genomics and insecticide resistance research. His work has advanced understanding of the molecular and evolutionary mechanisms driving resistance escalation in *Anopheles* mosquitoes across Africa. He has led large-scale genomic surveillance initiatives integrating population genomics, transcriptomics, and functional validation to identify resistance markers and design molecular markers relevant for public health action. His research directly informs vector control strategies and resistance management policies across multiple endemic countries. Speaker 2: Dr Estelle Mewamba Mezajou, Centre or Research in Infectious Diseases (CRID), Cameroon Talk 2: Genomic surveillance platforms and next-generation sequencing applications for vector control (15 min).

Brief biography 2: Dr. Estelle Mewamba is a Cameroonian postdoctoral research assistant at the Centre for Research in Infectious Diseases (CRID) in Yaoundé. She earned her PhD in biochemistry from the University of Dschang in 2023, where she also obtained her master's and bachelor's degrees. Specializing in schistosomiasis and insecticide resistance, she focuses on genetics to fight against infectious diseases. Currently, she is the sequencing unit lead of the AVecGen initiative and her work focuses on strengthening in-country sequencing platforms and integrating next-generation sequencing into malaria vector surveillance systems. She has played a central role in operationalizing genomic services that not only support national malaria control programs but also research institutions across Africa. Her work exemplifies sustainable, locally anchored genomic innovation.

Speaker 3: Professor Isabella Oyier, Kenya Medical Research Institute (KEMRI), Kenya **Talk 3:** Building Sustainable Genomic Capacity in Africa for Disease Surveillance (15 min) **Brief biography 3:** Prof.

Isabella Oyier is a Professor of Molecular Epidemiology and Head of Biosciences at the KEMRI-Wellcome Trust Research Programme. She is also affiliated with the University of Oxford as an Associate Professor and Global Research Fellow. Her work focuses on malaria molecular epidemiology, particularly integrating genomic tools into routine disease surveillance to track drug resistance and inform public health policy. She has led major genomic surveillance initiatives, including COVID-19 testing and sequencing efforts in East Africa. A leader in African genomics, she advances sustainable capacity for disease monitoring and strengthens evidence-based responses to infectious diseases across the continent. **Speaker 4:** Dr Eric Ochomo, Kenya Medical Research

Institute (KEMRI), Kenya **Talk 4:** Bridging Genomics and Vector Control: Translating Data into Public Health Tools (15 min) **Brief biography 4:** Dr. Eric Ochomo is a senior research scientist the Kenya Medical Research Institute (KEMRI). He is a leading medical entomologist specializing in malaria vector surveillance in sub-Saharan Africa. His research integrates genomics, ecology, and field trials to understand mosquito behavior, insecticide resistance, and transmission dynamics. He has contributed to evaluating innovative vector control tools, including insecticide-treated nets and spatial repellents.

Dr. Ochomo's work has informed malaria control policies, particularly in western Kenya, and bridges scientific research with public health implementation to strengthen evidence-based vector control strategies across Africa. **Speaker 5:** Dr Mahamat Gadj, Centre or Research in Infectious Diseases (CRID), Cameroon **Talk 5:** Strengthening Bioinformatics infrastructure for vector genomics:

Sustainable data systems and workforce development through AVecGen (15 min) **Brief biography 5:**

Dr Mahamat Gadj is a research assistant (RA) at the Centre or Research in Infectious Diseases (CRID), Cameroon, where he leads computational analysis and data systems development for vector genomics initiatives.

Through the AVecGen project, he supports the establishment of standardized genomic pipelines like the SnakePool, high-performance computing capacity, and regional data-sharing frameworks that enable in-country collaborative analysis of large-scale sequencing data. His work focuses on building sustainable bioinformatics infrastructure and training the next generation of African scientists in genomic data science for vector-borne disease surveillance. Speaker 6: Dr El Hadji Niang, University Cheick Anta Diop, Dakar, Senegal Talk 6: Strategy for malaria molecular surveillance in Africa and contribution of Centres of excellence such as AVECGEN Brief biography 6: Prof. El Hadji Amadou Niang is a medical entomologist at the University Cheick Anta Diop de Dakar specializing in the bio-ecology, population genetics, and genomics of malaria vectors, particularly *Anopheles gambiae* complex and *Anopheles funestus*. His research has advanced understanding of vector distribution, insecticide resistance, and adaptive dynamics, strengthening malaria control strategies across Africa. He is also actively involved in capacity building and mentorship, contributing to the training of African scientists and strengthening entomological surveillance systems across the continent. His experience aligns closely with the mission of Centres of Excellence such as AVECGen, which aims to build sustainable, Africa-led genomic expertise for disease surveillance. Panel Discussion (30 minutes)

Symposium Text: Malaria control in Africa faces a critical challenge: the rapid emergence and spread of insecticide resistance in *Anopheles* mosquito vectors. The increasing prevalence of resistance to pyrethroids and other insecticide classes threatens the effectiveness of current vector control tools deployed by national malaria control programs and therefore jeopardize decades of progress and efforts in malaria reduction. Advances in genetics, genomics, molecular biology, functional genomics and evolutionary science now provide unprecedented tools to fully characterize resistance mechanisms and monitor their spread across populations and borders. This symposium will examine the omics architecture of insecticide resistance in African malaria vectors, highlighting key mechanisms such as target-site mutations, metabolic resistance pathways, structural variants, and adaptive introgression. Presentations will explore the evolutionary dynamics driving resistance emergence, selection pressure, and gene flow across ecological and geographic gradients. Speakers will also showcase innovative genomic surveillance platforms, next-generation sequencing services, and bioinformatics pipelines that enable real-time resistance monitoring. Particular emphasis will be placed on translating genomic data into operational decision-making for national malaria control programs. A central focus of the session is sustainable African-led genomics capacity. Case studies from multiple regions will demonstrate how locally established sequencing hubs, regional data-sharing networks, and structured training initiatives are empowering scientists to lead discovery

research and inform evidence-based vector control strategies. By connecting molecular mechanisms to implementation science, this symposium illustrates how genomics-informed surveillance can strengthen vector control programs, enhance global health security, and accelerate progress toward malaria elimination across Africa.

Submission ID: 53304bb0-5ad7-454e-aab3-c4f4cee11cc0

Symposium 3

Organizer: Bernard Abong'o

Email: abongoben@gmail.com

Title: Assessing effects of housing modification on indoor thermal comfort and malaria vector densities in hot and humid zones of western and coastal Kenya

Symposium Chair: Dr Bernard Abong'o

Symposium Speakers: 1. Dancan Abala: Housing typology and risk of disease transmission and exposure to extreme heat in western and coastal Kenya 2. Teresa Bange: Community knowledge, perception and attitude towards housing improvement for reduced indoor heat and malaria transmission in western and coastal Kenya 3. Prof Francis Mutuku: Impact of housing improvement on mosquito population and biting behaviour 4. Dr Eric Ochomo: Impact of housing improvement on malaria burden in western and coastal Kenya 5. Dr Bernard Abong'o: Impact of housing improvement on indoor thermal comfort in western and coastal Kenya

Symposium Text: Exposure to high indoor temperatures results in heat-related illnesses and increased exposure to vector-borne diseases. Global warming is expected to exacerbate heat-related illnesses, especially in Africa. To mitigate these consequences, it is important to maintain indoor temperatures within recommended thermal comfort zones. Doors, eaves, and fenestrations facilitate heat transfers between the indoor and outdoor environment. Unfortunately, these also serve as entry routes for disease-carrying vectors such as mosquitoes. Additionally, these openings are usually not oriented or are disproportionate in size to the indoor environment to achieve meaningful cooling. Vector-proofing of these openings has the potential to increase indoor temperatures, hence jeopardizing the comfort of the occupants. We conducted a small-scale field trial with qualitative and quantitative data collection approaches to assess the impact of housing improvement on indoor thermal comfort and malaria transmission. Approximately 150 houses in western and coastal Kenya were modified with screened eaves, windows and doors for mosquito control. The houses received additional windows and white reflective paint on the roof for passive cooling. Data collection involved monitoring of indoor temperature and humidity, mosquito population, mosquito biting behaviour, malaria burden, community treatment-seeking behaviour and knowledge, perception and attitude

towards housing improvement for disease control. The results demonstrate the impact of housing improvement on indoor thermal comfort and disease control.

Submission ID: 8b39b798-4ebb-4470-b120-e2976ef6f434

Symposium 4

Organizer: Gerard Killeen

Email: gerard.killeen@ucc.ie

Title: Rethinking the population dynamics and control targets for malaria vector guilds in East Africa

Symposium Chair: Gerry Killeen

Symposium Speakers: Graham White-Historical characterizations of Africa's primary malaria vectors long before the scale up of effective control measures Fredros Okumu et al-Species sanitation and elimination targets informed by experiences of malaria vector guild transformations in the Kilombero Valley Gerry Killeen et al- Blood host preferences and competitive inter-species dynamics within the *Anopheles gambiae* complex inferred from signs of animal activity around aquatic larval habitats: Implications for vector control and elimination strategies Deo Kavishe et al- Persistence of residual *Anopheles gambiae* populations associated with frontier human settlements and nocturnal livelihood-related activities at the fringes of a large conservation area in southern Tanzania Nicodem Govella- Nationally representative programmatic surveillance of mosquito and human behaviours that influence human exposure to malaria transmission and the impact of vector control across Tanzania Laizer Tajiri-Mapping out persistence of *Anopheles gambiae* across Tanzania based on climatic stratification criteria Maneno Baravuga-The behavioural ecology and vectorial capacity of *Anopheles arabiensis*: Then and now.

Symposium Text: Several recent quantitative field studies, at scales ranging from a few villages up to the entire country of Tanzania, indicate that our understanding of how different primary vectors contribute to malaria transmission and respond to front line vector control interventions needs to be rethought. In this symposium, the authors of these studies present independent and complementary strands of evidence that the roles of *Anopheles gambiae*, *An. funestus*, *An. arabiensis* play in maintaining malaria transmission across east Africa today differs from what we might have expected based on historical characterizations of these species before insecticidal nets and indoor sprays were scaled up across the region. On the one hand, some of these studies shed light on the competitive population dynamics that have enabled surprising outright elimination of *An. gambiae* and *An. funestus* across much of east Africa, while others elucidate the bases of their robust persistence elsewhere, invariably associated with heavy residual disease burden. Also, while *An. arabiensis* has

proven every bit as resilient to control as anticipated, innovative new entomological survey methods help understand why it mediates far lower levels of transmission following sustained vector control scale up than might have been expected. Together, these findings indicate reasonable grounds for optimism about the prospect of eliminating *An. gambiae* and *An. funestus* across a far greater extent of their historical ranges with only incremental improvements to existing vector control strategies, while the levels of transmission mediated by well-managed *An. arabiensis* populations may be far more readily mitigated than previously imagined, albeit with the worrying caveat that *An. coluzzi* has now made its first problematic appearance in the region.

Submission ID: 60a21502-ee41-4da0-b69c-3497b42bfa52

Symposium 5

Symposium title: Building a Sustainable Modelling Capacity in Malaria-Endemic Countries

Conference theme: Reconnect and reimagine mosquito control in Africa

Sub-theme: Data information systems, modelling and IVM

Principal organizer

- Samson Kiware (Ph.D.) – Ifakara Health Insitute, skiware@ihi.or.tz

Co-organizer(s)

- Gloria Shirima — Ifakara Health Institute, gshirima@ihi.or.tz

Moderator

- Janice Maige and Praise Michael

Speakers

- Samson Kiware (Ph.D.) — tentative topic: Building a critical mass of data scientists and mathematical modellers in LMICs
- James Michael — tentative topic: Strengthening data management and surveillance systems for vector control
- Gloria Shirima — tentative topic: Disease modelling for decision-making in low-middle income settings
- Nicholas Mziraya — tentative topic: Modeling the impact of malaria chemoprevention with Sulfadoxine-pyrimethamine on the spread of *Plasmodium falciparum* dhps 581G mutation

Description

Mathematical modelling is increasingly recognized as a vital tool for malaria control, helping National Malaria Programs (NMPs) in sub-Saharan Africa improve planning, optimize funding, stratify malaria risk, and assess interventions. However, integration of modelling into routine decision-making remains limited by a shortage of local expertise, leaving many programs dependent on technical

support from the Global North. This symposium presents the achievements and progress of a multi-year initiative (2020–present) to build a sustainable network of data scientists and mathematical modellers supporting NMPs in Tanzania and other sub-Saharan African countries. Project members will present scientific work carried out across Phases I and II, covering capacity building, data systems for vector control, and applied disease modelling for intervention planning.

Justification

Building local, sustainable modelling capacity is directly relevant to PAMCA's mission of strengthening vector control and disease elimination expertise across Africa. This symposium offers PAMCA members — many of whom work within or alongside NMPs — practical lessons from a real, multi-country capacity-building effort, including honest discussion of challenges and lessons learned from Phases I and II. Countries considering similar in-house modelling investments will benefit directly from the ways-forward recommendations shared here, making this session valuable both to modellers and to program decision-makers across the PAMCA network.

Presentation 1

Title: Building a critical mass of data scientists and mathematical modellers in LMICs: A case of Tanzania

Description: This presentation will provide a general overview of the project, its aims and objectives, successes, and challenges, along with lessons learned from Phases I and II and ways forward for subsequent phases.

Presenter: Samson Kiware (Ph.D.),

Time: 15 min (10 min presentation, 5 min Q&A)

Presentation 2

Title: Strengthening data management and surveillance systems for vector control

Description: This presentation highlights the data management platform (VBDs360), deployed and used by medical entomologists and National Malaria Programs, including processes for data collection, storage, harmonization, integration, and accessibility to ensure consistency, quality, and usability across diverse research settings.

Presenter: James Michael

Time: 15 min (10 min presentation, 5 min Q&A)

Presentation 3

Title: Disease modelling for decision-making in low-middle income settings

Description: This presentation highlights how disease modelling can be used to understand the

impact of vector control interventions, demonstrating applications of the Vector Control Optimization Model (VCOM) in assessing the impact of biolarviciding.

Presenter: Gloria Shirima

Time: 15 min (10 min presentation, 5 min Q&A)

Presentation 4

Title: Modeling the impact of malaria chemoprevention with sulfadoxine-pyrimethamine on the spread of Plasmodium falciparum dhps 581G mutation

Description: This presentation will present modelling results on how sulfadoxine-pyrimethamine-based chemoprevention influences the spread of the dhps 581G resistance mutation in Plasmodium falciparum, with implications for chemoprevention policy.

Presenter: Nicholas Mziraya

Time: 15 min (10 min presentation, 5 min Q&A)

Panel Session

Panel members:

- Samson Kiware - Ifakara Health Insitute
- Charles Mwalimu - Tanzania National Malaria Control Program
- Gloria Shirima - Ifakara Health Insitute
- Nicholas Mziraya - Ifakara Health Insitute
- Brian Masanja - Ifakara Health Insitute
- Hirut Suraphel - Ifakara Health Insitute

Moderator: Janice Maige and Felx Brown

Aim of the panel/discussion: This session will critically discuss the successes, challenges, and lessons learned from Phases I and II and the support provided to NMCP. It will also give the audience the opportunity to share their views, ask questions, and take part in the discussion.

Time: 30 min

Expected number of attendees: 30–50 people

Overall symposium time: 90 minutes

List of Oral Abstracts

Scientific Session 1: Surveillance Data Systems & Digital Platforms

Paper ID# 112

Title: Validation of MALDI-TOF MS for rapid detection of antimalarial drug resistance-associated SNPs in Plasmodium falciparum

Rehema Gona^{1,*}

¹KEMRI-WELLCOME TRUST

Background: Emergence of *Plasmodium falciparum* resistance to artemisinin-based combination therapies (ACTs) and Sulfadoxine-Pyrimethamine (SP) threatens malaria control in endemic African settings. Routine molecular surveillance of resistance-associated single nucleotide polymorphisms (SNPs) is essential, but conventional next-generation sequencing platforms remain costly and technically demanding. There is a need for rapid, scalable, and cost-effective genotyping approaches suitable for routine surveillance.

Methods: This study is currently in progress and evaluates MALDI-TOF MS as an alternative platform for SNP genotyping. A primer extension assay targeting validated ACT- and SP-resistance-associated SNP loci has been designed and optimized for MALDI-TOF MS detection. Laboratory workflow development is ongoing, including assay validation steps and preparation for comparative analysis against Illumina next-generation sequencing reference data. Performance metrics to be assessed include genotype call concordance, discriminatory capacity, turnaround time, and operational feasibility.

Results: No experimental data is available at the time of submission. Sample processing, assay optimization, and data generation are ongoing and are expected to be completed prior to the conference.

Conclusion: This study will evaluate the utility of MALDI-TOF MS for routine surveillance of antimalarial drug resistance markers in *P. falciparum*. If validated, the platform may offer a scalable and cost-effective approach for molecular monitoring in resource-limited settings, supporting early detection of emerging resistance and strengthening malaria control strategies.

Keywords: MALDI-TOF MS; *P. falciparum*; Kelch 13, pfdhfr, pfdhps, antimalarial resistance; SNP genotyping; Illumina NGS

Paper ID# 5

Title: How malaria financing drifted away from the mosquito

Manuel LLuberas^{1,*}

¹Mosquito Den LLC

Background: ALMA's 2025 Africa Malaria Progress Report lays bare a truth: Africa remains off course toward elimination not because there's no money, but because the flows of malaria financing have increasingly and systematically shifted away from active mosquito population reduction

measures that historically did the heavy lifting on transmission reduction and elimination. The stark observation in the report that “we remain off-course and the ‘perfect storm’ of threats has intensified,” with shrinking Official Development Assistance and a shortfall in the Eighth Replenishment of the Global Fund, points to funding volatility as a symptom of deeper allocation choices rather than the root cause of stagnation.

Methods: A policy and financing review was undertaken using the 2025 ALMA Africa Malaria Progress Report and existing evidence on malaria intervention effectiveness and financing patterns. For decades, investment patterns that prioritized LLINs and IRS drove dramatic reductions in cases, and deaths prevented more than 1.2 billion cases and millions of deaths, far more than any single intervention. This underscores the centrality of mosquito reducing transmission. WHO continues to emphasize vector control for malaria prevention but keeps LSM and larviciding as supplementary.

Results: Funding trends in recent years tell a different story. The short-term focus has tilted toward biomedical innovations like vaccines, diagnostics, and treatments, which, while critically important, are complementary rather than substitutes for sustained vector control. The narrative that funding is simply too scarce obscures the reality that malaria financing is not always matched with the interventions that have the greatest epidemiological impact. The implications are clear: to reinvigorate progress, malaria financing must be re-oriented in ways that preserve and scale the preventive tools that keep mosquito populations in check while integrating them with other elements of malaria control.

Conclusion: Governments and donors can commit to ring-fencing funds for core vector control activities over multi-year cycles, thus reducing funding volatility on procurement and deployment schedules.

Keywords: Navigating Emerging Currents, Program durability, Action-oriented financing, Long-term continuity, Resource allocation

Paper ID# 217

Title: SMART MD: Redefining the “Gold Standard” in Malaria Diagnosis through Artificial Intelligence and Digital Innovation

Christiane Donkeu^{1,2,*}, Pierre Adorni³, Sylvie Kemleu⁴, Regis Grailhe³, Lawrence Ayong²

1.University of Yaounde

2.Centre Pasteur Cameroon

3.Technology Development Division, Institut Pasteur Korea

4.Centre Pasteur Cameroun

Background: Despite the widespread use of rapid diagnostic tests, microscopy remains the reference standard for malaria diagnosis. However, its accuracy is highly dependent on microscopist expertise, resulting in significant variability, particularly in resource-limited settings. Artificial intelligence (AI) offers new opportunities to standardize diagnosis and improve reliability. This study will clinically validate SMART MD, an AI-powered mobile platform for automated detection of Plasmodium parasites and parasitemia quantification from blood smears.

Methods: SMART MD integrates deep-learning algorithms within a standardized digital microscopy workflow. The model was trained on a locally curated dataset of expert-annotated malaria images and deployed in an Android application enabling real-time image acquisition and automated analysis through a smartphone-connected microscope. Clinical validation was performed using WHO quality assurance reference slides, including 53 positive samples with varying parasite densities and 18 negative samples. Diagnostic performance was evaluated against reference readings using sensitivity, specificity, and parasite density estimation accuracy.

Results: SMART MD provides fully automated malaria diagnosis in less than 2 minutes per slide. The platform achieved a sensitivity of 91.4% and a specificity of 88.9%. Among positive samples, 83.02% of parasite density estimates were within $\pm 25\%$ of reference values, demonstrating robust quantitative performance across a broad range of parasite densities.

Conclusion: SMART MD combines AI and digital microscopy to deliver rapid, accurate, and reproducible malaria diagnosis, with strong potential to standardize malaria microscopy and strengthen disease control programs in endemic settings.

Keywords: Plasmodium falciparum; artificial intelligence; digital microscopy; automated malaria diagnosis; mobile health technology

Paper ID# 142

Title: Spatiotemporal mapping of insecticide resistance mechanisms in malaria vectors in Africa

Sylviane Sylviane^{1,*}, David Duncan², Gerry Ryan², Emmanuel Mpolya³, Nick Golding²

1.Vector Atlas

2.The Kids Research Institute Australia

3.The Nelson Mandela African Institution of Science and Technology, Arusha

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 is 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 of 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 modeled to produce mechanism-specific spatiotemporal resistance maps for targeted intervention planning.

Keywords: Spatiotemporal modeling, insecticide resistance, target site resistance, metabolic resistance, malaria vectors

Paper ID# 129

Title: Community-driven biocuration for climate-sensitive infectious diseases: building FAIR, AI-ready knowledge systems for the global south

Henry Njoku^{1,*}

1.University of Ibadan

Background: Climate change is intensifying infectious disease outbreaks across the Global South by altering environmental conditions that drive transmission. Yet knowledge of climate-sensitive infectious diseases (CSIDs) remains fragmented across disciplines and regions.

Methods: The Climate-Sensitive Infectious Disease (CSID) Atlas was developed to address this gap by building a FAIR (Findable, Accessible, Interoperable, Reusable), AI-ready knowledge system that harmonises disease definitions, datasets, and visualisations to support surveillance and decision-making. Nigeria was chosen as a pilot due to its high vulnerability to climate hazards and recurrent outbreaks. Epidemiological data (2020–2024) were compiled for six priority CSIDs: malaria, cholera,

Lassa fever, typhoid fever, yellow fever, and hepatitis E. These were integrated with climate variables including rainfall variability, temperature anomalies, flooding, and drought, then mapped against socioeconomic indicators such as water and sanitation access, slum density, displacement, and surveillance gaps.

Results and conclusion: Spatial analyses revealed hotspots in Lagos, Kano, Edo, and Borno States, where climate extremes intersect with social and infrastructural vulnerabilities. Malaria and cholera correlated strongly with rainfall and flooding, while Lassa fever and hepatitis E were linked to drought, food insecurity, and displacement. All datasets were curated using FAIR principles to ensure interoperability and integration with AI-driven risk prediction.

Conclusion: Climate extremes and social vulnerabilities jointly drive the spatial distribution of climate-sensitive diseases, with Lagos, Kano, Edo, and Borno identified as major hotspots.

Keywords: Annotations, Data Analysis, Data Modeling, Fair Data Principles, Modeling

Paper ID# 29

Title: Integrating models and data for the next generation of vector maps with the Vector Atlas

Gerard Ryan ^{1,*}, Marianne Sinka ², Nick Golding ³

1.The Kids Research Institute Australia

2.University of Oxford

3.University of Western Australia

Background: Malaria control programs are eager to understand what mosquito species are where in order to efficiently target activities like vector control and bed net distribution. Here we present new distribution maps for dominant and secondary vectors in Africa, including the first such maps for several species.

Methods: Our work is based on the Vector Atlas, a new online data hub with a comprehensive collection of malaria vector occurrence records. Although previous maps exist for several dominant vector species, we update these with new data and develop new methods that allow us to account for the sampling biases inherent in collection data, and physiological limits on occurrence. Unlike most such exercises, our modelling framework incorporates a simple presence of records, presence-absence data, and count data to make effective use of all data available.

Results: We produce maps of the distribution and relative abundance of Anopheles species that will be a key resource for informing malaria control activities in Africa. With linkage to the Vector Atlas, they can be systematically updated as data collection continues, and in collaboration with in-country researchers and national malaria programmes, are augmented to answer specific questions in

malaria control with additional country-level data.

Conclusion: Our work can also directly support epidemiological modelling through understanding vectorial capacity.

Keywords: Model, bayesian, anopheles, ecological niche model, species distribution model

Paper ID# 4

Title: Invisible Wings

Manuel LLuberas^{1,*}

1. Mosquito Den LLC

Background: There are forces that announce themselves, earthquakes, wars, market crashes, and there are forces that arrive quietly, with no sound louder than a sigh. Mosquitoes belong to the second category. They do not roar. They hum. Their power lies not in spectacle but in persistence, and in humanity's remarkable talent for looking past what is small, familiar, and inconvenient. The mosquito has killed more humans than any other animal in history, including humans. This is not metaphor, nor provocation, nor rhetorical flourishing. It is arithmetic. Yet this fact rarely alters budgets, reorganizes ministries, or commands sustained attention. We respond to mosquitoes the way we respond to background noise, by tuning them out until the noise becomes unbearable. Then we react, briefly and loudly, before returning once more to forgetting.

Methods: The presentation uses systems-based analysis of mosquito-borne disease control, examining how prevention systems, institutional commitment, financing, accountability, and sustained public-health action influence the persistence and resurgence of mosquito-borne diseases. It considers historical experiences of mosquito control and the consequences of weakening or abandoning prevention systems. This presentation is about that: forgetting.

Results: Mosquitoes have shaped economies, redirected empires, stalled development, and quietly taxed the poor while remaining almost entirely absent from serious political discourse. Societies once learned to control mosquito-borne disease at scale, then dismantled the systems that made that control possible. This brings the dangerous illusion that modern technology, clever genetics, or better medicine can substitute for the unglamorous work of prevention. Every resurgence of mosquito-borne disease is accompanied by a familiar refrain: surprise. How could this happen? Why now? The honest answer is almost always the same: because the systems that once prevented it were weakened, defunded, fragmented, or abandoned. Mosquitoes do not defeat us because they are clever. They defeat us because they are constant. And we are not. Mosquitoes thrive where responsibility is diffuse and accountability is absent. They are not impressed by mission statements or pilot projects.

They respond only to action, repeated endlessly, even when nothing seems to be happening.

Conclusion: The wings are invisible. The consequences are not.

Keywords: Operational vector control, locally anchored partnerships, Sustainable financing, Public-private collaboration

Scientific Session 2: Insecticide Resistance Monitoring and Management

Paper ID# 10

Title: Pyrethroid resistance in the dengue fever vector *Aedes aegypti* in urban and semi-urban hotspot areas of Dar Es Salaam, Tanzania

George Ogwen^{1,*}, Valeria Silvestri², Jacklin Mosha³, Alphaxard Manjurano³, Jackie Cook⁴, Joe Biggs⁴, Jackline Martin³, Robert Kaaya⁵, Johnson Matowo⁵

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4.Department of Infectious Disease Epidemiology and International Health, London School of Hygiene and Tropical Medicine (LSHTM)

5.Department of Parasitology and Microbiology, KCMC University, P.O.BOX 2240, Moshi Tanzania

Background: Dengue fever remains a major public health concern in Tanzania and is mainly transmitted by *Aedes aegypti*. The increasing emergence of insecticide resistance threatens the effectiveness of vector control interventions. Despite recurrent outbreaks, data on insecticide susceptibility of *Aedes aegypti* in Tanzania are limited. This study assessed the resistance status of *Aedes aegypti* populations in Dar es Salaam.

Methods: A cross-sectional entomological survey was conducted in urban (Temeke) and semi-urban (Kigamboni) districts during the wet season (October 2024–June 2025). One hundred households from each district were randomly selected for larval sampling. Immature mosquitoes were collected, reared to adults, and morphologically identified. WHO standard susceptibility bioassays were performed with a total of 150 female *Ae. aegypti* per insecticide including control, and mortality was recorded at 24 hours following WHO criteria. Piperonyl butoxide (PBO) synergist assays were used to assess mono-oxygenase-mediated resistance.

Results: Complete susceptibility (100% mortality) was observed only to pirimiphos-methyl (60 mg/m²) in both districts. Full susceptibility to bendiocarb (0.2%) was detected in Kigamboni (98% mortality), while probable resistance was observed in Temeke (96%). Complete resistance to malathion (1.5%) and all tested pyrethroids were found in both districts. After PBO pre-exposure,

partial restoration of susceptibility to deltamethrin (0.03%) occurred in Kigamboni only, with no restoration observed for other pyrethroids.

Conclusions: *Aedes aegypti* populations in Dar es Salaam show widespread resistance to pyrethroids and malathion but remain susceptible to pirimiphos-methyl. Continuous resistance monitoring and evaluation of alternative insecticides are essential to guide dengue vector control in Tanzania.

Keywords: *Aedes aegypti*, Insecticide resistance, Vector control, Dar es Salaam, Tanzania

Paper ID# 65

Title: Malaria transmission and insecticide resistance across eco-climatic facies in Manjo and Manengoteng, Cameroon

Rolyne Sorelle Wakam Noubou^{1,*}, Jean Arthur Mbida Mbida¹, Herman Parfait Awono-Ambene², Carole Ornella Ghariegam¹, Rachel Ngaha¹, Idriss Nasser Ngangue Siewe^{1,2}, Patrick Akono Ntonga¹

1.The University of Douala

2.OCEAC Cameroon

Background: Vector control requires entomological insights specific to each ecological setting. This study aimed to document entomological data on malaria vectors, their transmission role, and insecticide susceptibility in the borough of Manjo, where such data were lacking.

Methods: Conducted quarterly from June 2022 to May 2023 in two ecologically distinct sites, Manjo town and Manengoteng village, the study used human landing catches to collect adult mosquitoes indoors and outdoors. Anopheline species were identified by PCR, infectivity was determined by circumsporozoite protein-ELISA, and insecticide susceptibility was assessed by WHO tube assays and resistance mechanisms were identified by *kdr* genotyping, and synergist assays.

Results: A total of 1,766 mosquitoes belonging to five genera were collected. *Anopheles* accounted for 36.0% and *Culex* for 58.1% of collections. In Manengoteng, *An. funestus* s.l. predominated (60.3%) with marked exophagic behaviour, while in Manjo, *Culex quinquefasciatus* was most abundant (94.4%) with predominantly endophagic behaviour. *Anopheles* densities were higher during the rainy season (79.87%). Malaria transmission was seasonal, with low EIR values recorded for *An. gambiae* s.s. (0.05 infectious bites/person/night) and *An. funestus* s.s. (0.02) at Manengoteng, and *An. coluzzii* (0.02) at Manjo. *An. gambiae* s.l. exhibited resistance to deltamethrin and permethrin at both sites. In Manengoteng, survival rates reached 22.54% and 15.94% respectively, and in Manjo 30.39% and 20%. This resistance was mediated by target site mechanisms, notably high *kdr* allele frequencies (0.84 and 0.97 in Manengoteng and Manjo respectively), and metabolic mechanisms confirmed by synergist assays.

Conclusions: High vector diversity and widespread pyrethroid resistance were found in the borough of Manjo, underscoring the urgent need for sustained local entomological surveillance and vector control strategies adapted to the observed resistance profiles.

Keywords: *Anopheles funestus*, *Anopheles gambiae* s.l., malaria transmission, insecticide resistance, Manengoteng, Manjo.

Paper ID# 59

Title: Behavioral plasticity and metabolic resistance in *Anopheles gambiae* s.l. as key challenges for malaria elimination in Senegalese Hotspots

Pape Cheikh Sarr^{1,*}, Mohamed A. Nourdine², Abdoulaye Kane Dia², Benoit Sessinou Assogba³, Oumou Kalsom Gueye², Lassana Konaté², Oumar Gaye⁴, Ousmane Faye², El Hadji Amadou Niang², Ousmane Sy²

1.University Cheikh Anta Diop

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3.Medical Research Council Unit, The Gambia at the London School of Hygiene and Tropical Medicine, Banjul, the Gambia

4.Laboratory of Medical Parasitology (MARCAD-Plus program) Faculty of Medicine, Pharmacy and Odonto-stomatology of University Cheikh Anta Diop of Dakar, Senegal

Background: Despite scale-up of core interventions (LLINs, IRS, SMC), residual malaria transmission persists in hotspots in Northern and Central Senegal. This study investigates bionomics and insecticide resistance of *Anopheles gambiae* s.l. populations sustaining transmission.

Methods: The study was conducted between June 2024 and February 2025 in three sites: Darou Salam (North), Keur Martin, and Mbine Coly (Center). Mosquitoes were collected using Human Landing Catches (HLC) and Pyrethrum Spray Catches (PSC) collections. Standard WHO susceptibility bioassays (1X, 5X, and 10X diagnostic doses) and PBO synergist tests were performed on the fresh and brackish-water population of Mbine Coly. Species identification was confirmed via PCR (Wilkins et al.).

Results: Out of 2,780 female anophelines collected (HLC and PSC), *An. gambiae* s.l. was the dominant vector (>92%). Significant behavioral plasticity was observed across sites. High exophagy (>52%) in Darou Salam and Keur Martin, contrasting with dominant endophagy (61.3%) in the coastal site of Mbine Coly. Susceptibility tests on the *An. melas* population from Mbine Coly revealed confirmed resistance to alpha-cypermethrin (81.7% mortality) of moderate-to-high intensity (persistence at 5X

dose). PBO pre-exposure fully restored susceptibility (100%), indicating major involvement of Cytochrome P450s. Full susceptibility was observed for pirimiphos-methyl and bendiocarb.

Conclusion: Malaria persistence in these hotspots is driven by a combination of behavioral avoidance (exophagy) and metabolic resistance. While exophagic behavior in the North and Center limits the efficacy of indoor tools, metabolic resistance in coastal *An. melas* further complicates control efforts. These findings support the prioritized deployment of next-generation nets (PBO-LLINs) and insecticide rotation (carbamates/organophosphates) to overcome residual transmission and achieve elimination in Senegal.

Keywords: Anopheles, hotspots, bionomics, exophagy, metabolic resistance, Senegal.

Paper ID# 232

Title: Investigating the multi-resistance mechanism of *Anopheles coluzzii* to insecticides in Osun State, Nigeria

Zarat Iwalewa^{1,*}

1.UNIOSUN

Background: The increasing insecticide resistance by *Anopheles* mosquitoes continues to threaten the effectiveness of core vector-control interventions. This study investigated resistance mechanisms in *Anopheles gambiae* s.l. populations in Olorunda and Osogbo local governments (LGs) in Osun State, Nigeria.

Method: Larval collection was conducted from 0700hr – 1100am between May and August 2024. Susceptibility testing was carried out on 2-3days old mosquitoes using the WHO insecticide susceptibility bioassay against pyrethroids and an organophosphate with varying discriminating concentrations. Similarly, the WHO synergist bioassay was used to assess the involvement of monooxygenases in resistance. Sibling species were identified using Polymerase Chain Reaction (PCR), and allele specific PCR was used to detect the L1014F knockdown resistance (Kdr) mutation. Metabolic enzyme activities were measured using biochemical assays.

Results: Resistance of *Anopheles* to pyrethroids alone was observed across the study areas, with between 39-82% mortality. Synergist bioassay showed varying mortalities. PBO+permethrin yielded 96% mortality in Osogbo and 75% in Olorunda, while PBO+deltamethrin produced 99% and 87%, respectively. Analysis of the *kdr* locus revealed allele frequencies of 0.84 and 0.88, indicating high levels of insecticide resistance in both LGs. Monooxygenase activity was low in resistant populations ($P = 0.000$), whereas glutathione S transferases were significantly overexpressed (59.52 ± 1.44 ; $P = 0.001$). β esterase activity was also elevated (18.86 ± 0.93 ; $P = 0.000$).

Conclusion: The present study reveals multiple resistance mechanisms in *Anopheles* in the study areas, with the predominance of *An. coluzzii*, including metabolic detoxification and target site mutation. Therefore, proactive, evidence-based resistance management strategies are urgently needed to restore and sustain the efficacy of current vector control tools and strategies in Osun State.

Keywords: *Anopheles gambiae* s.l., insecticide resistance, synergist, metabolic assay, vector control, Osun, Nigeria.

Paper ID# 128

Title: Profiling insecticide resistance in *Anopheles gambiae* s.l. and *Anopheles stephensi* from Kenya using in-country nanopore sequencing

Cynthia Odhiambo^{1,*}, Mulenga Mwenda², Cyprian Adala¹, Sylvia Milanoi¹, Diana Omoke¹, Brian Morgan¹, Karolina Mosler³, Brian Polo¹, Daniel Bridges², Eric Ochomo⁴, Jason Hendry³

1.Kenya Medical Research Institute

2.PATH

3.Max Planck Institute for Infection Biology

4.Kenya Medical Research Institute (KEMRI)

Background: Malaria remains a threatening disease in Kenya, with over 70% of the population at risk of getting infected. Existing vector control interventions such as indoor residual spraying (IRS) and insecticide treated nets (ITNs) have contributed to >70% of the decline in malaria transmission between 2000-2015 but recently, the progress has stalled and, in some cases, even increased, due to among other reasons, the emergence of insecticide resistance. There is a need for continuous insecticide resistance monitoring to ensure the vector control interventions remain effective.

Methods: Therefore, we developed a simple and cost-effective nanopore sequencing insecticide resistance method that targets key insecticide resistant (IR) markers, including target site and metabolic resistance markers i.e. VGSC, Gaba receptor, Ace1 and Gste2, and tested it in *An. gambiae* s.s, *An. arabiensis* and *An. stephensi* collected from different regions across the country to define their resistance profiles. This data was analyzed in realtime using Nomadic software.

Results: The panel achieved high sequencing coverage for most targets across different species. We investigated IR markers across species and observed the KDR East (L995S) mutation to be fixed in *An. gambiae* s.s but at low frequencies in both *An. stephensi* and *An. arabiensis*. The KDR West (L995F) and Gaba A296S variants were detected at low levels across all three species. The Gste2 L119V mutation was exclusive to *An. gambiae* s.s, and several previously unreported mutations were also identified through this approach. In conclusion, moderate to low levels of resistance mutation

frequencies identified here on *An. gambiae* s.l. and *An. stephensi* hinted resistance to permethrin, DDT, deltamethrin and Dieldrin insecticides.

Results: These results also provide the first Kenyan *An. stephensi* insecticide resistance profiling that will be very informative to the NMCP in controlling this invasive vector.

Keywords: Insecticide resistance, Targeted sequencing, *An. gambiae*, *An. stephensi*, Surveillance

Paper ID# 43

Title: Contribution of microbial larviciding to resistance management strategies: a multi-scale evaluation of its impact on resistant *Anopheles gambiae* s.l. population in Cameroon.

Diane Leslie NKAHE^{1,2,*}, Christophe Antonio-Nkondjio²

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Background: Larviciding using microbial compounds is considered appropriate for controlling outdoor biting mosquitoes. However, the influence of larviciding in managing pyrethroid resistance remains unexplored. This study investigated whether the microbial-based larvicide VectoMax G can increase the susceptibility of *Anopheles coluzzii* populations to pyrethroids.

Method: The susceptibility status of *An. coluzzii* field population was evaluated at different time points, before and during larviciding treatments. Simultaneously, *An. coluzzii* larvae were collected and split into four groups, each subjected to 21 generations of selection, as follows; (i): deltamethrin 0.05%_only, (ii): VectoMax only, (iii): VectoMax+deltamethrin0.05%, (iv): VectoMax+deltamethrin0.05%+susceptible. Life-traits parameters were measured in the progeny. Kdr frequency, then the expression profile of detoxification genes was checked using qPCR. All parameters were compared between the first and the last generation of each laboratory colony and between field samples collected before and during larviciding.

Results: First findings showed a decrease in resistance intensity to deltamethrin from high to low in field populations. The colony vectomax + deltametrin +susceptible displayed a fitness profile similar to the susceptible colony with short development time and long adult survival rate ($p=0.18$). Moreover, the kdr gene frequency was found to be unchanged in the field population and a significant decrease in the overexpression profile of detoxification genes was detected in field population after larviciding implementation ($p<0.05$).

Conclusion: The study suggests that, under larvicide treatment, resistance reversal is possible, but it may take longer to establish in a highly resistant population, subject to continuous insecticide selection pressure. Furthermore, the addition of new tools specifically targeting the larval stages

could improve malaria vector control and insecticide resistance management.

Keywords: Microbial larvicide, resistance reversal, *Anopheles coluzzii*

Scientific Session 3: Novel Vector Control Tools & Product Innovation

Paper ID# 86

Title: Development of second-generation passive emanators for malaria vector control

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Background: Spatial emanators were recommended by the WHO in 2025 and are now being rolled out. These rely on pyrethroids, raising concerns about resistance selection. We developed novel assays in two large systems; the Ifakara Ambient Chamber Test (I-ACT) and the semi-field system (SFS) to identify non-pyrethroids active ingredients for further development.

Methods: Eleven volatile compounds with known activity in smaller-scale assays were initially screened in the I-ACT against *Anopheles gambiae* s.s. using treated filter-paper. Doses were explored until feeding inhibition was observed at multiple exploratory doses. Compounds were subsequently evaluated individually in the SFS against *An. gambiae* s.s. and *An. funestus* and further tested in combination with transfluthrin, or a known synergist. The primary endpoint was feeding inhibition, and delayed mortality was recorded as a secondary outcome.

Results: All compounds showed blood-feeding inhibition in both test systems, with eight compounds achieving $\geq 60\%$ feeding inhibition at one or more doses in the I-ACT, performing comparably to or better than transfluthrin. In the SFS, efficacy declined slightly for both candidates and transfluthrin. Among individual compounds, capric acid and nootkatone retained the highest efficacy (50-70% feeding inhibition). Most combinations with transfluthrin showed little or no improvement over single compounds. In contrast, the 1:1 combination of TCA and GMR-189 produced the highest semi-field protection, reaching 70% feeding inhibition.

Conclusions: We developed a novel large assay for testing volatile active ingredients for second generation spatial emanators, investigating blood feeding inhibition and delayed mortality. All were efficacious, opening the pipeline for new methods and products that will be needed as current spatial emanators face insecticide resistance challenges.

Keywords: Spatial emanators, Volatile active ingredients, Semi-field, Feeding inhibition, Passive repellents, *Anopheles*

Paper ID# 216

Title: Efficacy of the spatial repellent SC Johnson Mosquito Shield™ against anophelines in free-flight chambers, semi-field systems, experimental huts, and in-home tests

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Background: Evaluation of vector control tools follows a phased approach, progressing from laboratory studies to semi-field trials in experimental huts, and finally to small-scale (in-home test) and large-scale (randomized control trials) field evaluations under user conditions. Method selection depends on the specific data objectives.

Methods: We assessed mortality, exophily, deterrence, landing- and blood-feeding reductions induced by SC Johnson Mosquito Shield™ in free-flight chambers, semi-field and field experimental hut trials, and an in-home test against Afro-tropical malaria vectors. Descriptive statistics were presented as means with 95% confidence intervals. Mixed effects of regression with appropriate distribution for count and proportion of outcomes were applied for inferential statistics. The semi-field, field experimental hut, and in-home test were run for 32 nights (label claim of the product).

Results: Landing reductions measured using human landing catches were of similar magnitude across experimental hut tests in the semi-field (71%) and field (70%), as well as in-home tests (66%), but were higher in the free-flight chambers (96%) using a susceptible mosquito strain. Other endpoints (blood-feeding, mortality, and exophily) generally showed higher estimates in controlled environments with lab-reared mosquitoes, compared to ambient conditions with wild, free-flying mosquitoes in experimental huts or residential homes.

Conclusion: The findings highlight the strengths and limitations of free-flight chambers, semi-field systems, experimental huts, and in-home tests in generating efficacy data for new spatial repellent products. Mosquito landing reduction estimated via human landing catches is a reliable metric for monitoring spatial repellent product longevity across efficacy testing methods. The efficacy gradient between controlled and ambient conditions highlights the importance of testing under realistic settings before public health deployment.

Keywords: Free flight chamber tests, semi field system tests, experimental hut tests, in-home tests, spatial repellent efficacy testing,

Paper ID# 47

Title: Entomological transmission parameters, Wolbachia detection, and anopheles salivary peptides (gsg6-p1) as complementary tools for malaria transmission assessment in Kekem and Njombé-Penja, Cameroon

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Background: Classical entomological indices alone are insufficient to fully capture malaria transmission complexity. This study combined entomological transmission parameters, Wolbachia detection in wild anophelines, and IgG antibody quantification against the Anopheles salivary peptide gSG6-P1 to propose an integrated, more sensitive framework for malaria transmission assessment in Kekem and Njombé-Penja, Cameroon.

Methods: Conducted from May 2021 to June 2023, mosquitoes were collected across 70 households using Human Landing Catches and CDC light traps, then processed for sporozoite detection by ELISA, molecular species identification by PCR, and Wolbachia screening by RFLP-PCR. Dried blood spots from 95 participants aged 2 to 60 years were analyzed for IgG anti-gSG6-P1 antibodies by ELISA. Data were analyzed using SPSS v3.0.

Results: A total of 3,694 mosquitoes from three genera (Anopheles, Aedes, Culex) were collected, with five anopheline species identified: An. gambiae, An. coluzzii, An. nili, An. ziemanni, and An. funestus s.l. Of 1,550 Anopheles screened, sporozoite infection rates of 0.34% and 1.28% were recorded in Kékem and Njombé-Penja respectively. The EIR reached 0.27 ib/h/n in Njombé-Penja and 0.16 ib/h/n in Kékem. Natural Wolbachia prevalence was below 5% at both sites. Anti-gSG6-P1 IgG titers showed positive concordance with locality, age group, LLIN use, and EIR.

Conclusion: Integrating entomological parameters, Wolbachia detection, and anti-gSG6-P1. IgG quantification enhances malaria transmission assessment. The low Wolbachia prevalence and concordance of gSG6-P1 titers with EIR support their adoption in routine malaria surveillance.

Paper ID# 50

Title: Intronic Homing Gene Drives to induce female-specific lethality or sterility for *Anopheles gambiae* population suppression

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Background: Homing Endonuclease Gene Drives (HEGs) are among the most promising genetic control strategies for *Anopheles gambiae* population suppression. The double sex gene drive is the most promising, mainly due to its high sequence of conservation and functional constraint at the intron-exon boundary. However, the rarity of such highly conserved female-specific targets and the emergence of resistance alleles limit the broader applicability of current HEG designs.

Methods: Therefore, we are developing an intronic HEG strategy that leverages sex-specific alternative splicing to convert bisexual traits into female-specific traits. As a proof-of-concept, we leveraged the sex-specifically spliced intron of the 007 gene to convert a bisexually expressed DsRed2 marker to a male-specifically expressed phenotype while hosting an X-shredder sgRNA. Briefly, the DsRed2 coding sequence was interrupted by the intron, resulting in its correct splicing in males and retention in females.

Results: Males showed strong 3xP3 DsRed2 fluorescence, while females had significantly reduced fluorescence both in larval and pupal stages. The intronic X-shredder sgRNA produced a strong male bias progeny when crossed to $\beta 2$ -Cas9 with trans-heterozygous males, generating 96% male offspring when crossed to wild-type females. This sex-specific expression and transgene hosting capacity demonstrate the feasibility of using this intron to develop novel HEGs. To transfer this to native genes, an analysis of highly conserved 20bp Cas9 target sites in the genome identified three genes natively expressed in both sexes. These genes will next be tested by a CRISPR knock-in strategy to examine the homing efficiency of HEG within the 007 sex-specifically spliced intron.

Conclusion: Our findings establish the use of the 007 sex-specifically spliced intron to convert a bisexual gene into a male-specific gene while expressing a functional transgene. Therefore, this strategy can be applied to a wide range of applications, such as population modification.

Keywords: *Anopheles gambiae*, Homing Endonuclease Gene Drives, population suppression, and 007 sex-specifically spliced intron

Paper ID# 74

Title: Investigating small molecule inhibitors targeting reproductive proteins in *Anopheles gambiae*. as an innovative pathway to reduce malaria transmission

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Background: Targeting key genes involved in mosquito fertility and susceptibility to *Plasmodium* using small molecule inhibitors represents a promising alternative approach to reduce malaria transmission. In this study, we investigated four candidate genes (MISO, HPX15, VG, and LP) associated with *Anopheles* reproductive success and vector competence in *Anopheles gambiae* s.l.

Methods: Using whole-genome SNP data from the Ag1000G project, we analyzed these genes in 2,784 wild-caught *Anopheles gambiae* s.l. collected across 19 sub-Saharan African countries. Population genetic analyses were conducted to assess structure, genetic diversity and differentiation, alongside neutrality tests and evaluation of nonsynonymous SNP (nsSNP) linkage.

Results: Our results revealed a high level of conservation across all four genes in natural populations, suggesting their essential biological roles and potential as robust molecular targets. These findings provide integrated insights into key reproductive and transmission-related traits of major malaria vectors within their natural genetic background, supporting the development of innovative and sustainable vector control strategies. To further explore functional implications, HPX15 was selected for experimental validation. Four candidate small molecules were tested for their impact on *Anopheles coluzzii* life-history traits. While no significant effects were observed on mating or insemination, inhibition of HPX15 disrupted critical physiological processes, including reduced fecundity, decreased embryonic viability, and shortened adult lifespan.

Conclusion: The combined impact on reproductive success and survival highlights the strong epidemiological relevance of this approach. Importantly, targeting highly conserved biological

functions may reduce the likelihood of rapid resistance emergence compared to conventional insecticide-based strategies that act on more adaptable traits.

Keywords: Small molecule inhibitors, Anopheles key gene target, innovative pathway to reduce malaria transmission

Scientific Session 4: Indoor environment and control tools

Paper ID# 235

Title: Impact of vector control interventions on paediatric malaria admissions in western Kenya: Interrupted time-series analysis

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Background: Evidence on the combined effect of indoor residual spraying (IRS) and insecticide-treated nets (ITNs) on severe malaria remains limited. We used interrupted time-series analysis to examine the impact of piperonyl butoxide (PBO) nets and IRS on paediatric malaria hospitalizations in Busia County.

Methods: We analyzed children aged 1 month to 14 years admitted with malaria to Busia County Referral Hospital from January 2018 to December 2025. A Bayesian negative binomial segmented regression interrupted time-series model was fitted to monthly malaria admission incidence to assess changes following the introduction of PBO nets and IRS. Three periods were defined: a baseline period with pyrethroid-only ITNs (January 2018–June 2021), a post-PBO net period (July 2021–January 2024), and a post-IRS period (February 2024–December 2025), which included a return to pyrethroid-only ITNs from July 2024. Two IRS rounds were implemented in 2024 and 2025.

Results: There were 1,993 malaria admissions in the baseline period, 1,275 in the PBO net period, and 233 in the IRS period. We found no evidence of an immediate or sustained change in admissions after PBO net distribution compared with the pyrethroid-only ITN period. After IRS began in February 2024, there was no evidence of an immediate reduction in malaria admissions (adjusted incidence rate ratio, aIRR = 0.68; 95% CI: 0.29–1.60). However, IRS was associated with a significant monthly decline in admissions over time (aIRR = 0.91; 95% CI: 0.88–0.95), corresponding to an overall 73% reduction in malaria hospitalization rates (aIRR = 0.27; 95% CI: 0.21–0.35).

Conclusion: These findings suggest that sustained malaria control gains will require integrated vector control strategies rather than reliance on ITNs alone. Hospital surveillance provides a valuable approach for evaluating the impact of vector control policy changes as interventions are scaled up or withdrawn.

Keywords: IRS, ITNs, Busia, hospitalization

Paper ID# 149

Title: Design matters: structural variation in experimental huts significantly alters entomological endpoints in insecticide-treated net (ITN) evaluation – a comparative experimental hut trial using a latin square design in Tanzania and Côte d'Ivoire

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Background: Experimental huts are the gold standard for semi-field evaluation of insecticide-treated nets (ITNs), but designs vary markedly across regions. This study aimed to assess the influence of four common hut designs—East African, West African, Ifakara, and Rapley—on key entomological endpoints and to determine if they produce consistent estimates of relative product efficacy.

Methods: A 126-night comparative trial was conducted in Tanzania using 18 experimental huts in a 9×9 Latin square design. Four hut types were tested with Pronet Duo, interceptor® g2, magnet®, and untreated nets. Findings were benchmarked against a simultaneous sister trial conducted exclusively in West African huts in Côte d'Ivoire. The primary outcome was 72-hour mortality (m72), with secondary outcomes of mosquito density, blood-feeding success, and exiting.

Results: a total of 22,611 *Anopheles gambiae* s.l. were collected in Tanzania. Rapley and Ifakara huts captured over six times more mosquitoes than East African huts (rate ratio [err] = 6.50 and 6.22, respectively; $p < 0.0001$), while West African huts caught 88% fewer ($rr = 0.12$, $p < 0.0001$). West African huts recorded the highest adjusted mortality (70%) and blood feeding (15%), whereas other types ranged from 40-46% mortality and 3-8% blood feeding. Despite these variations, all hut designs predicted the same direction of effect for relative product performance.

Conclusions: Experimental hut architecture substantially affects key entomological outcomes, influencing both the measured efficacy of magnitude and statistical power. While relative product performance remains broadly consistent, the variation in absolute values underscores the urgent need for greater standardization of hut design and reporting standards to improve cross-site comparability and the reliability of global malaria control policy evidence.

Keywords: experimental hut trials, insecticide-treated nets, ITN, *Anopheles gambiae*, malaria, hut design, Tanzania, Côte d'Ivoire

Paper ID# 218

Title: Estimating the hole surface area of insecticide-treated nets using image analysis, manual hole counting and exact hole measurements

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Background: The physical integrity of insecticide-treated nets (ITNs) is a key determinant of their effectiveness in preventing malaria transmission. Current World Health Organization (WHO) guidelines rely on manual hole counting to assess net condition, but this approach is labor-intensive and may underestimate damage, particularly for large or irregularly shaped holes. Automated image-based methods offer a potential alternative for improving the accuracy, consistency, and efficiency of ITN integrity assessment.

Methods: Seventy-five ITNs from an ongoing study were purposively selected. Physical integrity was assessed using manual hole counting, image analysis, and ground truth measurements. A graphical user interface was developed to segment holes from photographs taken on each side of the nets, and the whole surface area was computed. Agreement between methods was evaluated using Bland-Altman analysis.

Results: Substantial agreement was observed between image analysis and ground truth measurements. The overall bias was small, with a mean ratio of 0.70 and 95% limits of agreement ranging from 0.35 to 1.38. Manual hole counting underestimated hole surface area, particularly for holes larger than 10 cm in diameter.

Conclusion: Image-based analysis provides sufficient information to estimate hole surface area and represents a promising approach for automated assessment of ITN physical integrity. Although the WHO method underestimates hole surface area, it remains appropriate for classifying nets due to method-specific thresholds.

Keywords: Insecticide-treated nets, ITN, image analysis, physical integrity, physical condition, hole

counting, functional survival

Paper ID# 166

Title: The non-inferiority efficacy of four pyrethroid-piperonyl-butoxide insecticide-treated nets in Tanzania and Côte d'Ivoire: evidence from experimental huts and Ifakara ambient chamber test

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Background: Pyrethroid-piperonyl butoxide (PBO) insecticide-treated nets (ITNs) are recommended for malaria control in areas with metabolic pyrethroid resistance. Multiple pyrethroid-PBO products are WHO-prequalified, but evidence on their comparative efficacy is limited. This study assessed the non-inferiority of three second-in-class pyrethroid-PBO nets (PermaNet® 3.0, Tsara Boost®, and VEERALIN®) relative to the first-in-class Olyset® Plus.

Methods: Experimental hut trials using 6x6 Latin square design were conducted against wild free-flying pyrethroid-resistant *Anopheles gambiae* sensu lato in M'Bé, Côte d'Ivoire (West African huts) and Lupiro, Tanzania (new Ifakara huts), with a complementary Ifakara Ambient Chamber Test (IACT) using laboratory-reared resistant *Anopheles arabiensis*. Non-inferiority was assessed primarily on 24-hour mosquito mortality, using logistic regression based on a 7% non-inferiority margin.

Results: Across all three studies, the pyrethroid-PBO nets were superior to standard pyrethroid-only nets ($p < 0.0001$). The second-in-class products were non-inferior to the first-in-class Olyset® Plus in Côte d'Ivoire and superior to it in both Tanzanian trials. These results confirm that all three new net candidates are highly effective tools for killing resistant mosquitoes.

Conclusion: PermaNet® 3.0, Tsara Boost®, and VEERALIN® proved just as effective as the industry-standard Olyset® Plus at killing mosquitoes in both study regions. These results validate the WHO's broader strategy for PBO nets and offer clear evidence to guide the purchase of life-saving malaria tools.

Keywords: non-inferiority, superior, insecticide-treated nets, piperonyl butoxide, experimental huts, IACT, pyrethroid resistance,

Paper ID# 141

Title: When chemistry holds, holes matter less: a framework for ITN functional durability and design

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Background: Insecticide-treated nets (ITNs) should protect for 3 years, but products differ in fabric durability and bioavailable insecticide persistence. Quantifying their relative contributions under use conditions is critical to developing ITNs with sustained efficacy.

Methods: Physical and chemical decay of pyrethroid ITNs obtained from a three-year longitudinal field trial in Tanzania were assessed. Effects of insecticide content, hole location, and holed surface area on 24-hour mortality and blood-feeding of pyrethroid-susceptible *Anopheles gambiae* sensu stricto were evaluated using the Ifakara Ambient Chamber Test (I-ACT). Outcomes were analyzed using a differential equation model with a hyperbolic function for holed area and a saturating function for insecticide content, allowing separation of barrier and insecticide effects.

Results: Fabric integrity and insecticide declined over time, varying by brand. Half of damage occurred in the bottom quadrant, typically tucked under mattresses. Only 27% of holed area was accessible to mosquitoes, concentrated in lower side panels above the mattress—an area amenable to reinforcement. Increasing holed area increased blood-feeding success, but residual insecticidal activity maintained low mosquito survival. The model showed excellent fit and separated barrier and insecticidal effects. Differences in mortality between brands were explained by linear scaling of insecticide concentration, with a shared parameter describing the concentration required to achieve half-maximal insecticidal effect; after scaling, deltamethrin was 780-fold more potent than permethrin.

Conclusion: Conditional on holed area, efficacy was largely explained by insecticide performance – heavily damaged nets were effective when insecticidal activity remained high. This framework enables prediction of chemical durability from insecticide properties, supporting rational product design through targeted reinforcement and improved formulation to maximise sustained efficacy and cost-effectiveness

Keywords: Insecticide Treated Nets (ITN), durability, physical integrity, mosquito, *Anopheles*,

mortality, feeding inhibition, bioassay

Paper ID# 32

Title: Chlorfenapyr bednets effectively overcome pyrethroid resistance escalation in highly resistant *Anopheles malaria* vectors in Uganda

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Background: Escalating insecticide resistance threatens the efficacy of LLINs, undermining malaria control.

Methods: We conducted the first experimental hut trials in Uganda using highly resistant free-flying wild *Anopheles* mosquitoes (surviving 10x diagnostic dose of pyrethroids) and F2 hybrids of FANG and Ugandan *An. funestus* to evaluate the performance of bednets.

Results: The Interceptor G2 (chlorfenapyr) net demonstrated superior efficacy compared to Interceptor (pyrethroid-only) [mortality OR: 18.7 (8.05–48.6) $P < 0.0001$], achieving an overall mortality rate of 70.6% and 63.2% against *An. funestus* and *An. gambiae* respectively. In contrast, PBO and PPF-treated bednets exhibited significantly lower mortality against *An. funestus* (<40% mortality) though performance against *An. gambiae* was moderate (>50% mortality). Regarding blood-feeding inhibition (BFI), PBO nets, outperformed Interceptor G2 and Royal Guard, while Interceptor produced minimal BFI. Further evaluation of Royal Guard's PPF effect on oviposition revealed no significant reduction in oviposition rates compared to controls with *An. funestus*. Genetic analysis using the hybrid crosses revealed that pyrethroid resistance markers (4.3 Kb-SV and G454A-Cyp9K1) were significantly associated with mosquito survival and blood-feeding success against pyrethroid-only and PBO nets but showed no significant association with Interceptor G2 net. These findings support Interceptor G2 as a promising intervention for regions dominated by both highly resistant *An. funestus* s.l. and *An. gambiae* s.l. Piperonyl butoxide and PPF nets emerge as a good alternative for areas mostly dominated by resistant *An. gambiae* s.l. populations.

Conclusion: Critically, the demonstrated variable impact of insecticide resistance on bednet efficacy calls for comprehensive local vector population mapping and systematic resistance monitoring. The

evidence should guide strategic LLIN distribution and timely interventions to sustain malaria control efficacy in resistance-prone settings.

Keywords: Anopheles funestus, Anopheles gambiae, Experimental huts, Interceptor G2, Malaria, LLINs; Resistance, Uganda

Paper ID# 84

Title: Hut trial evaluation of SOVRENTA as a vector control tool against malaria vectors in Zambia

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Background: Malaria vector control in Zambia relies heavily on use of insecticides in indoor residual spraying (IRS) and long-lasting insecticidal nets (LLINs) distribution. Insecticide resistance among malaria vectors threatens its effectiveness. This study evaluates a novel IRS formulation, SOVRENTA (plinazolin-based), designed to overcome resistance and provide prolonged residual activity. The primary objective is to assess the efficacy and duration of action of SOVRENTA against both susceptible and resistant mosquito populations. It is hypothesized that SOVRENTA will demonstrate superior or comparable performance to the standard IRS product, Actellic 300 CS, across different wall substrates, addressing the problem of declining IRS effectiveness due to resistance.

Methods: A Phase II experimental hut trial is being conducted in Shikapande village, Nchelenge District, Zambia, since June 2025 and expected to end by July 2026. Fifteen huts with cement, mud, and brick surfaces were randomized to receive SOVRENTA (120 mg/m²), six huts, Actellic 300 CS (1000 mg ai/m²), six huts, or no treatment, three huts. Monthly WHO cone bioassays using laboratory-reared susceptible Anopheles gambiae and wild resistant An. funestus will assess residual efficacy. Entomological indices, exiting & resting densities are measured via exit traps, and aspiration. Data on mosquito mortality is collected and analyzed using mortality thresholds (≥80%) and Abbott's correction where applicable. Additional data on user acceptability is gathered.

Results: After 8 months of the evaluation, SOVRENTA has shown good residual efficacy above 80% mortality on all surfaces, after 72 hours of exposure in both the laboratory reared and wild vector populations. Final results, ready, at the end of July 2026, will be shared at the conference.

Conclusions: SOVERENTA is efficacious and has shown acceptable residual activity and should be considered as an additional insecticide option in IRS programmes in Zambia.

Keywords: Zambia, Hut trials, SOVRENTA, Indoor Residual Spraying

Paper ID# 131

Title: Durability monitoring of PermaNet 3.0 and Olyset Plus LLINs: A 24-month assessment in Western Kenya

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Background: Global progress towards malaria control and elimination has stalled in recent years, and the long-term effectiveness of malaria vector control is threatened by the emergence and intensification of insecticide resistance in key mosquito populations. New types of ITNs that use more than one active ingredient and are effective against pyrethroid-resistant mosquitoes have been developed, but large-scale uptake has been slow prior to 2020, and very limited durability monitoring data exists for these new products. In Kenya, PermaNet 3.0 and Olyset Plus were distributed in Teso South in Busia County and Khwisero Sub-County in Kakamega County in June through August in 2021 through mass campaign. This study monitored efficacy, physical integrity, and chemical content of the 2 brands 12 & 24 months post distribution.

Methods: A longitudinal survey was conducted following the distribution campaign. Attrition rates were calculated, and bioefficacy was assessed via 24-hour mortality rates against susceptible and resistant mosquito strains using WHO cone bioassay.

Results: Bioefficacy for PermaNet 3.0 roofs against resistant strains declined from 43.3% (12M) to 12.2% (24M). Olyset Plus showed low mortality against resistant strains (15.2%). Attrition rates reached 37.5% in Kakamega and 46.4% in Busia, a significant increase from 12-month figures (~13%). The primary driver was net reallocation (64.7%). Chemical analysis revealed significant degradation: PermaNet 3.0 side panels lost 67.9% of deltamethrin, and roof PBO content deviated by 58% from manufacturer's targets. Olyset Plus showed a 39% reduction in permethrin and a 75% reduction in PBO. Notably, PermaNet 3.0 roof deltamethrin remained stable at 4.0 g/kg. After 24 months, both LLIN brands exhibited high attrition and substantial chemical loss, particularly in synergist (PBO) levels.

Conclusion: The sharp decline in bioefficacy against resistant mosquitoes raises concerns regarding

the effective lifespan of these nets in high-resistance areas.

Keywords: Durability, LLINs, PermaNet 3.0, Olyset, PBO

Scientific Session 5: Larval Source Management

Paper ID# 265

Title: Botanical phytochemical blends as next-generation larval growth regulators against *Anopheles gambiae*

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3.Kenya Medical Research Institute

Background: Malaria vector control in Africa remains dominated by adult-stage interventions, yet productive aquatic habitats continue to replenish vector populations. Botanical insect growth regulators (IGRs) offer a complementary larval source management strategy by disrupting mosquito development rather than relying on rapid knockdown.

Methods: Methanolic leaf extracts from curry tree (*Murraya koenigii*) plants collected across contrasting Kenyan ecological zones were screened against third-instar *Anopheles gambiae* s.s. larvae. The most active extract was subjected to bioassay-guided fractionation and LC-QTOF-MS profiling. Sublethal assays monitored larval survival, locomotion, pupation, adult emergence and developmental abnormalities. To examine mode of action, exposed late third/early fourth instar larvae and controls were profiled by RNA sequencing, followed by RT-qPCR validation.

Results: Semi-arid plant material, particularly from Kibwezi, showed strong larvicidal activity. Fractionation yielded an alkaloid-rich bioactive fraction with a 72-hour LC₅₀ of 2.43 ppm, approximately 20-fold more potent than the crude extract. Sublethal exposure caused reduced locomotion, anterior midgut/gastric caeca darkening, larval-pupal intermediates, delayed pupation, and severely impaired adult emergence. Transcriptomic analysis identified 730 differentially expressed transcripts, with 65.75% induced in exposed larvae. Affected pathways included cuticle formation, juvenile hormone regulation, sterol/ecdysteroid-associated processes, Osiris genes, detoxification, oxidative stress response, putrescine metabolism, and cell growth.

Conclusions: *M. koenigii* phytochemicals induce multi-endpoint developmental disruption consistent with botanical IGR activity. By linking visible larval arrest to molecular signatures of cuticle, endocrine and stress-pathway disruption, this work supports a mechanism-informed pipeline for locally sourced mosquito larval control products.

Keywords: Botanical insect growth regulators; *Murraya koenigii*; *Anopheles gambiae*; larval source management; cuticle disruption

Paper ID# 269

Title: Sibship analyses reveal larval habitat size preferences and skip oviposition behaviour in female *An. arabiensis*

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Background: Long-lasting insecticide-treated nets (ITNs) and indoor residual spraying (IRS) have played a significant role in malaria control. However, the effectiveness of ITNs and IRS is declining due to the development of insecticide resistance and other factors. There is a need for complementary strategies. Larval source management, through the autodissemination of larvicides by ovipositing female mosquitoes, is potentially a promising strategy. The effectiveness of this strategy requires an understanding of the oviposition site selection behaviour of female mosquitoes. This study investigated the oviposition response of gravid *Anopheles arabiensis* to artificial larval habitats of contrasting sizes in a semi-field.

Methods: Twelve small (30 cm diameter, 20 l) and large (60 cm diameter, 40 l) artificial larval habitats were established in two compartments of a semi-field. In quadruplicated experiments, forty wild gravid *An. arabiensis* were released into each compartment and allowed to lay eggs in habitat of their choice(s). The resulting 3rd larval instar was collected, counted, and preserved in 80% ethanol. DNA extraction and microsatellite genotyping were conducted on larvae collected from one replicate of the two compartments. Sibship analysis using Bayesian-likelihood methods was conducted to construct individual female oviposition habitat choice(s).

Results: More eggs were significantly laid in smaller habitats. Females skip-oviposited across two to four habitats, while others laid all their eggs in individual habitats. Overall, skip-ovipositing females laid more eggs, but fewer eggs per habitat, and were more likely to alternate between small and large

habitats than habitats of the same size.

Conclusion: Females preferred to lay eggs in smaller habitats and practiced skip-oviposition. This behavioral trait is informing the design and application of autodissemination and attract-and-kill strategies for malaria vector control.

Keywords: Semi field, *Anopheles arabiensis*, Oviposition, Habitats

Paper ID# 95

Title: Breaking the Cycle: Community-Led environmental management for outdoor breeding and harbourage site reduction

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Background: Vector-borne and other environmentally mediated infectious diseases impose a disproportionate burden on LMICs. Malaria and dengue, transmitted by mosquitoes, and Lassa fever, a rodent-borne disease, share common peridomestic environments that sustain their respective vectors or reservoirs. Community-led environmental management (CLEM) has emerged as a cost-effective, locally owned method of disease control, yet a synthesis across these contexts has been lacking.

Methods: We followed PRISMA 2020, searching five databases and grey literature from January 2010 to December 2024 for community-led interventions against outdoor breeding and rodent harbourage. Designs ran from cluster RCTs to comparator-controlled cross-sectional studies. Two reviewers independently screened, extracted, and rated bias. Heterogeneity ruled out meta-analysis, so we used a structured narrative synthesis (SWiM) and read results by design and bias rating.

Results: Of 4,217 records, 59 studies qualified: malaria 31, dengue 22, Lassa 3, mixed 3. Five intervention types recurred: sanitation, waste and container management, water-source control, mobilisation and IEC, and drainage. Direction was consistent: larval density fell 43.2% (28–65%), breeding-habitat prevalence 44.7% (31–61%), incidence 28–52%. Cluster RCTs showed smaller gains (38.6%) than quasi-experimental studies (48.4%), which fits residual confounding; the strongest adjusted estimate was an odds ratio of 0.44 (95% CI 0.31–0.63) for stagnant-water sites. Lassa contributed just three studies, so that signal stays thin.

Conclusion: CLEM is consistently associated with meaningful reductions in outdoor breeding and harbourage sites and in disease indicators across malaria, dengue, and, more tentatively, Lassa fever.

Because the evidence base spans heterogeneous study designs, diseases, and settings, policy translation should be context-specific and adaptive rather than uniform.

Keywords: Community-led vector control; outdoor breeding sites; peridomestic environmental management; malaria; dengue; Lassa

Paper ID# 116

Title: Semi-field evaluation of the residual efficacy of natular™ mini-DT larvicide against an invasive malaria vector *Anopheles stephensi* in Northeastern Ethiopia

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Background: The new emerging spread of *Anopheles stephensi*, an invasive malaria vector, in Ethiopia and other parts of the Horn of Africa has raised concerns about increased malaria transmission due to its adaptability to urban environments. A better understanding of effective vector control strategies, including larviciding, is crucial to combat this challenge, especially given the limitations of traditional insecticide-based methods. This study aims to determine the efficacy and residual effect of Natular Mini DT, a Spinosad larvicide at a content of 7.48% (w/w) solid, bilayer tablet against *An. stephensi*.

Methods: A longitudinal study was conducted in Jimma University Tropical and Infectious Disease Research Center Field Research Station at Awash Subac Kilo, Afar, Ethiopia, from November 2024 to January 2025. Under semi-field conditions, the evaluation utilized 16 containers, each filled with 50L of water, 8 treated with a single tablet with respective controls of 50% weekly water replacement, and no water replacement. Each week, 25 larvae were introduced into each container; larval mortality was recorded at 24, 48 and 72 hours post-exposure for each weekly batch for 12 weeks. Data were analyzed using descriptive statistics for summarization, and binary logistic regression analysis was employed to evaluate treatment differences and residual efficacy.

Result: Natular Mini DT exhibited a rapid larvicidal effect, but 100% mortality was not recorded for only the first two weeks for both water regimens. The comparison of treated water regimens revealed that the absence of water replacement resulted in a 75% lower likelihood of larval mortality. Furthermore, the larvicide showed significant residual efficacy for 12 weeks.

Conclusion: There was greater larval mortality from Natular Mini DT larviciding linked to prolonged duration in weeks and more effective in temporary water storage types. However, field efficacy and non-target effects of the larvicide should be studied.

Keywords: *Anopheles stephensi*, Larvicide, Vector control, Malaria, Natular™ Mini DT, Residual

efficacy, Ethiopia

Paper ID# 94

Title: Semi-field Evaluation of the Natular DT Mini®, Spinosad Larvicide in the control of pyrethroid-susceptible and resistant *Aedes aegypti* in Urban Water Habitat in Tanzania

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Background: Discarded and domestic water storage containers in urban settings are common larval habitats for *Aedes aegypti*. Many larvicides face resistance and show limited residual efficacy, especially in containers with frequent water replenishment. Natular® DT Mini, a Spinosad-based larvicide with a novel mode of action, has been used outside Africa; however, evidence of its efficacy and residual activity in African urban settings remains limited. This study evaluated its efficacy over 12 weeks under conditions simulating discarded and domestic containers with and without water replenishment.

Methods: The study was conducted at Ifakara Health Institute, Bagamoyo, Tanzania. Sixteen plastic containers were filled with 50 L of water; eight had no replacement, while eight underwent 50% water exchange weekly. Within each group, four containers were treated with a single Natular® DT Mini tablet, and four served as controls. Second instar larvae were introduced into floating devices, each holding 25 pyrethroid-susceptible or resistant *Ae. aegypti*. Larval mortality was recorded up to 72 hours, and adult emergence was monitored.

Results: One application of Natular® DT Mini leads to high larval mortality and sustained emergence inhibition for up to 12 weeks under both water regimes. No significant difference in 72-hour larval mortality was observed between susceptible and resistant strains in containers without water replacement (OR = 1.07; 95% CI: 0.71–1.59; $p = 0.759$) or with replenishment (OR = 1.33; 95% CI: 0.89–1.97; $p = 0.160$). Emergence inhibition exceeded 80% from week 2 onward, while controls showed near-complete emergence.

Conclusion: Natular® DT Mini is highly effective against both susceptible and resistant *Ae. aegypti* in containers with stable or replenished water. Comparable efficacy across strains suggests no cross-resistance, supporting its potential as an easy-to-deploy, long-lasting larvicide for urban vector control.

Keywords: *Aedes*, *Ae. aegypti*, Larvicide, Spinosad, breeding habitat, Dengue, Natular® DT Mini, Vector control, Tanzania

Paper ID# 162

Title: Efficacy and Residual Activity of Novaluron on *Anopheles coluzzii* and *Anopheles arabiensis* in laboratory and semi-field conditions in Senegal

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Background: Vector control methods have significantly reduced malaria transmission. However, challenges such as insecticide resistance and behavioral adaptation of vectors highlight the urgent need for alternative control measures. Novaluron, an insect growth regulator, was evaluated following the World Health Organization Pesticide Evaluation Scheme.

Methods: Laboratory bioassays were carried out using third (L3) fourth instar larvae (L4) of *Anopheles coluzzii* (laboratory strain) and *Anopheles arabiensis* (collected from the Dakar suburbs) at 10 concentrations ranging from 0.01 to 6 µg/l. Pupae were also exposed to 6 concentrations ranging from 100 to 750 µg/l using same species. Concentrations inhibiting adult emergence at 50% (EI50) and 99% (EI99) were determined using log-dose-response analysis. At the experimental station, efficacy and residual activity were assessed exclusively on L3, with multiple diagnostic doses (DD) for each species.

Results: In the laboratory, emergence inhibition (EI) 50% and 99% values on L3 were 0.145 and 0.29 µg/l for *An. coluzzii* and 0.37 and 0.69 µg/l for *An. Arabiensis*, on L4, 1.95 and 3.61 µg/l for *An. coluzzii* and 2.76 and 5.02 µg/l for *An. arabiensis*. For pupae, EI50 and EI99 values were 145 and 265 µg/l for *An. coluzzii* and 428.37 and 714.13 µg/l for *An. arabiensis*. At the experimental station, *An. coluzzii* showed respectively 86 and 77,08% cumulative mortality (CM) and emergence inhibition rate (EI) by day 33 at 6 µg/l. For *An. arabiensis*, 84% CM and 77,08% EI were observed by day 40 at 15 µg/l. *Anopheles coluzzii* and *An. arabiensis* are susceptible to Novaluron at low concentrations under laboratory conditions. At optimal doses, Novaluron effectively inhibits both pupation and adult emergence. Its efficacy and residual activity under semi-field conditions its potential as a component of integrated malaria vector control strategies.

Conclusion: These results provide insights into optimizing application frequency and operational costs for potential field deployment.

Keywords: Insect growth regulator, Novaluron, vector control, semi-field evaluation, mosquito larvae

Paper ID# 53

Title: Development of a Comprehensive Larviciding Evaluation and Assessment Framework

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Background: Larviciding is increasingly prioritized by NMPs for its potential to complement existing interventions. Although historically proven as an effective intervention, implementation expertise is piecemeal, preventing the generation of robust data in modern malaria vector control programs.

Methods: To meet this need, we developed the Comprehensive Larviciding Evaluation and Assessment Framework (CLEAR) using available evidence, best practices, and expert opinion. The framework was developed through the RBM Vector Control Working Group and involved input from national malaria programs, WHO, academia, donors, industry, and implementation partners.

Results: CLEAR is a comprehensive monitoring and evaluation framework consisting of three modules: evaluation design, impact evaluation, and process evaluation. Evaluation designs, including interrupted time series, difference-in-differences, and controlled interrupted time series approaches, are discussed in the context of typical malaria program surveillance capacity. CLEAR defines a standardized set of indicators spanning intervention coverage, operational performance, entomological impact, epidemiological impact, cost-effectiveness, and community engagement. The framework also shows how technology can strengthen habitat mapping, intervention delivery, and program monitoring. The presentation will describe the CLEAR development process, its key components, and planned pilot applications in Ghana and Uganda to assess feasibility and utility under programmatic conditions.

Conclusions: CLEAR provides NMPs with a standardized approach for generating high-quality evidence on the implementation, effectiveness, and cost-effectiveness of larviciding interventions. By strengthening monitoring and evaluation, the framework may support evidence-based decision-making and facilitate the integration of larviciding into routine malaria vector control strategies.

Keywords: larviciding, evaluation

Paper ID# 248

Title: Spatial analysis and characterization of Anopheles spp. larval breeding sites in three villages of Burkina Faso: implications for targeted vector control

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Background: The persistence of malaria in sub-Saharan Africa requires a detailed understanding of the spatial distribution of vectors. Mass interventions could be more effective if they were guided by accurate mapping of areas of high larval productivity (hotspots). This study aims to characterize the spatial distribution of larval sites of *Anopheles* spp. and non-target entomofauna (NTO) in the villages of Souroukoudingan, Bana and Pala, in order to identify priority areas for targeted and ecologically sound larval control.

Methods: Entomological surveys carried out between 2012 and 2017 have made it possible to map the larval sites. The spatial analysis mobilized the minimum convex envelope and the directional distribution to compare the spatial extent of the deposits in relation to the dwellings (compounds); analyses of hotspots (Getis-Ord Gi statistics*) with confidence levels of 95% to 99% and an inventory of the diversity of non-target insects (Dytiscidae, Baetidae, Corixidae, Chironomidae, etc.) in order to assess the ecological balance of the roosts.

Results: The results reveal a strong spatial heterogeneity of larval productivity. In Souroukoudingan, the distribution of larvae mainly follows the axis of the R18 regional road, suggesting a structuring effect of the infrastructure. In Pala, a statistically significant hotspot (99% confidence) is identified in the center of the village. The most productive roosts (289 to 779 larvae) also have a high entomological biodiversity, highlighting the importance of control approaches that respect ecological balances.

Conclusion: The close spatial correlation between larval hotspots and settlement areas suggests that integrated management based on digital mapping and spatial analysis would optimize vector control, reduce malaria transmission, and preserve local biodiversity.

Keywords: Burkina Faso, Cartography, *Anopheles*, Hotspots, Vector control

Paper ID# 11

Title: Biorational Larvicides, Larviciding and Resistance Management for Mosquito Control – Then, Now and the Future

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Background: While ITNs and IRS effectively target indoor-biting mosquitoes, documented shifts toward outdoor biting across sub-Saharan Africa underscore the urgent need for complementary outdoor tools as the continent moves toward malaria elimination. Emerging interventions are increasingly context-specific rather than broadly applied. Repellent-based strategies remain important for reducing human–vector contact and preventing infections. The study assessed feasibility and acceptability of the E55 Rechargeable Portable Mosquito Repeller as a routine tool for outdoor mosquito control in a malaria-endemic setting.

Methods: The study was conducted in Kisumu and Siaya counties, with 80 participants (40 per site). Using purposive sampling, household surveys, and in-depth interviews (IDIs) assessed feasibility and acceptability of the device. Surveys were conducted for one-month post-intervention in 20 households per site, while IDIs were done in two rounds (one and two months) with 10 households per site. Survey and IDI participants were distinct, with repeat IDIs tracking changes over time.

Results: The device was mainly used outdoors in the evenings around homes, though indoor use increased over time. Participants reported high perceived efficacy, ease of use, and portability, with strong willingness to continue use. Participants reported reduced mosquito presence resulting to less reliance on coils, other repellents, and slightly on ITNs. Suggested design improvements included modifications to enhance indoor suitability and longer cartridge and battery life. Adverse effects were minimal, mainly mild eye, nose, and skin irritation following contact with the insecticide.

Conclusion: The findings show that the intervention is a feasible and well-accepted outdoor vector control tool in malaria-endemic areas. Its effectiveness and ease of use suggest it can complement existing strategies for outdoor transmission. The design improvements suggested could enhance acceptability.

Keywords: Spatial repellent; Outdoor mosquito control; Community acceptability; Feasibility; Residual malaria transmission; Kenya

Paper ID# 78

Title: Long-lasting ivermectin in livestock for malaria control in pastoralist communities of Turkana, Kenya

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Background: Malaria control in arid regions of sub-Saharan Africa remains challenging due to outdoor biting and insecticide resistance among key vectors such as *Anopheles arabiensis* and the emerging invasive *Anopheles stephensi*. In pastoralist communities of Turkana, Kenya, close human–

livestock interactions and predominantly zoophilic vector behaviour present an opportunity for alternative control strategies. This study evaluates a One Health approach using long-lasting ivermectin (LLI) administered to livestock to reduce malaria transmission.

Methods: We will conduct a controlled before-and-after study with a difference-in-differences design in two sites in Lokichogio subcounty, Turkana County. Following a one-year baseline period, biannual LLI mass drug administration will be delivered to livestock in intervention areas, with control areas receiving no intervention. Entomological surveillance includes human- and livestock-baited traps, larval sampling, and CO₂-baited collections. Outcomes include mosquito abundance, survival, species composition, and host preference. Epidemiological impact will be assessed through longitudinal active case detection at household level of malaria case incidence using community health promoters. Molecular analyses will characterize vector species and population structure.

Results: Preliminary entomological collections indicate that transmission is dominated by highly zoophilic *An. arabiensis*, with evidence of *An. stephensi* presence. High levels of outdoor biting and substantial livestock feeding support the rationale for a livestock-targeted intervention.

Conclusion: The LLIMA trial will generate critical evidence on the effectiveness of livestock-based ivermectin mass drug administration as a complementary malaria control strategy in pastoralist settings. If effective, this approach could provide a scalable and context-appropriate intervention where conventional tools are less effective.

Keywords: malaria one-health ivermectin Turkana Kenya

Paper ID# 111

Title: Physiological status and species identity influence ATSB uptake in malaria vectors: semi field structures evidence from Kenya

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Background: Attractive targeted sugar baits (ATSBs) are a promising malaria vector control tool exploiting mosquito sugar-feeding behavior. However, uncertainty remains on how mosquito species, physiological status, and competing host cues affect ATSB uptake. This study examined determinants of ATSB feeding among malaria vectors in western Kenya.

Methods: Exploratory semi-field studies were conducted using wild and laboratory-reared *Anopheles* mosquitoes, including *An. gambiae* s.l. (predominantly *An. arabiensis*), *An. gambiae* s.s., and *An. funestus* s.l. (predominantly *An. funestus* s.s.). Mosquitoes were exposed to attractive sugar

bait (ASB) or attractive toxic sugar baits (ATSB) in semi-field structures, and feeding was assessed using dye markers. Logistic regression models were used to evaluate the effects of blood-feeding status and the presence of human host cues (occupied vs unoccupied huts) on ATSB uptake. Species- and strain-specific differences in feeding were also assessed over time.

Results: ATSB feeding varied significantly by species, physiological status, and the presence of host cues. Blood-feeding status had no significant effect on *An. gambiae* s.l. (OR=0.94, 95% CI: 0.26–3.40; p=0.919) or *An. gambiae* s.s. (OR=0.72, 95% CI: 0.31–1.66; p=0.435), But significantly increased feeding in *An. funestus* s.l. (OR=3.45, 95% CI: 1.07–11.2; p=0.038). Human host cues significantly reduced ATSB feeding across species, suggesting a shift toward host-seeking when a blood source was available. Feeding proportions also varied by species and strain, with consistently higher uptake in *An. funestus*. Temporal variation was observed.

Conclusion: ATSB feeding behavior showed clear species-specific differences, with *An. Funestus* demonstrating higher and physiologically influenced uptake than *An. gambiae* populations. Vector species composition and behavioral ecology should be considered when deploying ATSBs. Tailored strategies may improve ATSB effectiveness across diverse malaria transmission settings.

Keywords: Malaria vector control; ATSB; sugar feeding; *An. funestus*; *An. gambiae*; physiological status; species-specific behavior

Paper ID# 97

Title: Optimizing acacia-based attractants for outdoor control of *Anopheles gambiae* in Africa

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1.icipe

Background: Outdoor mosquito control remains a major challenge in Africa, requiring innovative, ecologically grounded approaches. Plant-derived semiochemicals play a critical role in mosquito sugar-feeding behaviour and may provide novel attractants for vector management. This study evaluated acacia-derived semiochemical blends as potential tools for outdoor surveillance and management of malaria vectors.

Methods: Synthetic blends mimicking the natural ratios of four key volatile: 1-octen-3-ol, linalool oxide, sulcatone, and nonanal identified from *Acacia tortilis*, *Acacia laeta*, and *Acacia nilotica* were evaluated on adult *Anopheles gambiae* of both sexes using a Y-tube olfactometer. The most attractive doses were compared among blends and against linalool oxide (LO), a known plant-derived attractant.

Results: Dose–response assays showed that attraction varied with blend composition, concentration,

and mosquito sex. The *Acacia tortilis* blend (TB) consistently elicited the strongest responses in both female and male *Anopheles gambiae*. At their optimal doses, females showed a 67.6–73% preference for TB, compared with 27% for the *A. laeta* blend (LB) and 32.4% for the *A. nilotica* blend (NB). Similarly, males preferred TB over LB (65.8% vs 34.2%) and TB over NB (75.7% vs 24.3%). When compared with the standard plant-derived attractant linalool oxide (LO), TB elicited significantly stronger responses in both females (68.6% vs 31.4%) and males (62.9% vs 37.1%).

Conclusion: These findings highlight the potential of ecologically relevant semiochemical blends for enhancing outdoor mosquito surveillance and control. Incorporating plant-based attractants such as TB into Attractive Toxic Sugar Bait (ATSB) systems offers a promising, sustainable strategy for targeting vector populations in African dryland ecosystems.

Keywords: Acacia, Malaria, *Anopheles gambiae*, management

Paper ID# 58

Title: Laboratory establishment of *An. gambiae* s.l. colonies with *Microsporidia* sp. MB and development of molecular diagnostic assays for MB release programmes

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Background: *Microsporidia* sp. MB is a naturally occurring microsporidian in *Anopheles* mosquitoes and has been shown to inhibit Plasmodium transmission. One of the two feasible malaria control strategies would involve disseminating MB either through mosquito releases or via spores capable of infecting mosquito larvae. Either strategy requires the establishment of *An. gambiae* colonies with stable MB infection and diagnostic methods capable of monitoring infections and MB prevalence in the field.

Methods: The progeny (G1s) of field-caught mosquitoes (G0s) from Burkina Faso were individualized and screened for MB. Progeny (G2s) from MB-positive mosquitoes were pooled, and the same process was repeated until a stable, high-prevalence MB colony was established. A new end-point PCR, a duplex TaqMan PCR, and a simple, cost-effective Colourimetric LAMP assay targeting the MB 18S rRNA were developed. MB density across mosquito life stages and tissue tropism in both males and females, including those that are mated and blood-fed, was assessed using a TaqMan qPCR assay. Four different MB colonies (G+, Z+, BQ+, E+) were established and maintained stably in the laboratory for

over two years with minimal intervention.

Results: All three diagnostic methods developed for MB were highly specific and more sensitive than previously published detection methods, with duplex qPCR efficiency of 90–110% ($R^2 > 0.98$) and a detection limit of 1000 copies in both TaqMan qPCR and LAMP assay. The home-brew reagents developed the LAMP assay to reduce reaction costs to ~20% of commercially available kits while maintaining high sensitivity. MB prevalence was higher in eggs and adult females than in other life stages and was predominantly present in gonadal tissues. MB density also increased after a blood meal (4.3-fold, $p=0.003$), suggesting activation of sporogony in Microsporidia MB.

Conclusion: Thus, the laboratory colonies established, and diagnostic methods developed would be a significant step forward in using MB for malaria control.

Keywords: Malaria, *Anopheles gambiae*, Burkina Faso, Microsporidia sp. MB, LAMP assay, Diagnostics

Paper ID# 57

Title: Natural transmission routes of Microsporidia sp. MB are promising avenues to use for malaria control

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Background: Microsporidia sp. MB is a microsporidian symbiont of the *Anopheles gambiae* complex. Mosquitoes carrying MB have been shown to have reduced prevalence and density of *Plasmodium falciparum* infections in field and laboratory settings. If we can increase the proportion of field mosquitoes carrying MB, this would reduce malaria cases. As microsporidia has complex life cycles including several intracellular and environmental stages, it could be possible to exploit aspects of the natural life cycle to introduce more MB into field populations. Working with laboratory established MB infected *Anopheles coluzzii* colonies from Burkina Faso we set up crosses with MB positive and negative mosquitoes and used TaqMan qPCR, fluorescent microscopy and comparative transcriptomics to examine vertical transmission of MB across multiple oviposition's, the development and infectivity of spore stages in different potential hosts and gene expression in response to blood feeding.

Results: Our results show that the primary route of MB transmission is vertically through the gonadal

tissues of female mosquitoes into their progeny at over 95% frequency. Although transmission from male to female occurs during mating, onward transmission to progeny is rare at <2% frequency. This pattern is consistent across multiple oviposition's. Interestingly, MB sporogony occurs in ~11% of developing ovarioles, in response to the mosquito host taking a bloodmeal. These spores are environmentally stable, and experiments are ongoing to understand this likely horizontal transmission route in several potential hosts. Preliminary analysis of transcriptome data examining ovaries has indicated that MB is influencing host gene expression. This analysis is ongoing and a summary of the results will be presented.

Conclusion: This understanding of MB transmission leads us to believe that release of MB infected female mosquitoes and MB spores into the environment are promising avenues for increasing MB prevalence in the field to combat malaria.

Keywords: Malaria, *Microsporidia* sp. MB, Burkina Faso, Transmission, *Anopheles* mosquitoes, Control, Spores

Paper ID# 42

Title: Status of domestic anti-mosquito control tools, human exposure to anopheles bites and malaria prevalence in Bélabo and Ouami, East Cameroon

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Background: In the forest regions of Cameroon, communities face high vector nuisance and high malaria endemicity. To control this nuisance, households use insecticides; however, these products are used at home without evidence of their efficacy against targeted mosquito populations. This study presents a sample of anti-mosquito tools used in households, human exposure to *Anopheles* bites, and malaria prevalence in Bélabo and Ouami, two localities in the forest region.

Methods: Study was conducted in Bélabo and Ouami in October 2022. The study protocol included : A survey in 200 randomly selected households to assess different anti-mosquito tools used ; WHO cone and susceptibility bioassays using reared *An. gambiae* s.l. were conducted, respectively, to assess the efficacy of LLINs collect in households and domestic anti-mosquito tools (coils and aerosols) ;

immunological analyses of exposure to *Anopheles* bites using salivary peptide gSG6-P1 on blood samples and microscopy to determine the prevalence of *Plasmodium* spp. infection in the study population.

Result: The household survey revealed that long-lasting insecticidal nets (LLINs) (59.81%), insecticide aerosols (38.82%), and insecticide coils (16.47%) were the most commonly used anti-mosquito tools. Aerosols showed optimal efficacy against *Anopheles gambiae* s.l with 100% mortality. Coils showed minimal efficacy (82.5%), while LLINs showed no efficacy (12.53%) against *An. gambiae* s.l. Of the 370 blood samples analyzed, 133 tested positive, giving an overall infection prevalence of 35.94%. Participants who did not regularly use control tools were more exposed to *Anopheles* bites and had higher infection rates compared to those who used them regularly.

Conclusion: The study reveals a high level of exposure to *Anopheles* bites among participants who do not regularly use anti-mosquito control stools, optimal efficacy of aerosols, minimal efficacy of mosquito coils and a no efficacy of LLINs against *An. gambiae* s.l.

Keywords: Efficacy, anti-mosquito tools, *Anopheles gambiae* s.l., Aerosols, Coils, LLINs

Paper ID# 60

Title: Nationally representative programmatic surveillance of mosquito and human behaviours that influence human exposure to malaria transmission and the impact of vector control across Tanzania

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Background: Integrated entomological and anthropological surveillance is critical for understanding malaria transmission risks and tailoring intervention packages but has not been implemented at scale due to lack of practical, affordable procedures for nationally representative monitoring. This study in Tanzania introduces and field-tests the first scalable framework design and reports early data summaries, demonstrating its feasibility and utility for generating programmatically informative indicators of mosquito and human behaviours.

Methods: One village was randomly selected from each of twenty-five ecologically and epidemiologically diverse districts across Tanzania for simultaneous surveys of malaria vector and human behaviours, using a rolling cross-sectional design. Surveys were repeated approximately annually over three years, with each village assessed across wet and dry seasons to capture temporal variation. A total of 25,663 host-seeking mosquitoes were sampled indoors and outdoors using METs, while human behaviour was assessed using a standard questionnaire across 864 households.

Results: *Anopheles arabiensis* was widespread, while *Anopheles gambiae* and *Anopheles funestus* were more localized. Most fed *An. funestus* and *An. gambiae* contained human blood, whereas *An. arabiensis*, *An. quadriannulatus*, and *An. lesoni* fed predominantly on cattle. Higher proportions of host-seeking *An. arabiensis* were caught outdoors (64.9%) than *An. gambiae* (58.3%) or *An. funestus* (42.4%). Across all age groups, people were more likely to be outdoors in the early evening (18:00–21:00), especially adolescents (13–17 yrs) and adults compared to younger children. Adolescent males were less likely to use bed nets. Bed net use increased in the rainy season and declined in the dry season.

Conclusion: This national surveillance framework demonstrated feasibility for measuring mosquito and human behaviour metrics to inform optimization of malaria control strategies.

Keywords: vector surveillance, malaria transmission, human behaviours, malaria vector behaviour, vector control, outdoor exposure

Paper ID# 219

Title: Establishing a network of permanent observatories for mosquitoes and mosquito-borne diseases in East and Southern Africa (VectorGrid-Africa)

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Background: Mosquito-borne diseases remain a major public health threat in sub-Saharan Africa, yet surveillance systems are often fragmented, short-term, and poorly standardised. This limits understanding of long-term transmission dynamics, climate and land-use impacts, emerging arboviruses, insecticide resistance, and zoonotic spillover risks.

Methods: VectorGrid-Africa is establishing permanent mosquito observatories across Kenya, Madagascar, Mozambique, South Africa, and Tanzania from 2026. In each country, 3-5 ecologically diverse districts will be selected through a structured consultative process, with sentinel villages and urban neighborhoods conducting standardised monthly mosquito sampling and intensified seasonal surveys. Surveillance will generate harmonized longitudinal data on vector densities, species composition, biting behaviour, host-feeding patterns, pathogen infection rates, genetic variation, insecticide resistance markers, climate, land use, vector control coverage, human activity, routine malaria trends, non-malaria febrile illness, and animal health indicators.

Implementation status: As an early-stage platform, VectorGrid-Africa has developed a multi-country observatory architecture, standardised sampling and laboratory protocols, site-selection framework, data-governance pathway, and One Health integration model. Planned analyses will assess temporal and spatial trends, ecological drivers of vector abundance and pathogen risk, and links between entomological, environmental, human health, and animal health indicators. Rift Valley fever will serve as the initial zoonotic surveillance model, beginning in Tanzania.

Conclusion: VectorGrid-Africa will provide long-term infrastructure for integrated mosquito-borne disease surveillance, improving outbreak detection, climate-responsive risk assessment, insecticide resistance monitoring, and preparedness for emerging and zoonotic diseases.

Keywords: VectorGrid-Africa; mosquito observatories; mosquito-borne diseases; One Health surveillance; arboviruses

Scientific Session 7: Vector Surveillance & Bionomics

Paper ID# 237

Title: Ecofriendly malaria control strategies: contribution of plant-based essential oils as bioinsecticide to control *Anopheles spp.*

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Background: Environmental and human health concerns added to the widespread resistance of malarial vectors to synthetic insecticides currently used has led researchers to look for sustainable alternatives in botanicals with a great interest in plant essential oils. Essential oils contain diverse volatile monoterpenes, diterpenes and sesquiterpenes compounds that possess ovicidal, larvicidal, adulticidal, repellency, antifeedant, growth and reproduction inhibitors activities.

Methods: Essential oils of 11 plant species grouped in 8 families harvested in Cameroon flora were tested in laboratory for their ovicidal, larvicidal and adulticidal activities against *Anopheles gambiae* s.l. according to WHO standard protocol.

Results: Among 11 plant essential oils tested, 7 plant oils exhibited a significant insecticidal activity including ovicidal activity [5 plants, yield (0.24-1.677%), compound number (12-52) and LC50 after 24hrs (0.14-17.8 ppm)], larvicidal activity [7 plants, yield (0.07-1.67%), compound number (16-52) and LC50 after 24hrs (0.10-82.22 ppm)] and adulticidal activity [6 plants, yield (0.04-1.67%), number of compounds (7-52) and LC50 after 24hrs (0.10-7.6 ppm)]. Their major phytochemical constituents were Linalol (20.45%) for *Cananga odorata*, Myrcene (31.75%) for *Cannabis sativa*, Caryophyllene (31.8%) for *Capsicum annum*, Isolimonene (77.93%) for *Citrus aurantiifolia*, (z) Anethole (34.24%) for *Clausena anisata*, Eucalyptol (34.25%) for *Eucalyptus globulus*, Terpinolene (24.97%) for *Hyptis spicigera* and β -Curcumene (15.24%) for *Zingiber officinale*.

Conclusion: Since some essential oils showed a high insecticidal efficacy against *An. gambiae* s.l., small scale field tests should be conducted furthermore. As future prospects, these plant-based essential oils will be used singly or in combination recipe to develop new potential mosquito bioinsecticides to control malaria vectors in small-scale fields and then in the population inhabitants.

Keywords: Bioinsecticides, Plant essential oils, malarial vector, *Anopheles gambiae*.

Paper ID# 126

Title: Molecular detection and maternal transmission of *Microsporidia* MB in the field-caught *Anopheles coluzzii* in Cameroon

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Background: Recent discoveries of *Microsporidia* MB in *Anopheles* mosquitoes and its demonstrated capacity to block malaria transmission suggest that it could be a promising candidate for a symbiont-based malaria control strategy. However, the diversity of *Microsporidia* MB, particularly in major malaria vector such as *An. coluzzii*, remains unstudied in Cameroon. In this study, we investigated the prevalence and phylogenetic analysis of *Microsporidia* MB, along with its maternal transmission in natural populations of *Anopheles* mosquitoes in Cameroon.

Methods: An entomological survey was conducted across four localities in Cameroon. PCR targeting the ribosomal RNA gene was used to detect the *Microsporidia* MB 18S sequence. Positive samples were validated by sequencing and phylogenetic analysis. Subsequently, the maternal transmission of *Microsporidia* MB was assessed by detecting its presence in F1 mosquitoes derived from F0 females that tested positive. Additionally, we examined the potential correlation between *Microsporidia* MB and *P. falciparum*.

Results: A total of 2,559 mosquitoes, belonging to three species (*An. coluzzii*, *An. arabiensis*, and *An. gambiae*) were collected. *Microsporidia* MB infection was detected exclusively in *An. coluzzii* from Gounougou, with a prevalence of 1.13% (n = 29). Phylogenetic analysis showed that the *Microsporidia* MB strains detected in Cameroon were closely related to those found in Kenya. Evidence of vertical transmission was confirmed, with rates ranging from 50% to 100%, from F0 parents to F1 offspring, regardless of sex. Notably, none of the *Microsporidia* MB-positive mosquitoes carried *P. falciparum*.

Conclusions: This study provides field-based evidence of *Microsporidia* MB presence in *Anopheles* mosquitoes in Cameroon. Further research should explore the stability of vertical transmission and the influence of this *Microsporidia* MB symbiont on *Plasmodium* development.

Keywords: Malaria, *Anopheles*, *Microsporidia* MB, Phylogenetic analysis, Maternal transmission, *Plasmodium* detection, Cameroon

Paper ID# 122

Title: Ento-virological surveillance of Rift Valley fever and human exposure risk in a pastoralist-dominated ecology of Southern KenyaFaith Cherop^{1,*}, Rosemary Sang², David Tchouassi³, Florence Oyieke⁴

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Background: Rift Valley fever virus (RVFV) has consistently presented a veterinary and public health challenge in Africa and beyond. However, the extent of human exposure and associated disease burden, especially during the inter-epidemic period, remains poorly evaluated. We investigated arbovirus entomological risk and seroprevalence of RVFV in the febrile human population in Nguruman.

Methods: Cross sectional monitoring of adult mosquitoes using CO₂-baited CDC light traps was undertaken after long rains between 2021 and 2023 in twelve villages represented by three ecological zones in Nguruman. The sources of blood meals in engorged specimens were identified by PCR. The generalized linear mixed-effects model was used to analyze ecology- and village-level effects on mosquito abundance. Outpatients in a health facility in Nguruman were randomly sampled for blood and interviewed. Exposure to RVFV was determined by using PRNT. The association between RVFV seroprevalence and human demographic characteristics was assessed using regression analysis.

Results: A total of 22,985 mosquitoes were collected comprising 32 species belonging to eight genera. The primary RVFV vector *Aedes mcintoshi* (58.3%) was the predominant species and occurred almost exclusively in the Conservancy (>97%). The secondary vectors constituted 23%. *Ae. mcintoshi* comprised most of the blood-fed specimens and analysis revealed a shift in host feeding obtaining blood meals from diverse wildlife mammalian hosts in the conservancy to exclusively humans in farmlands. *Cx. univittatus* maintained an opportunistic feeding; birds, buffalo, goat, antelope and human (HBI = 0.11). Among the 179 individuals, the estimated RVFV antibodies seroprevalence was 7.8% (95% CI: 4.50 – 13.03), with age being an important predictor of seropositivity (OR = 1.05, 95% CI: 1.01–1.09, p = 0.01).

Conclusion: The findings demonstrate that the study area supports a diverse mosquito fauna, with the primary Rift Valley fever virus (RVFV) vector, *Aedes mcintoshi*, predominating in the conservancy and exhibiting a marked shift in blood-feeding behavior from wildlife hosts in the conservancy to

humans in adjacent farmlands.

Keywords: Rift valley fever, seroprevalence, inter epidemic, pastoralist

Paper ID# 171

Title: Revisiting the epidemiological role of *Anopheles arabiensis*: host use, spatial patterns, and evidence for paradigm reappraisal from Tanzania

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Background: The findings demonstrate that the study area supports a diverse mosquito fauna, with the primary Rift Valley fever virus (RVFV) vector, *Aedes mcintoshi*, predominating in the conservancy and exhibiting a marked shift in blood-feeding behavior from wildlife hosts in the conservancy to humans in adjacent farmlands. *Anopheles arabiensis* is widely regarded as a primary malaria vector across Africa, but its contribution under contemporary ecological and intervention conditions remains uncertain. We present evidence from Tanzania suggesting that its independent epidemiological role may be more limited and context-dependent than established paradigms imply.

Methods: Data were drawn from a national entomological survey across 25 districts in Tanzania. Blood-meal analysis estimated human blood index (HBI) by trap type and livestock context. Primary-vector composition was assessed across transmission strata, and species distribution models compared predicted vector occurrence with malaria prevalence.

Results: *An. arabiensis* blood meals were predominantly bovine, with low overall HBI (28/834; 3.4%). HBI was higher in human-baited traps (8/16; 50.0%) and indoor aspirators (2/6; 33.3%) than in passive barrier screens (18/812; 2.2%) and was higher where livestock were absent (13/86; 15.1%) than present (15/748; 2.0%). Despite small numbers, blood-fed *An. funestus* and *An. gambiae* were predominantly human-fed. Districts where *An. arabiensis* occurred without other primary vectors were concentrated in very-low and low-transmission strata, whereas co-occurrence with *An. funestus* and/or *An. gambiae* aligned with higher-transmission districts. Species distribution models showed that predicted occurrence of *An. gambiae* and *An. funestus* broadly mirrored malaria prevalence, while *An. arabiensis* was widespread but showed little correspondence with prevalence.

Conclusions: The low human feeding observed here, together with spatial patterns, suggests that *An. arabiensis* may not consistently function as an independent dominant vector in Tanzania. Its epidemiological importance may be greatest where it occurs alongside *An. funestus* and *An. gambiae*, which may sustain more robust reservoirs. We recommend reassessment of its role in surveillance interpretation and vector control prioritization.

Keywords: *Anopheles arabiensis*; Human Blood Index; Tanzania; Malaria Vector Surveillance

Paper ID# 215

Title: Exploiting natural symbionts of the *Anopheles gambiae* complex to block *Plasmodium falciparum* development

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Introduction: The emergence and rapid spread of insecticide and antimalarial drug resistance are undermining malaria control efforts, underscoring the need for new control tools. One of the most promising strategies involves exploiting mosquito symbionts that inhibit parasite development.

Methods: This study assesses the ability of bacterium *Serratia* and *Pantoea* to inhibit the development of *Plasmodium falciparum* in *Anopheles gambiae*. Field-collected mosquitoes were morphologically identified and dissected to isolate organs. PCR detected bacterial genera, and their identity was confirmed by 16S rRNA sequencing. Laboratory-reared *Anopheles coluzzii* were co-infected with bacterial *Serratia* sp._Soumouso (S_Soum) or *Pantoea* sp._Bobo1 (P_Bobo) and *Plasmodium falciparum*.

Results: Molecular analysis of 783 *Anopheles gambiae* mosquitoes revealed prevalence rates of 13.3%, 22.0%, and 13.2% for the bacteria *Serratia* spp., *Pantoea* spp., and *Asaia* spp. Furthermore, studies on natural *Plasmodium falciparum* infections have shown that the strain S_Soum and P_Bobo and their co-inoculum significantly reduce both oocyst prevalence (91% and 77%) and sporozoite prevalence (72% and 74%) in mosquito vectors and extend the parasite's extrinsic incubation period.

Conclusion: These results confirm the inhibitory effect of the bacterial S_Soum and P_Bobo on the development of *Plasmodium falciparum*. Further semi-field studies are needed to support the integration of these symbionts into malaria control strategies in the face of increasing insecticide and antimalarial drug resistance.

Keywords: Malaria, *Serratia*, *Pantoea*, *Plasmodium*, *Anopheles*, Phylogenetic, West Africa.

Paper ID# 260

Title: Influence of ground marker shape on *Anopheles coluzzii* swarm spatial structure and flight kinematics: a 3D video-tracking study

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Background: Mating in *Anopheles* mosquitoes depends on swarming: males aggregate at dusk above visual ground markers and females enter to copulate. Ground markers anchor swarm location, but whether marker geometry influences swarm spatial structure and individual flight dynamics had not been quantified. We combined semi-field experiments with 3D infrared video-tracking to test how ground marker shape affects swarm organization and flight behavior in *Anopheles coluzzii*.

Methods: Five marker shapes of identical surface area (1 m²) were tested in four replicate trials at the Mosquito Ecology Research Facility (MERF, Bama, Burkina Faso), yielding 7,060 swarming trajectories across 20 sessions.

Results: Swarms formed above all marker shapes and centroid positions remained stable across shapes ($q > 0.3$), confirming that swarm localization is determined by marker presence rather than marker geometry. Mean flight speed, acceleration magnitude, and angular velocity showed overlapping distributions across shapes ($q = 0.75 - 0.92$), indicating that global flight kinematics were conserved regardless of marker shape. In contrast, marker geometry significantly influenced swarm horizontal dispersion ($q < 0.001$) and inter-saccade displacement along both horizontal axes ($q < 0.05$ and $q < 0.001$), with marker width along the N-S axis predicting swarm dispersion along that axis ($p < 0.01$, effect size = 0.226).

Conclusion: Visual ground cues shape swarm organization at two levels: marker presence determines swarm location, while marker width predicts inter-saccade displacement and swarm horizontal dispersion.

Keywords: *Anopheles coluzzii*, Mosquito swarming, Ground marker geometry, 3D video-tracking, Flight kinematics

Paper ID# 247

Title: Species-Specific Interactions Between Piperonyl Butoxide and Chlorfenapyr in *Anopheles gambiae* s.l. and *Anopheles funestus* s.l.

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Background: *Chlorfenapyr* (CFP) and piperonyl butoxide (PBO) insecticide-treated nets are deployed against pyrethroid-resistant malaria vectors. Their interaction is biologically complex: CFP is a pro-insecticide requiring oxidative activation by CYP450s, while PBO inhibits these enzymes. This study assessed PBO pre-exposure effects on CFP susceptibility in wild *Anopheles gambiae s.l.* and *Anopheles funestus s.l.* in Tiébissou, central Côte d'Ivoire.

Methods: Mosquitoes were collected from six villages in 2023 and 2024 following LLIN distribution. CFP susceptibility was assessed using a diagnostic dose (100 µg/bottle) and a lower dose (10 µg/bottle) with or without 4% PBO pre-exposure via CDC bottle bioassays. Mortality was recorded at 72 h post-exposure and compared using Fisher's exact tests.

Results: All *An. gambiae s.l.* and *An. funestus s.l.* populations were susceptible to the diagnostic CFP dose. Lower-dose assays revealed marked variation across species, sites, and time periods. PBO pre-exposure increased CFP-induced mortality in *An. funestus* across multiple sites and collection periods, indicating synergism. In *An. gambiae s.l.*, responses were heterogeneous, ranging from no detectable effect to partial synergism, with no antagonistic effects observed.

Conclusion: PBO–CFP interactions were species, sites, and period-dependent. No antagonistic effect was detected in either species. PBO produced synergism in *An. funestus*, whereas *An. gambiae s.l.* showed variable responses. All populations remained susceptible to the diagnostic CFP dose, supporting the co-deployment of PBO-based and CFP-based insecticide-treated nets for malaria vector control.

Keywords: *Anopheles gambiae*; *Anopheles funestus*; Chlorfenapyr; Piperonyl butoxide (PBO); Metabolic resistance; Vector control

Paper ID# 33

Title: Spatial heterogeneity in anopheles vector diversity, Plasmodium falciparum infection rates, and symbiont prevalence in eight Cameroonian villages: insights for targeted malaria control

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Background: Malaria transmission in Cameroon shows spatial variability due to diverse anopheles vectors. This study aimed to characterize species composition, *plasmodium falciparum* infection

rates, and symbiont (*Wolbachia*, *Microsporidia*) presence across eight sites to inform targeted control.

Methods: A total of 6033 *Anopheles* mosquitoes were collected from eight sites using human landing catch (HLC, n=5724) and CDC light traps (n=309), plus 391 *Mansonia* spp. And 2203 *Culex* spp. species identification used morphology, Wilkins PCR-ID (n=316), and Minion Sequencing (n=266, Hotshot DNA extraction). *P. falciparum* was detected by CSP Elisa (n=5131) and qPCR (n=266). *Wolbachia* sp. And *microsporidia* were screened by PCR-gel electrophoresis (n=266).

Results: *Anopheles gambiae* s.l. dominated (5009, 83%), followed by *A. pharoensis* (709), *A. ziemanni* (117), and minor species. Wilkins PCR-ID revealed *A. gambiae* s.s. predominant, with *A. coluzzii* (76), *A. arabiensis* (11), and *A. funestus* s.s. (30). Minion sequencing (n=266) explicitly confirmed: *A. gambiae* s.s., *A. coluzzii* and *A. arabiensis* in Ngong, *A. coluzzii* in Tibati, *A. funestus* in Esse, Kekem and Tibati, *A. pharoensis* in Yangha, Tibati and Mbe, and others in low density. CSP Elisa detected 126 *P. falciparum* positives (2.5%): 80 *gambiae* (Esse), 37 (Belabo): 36 *gambiae*, 1 *funestus*, 5 *gambiae* (Maka), 2 (Tibati: 1 *funestus*, 1 *gambiae*), 2 (yangha: 1 *gambiae*, 1 *pharoensis*). QPCR confirmed 19 positives (7.1%), mainly *A. funestus* in Esse/Kekem. *Wolbachia* infected 23/266 (8.6%); *microsporidia* 45/266 (16.9%) was mainly found in *A. gambiae*.

Conclusion: *A. gambiae* s.l. was found more infected, with localized *A. funestus* contributions and rare *A. pharoensis* involvement. Minion revealed finer diversity. Moderate infection rates and symbiont prevalence suggest potential for innovative, site-specific interventions (e.g., *Wolbachia*-based) in Cameroon.

Keywords: Vector Diversity, Heterogeneity, *Plasmodium* Infection, Malaria Control, Vector Surveillance

Paper ID# 103

Title: Understanding malaria vector dynamics and transmission in Pouth-Kelle Community, Nyong et Kelle Division, Centre Cameroon

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Background: Malaria remains a major public health concern in tropical regions, sustained by multiple vector species with diverse traits. In transitional zones like the forested Pouth-Kelle community, vector dynamics are poorly characterized. This study aimed to detail *Anopheles* species composition, biting behaviour, and malaria transmission indicators to guide control strategies.

Methods: From February 2021 to January 2022, adult mosquitoes were collected indoors and outdoors in three houses via human landing catches over two consecutive nights monthly.

Morphological and molecular methods identify species. Entomological indicators and ELISA tests for *Plasmodium falciparum* circumsporozoite proteins assessed infection rates. Concurrently, 107 residents were screened for malaria by microscopy. Associations between variables (sex, age) and malaria infection were evaluated using bivariate analysis with the Chi-square test

Results: Among 790 *Anopheles* collected, 64.7% were *An. gambiae* s.l. (98% *An. gambiae*, 2% *An. coluzzii*), followed by *An. nili* (20%), *An. funestus* (15.2%), and *An. paludis* (0.1%). Outdoor and indoor biting rates for *An. gambiae* s.l. were similar (~6.8 b/p/n). Infection rates were higher indoors for *An. gambiae* s.l. (11.3% vs. 6.48%, $p=0.039$); other species had similar indoor/outdoor rates. Entomological inoculation rates were higher indoors for *An. gambiae* s.l. (0.75 vs. 0.45 ib/p/n). Malaria prevalence was 30.8%, with no sex differences but decreased with age; children <10 years had 28.5 times higher odds than adults 30–40 years.

Conclusion: Malaria transmission in Pouth-Kelle is maintained by multiple *Anopheles* species with varying biting and infection patterns indoors and outdoors. Higher indoor infection rates support indoor control, but outdoor transmission requires integrated vector management, prioritizing vulnerable children.

Keywords: Anopheline dynamics - Vector behaviour - Malaria transmission - Pouth-Kelle Community – Cameroon

Paper ID# 153

Title: Detection of the desert malaria vector *Anopheles gambiae* with high vectorial capacity for malaria parasites in the dryland ecosystem of Kenya

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Introduction: In Kenya, parts of the dryland ecosystems have disproportionately witnessed a surge in malaria burden amidst poor understanding of the entomologic risk factors.

Methods: Wild female *Anopheles* mosquitoes were sampled using CDC light traps in a village in the arid Marigat subcounty, Baringo County of the Kenyan Rift Valley. A subset of the samples was processed by PCR and sequencing for species identification, malaria parasite infection, and host meal sources. In addition, cone bioassay was used to assess efficacy of single and dual-ingredient insecticide-treated nets on the mosquito population.

Results: The data revealed the presence of *Anopheles sergentii* and found to exhibit high *Plasmodium falciparum* sporozoite infection rates (8.9%), yet zoophagic tendency. Despite high exophilic tendencies, the mosquito displayed strong resistance phenotypes based on low-moderate mortalities (8-55%) induced by new generation PBO- and pyriproxyfen (PPF)-based nets to a population of the species.

Conclusion: The data provide evidence incriminating *An. sergentii* as a potential malaria vector beyond its historical record in Kenya. The results underscore the need for mainstream molecular analysis into routine malaria surveillance activities. In addition, the reduced efficacy of dual ingredient nets against *An. sergentii* could present a challenge to their future deployment in the region, including outdoor control tools with similar active ingredients.

Keywords: Malaria surveillance, insecticide resistance, bednet efficacy, novel vectors, dryland ecosystems

Paper ID# 108

Title: Genomic surveillance of Trehalose-6-Phosphate Synthase in *Anopheles gambiae*: A promising target for Next-Generation insecticides

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Background: The increasing prevalence of insecticide resistance in *Anopheles gambiae* threatens malaria control efforts across Africa, highlighting the need for novel molecular targets. Trehalose-6-phosphate synthase (TPS), a key enzyme in trehalose biosynthesis, is essential for survival and development and is absent in humans, making it a promising insecticide target. Its genetic variability and evolutionary stability in natural populations remain unclear.

Methods: We analysed whole-genome sequence data from the Ag1000G Phase 3.0 dataset, comprising populations of the *Anopheles gambiae* complex from 19 African countries. The SNPs and amino acid changes allele frequencies, nucleotide diversity, and Tajima's D were analysed using malariagen data toolkit. Analyses focused on non-synonymous variants with allele frequency ≥ 0.05 in at least one cohort. Linkage disequilibrium was assessed using Lewontin's D' method. Functional impacts were predicted using SIFT and PROVEAN.

Results: A total of 4590 variants were identified in TPS, including 459 non-synonymous mutations, of which 19 occurred at appreciable frequencies. These variants were found to be generally rare, geographically restricted and species-specific, and to have no mutations shared across all species. LD analysis showed that the variants were either in complete linkage or not linked. Functional

predictions identified 32% of variants as deleterious, with high-confidence mutations restricted to *Anopheles* pwani populations in Tanzania. Low nucleotide diversity ($\pi < 0.01$) and predominantly negative Tajima's D indicate strong purifying selection and functional constraint.

Conclusion: TPS showed low genetic diversity, limited functional variation, and strong signatures of purifying selection across the *Anopheles gambiae* complex. These suggest that TPS represents a genetically stable molecular target for vector control interventions, although further functional and experimental studies are required to validate it.

Keywords: *Anopheles gambiae*, Trehalose-6-phosphate synthase (TPS), Genomic surveillance, Insecticide target, Population genetics

Scientific Session 8: Parasite tracking and Genomics

Paper ID# 90

Title: Computational identification of DsiRNA candidates targeting arginase in *Anopheles gambiae* for RNAi-based vector control

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Background: The rapid increase of insecticide resistance in *Anopheles gambiae* threatens current malaria control efforts and highlights the need for new control methods. RNA interference (RNAi) offers a targeted and environmentally sustainable alternative. Arginase, a key regulator of nitrogen metabolism, is important for mosquito immunity and parasite development, representing a promising molecular target. This study used computational modeling to identify effective Dicer-substrate small interfering RNAs (DsiRNAs) for arginase silencing.

Methods: DsiRNAs targeting the arginase gene were designed using Integrated DNA Technologies (IDT) and screened based on GC content, thermodynamic properties, secondary structure, and off-target potential. Binding affinity to target mRNA was also evaluated, and melting temperatures were determined. The derived 21-mer guide strand siRNA was used for molecular docking with *Anopheles gambiae* Argonaute-2 (Ago2) using a validated homology model (HDOCK). The stability of the top-ranked complex was further assessed using 100 ns molecular dynamics simulations.

Results: Eight DsiRNAs met all selection criteria, with optimal GC content (37–51.9%) and strong binding affinities (–43.4 to –52.2 kcal/mol). Docking analysis identified DsiRNA8, DsiRNA6, and DsiRNA1 as top candidates, showing favorable binding energies and interactions within key Ago2 domains (PAZ and MID). Molecular dynamics simulations of the Ago2–DsiRNA6 complex confirmed structural stability, with stable RMSD, stable hydrogen bonding, and maintained compactness

throughout the simulation period.

Conclusion: This study identifies DsiRNA6, DsiRNA8, and DsiRNA1 as robust candidates for silencing of arginase in *Anopheles gambiae*. The findings demonstrate the potential of RNAi-based strategies as innovative vector control methods and provide a foundation for experimental validation to confirm gene knockdown efficiency and applicability in malaria control.

Keywords: RNA interference, DsiRNA, *Anopheles gambiae*, Arginase, Mosquito control, Computational modelling

Paper ID# 81

Title: Spatial distribution of 2La, 2Rb, and 2Rc chromosomal inversion polymorphisms in *Anopheles gambiae*.I. mosquitoes in Ghana

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Background: *Anopheles* mosquitoes are rapidly adapting to heterogeneous environments through chromosomal inversions. Vector populations harbouring advantageous inversion combinations can spread and persist under multiple environmental conditions, contributing disproportionately and cryptically to sustained malaria transmission. However, little is known about current inversion distribution patterns, limiting the design of adaptive control strategies. This study investigated the spatial distribution of inversion polymorphisms (2La, 2Rb, 2Rc) across Ghana.

Methods: *Anopheles* immatures were sampled from breeding habitats, and resting adults were sampled in and around human habitations using Prokopack aspirations. Adult samples were speciated and karyotyped using PCR to determine inversion distributions in the Coastal savannah, Forest and Guinea-savannah ecological landscapes of Ghana.

Results: A high number of *An. Coluzzi* was sampled in the Guinea-savannah [2La/2La (53.33%, 112/210), 2La/2L+a (30%, 63/210)] and Coastal [2La/2La (30%, 60/200), 2La/2L+a (31%, 62/200)] landscape had inverted 2La karyotypes, probably to adapt and survive the warmer environmental conditions. The 2Rb inversion was observed in 76.67% (69/90) of *An. gambiae* s.s sampled in the Forest landscape, reflecting adaptation to local environmental conditions. All *An. gambiae* s.s. sampled in the highlands had either the 2Rb/2Rb (68%, 51/75) or 2Rb/2Rb+ (32%, 24/75) karyotype, likely reflecting adaptation to desiccation stress associated with reduced humidity in highland environments. In the Coastal landscape, 47.59% (69/145) of the *An. coluzzii* sampled

were 2Rc/2R+c heterozygotes.

Conclusion: Study findings show a high number of *An. gambiae*.l. in Ghana had inverted 2La, 2Rb, and 2Rc chromosomes as adaptive response to unfavorable conditions, likely aiding their survival and proliferation. Integrating inversion monitoring into routine vector surveillance could inform adaptive malaria control strategies.

Keywords: *Anopheles gambiae* s.l. 2La, 2Rb, 2Rc, Adaptation

Paper ID# 161

Title: Genetic Structure and Diversity of *Anopheles gambiae* s.l. Populations: Mechanisms Involved in Insecticide Resistance

Moussa Diop^{1,*}, Ndeye Seny Diagne¹, Mame Fatou Tall¹, Abdoulaye Niang¹, El Hadji Amadou Niang¹

Background: *Anopheles gambiae* complex species are among the main malaria vectors in West Africa, exhibiting great phenotypic and genotypic diversity. Genetic structure and diversity of *An. gambiae* s.l. populations and complexity of mechanisms involved in population evolution remain unclear. This study aims to determine genetic structure and diversity of *An. gambiae* s.l. populations and mechanisms involved in insecticide resistance.

Methods: Indoor and outdoor resting mosquitoes were collected using Pyrethrum Spray Catches and Prokopack aspirators, respectively, from July 2020 to September 2022 in Djicomol, Cadjinolle and Wendaye sites in Senegal. Amplicon sequencing was performed to identify samples using the ANOSPP panel, and whole genome sequencing (WGS) was carried out.

Results: A total of 269 *An. gambiae* s.l. specimens were identified by ANOSPP, *An. gambiae* s.s. and hybrid *An. gambiae/An. coluzzii* were the most common species with 38.29% and 40.89%, respectively. WGS revealed a new taxon (Bissau) in *An. gambiae* complex with 80% on 15 specimens sequenced. Principal component analysis does not show a homogeneous group of *An. gambiae* s.l. populations. Pairwise *F_{st}* showed that there was little genetic differentiation between Bissau molecular form and *An. coluzzii* (0.0128), whereas there was significant genetic differentiation between Bissau molecular form and *An. melas* (0.6693). Genetic diversity showed that nucleotide diversity is low between these species, with a positive Tajima D indicating that the population is in equilibrium. Insecticide resistance genes L995F, Ace-1, Rdl and Gste2 were detected in Bissau molecular form.

Conclusion: These findings highlighted the existence of a new molecular form in the *An. gambiae* complex genetically different from other species and showed the presence of insecticide resistance genes. Genomic surveillance of malaria vectors is essential to understanding genetic variations in

natural vector populations and to guide implementation of new innovative vector control tools.

Keywords: *Anopheles gambiae s.l.*, Genetic Structure, Diversity, Insecticide, Mechanisms, Resistance

Paper ID# 144

Title: Divided by the Rift: Genomic diversity of key malaria vectors in East and Southern Africa.

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Background: The Great Rift Valley has long been hypothesized as a major biogeographical barrier, restricting gene flow between *Anopheles* mosquito populations across East and Southern Africa. Identifying the precise drivers of population isolation is important for malaria vector control as it can impact the efficacy of conventional (LLINs, IRS) and next-generation (genetically modified organisms) intervention strategies. This study employed a landscape genetics framework using whole genome sequence (WGS) data generated in association with MalariaGEN.

Methods: Fine-scale genetic variation was first quantified by identifying biallelic single-nucleotide polymorphisms (SNPs). Population structure was characterized using Principal Component Analysis (PCA) and Bayesian clustering (ADMIXTURE analysis) to visualize broad genetic groups. To measure the degree of isolation between populations, pairwise fixation indices and genomic distances were calculated. To test the "barrier" effect of the Rift Valley versus other factors, the landscape was converted into resistance surfaces with spatial grids where each cell was assigned a cost value based on its hypothesized resistance to mosquito movement. Multiple models representing different hypotheses were then developed, validated, and tested. The fit of each model was used to determine whether the Rift Valley is the primary driver of genetic isolation or if gene flow is more significantly constrained by climatic and human-driven environmental factors.

Results: In general, the population structured in both *An. gambiae s.l.* and *An. funestus s.l.* in the region was best explained with respect to the Great Rift Valley. However, there was unique population cluster of *An. funestus s.l.* in Malawi which wasn't explained by its location with respect to the Rift and in south-eastern Tanzania where the population was highly inbred.

Conclusion: This preliminary analysis of gene flow across the region will, we hope, help to inform regional implementation of vector control tools.

Keywords: Gene flow, landscape genetics, *Anopheles funestus*, Insecticide resistance

Paper ID# 76

Title: Genetic surveillance of target site mutations and copy number variants associated with the escalating insecticide resistance in *Anopheles gambiae* (s.l.) in Ghana

Anisa Abdulai^{1,*}, Isaac Kwame Sraku¹, Christopher Mfum Owusu-Asenso¹, Yaw Akuamoah-Boateng¹, Abdul Rahim Mohammed Sabtiu¹, Fred Aboagye-Antwi¹, Patrick F. Ayeh-Kumi¹, Yaw Asare Afrane¹

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Background: Insecticide resistance in malaria vectors threatens control efforts, as increased insecticide use selects for resistance alleles, making it crucial to understand their genetic basis in local *Anopheles* populations. This study characterized target-site resistance mutations and copy number variants (CNVs) in *Anopheles gambiae* s.l. from nine sites with varying interventions and ecological settings in Ghana.

Methods: Study site included indoor residual spraying (IRS) locations (Kpalsogu, Obuasi), pyrethroid-PBO net sites (Tolon, Kade), chlorfenapyr net sites (Takoradi, Elubo), and standard pyrethroid LLIN sites (Ada, Konongo, Libga) across Ghana's ecological zones. Larvae were collected, reared, and tested using WHO susceptibility bioassays for pyrethroids and organophosphates. Resistance markers (L995F/S, N1570Y, V402L, I1527T, Ace1 G280S) were genotyped using TaqMan PCR, while Ace-1 and carboxylesterase duplications were assessed by PCR.

Results: WHO bioassays revealed moderate-to-high pyrethroid resistance (4–65%) at all sites. Obuasi (IRS) showed higher organophosphate resistance (1.7%) compared to other sites. The L995F kdr mutation was strongly associated with pyrethroid resistance ($P < 0.05$) and occurred at high frequencies (0.82–1.0) in IRS and standard LLIN sites. Other kdr variants (L995S, N1570Y, I1527T, V402L) appeared at variable frequencies (0–0.59). The Ace-1 G280S mutation was significantly associated with pirimiphos-methyl resistance ($OR=2.20$, $P<0.001$). Ace-1 gene duplications occurred in 22.8% of mosquitoes, predominantly in individuals carrying the G280S resistance allele ($P<0.001$). Carboxylesterase CNVs were also identified, with Coexf_Dup1 (30.4%) significantly associated with pirimiphos-methyl resistance ($OR = 1.68$, $P = 0.02$).

Conclusion: These findings reveal that target-site mutations and CNVs are widespread in *An. gambiae* s.l. across Ghana, indicating that multiple mechanisms may be driving insecticide resistance in malaria vectors.

Keywords: Insecticide resistance, *Anopheles gambiae* s.l, malaria, Ghana

Paper ID# 176

Title: Male Mating Competitiveness of the MMCP Mosquito Line in Laboratory Cage Competition Assays

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Background: Male mating competitiveness is a critical fitness parameter for evaluating the potential performance of genetically modified mosquito strains intended for vector control. This study assessed the mating competition ability of the genetically modified mosquito line MMCP in comparison with wild-type mosquitoes under controlled insectary conditions.

Methods: Mating competition experiments were conducted using cage assays in which MMCP and wild-type males competed for wild-type virgin females at defined ratios. Each replicate cage contained a fixed number of 100 virgin wild-type females, exposed to a total of 100 males under three experimental treatments: 1:1 ratio (50 MMCP: 50 wild-type males), 3:1 ratio (75 MMCP: 25 wild-type males), and 1:3 ratios (25 MMCP: 75 wild-type males). A control group containing 100 wild-type males and 100 wild-type females was included to confirm normal mating performance. Mosquitoes were allowed to mate for 72 hours (3 nights) under standard insectary conditions. After the mating period, females were collected and processed to assess insemination status, and progeny were subsequently analyzed by genotyping to determine paternity.

Results: Preliminary findings show that mating was successfully achieved in all experimental groups, with observable differences in mating performance between MMCP and wild-type males across the tested competition ratios. Laboratory analyses and progeny screening are currently underway to determine paternity and quantify the relative mating competitiveness of MMCP males.

Conclusions: The results will generate comparative competitiveness estimates and provide essential evidence to support fitness evaluation and biosafety assessment of the MMCP line.

Keywords: mating competition, male competitiveness, MMCP, wild-type, gene drive mosquitoes, fitness evaluation, cage assays

Paper ID# 197

Title: Genomic signatures of selection in *Anopheles funestus* reveal shared and population-specific adaptive variation across African populations

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Background: Insecticide resistance in *Anopheles funestus* threatens malaria control across Africa.

While metabolic resistance is well characterized, broader genomic signatures of selection may reveal both known and previously uncharacterized mechanisms of resistance and adaptation across structured populations.

Methods: We analyzed whole-genome sequence data from 635 *An. funestus* from West (Senegal, Guinea, Nigeria), Central (Cameroon), and East Africa (Kenya). Population structure was assessed using PCA, neighbour-joining trees, and pairwise *F*_{ST}. Selection scans used H12, with candidate variants prioritized using iSAFE. Selective regions were further explored through diplotype clustering and CNV analysis.

Results: We observed strong differentiation between East and West/Central Africa, with sub-structure within West Africa. A major sweep on chromosome arm 2RL overlapped a cytochrome P450 cluster, where non-synonymous variants in CYP6A14 were shared across West and Central populations at near fixation. Within this sweep, octopamine receptor genes showed signals restricted to Guinea and Nigeria, indicating localized adaptation within a shared genetic background. A second signal on 3RL encompassed the gamma-aminobutyric acid (GABA) receptor locus. In both regions, variants occurred in extended haplotypes of reduced heterozygosity, consistent with recent positive selection. CNVs affecting detoxification genes within the 2RL sweep further supported structural adaptation. Metabolic signals were broadly shared, whereas neuromodulatory signals were spatially restricted.

Conclusion: Adaptive evolution in *An. funestus* reflects both shared and local processes. While widespread selection on detoxification pathways indicates common pressures, localized signals in neuromodulatory loci, including GABA and octopamine genes, suggest additional adaptive responses. This highlights the value of whole-genome approaches for detecting shared and uncharacterized adaptation.

Keywords: *Anopheles funestus*, Genome-wide selection scans, Adaptive evolution, Neuromodulation, Vector control

Paper ID# 89

Title: A targeted nanopore amplicon sequencing panel for simultaneous identification of six *Anopheles* species and Plasmodium detection

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Background: Malaria vector surveillance is constrained by low-throughput, labor-intensive methods requiring multiple assays for *Anopheles* species ID and Plasmodium detection. Although amplicon sequencing (ANOSPP panel) enables multiplex species ID and parasite detection, reliance on short targets and centralized platforms limits uses in resource-limited settings. This highlights sequencing enabling rapid, accurate vector, and parasite detection in a single workflow.

Methods: We developed a multiplex nanopore amplicon sequencing panel targeting ten loci across six *Anopheles* species (*An. gambiae*s.s., *An. arabiensis*, *An. coluzzii*, *An. funestus*, *An. coustani*, *An. stephensi*) and a Plasmodium 18S rRNA marker, selected through multiple sequence alignment. Amplicons were optimized for Oxford Nanopore MinION long-read sequencing. Taxonomic classification was performed using Kraken2 and Bracken. The panel was evaluated on 480 Kenyan mosquito samples (80 per species).

Results: High concordance with reference identification was seen with clear species clustering and minimal cross-assignment. Sensitivity and specificity exceeded 90% for *An. arabiensis*, *An. funestus*, and *An. stephensi*, while *An. gambiae* also performed strongly with slightly lower specificity. Lower sensitivity was observed for *An. coluzzii* (62%) and *An. coustani* (43%), though specificity remained high. Long-read sequencing improved discrimination within species complexes. The Plasmodium 18S marker enables detection of Plasmodium; primers are still being optimized.

Conclusion: This nanopore approach integrates vector species identification and parasite detection into a single workflow, reducing cost, time, and labor while increasing throughput. Its portability supports use in endemic settings, showing potential as a scalable tool for improved malaria surveillance. Further optimization is required to improve the resolution of *An. coluzzii*, *An. Coustani*, and plasmodium detection.

Keywords: Nanopore sequencing; *Anopheles* species identification; Plasmodium detection; malaria vector surveillance; multiplex amplicon

Paper ID# 16

Title: Cis-regulatory elements and allelic variation in the arginosuccinate lyase gene exacerbates pyrethroid resistance in the major African vectors *Anopheles funestus*

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Background: Deciphering the genetic drivers mechanisms of escalated pyrethroid resistance in mosquitoes is paramount to mitigating resistance impact on malaria control. Understanding the molecular and physiological mechanisms underlying this resistance therefore remains a priority in order to guide the development of sustainable management tools. This research aimed to determine the involvement of arginosuccinate lyase (ASL) in insecticide resistance escalation in *Anopheles funestus*, combining different transcriptomic and functional validation approaches.

Methods: This included (i) phenotypic and molecular characterization (biological insecticide tests, qPCR, PCR, and cloning); (ii) detection of gene polymorphisms associated with resistance and (iii) in vivo functional validation through transgenic expression in *Drosophila melanogaster* and RNA interference (RNAi) in *Anopheles funestus* collected in Mibellon, Cameroon.

Results: Multi-omics analyses revealed ASL upregulation Africa wide with a significant overexpression in Uganda resistant to permethrin compared to the control population and detected a strong signal of genetic differentiation around ASL in resistant populations, exhibiting copy number variation (CNV). Predominant haplotypes harboring T-277A promoter mutation and/or R125H mutation in the ASL protein coding region were detected in resistant mosquitoes to permethrin. Transgenic expression of ASL and RNAi confirms its ability to confer pyrethroid resistance. A T-277A-ASL DNA-based assay confirmed its association with resistance escalation, revealing a marked temporal increase in Uganda (2010-2023) but with a drastic reduction in 2024 after deployment of chlorfenapyr-based bed nets.

Conclusion: This study elucidates a novel resistance pathway driven by ASL highlighting the decisive role of ASL and introducing a new DNA-based diagnostic tool to monitor its spread and impact in Africa.

Keywords: Malaria, insecticide resistance, *Anopheles funestus* s.s, arginosuccinate lyase, overexpression, allelic variation

Scientific Session 9: Emerging & Invasive Vectors

Paper ID# 49

Title: First field characterization of *Aedes aegypti* swarming behavior in Burkina Faso

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Background: *Aedes aegypti* is a major vector of arboviruses, yet its mating behaviour in natural environments remains poorly understood. Unlike *Anopheles* mosquitoes, for which swarming is well documented, evidence of swarming in *Ae. aegypti* has largely been limited to laboratory and semi-field studies. Understanding its mating system is critical for optimizing male-based vector control strategies.

Methods: Field observations were conducted in Bobo-Dioulasso, Burkina Faso, to characterize swarming behaviour under natural conditions. A total of 96 swarm events were monitored across June and July. Swarm structure, timing, height, size, and mating activity were recorded, and derived metrics such as mating rate and coupling success were analyzed using descriptive statistics and regression models.

Results: Swarms consistently formed at low altitude (0.15–0.35 m) above ground-level visual markers, indicating marker-dependent aggregation. Three behavioral phases were identified: stable formation under calm conditions, compression under wind disturbance, and post-copula ascent of mating pairs (1.5 m). Swarm size ranged from 50 to 500 males and was significantly larger in July than June, while duration (130 min) remained stable. Swarms produced an average of 33 couples, including 25 true copulations. Swarm size positively predicted mating output, but mating efficiency declined with increasing density due to male–male interference.

Conclusion: *Aedes aegypti* forms structured, reproductively active swarms in natural environments, shaped by microclimatic conditions and density-dependent dynamics. These findings provide the first field-based framework for understanding *Ae. aegypti* mating ecology and have important implications for improving male-based vector control strategies such as SIT, Wolbachia, and gene drive approaches.

Keywords: *Aedes aegypti*; swarming behavior; mating ecology; density dependence; vector control; Burkina Faso

Paper ID# 68

Title: Human mobility pathways and the spread of *Anopheles stephensi*: insights from participatory mapping in a high mobility border setting in northern Kenya

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Background: The rapid expansion of *Anopheles stephensi* across Africa threatens malaria control due to its adaptability to urban environments and potential for human-mediated dispersal. While spreading transport corridors is documented, underlying mobility processes remain poorly understood. Nested within the AnoSTEP-Afrika study, this study examined how human mobility shapes vector dispersal and exposure risk in a high-mobility border setting in northern Kenya.

Methods: A retrospective qualitative study using participatory mapping and focus group discussions was conducted in Illeret, Marsabit County, along the Kenya–Ethiopia border. Pastoralists, traders/truck drivers, and mobile women (n=30) mapped routes, stopovers, and movement drivers. Discussions explored water use and mosquito exposure. Maps were digitized to reconstruct pathways. Spatial overlay identified convergence points, and thematic analysis captured risk patterns.

Results: Mobility was structured and repetitive, including seasonal pastoralist circuits driven by water and pasture search, National trade corridors transporting goods from Kenya-Ethiopia to Kenya-Uganda borders, and frequent women local and cross-border movements. Convergence points, Lake Turkana shores, fish camps, trade hubs, and border towns emerged as key nodes with water access, overnight stays, and increased exposure. Participants reported mosquito biting at these sites and during transit. These nodes likely facilitate passive vector exposure and dispersal via movement of people, water and goods, with risk concentrated along mobility pathways.

Conclusions: Mobility pathways and convergence nodes are critical but under-addressed sites for vector exposure and dispersal. Targeting them with mobility-informed surveillance and interventions offers a strategic opportunity to reduce transmission and limit the spread of *An. stephensi*. Participatory mapping provides a scalable approach for identifying dynamic risk landscapes in mobile populations.

Keywords: *Anopheles stephensi*, Human mobility, Vector dispersal, Malaria transmission, Participatory mapping, vector surveillance

Paper ID# 132

Title: Insecticide susceptibility status of populations of an invasive vector *Anopheles stephensi* to novel chemical insecticides and an insect growth regulator from Eastern Ethiopia

Ephrem Ejigu 1*

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Background: The presence of the invasive malaria vector *Anopheles stephensi* has been confirmed in urban, peri-urban, and rural areas of Ethiopia. Recent studies also show resistance to pyrethroids, carbamates, and organophosphates. This study assessed the susceptibility of *An. stephensi* to candidate insecticide (broflanilide, clothianidin, chlorfenapyr) for indoor residual spraying (IRS) and the insect growth regulator pyriproxyfen for larval control in eastern Ethiopia.

Methods: WHO bottle bioassays were conducted using adults reared from field-collected larvae. Bottles were treated with diagnostic doses: broflanilide (9 µg), clothianidin (10 µg), chlorfenapyr (100 µg), and pyriproxyfen (100 µg). Solvent controls were included. Mortality was recorded at 24 hours for all insecticides and extended to 72 hours for chlorfenapyr and pyriproxyfen. Pyriproxyfen effects on oviposition were assessed four days after exposure.

Results: Mortality at 24 hours was 100% for broflanilide and clothianidin. Chlorfenapyr caused 66% mortality at 24 hours and delayed mortality 100% at 48 hours, indicating high susceptibility. Pyriproxyfen effectiveness was assessed through oviposition inhibition rather than adult mortality. As a result, pyriproxyfen showed low mortality (0–15% by 72 hours) but completely inhibited oviposition (100%), while controls showed normal egg-laying.

Conclusion: *An. stephensi* populations were fully susceptible to the tested insecticides (although chlorfenapyr mortality reached 100% only after delayed observation at 48 hours), and pyriproxyfen effectively blocked reproduction. These products show strong potential for IRS and larval control. Further studies on residual efficacy in different settings are recommended.

Keywords: Insecticide susceptibility, *Anopheles stephensi*, chemical insecticides, insect growth regulator, Ethiopia

Paper ID# 231

Title: Transcriptomic signatures of high-intensity pyrethroid resistance in *Anopheles gambiae* from a Cameroonian agricultural hotspot

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Background: Pyrethroid resistance threatens malaria vector control across Africa, yet the mechanisms underlying extreme resistance in *Anopheles gambiae* remain unclear.

Methods: We investigated transcriptomic responses, allele frequency shifts, and selection signatures linked to high permethrin resistance in *An. gambiae* from Mangoum, Cameroon.

Results: RNA seq analyses showed strong overexpression of detoxification genes in both unexposed and exposed mosquitoes. UGT308G1 displayed the highest expression (FC = 105.1; 50.8). The CYP6Z cluster was markedly upregulated, including CYP6Z3 (FC = 68.8; 41.4), CYP6Z2 (29.0; 17.2), and CYP6Z1 (12.3; 6.0). Other genes such as CYP9K1, CYP6M2, and CYP4G17 were also elevated.

Increasing permethrin doses (1×–10×) enhanced oxidative stress, mitochondrial, and translational pathways. Population genetic analyses revealed strong selective sweeps at VGSC and the rp1 region. High-frequency nonsynonymous variants in CYP6AA1, CYP6AA2, CYP6P1, and Glu205Asp CYP6P3 were nearly fixed in field populations but absent in susceptible strains, indicating strong selection. Additional variants in CYP12F2, UGT49A3, UGT308A2, and ABCA2 further discriminated against resistant backgrounds. RNAi silencing of CYP6Z1–Z4 significantly increased mortality under pyrethroid exposure, confirming their functional role.

Conclusion: These results indicate that resistance intensity arises from combined target sites and metabolic mechanisms, with the CYP6Z cluster playing a central role, and highlights the value of integrating metabolic markers into resistance surveillance.

Keywords: *Anopheles gambiae*; malaria; pyrethroids; resistance escalation; transcriptomic analysis; CYP6Z genes

Paper ID# 121

Title: Does feeding on the invasive weed *Parthenium hysterophorus* alter insecticide susceptibility and detoxication gene expression in *Aedes aegypti* and *Anopheles arabiensis*?

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Background: Plant feeding is common biological behavior among mosquito vectors. Although

Parthenium hysterophorus is an invasive and toxic plant, mosquitoes readily feed it. Detoxification of its secondary metabolites may involve metabolic pathways similar to those responsible for insecticide detoxification. This study investigated whether pre-exposure to *P. hysterophorus* through sugar feeding alters pyrethroid susceptibility and the expression of detoxification genes in *Aedes aegypti* and *Anopheles arabiensis*.

Methods: Crude methanolic leaf and flower extracts of *P. hysterophorus* were prepared using Soxhlet extraction. Extract concentrations were dissolved in DMSO and mixed with 10% glucose solution before being offered to adult female mosquitoes. Mosquitoes were then exposed to permethrin and deltamethrin using WHO tube susceptibility tests. Three biological replicates of 25 mosquitoes were tested per insecticide and treatment. Mortality data were analyzed using generalized linear models. Expression of CYP9J26, CCEae3a, and GSTD4, with RPL8 as the reference gene, was quantified by RT-qPCR.

Results: Compared to the control group, mosquitoes fed with *P. hysterophorus* leaf extracts exhibited significantly lower mortality following insecticide exposure, while flower extracts did not differ significantly from the control. RT-qPCR analysis revealed differential expressions of CYP9J26, CCEae3a, and GSTD4, indicating that feeding on *P. hysterophorus* influenced metabolic detoxification pathways.

Conclusion: Feeding on *Parthenium hysterophorus* altered mosquito responses to pyrethroid exposure and was associated with changes in the expression of metabolic detoxification genes. These findings suggest that the toxic effects of *P. hysterophorus* and the associated detoxification response may influence mosquito susceptibility to insecticides, warranting further investigation over successive mosquito generations.

Keywords: *Parthenium hysterophorus*; *Aedes aegypti*; *Anopheles arabiensis*; pyrethroid susceptibility; detoxification genes; Kenya.

Paper ID# 258

Title: Surveillance of the invasive *anopheles stephensi* and other mosquito vectors in Kenya

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Background: The aggressive expansion of the invasive *Anopheles stephensi* in Kenya, from Marsabit, Turkana and Kisumu to the rest of the country, is concerning. The spread of this species threatens to

undermine the vector control efforts in the country. To inform targeted control, we conducted a comprehensive assessment of adult mosquitoes in 3 counties in Kenya with diverse malaria transmission profiles. Here, we report the findings of an entomological survey for this species and other mosquito vectors using both morphological and molecular methods for species identification.

Methods: Adult mosquito collections were conducted in Marsabit, Nandi and Kisumu counties in Kenya using the standard trapping tools. The collections were done in 10 randomly selected households, per site, both indoors and outdoors, every two months. CDC-UV light traps, Prokopack aspirations, and BG sentinel traps were used from August 2025 to May 2026. The *Anopheles* specimens were identified using standard morphological keys and genetic analysis.

Results: In total, 2324 morphologically identified *Anopheles* mosquitoes were collected with the vast majority *An. gambiae s.l.* (114), *An. funestus* (283), *An. coustani* (273), *An. gibbinsi* (243) with several others in small numbers. Only 2 *An. stephensi* were collected and identified morphologically. A molecular approach incorporating both PCR endpoint assay and sequencing of portions of the internal transcribed spacer 2 (ITS2) and cytochrome c oxidase subunit 1 (cox1) loci confirmed the identity of the *An. stephensi* in Marsabit county (13/56) of the morphologically identified *An. stephensi* confirmed molecularly. The study is ongoing, and additional results will be presented during the conference.

Conclusions: Our findings show that *An. stephensi* is firmly established in Marsabit County, while absent in Nandi and Kisumu Counties. Continuous surveillance is critical in unravelling the incursion of this invasive species and informing control interventions.

Keywords: *Anopheles stephensi* *Anopheles gambiae* *Anopheles funestus* Vector surveillance

Paper ID# 100

Title: Ecology and insecticide resistance status of the invasive *Aedes albopictus* in Ghana

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Background: In mid-2023, *Aedes albopictus*, a key dengue vector, was found breeding in Takoradi, a seaport city in southwestern Ghana, during routine *Anopheles* surveillance. *Aedes albopictus* were previously identified sparingly breeding in Accra, Ghana, until this encounter. The invasion expansion coincided with the 2024 dengue fever outbreak in Ghana. This study investigated the ecology and insecticide susceptibility of *Ae. albopictus* near the initial detection sites, and its spread into the forest areas.

Methods: Larval surveys were conducted in 3 localities in Takoradi during the rainy (September 2023) and dry (February 2024) seasons by sampling *Aedes* immatures from water-holding containers close to human settlements. Adult *Aedes* mosquitoes were sampled using the Biogents Sentinel traps, Human Landing Catch, and Prokopack aspirators. Phenotypic resistance to 0.05% deltamethrin, 0.75% permethrin, and 0.25% pirimiphos-methyl were determined using the WHO bioassay protocol. PCR was used to genotype the resistance mutations in the samples collected.

Results: Among 2,666 *Aedes* larvae collected, *Ae. Aegypti* (97.3%) was the most abundant, followed by *Ae. albopictus* (2.7%). Car tyres were the most productive habitat (66.4%). Out of the 960 adult *Aedes* mosquitoes sampled during the study, *Ae. aegypti* (87.2%) was the predominant species, followed by *Ae. Albopictus* (12.2%). Follow-up surveys conducted two years later revealed *Ae. albopictus* had expanded from the coastal savannah into forest zones. *Aedes albopictus* was susceptible to pyrethroids and pirimiphos-methyl while *Ae. aegypti* was resistant to pyrethroids. *Aedes albopictus* had low frequencies of F1534C (0.18), V410L (0.02), V1016I (0.00) whilst *Ae. aegypti* had high frequencies of F1534C (0.72), V1016I (0.50), and V410L (0.06).

Conclusion: The study findings provide baseline data for public health action and necessitate the urgent need for enhanced vector surveillance and resistance monitoring for *Ae. aegypti* in Ghana.

Keywords: *Aedes albopictus*, Ecology, Insecticide resistant, Dengue

Paper ID# 48

Title: Patterns of insecticide resistance in *Aedes aegypti* and *aedes albopictus* in different cities across Cameroon

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Background: The large distribution of the main *Aedes* vector species alongside the increasing frequency of arboviral outbreaks in Cameroon necessitates evidence-based vector control, yet the efficacy of chemical interventions is threatened by increasing insecticide resistance in *Aedes* populations. This study investigated resistance profiles of *Aedes aegypti* and *Aedes albopictus* across ecologically diverse Cameroonian landscapes.

Methods: Larvae were collected from eight cities representing equatorial forest, coastal, highland, and savannah zones. WHO susceptibility bioassays were conducted on F1 adults against pyrethroids, carbamates, and organophosphates. Resistance mechanisms were characterized using multiplex TaqMan qPCR for *kdr* mutations and RT-qPCR for detoxification gene expression (P450s, GSTs, CCEs).

Results: *Aedes aegypti* displayed widespread pyrethroid resistance, with mortality as low as 17.4% (permethrin, Kribi). This was linked to high frequencies of F1534C (up to 95%) and V1016I (up to 46.3%) mutations, with the CC-II homozygote haplotype reaching 15%. Furthermore, massive metabolic upregulation was observed, notably a 184.8-fold increase in GSTD4 expression in Bafoussam. Conversely, *Ae. Albopictus* remained susceptible to most insecticides in most sites, though resistance to permethrin and deltamethrin was detected in Douala and Nkongsamba. While both species were susceptible to bendiocarb and pirimiphos-methyl, resistance to propoxur was common.

Conclusion: Findings reveal a wide spread of pyrethroid resistance in *Ae. aegypti* across Cameroon. The emerging resistance of *Ae. albopictus* in urban centers, contrasted with its general susceptibility elsewhere, underscores the need for species-specific and geographically tailored control strategies. These data provide a critical baseline for mitigating urban arboviral transmission.

Keywords: Arboviral diseases, *Aedes aegypti*, *Aedes albopictus*, Insecticide resistance, Vector control, Cameroon

Paper ID# 264

Title: Evaluation of eDNA qPCR for *Aedes albopictus* surveillance in larval habitats on La Réunion Island

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Background: On La Réunion island, *Aedes albopictus* is widespread across diverse urban and peri-urban habitats. Larval surveillance currently relies on morphological identification, a time-consuming method. Environmental DNA (eDNA) offers a promising alternative, but its field performance in tropical habitats remains poorly documented.

Methods: We evaluated an eDNA tool based on a TaqMan qPCR assay targeting *Ae. albopictus*. Analytical validation used 10-fold genomic DNA dilutions. Field validation was conducted at 28 sentinel breeding sites, monitored over six months (November to April), for a total of 119 samples. eDNA positivity required ≥ 2 valid replicates out of 3. Morphological identification of larvae was performed simultaneously. Breeding sites with excessive turbidity or organic matter were excluded.

Results: The eDNA assay showed high replicability for *Ae. albopictus* (ICC = 0.954, 95% CI: 0.930–0.971). Using eDNA, *Ae. albopictus* was detected in 54.6% (65/119) of samples, compared to 38.7% (46/119) by morphological identification. Concordance between eDNA and morphology was low to moderate (Kappa = 0.292, 95% CI: 0.130–0.454). eDNA sensitivity was 73.9% for *Ae. albopictus*. GLMM detected no significant effect of period, volume, turbidity, habitat type, or exposure on detection probability (all $p > 0.05$).

Conclusion: This eDNA method is reliable for *Ae. albopictus* surveillance in tropical settings. Exclusion of highly turbid sites may have underestimated prevalence in organic-rich habitats, a limitation to address in future studies.

Keywords: eDNA, multiplex qPCR, *Aedes albopictus*, vector surveillance

Scientific Session 10: Climate, Environment & Vector Ecology

Paper ID# 222

Title: Impact of acute thermal stress on survival and development rate of immature stages of the major malaria mosquito *Anopheles funestus* s.s. from the Sahel

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Background: Temperature and by extension climate change are modifying the distribution of malaria mosquitoes like *An. funestus* s.s. and their ability to transmit disease pathogens. This study investigated the impact of single exposure to various static temperatures on the survival and development rates of immature stages of the major malaria vector *An. funestus* s.s., establishing optimal temperature for survival and critical thermal minima and maxima for their growth.

Method: Blood-fed female *An. funestus* mosquitoes collected indoors from Katsina State, Nigeria,

were forced to lay eggs, and F1 eggs, larvae, and pupae were utilized for thermal assays for 1h at temperature ranging from 0°C to 45°C.

Result: Temperature impacts survival and development rates for all the life stages. For eggs, hatching rate was highest at 25°C (75%), which reduced to 15% at 0°C, 9% at 10°C, and was completely inhibited at $\geq 42^\circ\text{C}$. Larval survival and pupation were optimal at 25°C (10% and 90% respectively), but declined at 40°C (45% and 56% respectively), 41 °C (69% and 31% respectively) and $\geq 42^\circ\text{C}$ where mortality reached 100%. Emergence was highest at 25°C (74%), moderate at 10–20°C (73% and 61% respectively), but significantly impaired at 15°C (40%), 30–35°C (54%), and fully inhibited at $\geq 42^\circ\text{C}$. Pupal mortality remained low up to 35°C (0%) but rose sharply, reaching 100% at 42–45°C. Taken together, 0–10°C was predicted to be the critical thermal minima, and $\geq 42^\circ\text{C}$ the critical thermal maxima.

Conclusion: These findings highlight the narrow thermal window for survival and development of *An. funestus* s.s. suggesting that rising global temperatures may reshape its survival and distribution.

Keywords: Malaria, *Anopheles funestus*, climate change, Temperature

Paper ID# 83

Title: Ecological drivers of urban malaria in Accra, Ghana: Irrigated agriculture and vector adaptation to polluted habitats

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Background: Urban malaria transmission in Sub-Saharan Africa is an increasing public health concern, underestimated due to scarcity of natural *Anopheles* breeding habitats in cities. However, in Accra, vectors are increasingly adapting to polluted habitats, including domestic and industrial wastewater. This study assessed the distribution, abundance, behavior, and *Plasmodium* infection of malaria vectors across five ecological settings: irrigated urban farming (IUF), low (LS), middle (MS), and high (HS) socioeconomic areas, and peri-urban (PU) areas.

Methods: Larvae were collected using WHO dipping method, and adults through human landing catches (HLC) and Prokopack aspiration, during rainy and dry seasons of 2022 and 2023.

Physicochemical characteristics of breeding habitats were measured. Molecular analyses were conducted to determine vector species, sporozoite infection, blood meal sources, and resistance

markers.

Results: A total of 41,747 adult mosquitoes were collected, 95.49% host-seeking, and 4.51% resting. *Anopheles* species dominated among host-seeking mosquitoes, with the highest densities of *An. gambiaes.l.* in IUF sites. Indoor *An. gambiae* s.l. showed higher sporozoite rates (4.56%, 16/351) compared to outdoor (3.78%, 9/238) ($\chi^2 = 6.78$, $P = 0.009$). Of the 727 breeding habitats, 65.34% were positive for *Anopheles* larvae. Vectors were found breeding in highly polluted water with low dissolved oxygen and elevated dissolved solids, conductivity, and $\text{NH}_4\text{-N}$ levels. *An. coluzzii* was the predominant species. Molecular analysis detected the invasive vector *An. stephensi* in Accra, being the first report of the species in Ghana.

Conclusion: Irrigated urban agriculture sustains malaria transmission in Accra by maintaining high vector densities, human blood feeding, and sporozoite infection. These findings support targeted interventions and larval source management. The detection of *An. stephensi* highlights the need for enhanced surveillance and environmental control.

Keywords: *Anopheles*, Ecology, Malaria, Urban, habitat, pollution.

Paper ID# 82

Title: Temperature extremes impact survival and development rate of the major malaria vector, *Anopheles coluzzii* constraining its climate-sensitive life traits threshold

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Background: Climate change is constraining survival, lifespan, distribution, blood-feeding, and reproduction of malaria mosquitoes, as well as their ability to transmit *Plasmodium*.

Methods: This study investigated the impact of single temperature exposures on survival and development of immature stages of malaria vector, *Anopheles coluzzii*. Larvae were collected from Auyo, Jigawa State, in northern Nigeria, raised to adulthood and blood fed. The F1 eggs, larvae, and pupae were exposed for 1 h to temperature gradients spanning 0 to 43°C and the mean egg hatching, mortalities of larvae and pupae, as well development rates recorded.

Results: Highest egg hatching (80%) occurred at 25°C, significantly decreasing linearly to 0% at 43°C and 17% at 0°C. Larval mortality was lowest at 25°C (15%), but increased significantly to 100% at 43°C and 65% at 0°C. Pupation was 0% at 43°C and 45% at 0°C, with 85% observed at 25°C. Emergence peaked significantly at 25°C (85%) but dropped to 0% at 43°C and 35% at 0°C. Thermal performance curve, coupled with compartmental modelling predicted optimal temperatures of 22.10°C for egg hatching, 22.01°C for larval survival, 22.44°C for larval pupation, 22.41°C for pupal survival, and 24.19°C for pupal emergence. Genotyping of contrasting phenotypes (larvae and pupae alive at 41°C and dead at 38°C) revealed significant association between the 2La chromosomal inversion arrangements (2La/2La and 2La/2L+a) and larval survival, compared with standard arrangement, 2L+a/2L+a (odds ratio = 12.5, $p < 0.001$). Similar pattern was observed with respect to insecticide resistance L1014F VGSC kdr mutation, with heterozygote larvae (L1014/1014F) significantly surviving heat (OR = 12, $p < 0.001$) more than their homozygous resistant (1014F/1014F) and susceptible (L1014/L1014) counterparts.

Conclusion: Temperature extremes constrain the fitness of immature *An. coluzzii* mosquitoes, but the 2La inversion and L1014F kdr mutation confer heat tolerance in the larvae.

Keywords: *Anopheles coluzzii*, malaria, temperature, tolerance, climate change, chromosomal inversion, kdr mutation

Paper ID# 45

Title: One health lens: Malacological and Parasitological determinants of human and bovine schistosomiasis at Bwanje Valley Irrigation Scheme in Dedza district, Malawi.

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Background: Irrigation systems create interdependence between humans, animals, and the environment. This mixed-method cross-sectional study was conducted in October 2023 and July 2024 to assess the burden and determinants of schistosomiasis in snails, cattle, and humans to inform disease control.

Methods: Eight snail habitats (main dam, irrigation canals, rice fields and drainage dam) were mapped and sampled, in October 2023, using Quantum GIS and, purposive and simple random sampling. 385 snails were collected, identified, and examined by Cercariae shedding and Microscopy. A Structured questionnaire was administered to households to assess the risk factors of schistosomiasis. 406 Urine and 180 stool samples were collected and examined using cluster and systematic random sampling, and microscopy. Ten cattle were examined postmortem using

convenience sampling. Data entry, descriptive statistics, Chi-square test, binary logistics regression analysis and Pearson correlation were performed using SPSS at $P < 0.05$.

Results: *Bulinus globosus* snails ($n=362$, 94.0%) were more abundant than *Bulinus pfeifferi* ($n=14$, 4.0%) and *Bulinus africanus* ($n=9$, 2.0%). Only *Bulinus globosus* ($n=104$) snails were shedding cercariae, registering a 27.01% infection rate. 168/406 urine samples were positive for urinary schistosomiasis, representing 45.81% prevalence. 13/180 stool samples were positive for bovine schistosomiasis, representing 7.22% prevalence. All postmortem samples were negative for Bovine Schistosomiasis. Gender, age, occupation, history of Mass Drug Administration, use of PPEs, and water source were associated with urinary Schistosomiasis ($P < 0.005$). Respondents who did not receive Praziquantel ($COR = 2.481$, 95%, $CI: 1.020 - 6.031$) were 2.48 times more at risk of Schistosomias.

Conclusion: The scheme poses a multidisciplinary challenge as evidenced by the infection rates of 27.01% snails, 45.81% humans, and 7.22% cattle. This would require a multidisciplinary approach to overcome.

Keywords: Malacological, Parasitological, Bwanje Valley, Schistosomiasis,

Paper ID# 27

Title: Abundance and infection rate of *Schistosoma haematobium* in snail vectors and prevalence of urogenital schistosomiasis in Limphasa irrigation scheme in Nkhatabay district

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1. Mzuzu University

Background: Schistosomiasis is a Neglected Tropical parasitic Disease that is prevalent in sub-Saharan Africa including Malawi, the disease is a threat to young children and other high-risk population in areas where there are freshwater bodies. For effective implementation of the prevention measures to control and eradicate schistosomiasis and its intermediate vector snails along irrigation schemes, an understanding of the epidemiology and transmission of urogenital schistosomiasis in this area is important. This study investigated the abundance of *Schistosoma haematobium* intermediate host snails, the infection rate of *Schistosoma haematobium* in snail vectors and the prevalence of urogenital Schistosomiasis among school-going children in the Limphasa Irrigation Scheme in Nkhatabay District.

Methods: A cross-sectional study was conducted at Limphasa irrigation scheme in Nkhatabay District. The study enrolled 200 school-going children that were tested for *Schistosoma haematobium* infection. Urine samples were also collected and examined for the presence of *Schistosoma haematobium* eggs using urine centrifugation microscopy. *Bulinus* snails were sampled from

Limphasa irrigation scheme and examined patent *Schistosoma* infections using cercarial shedding techniques.

Results: A malacological survey indicated that *Bulinus* snails were found with an infection rate of 48.05% (n=206); the overall prevalence rate of urogenital schistosomiasis was 62.5%(n=200).

Conclusion: This study provides an understanding of the transmission and presence of urogenital schistosomiasis in irrigation schemes and improves our understanding on the epidemiology and transmission of urogenital schistosomiasis in irrigation schemes and this can provide a starting point on the introduction and integration of prevention and control measures of urogenital schistosomiasis in irrigation schemes.

Keywords: *Schistosoma Haematobium*, Limphasa Irrigation and Schistosomiasis

Paper ID: 224

Title: Seasonal Variation in Daily Indoor and Outdoor Biting Activity and Indoor/Outdoor Resting Behaviour of *Aedes aegypti* Along an Urbanisation Gradient in Burkina Faso

Author: Athanase Badolo¹

Background: In 2023, Burkina Faso recorded 154,867 dengue cases and 709 deaths, making it one of the deadliest dengue outbreaks in West Africa. However, the bionomics of *Aedes aegypti*, the primary dengue vector, remain poorly understood, particularly its resting and biting behaviours.

Methods: The study was conducted over six months in 2023 across three sites representing an urbanisation gradient: Paspanga (urban), Zongo (peri-urban), and Goundry (rural). Biting rates were assessed using 48-hour human landing catches (HLC) conducted indoors and outdoors, while resting mosquitoes were collected concurrently using Prokopack aspirators.

Results: A total of 5,851 mosquitoes were collected through HLC and 3,588 through Prokopack aspiration. Contrary to the assumption of strictly diurnal activity, continuous 24-hour biting was observed, with two major peaks occurring in the morning (05:00–09:00 h) and evening (16:00–19:00 h). Biting rates were substantially higher in urban areas, reaching up to 1,000 bites/person/48 h outdoors, compared with approximately 100 bites/person/48 h indoors in rural areas. The morning biting peak was absent in rural areas, suggesting possible behavioural adaptation along the urbanisation gradient. *Ae. aegypti* showed a preference for outdoor resting across all sites, with outdoor-to-indoor ratios ranging from 1.5 to 2.6. However, indoor resting increased during the dry season in urban and peri-urban areas.

Conclusion: The findings challenge the assumption that *Ae. aegypti* is exclusively diurnal and highlight substantial spatial and behavioural variation associated with urbanisation and seasonality.

The predominance of outdoor resting and biting suggests that conventional indoor-focused interventions, including indoor residual spraying and insecticide-treated nets, may provide incomplete protection against dengue transmission. Further research should investigate genomic variation and climate-related disruption of circadian rhythms to better understand behavioural adaptation. Vector control strategies in Burkina Faso and across West Africa should therefore be revised to incorporate the full range of *Ae. aegypti* biting and resting behaviours.

Keywords: *Aedes aegypti*, Dengue, Vector bionomics, Urbanisation, Biting behaviour, Burkina Faso

Paper ID# 110

Title: Eco-epidemiological study of schistosomiasis in Karonga: Linking intermediate host infection to human schistosomiasis.

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1. Mzuzu University

Background: Despite over a decade of Mass Drug Administration (MDA) with Praziquantel Karonga district, Malawi, urinary schistosomiasis remains a significant public health challenge. The absence of recent surveillance data on snail vectors and human infection has masked current transmission dynamics. The study assessed the eco-epidemiological status of urinary schistosomiasis in Karonga.

Methodology: A cross-sectional study was conducted from July 2023 to July 2024 in the Songwe valley involving 533 SAC and 16 water bodies. Water bodies were purposively selected based on high human-water contact activities. The snails were collected via scooping and hand-picking, morphologically identified, and subjected to cercariae shedding. Urine samples were processed via centrifugation and microscopically examined for *Schistosoma haematobium* eggs. Descriptive and inferential statistics were done using SPSS v25.

Results: Intermediate hosts of the *Bulinus* and *Biomphalaria* genera were present in 75% of water bodies, with 58% of habitats containing snails actively shedding cercariae. Among the cohort, 250 children (45%) tested positive for *S. haematobium*. Females exhibited a significantly higher prevalence (47.3%) than males ($p=0.044$). Significant relationships were observed between prevalence and Age ($\chi^2 = 6.753$, $p = 0.009$), Fishing in waterbodies ($\chi^2 = 6.615$, $p = 0.010$) and involved in rice cultivation ($\chi^2 = 6.225$, $p = 0.013$). Direct water contact through fishing (AOR=1.657, $p=0.010$) and rice cultivation (AOR=1.810, $p=0.013$) were strong predictors of infection. The mean intensity was 54.47 eggs/10ml, with heavy infections among those involved in rice cultivation (30%).

Conclusion: The high prevalence and abundant infected snail population underscore the limitations of current MDA-only strategies in the area. Achieving sustained control requires transitioning to an

integrated approach that pairs expanded preventive chemotherapy with targeted snail control and environmental management.

Keywords: Snail vectors, Urinary schistosomiasis, Primary school-aged children

Paper ID# 137

Title: Predicting the ecological niches of dengue and chikungunya *Aedes spp.* in Kenya between 2000 and 2025

Samuel Muchiri^{1,*}

1. KEMRI-Wellcome Trust Research Programme

Background: Reliable maps are essential for controlling the growing threat of *Aedes*-borne diseases in Kenya, but current modelling is limited by poor data and a narrow focus on *Aedes aegypti*. This study overcomes these barriers by building a national *Aedes* database and comparing multiple modelling methods to accurately map the habitats of all key local vector species, creating the foundation for targeted disease control.

Methods: We compiled a national *Aedes* occurrence database for Kenya (2000–2024) through a systematic review of published and unpublished sources supplemented with global inventories. Environmental covariates were prepared and assessed for multicollinearity. The ecological suitability was modeled for *Ae. aegypti*, *Ae. mcintoshi* and *Ae. ochraceus* using Boosted Regression Trees with performance evaluated via out-of-sample AUC and the Sørensen's index (SIppc).

Results: This analysis will generate the first high-resolution, multi-model ecological suitability maps for major *Aedes* vectors across Kenya. We anticipate that the BRT model will achieve the highest predictive performance (AUC > 0.8; SIppc > 0.6), outperforming individual algorithms. The results will identify key environmental drivers—such as specific temperature ranges, rainfall patterns, and urban land cover—associated with vector suitability and will reveal distinct spatial niches for primary (*Ae. aegypti*) and secondary dengue and chikungunya vectors, highlighting previously under-surveyed high-risk regions.

Conclusion: This study will establish a critical evidence base for arbovirus control in Kenya by producing the first comprehensive, high-resolution ecological suitability maps for the full suite of local *Aedes* vectors. By identifying the most robust modelling framework and key environmental drivers, the findings will enable precise spatial targeting of surveillance and interventions.

Keywords: Ecological niche modelling, *Aedes*, arbovirus

Paper ID# 25

Title: Climate-driven modelling of malaria transmission and future risk projections in Bonaberi and Tombel districts, Cameroon: A vectri and cordex-core multi-model approachSharlot Fosah^{1,*}

1. Buea University

Background: Malaria is a major public health issue in Cameroon. Transmission is sensitive to climate change. As climate change affects rainfall and temperature, understanding how vector ecology will change in the future is crucial for effective malaria control. This study looks at how climate factors influence malaria cases in the coastal district of Bonaberi and the inland district of Tombel, offering data-driven projections for future risk.

Methods: The research combined historical malaria case data from health facilities with detailed historical climate records. We used the Vector-borne Disease Community Model from the International Centre for Theoretical Physics (VECTRI), a mathematical model that simulates complex interactions between climate factors, mosquito populations, and Plasmodium development. To evaluate future risk, we ran the model using regional climate projections from the CORDEX-CORE dataset under standardized climate scenarios. We then conducted a temporal analysis to spot seasonal changes and transmission thresholds.

Results: The findings show that rainfall and temperature play a significant role in determining transmission intensity. Peak malaria cases occur about one to two months after heavy rainfall. VECTRI simulations accurately reflected the observed seasonal peaks and identified the best temperature ranges for parasite development. Future projections indicate a change in the malaria "calendar." There could be higher transmission risk during the current shoulder seasons and a geographical spread of risk zones as temperatures increase.

Conclusions: This study shows that combining dynamic epidemiological models like VECTRI with regional climate projections from CORDEX-CORE creates a strong framework for predicting malaria outbreaks. These results highlight the need to develop climate-focused early warning systems to improve vector monitoring and resource distribution in Cameroon's National Malaria Control Program.

Keywords: Malaria, VECTRI, CORDEX-CORE, Climate Change,

Paper ID# 262

Title: Container breeding *Anopheles arabiensis* in Kenya: an old habit or climate change induced?

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Background: *Anopheles arabiensis* is one of the principal vectors of malaria in Africa responsible for many deaths annually. Although it is widely distributed in Africa, it has more presence in arid and semi-arid areas. Following an accidental observation of container breeding *Anopheles* mosquitoes, a rapid survey was carried out in January of 2023 in Merti town, within Isiolo County in Northern Eastern Kenya. The main objective was to determine the extent of container breeding and establish the potential role in malaria transmission of the container-breeding *Anopheles* species.

Methods: Larval stages of *Anopheles* mosquitoes were collected from 8 randomly sourced man-made containers. The larvae were reared to adults. Emerging adults were morphologically identified to species. PCR techniques were used to determine the sibling species. To establish the contribution in disease transmission, malaria incidence data was obtained from the local health facility for the month of January and February 2023.

Results: All sampled containers were positive for *Anopheles* mosquitoes. Seventeen adults successfully emerged. All were identified morphologically as *Anopheles gambiae* s.l. Fourteen were identified by PCR as *Anopheles arabiensis*. Malaria positivity rate for the month in Merti health facility was 5.4 and 6.2 for under 5 and over 5 years respectively.

Conclusion: Container breeding by native species of *Anopheles* had not been reported in Kenya hitherto this observation. Having malaria incidences in the driest of months points to a potential transmission by the container breeding *Anopheles arabiensis*. Occurring in an area that has recently reported *Anopheles stephensi*; an invasive container breeding species from Asia, poses a great challenge. Whether this is climate change induced or a normal behavior by *Anopheles arabiensis* that went unnoticed needs further investigation.

Keywords: *Anopheles*, Mosquitoes, Vectors, Malaria

Scientific Session 11: Social & Behavioral Science for Vector Control

Paper ID# 56

Title: Dynamics influencing retention or discarding of insecticide-treated nets among study participants in the field durability trial of ITNs in Bagamoyo District, Tanzania

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1. Ifakara Health Institute

Background: Insecticide-treated nets (ITNs) are a key malaria prevention tool. Understanding the factors influencing users' decisions to retain or discard ITNs is essential for improving their effectiveness. This study examined factors influencing decisions among participants in a community based ITN durability study in Bagamoyo, Tanzania.

Methods: A cross-sectional qualitative approach was used; 51 in-depth interviews (IDIs) and observational were conducted across four villages. Twenty-five ITNs representing six brands with different attributes were displayed for participants to evaluate whether they would retain, discard, or repurpose them. Analysis followed the thematic framework approach: Audio recordings were transcribed, translated into English, then imported into NVivo12Pro for coding. Data were analyzed deductively and inductively to identify themes, patterns, and categories

Results: ITNs were widely recognized as the primary malaria prevention strategy due to their affordability and accessibility. Key factors influencing retention included larger net size (average 182 × 164 × 174 cm), smaller mesh size (>25 holes/cm²), and soft fabric texture. White was the most preferred color, followed by blue; some reported no color preference. Men were more likely to discard nets based on physical deterioration, while women tended to repair and reuse them unless severely damaged. Factors influencing discarding included smaller net size (average 164 × 149 × 158 cm), larger mesh size (<25 holes/cm²), and household economic status.

Conclusion: The findings suggest that ITN design significantly influences user behavior. Manufacturers should prioritize larger net dimensions, smaller mesh sizes, and softer fabrics to better align with user preferences. Improving these attributes may enhance utilization, encourage better care practices, and extend the net lifespan. While users may accept distributed ITNs, their continued use depends on perceived suitability and condition.

Keywords: Insecticide treated nets, Malaria, User preferences, Retention and disposal behavior

Paper ID# 259

Title: Gene Drive, complex technology? Communities' knowledge and perception on Gene Drive for malaria vector control in Burkina Faso

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Background: Malaria remains a major challenge in sub-Saharan Africa despite the progress made. Gene drive is considered an innovative approach, but its acceptance depends strongly on the social context and public perception. If this technology represents a significant scientific advance, it must be recognized that innovations in health are perceived in different ways depending on the social context, a factor that influences their acceptance by society. Consequently, one of the relevant research questions to be analyzed is the public understanding and perception of this technology.

Methods: A qualitative approach was adopted for this study. It combines literature review, primary data collection, and consultation workshops. A total of one hundred and fifty-five (155) interviews were conducted with community members, workers in the informal sector, members of civil society, staff from decentralized and devolved public services, as well as religious and traditional leaders. All interviews were recorded, transcribed, analyzed, and processed using Atlas.Ti software.

Results Gene Drive is perceived as a new and complex technology that is difficult for the general public to understand. The majority associate it with risks to health and the environment, and even with the emergence of new diseases such as dengue fever. Some social actors view it as a neo-colonialist approach aimed at controlling Africa. However, a minority regard this innovation as an effective tool for directly tackling the causes of malaria and accelerating its elimination. The views of this minority, who have had access to accurate information on Gene Drive, make a positive contribution to overcoming the challenge of misunderstanding.

Conclusion: Negative perceptions are a barrier to the adoption of gene drive. Its integration into the social system requires the involvement of public authorities, simplified communication, strong community participation, and a regulatory framework to counter misinformation.

Keywords: Gene Drive, Perception Knowledge, Complex Technology, Burkina Faso

Paper ID# 239

Title: Mosquitoes and biodiversity: a socio-anthropological perspective on human health primacy over ecosystem balance in Burkina Faso

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Introduction: Mosquitoes are part of biodiversity and their relationships between humans are shaped by social and cultural factors. This study explores community social representations regarding mosquitoes and their ecosystem interactions to understand the social and cultural factors influencing the social acceptance of emerging biotechnological vector control tools.

Methods: A qualitative study was conducted in western Burkina Faso (Bobo-Dioulasso and Kouentou) between April 2023 and January 2024. Data collection involved 54 in-depth semi-structured interviews (conducted in French, Dioula, and Bobo) with community, exploring the themes of health risk, mosquito ecological roles, and novel vector control technologies such as modified genetical mosquitoes. Audio recordings were transcribed and analysed through manual thematic content analysis.

Results: Our analysis reveals a dualistic, predominantly anthropocentric view. Participants define biodiversity as the sum of all living beings created by God, while emphasizing that humans remain God's primary and most important creation. Consequently, when interacting with humans, mosquitoes are perceived strictly as pathogens and harmful pests. Conversely, when it interacts with fauna (serving food for animals) and flora (participating in pollination), participants recognize a distinct ecological utility.

Conclusion: This dichotomy highlights a hierarchy of biodiversity attributes where human health pragmatic concerns take precedence over ecosystem considerations. These findings suggest that local anthropocentric prioritization could serve as a potential entry point or favourable lever for the social acceptability of novel genetic and biotechnological vector control tools, provided community engagement addresses these dual representations.

Keywords: Mosquito, biodiversity, biotechnology, health, anthropology

Paper ID# 63

Title: Temporal trends and impact of malaria-helminth co-infection among children in Olama, central Cameroon

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Background: Co-infection with malaria and intestinal helminthiasis represents a significant health burden among children in endemic areas. Our study evaluated, on the one hand, the temporal trends of these parasitic diseases and, on the other, measured the influence of intestinal parasite carriage on the intensity of plasmodial infection in children in Olama, central Cameroon.

Methods: A longitudinal, analytical study was conducted from April 2023 to November 2024, involving 200 children aged 1–12 years were monitored over six distinct periods to capture seasonal

fluctuations. malaria was diagnosed using thick blood smears, and helminths via the Kato Katz technique. temporal trends were analyzed using chi-square tests, while malaria parasite densities were compared between mono- and co-infected groups using Mann Whitney u tests.

Results: Prevalence rates varied significantly across collection periods ($p < 0.05$). Malaria prevalence peaked at 33.05% in April 2023, fluctuating to 19.59% by November 2024. Intestinal helminthiasis, primarily *ascaris lumbricoides* and *Trichuris trichiura*, showed a prevalence ranging from 23.42% to 6.41%. co-infection rates peaked at 5.08% (April 2023) and reached 2.06% by the end of the study ($p < 0.05$). children aged 5–12 years were the most affected group. a critical finding was that co-infected children exhibited a consistently higher malaria parasite load compared to those with malaria mono-infection, regardless of age. Despite an overall downward trend in prevalence for both malaria and helminthiasis in Olama, the 5–12 age group remains particularly vulnerable. The significant increase in malaria parasite density among co-infected children suggests that intestinal helminths may exacerbate malaria severity.

Conclusion: These results highlight the necessity of integrating deworming programs with malaria control strategies. further transcriptomic study is recommended to elucidate the biological mechanisms driving this parasitic synergy.

Keywords: Malaria, Helminthiasis, Co-infection, Olama

Paper ID# 164

Title: Knowledge, attitude and practice of undergraduate students of the University of Port Harcourt to mosquito vectors, disease transmission and preventive measures.

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Background: Mosquito vectors and the disease they transmit need to be understood by all and sundry especially those in the corridors of learning, to enhance advocacy and community involvement.

Methods: Student's knowledge of mosquito vectors, disease transmitted and preventive measures were assessed using a structured questionnaire among undergraduate students residing in the University of Port Harcourt Hostels, data pooled were analysed using descriptive statistics and presented in charts and tables.

Results: A total of 100 students were recruited for this survey; 42 males and 58 females, from the age of 15 -35 years from the undergraduate hostels at the Abuja and Delta Campus of the institution. The respondents were from 6 hostels; Mandela Hostel (41.4%), Niger Delta Development Commission

Hostel (31.6%), and Nigerian University Hostel, King Jaja, Goodluck Jonathan, Dan Etete (5.3%) each, distributed in different levels (100 - 400) with varying length of stay (less than 6 months to over 2 years) in the hostels. Knowledge of mosquito vectors was unanimous (100%), with biting more frequently at night (69%) than evenings (31%) and a high nuisance rate of 90.5%. The disease mostly attributed to mosquito was malaria with 85.7% of the respondent having been treated in the last six months, either by self-diagnosis (59%) or confirmed laboratory diagnosis (41%). Preventive measures were noted to be the use of treated nets (42.9%), repellent (21.4%), window closure (19%), ignore mosquitoes (9.5%), insecticides (2.4%) hand kill (2.4%) or covered properly while sleeping (2.4%).

Conclusion: This study reveals that the respondents were conversant with mosquito vectors, their disease, diagnosis and preventive measures, and with proper guidance can enlighten others on proper control of mosquito vectors. However, knowledge of the impact of human activities and how to reduce their influence is greatly needed in controlling the vector and the disease they transmit.

Keywords: Mosquito, Knowledge, Practice, Disease, Diagnosis, Prevention.

Paper ID# 79

Title: “Client Is King”: Construction workers' perceptions of house modification for malaria control and thermal comfort in rural Western and Coastal, Kenya.

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Background: Malaria and indoor heat remain major public health challenges in rural Kenya, particularly in hot, humid settings where climate change is expected to raise temperatures and health risks. Cross ventilation, reflective roofing, and screened openings can reduce indoor heat and malaria risk, yet uptake is low. This study explored workers' perceptions on climate-smart housing and the factors influencing thermal comfort and vector control through housing design.

Methods: A qualitative cross-sectional study was conducted during a six-month baseline phase in Kwale and Siaya counties, two hot, humid malaria-endemic regions. Four FGDs were conducted (two per site), each with 12 male artisans to inform intervention strategies. Participants were purposively selected from artisan networks, community engagement, and snowball sampling. Data were analyzed thematically using a framework approach.

Results: Artisans identified increased roof height, ceiling installation, window screening, improved ventilation, and sealing roof-wall gaps as ways for enhancing thermal comfort and vector control.

Most acquired skills through informal jua kali apprenticeships. Although artisans supported improved housing, their ability to influence design was limited by homeowner preferences, while financial constraints often outweighed health and comfort factors, with suggested modifications viewed as added costs. Where trust existed, homeowners relied on artisans' advice, highlighting their potential as ambassadors for healthy housing. Participants also called for additional training in climate-smart practices.

Conclusion: Artisans can promote healthier homes, but adoption depends on homeowner priorities. Improving thermal comfort and vector control requires artisan training, homeowner sensitization, and policies that promote healthy housing. Integrating climate-smart features into training, regulations, and education could hasten uptake of climate-resilient, malaria-protective homes.

Keywords: Malaria prevention, Climate-smart housing, Thermal comfort, Construction workers, Informal training, decision-making, Adaptation

Paper ID# 194

Title: Review of schistosomiasis information from health centers in Kilifi County, Kenya

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Background: Schistosomiasis, caused by *Schistosoma haematobium*, remains a neglected tropical disease of public health importance in coastal Kenya. Kilifi County is recognized as a transmission hotspot, where water contact patterns sustain endemicity despite mass drug administration. While malaria dominates vector-control priorities, schistosomiasis surveillance through health facilities provides critical evidence for integrated vector management (IVM) and neglected tropical disease control.

Methods: A retrospective review of outpatient and inpatient records from 14 health facilities in Kilifi County was conducted using standardized extraction tools. The intended study period was 2015–2025, but record availability varied by facility, with some beginning in 2016 and others in 2017. Data included demographics, diagnosis, treatment regimens, complications, and outcomes. Preliminary

analysis from six facilities was performed using descriptive statistics, chi-square tests, confidence intervals, and logistic regression models in R.

Results: Schistosomiasis accounted for ~11.4% of diagnoses (CI 10.9–11.9%). Distribution varied significantly across facilities and age groups (Chi-square $p < 0.001$), with higher burden among school-aged children and adults aged 16–49. Facility-level analysis identified Chasimba as a hotspot with 18.2% prevalence compared to Rabai (9.6%) and Ganda (7.8%). Logistic regression confirmed age and facility location as predictors of infection. The analysis is preliminary and limited to six facilities, with treatment outcome data being compiled and full dataset expected by end of July 2026.

Conclusion: Preliminary findings highlight schistosomiasis as a persistent disease burden in Kilifi County, with facility-specific hotspots and demographic risk factors. Integrating retrospective facility evidence into vector surveillance frameworks strengthens case management and supports integrated control strategies alongside malaria programs.

Keywords: Schistosomiasis, Vector Surveillance, Kilifi County, Epidemiology, Integrated Control

Paper ID# 228

Title: Rice Cultivation and Malaria in Nigeria: Re-Examining the Relationship.

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8. NC

Background: Nigeria accounted for 24.3% of global malaria cases in 2025 and aims to eliminate malaria by 2030 through the National Malaria Strategic Plan. Progress from insecticide-treated nets (ITNs), artemisinin-based combination therapies (ACTs), and other interventions is threatened by insecticide and drug resistance, as well as suboptimal intervention uptake. Rice Agro-ecosystems provide suitable breeding habitats for malaria vectors, particularly *Anopheles gambiae* s.l., and may increase human-vector contact during cultivation. While rice farming has been associated with increased mosquito abundance, evidence linking it to malaria burden in Africa remains limited. This

study will investigate the association between rice cultivation and malaria transmission risk in Nigeria.

Methods: A comparative cross-sectional study will be conducted in rice-growing and non-rice-growing villages in Jigawa and Gombe States. Approximately 1,250 households will be enrolled across study sites. Children aged 3 months to 15 years will be screened for malaria using rapid diagnostic tests; haemoglobin levels will be measured for anaemia assessment, and dried blood spots collected for species identification. Behavioural risk factors and vector-control use will be assessed using structured observations and Malaria Indicator Survey-based questionnaires. Informed consent and child assent will be obtained where applicable.

Conclusion: The study will generate evidence on the relationship between rice cultivation and malaria risk, integrating parasitological and socio-behavioural determinants to inform agriculture-sensitive malaria control strategies in endemic settings.

Keywords: Rice; malaria risk; vector control interventions; human behavioural; Nigeria

Paper ID# 71

Title: Baseline knowledge, attitudes, and practices related to housing modifications for thermal comfort and vector control in hot and humid malaria-endemic rural Kenya

Teresa Bange^{1,*}, Khadija Nuru², Sharon Okaka², Isaac Opella², Paul Mutuku², Hilda Otanga², Phaustine Indeché², Vincent Moshi², Wendy Gaitara³, Francis Mutuku⁴, Eric Ochomo², Bernard Bange²

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Background: Housing is recognized as an intervention for malaria control and thermal comfort in hot, humid settings, particularly for residual transmission driven by indoor mosquito exposure. Structural features influence mosquito entry and heat, yet research often focuses on risk features with limited attention to lived decision-making and indigenous knowledge shaping building practices. This study aimed to understand why people build the way they do and generate user requirements to inform co-creation of housing modifications.

Methods: A qualitative study was conducted in Siaya and Kwale counties, Kenya. Data were collected through 12 FGDs with homeowners and construction workers, 160 KAP surveys, and 20 KIIs with stakeholders from the built environment, public health, and vocational training sectors. Participants

were purposively selected. Data were analyzed thematically using a framework approach.

Results: Housing reflected incremental, resource-constrained building shaped by affordability, material availability, durability, security, and socio-cultural norms. Features linked to mosquito entry and heat persist because they serve key functions, including rainwater harvesting, termite control, ventilation, and cost management. Participants showed strong awareness of malaria risk but described unavoidable trade-offs. Over 97% were willing to adopt housing modifications, indicating some knowledge–practice gap. Indigenous knowledge informed user requirements: improving ventilation while reducing mosquito entry, cooling roofs while preserving water harvesting, screening eaves without increasing termite risk, and aligning solutions with affordability and incremental building.

Conclusions: Housing is a negotiated outcome of competing needs that shapes residual malaria transmission. Embedding social science to generate user requirements enables co-created housing solutions that are effective, acceptable, feasible, and scalable for malaria prevention in endemic settings.

Keywords: Housing modifications, Malaria, Residual malaria transmission, Vector control, Indigenous knowledge, Co-creation, social science

Scientific Session 12: Gender & Community Engagement

Paper ID# 156

Title: Why aren't there more African female medical entomologists? Deciphering the challenges, opportunities and missed opportunities in Burkina Faso and Cameroon.

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Introduction: Women's role in the fight against malaria is undeniable at the level of the home and the community. While the fight against malaria continues to stall, Africa fights with far less than half of the female gender. Investments made globally to increase women's participation in science have not translated into more than 27% of African women working as medical entomologists. This study aimed to determine why by examining missed opportunities for women to participate professionally as entomologists, vector biologists and other relevant roles within vector surveillance systems and national malaria control programs in Burkina Faso and Cameroon.

Methods: We conducted a qualitative study using in depth interviews with key stakeholders from national malaria control programs, universities, research centers and international organizations in Burkina Faso and Cameroon. In an attempt to understand the inception of women's limited

participation in medical entomology, we also conducted focus group discussions with female and male entomology students in master's and PhD programs in both countries.

Results: A few factors are at play in women's relative lack of participation in medical entomology: a) gender discrimination at school and work by peers and supervisors; b) sexual harassment; and c) work/life balance compounded by societal pressure to abide by gender roles. When faced with these circumstances, some women decide not to pursue or complete their graduate studies, while others, persevere until they find work, only to find themselves leaving after such extenuating circumstances. While some male peers and supervisors value women's strong work ethic, some conversely view women as lazy sexual prey who are given scholarship and other opportunities in exchange for sexual favors.

Conclusion: From the results, such occurrences act as a serious impediment to some women's participation and ascension in medical entomology. Creating conducive environments in the home, the lab and the office for women scientists to succeed is crucial.

Keywords: women, gender, African, medical entomology, discrimination, harassment

Paper ID# 102

Title: Strengthening Community-Based Vector Control Through Integrated Surveillance and Youth Engagement in Kenya

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Background: Mosquito-borne diseases remain a major public health burden in Africa, worsened by climate change, insecticide resistance, and gaps in community engagement. Integrated Vector Management (IVM) requires technical and community participation with data-driven decisions. This study explores community-based surveillance and youth engagement in mosquito control.

Methods: A mixed-methods study in peri-urban Kenya. Household KAP surveys assessed knowledge, attitudes, and practices on mosquito control. Larval source mapping and environmental assessment identified breeding sites. Focus on group discussions with youth volunteers and community health workers explored barriers and facilitators. Data were analyzed using descriptive statistics and thematic analysis.

Results: Moderate awareness of prevention methods but inconsistent application. Major breeding sites included stagnant water and poorly managed waste areas. Youth-led initiatives improved participation in source reduction and environmental cleanliness. Challenges included limited data tools, low policy awareness, and inconsistent engagement. Integration of local data collection and

community action improved responsiveness to vector risks.

Conclusion: Community-based surveillance combined with youth engagement strengthens vector control and sustainability of IVM. Investment in data systems, youth empowerment, and community-driven interventions is essential. Policymakers should adopt inclusive social, environmental, and technological approaches for effective vector management.

Keywords: Integrated Vector Management (IVM) Community-Based Surveillance Youth Engagement Mosquito Control Environmental Health

Paper ID# 220

Title: Youth perspectives on gene drive technologies for malaria control in Tanzania

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1. African Conversations Initiative

Background: Gene drive-modified mosquitoes (GDMMs) are a promising innovation for malaria control in sub-Saharan Africa. Their success, however, depends on public understanding and acceptance, particularly among youth, who form a large proportion of the population. This study explored Tanzanian youths' perceptions of malaria, GDMMs, and their potential role in supporting novel malaria control technologies.

Methods: This exploratory qualitative study involved nine focus group discussions with six youth groups, including motorcycle taxi riders, soccer teams, arts and crafts groups, sports coaches, and medical students. Participants received brief presentations on GDMMs followed by guided discussions. Data were analyzed in NVivo 12 Plus using inductive and deductive thematic analysis.

Results: Youth expressed strong interest in malaria control and enthusiasm for innovative technologies such as GDMMs. However, understanding of malaria transmission, especially the role of mosquitoes, was limited. Malaria was often perceived as a routine and manageable illness, contributing to low-risk perception. Participants were surprised by the burden of malaria and expressed frustration at being excluded from national control efforts. Although some initial skepticism toward GDMMs existed, most participants were willing to support malaria control if engaged early through trusted messengers, peer education, creative outreach, and sustained involvement. Many also expressed willingness to educate communities about GDMMs.

Conclusion: Youth in malaria-endemic settings are eager to contribute to malaria control and are open to emerging technologies such as GDMMs. However, limited malaria knowledge and feelings of exclusion may hinder meaningful engagement. Early, inclusive, and sustained youth involvement is essential to strengthen informed participation and public support for GDMMs.

Keywords: Youth, malaria, gene drives, engagement

Paper ID# 152

Title: Countering the scramble for African faces and voices: Objective criteria for distinguishing friend from foe and managing those distinct relationships accordingly

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Background: Distinguishing authentic capacity-building partnerships from pseudo-capacity-building models is essential for promoting equitable and sustainable research development.

Methods: Here I present a conceptual framework for distinguishing between strategic system strengthening investments that enable the sustainable development of African institutional capacity over the long term and tactically expedient system support expenditures that undermine it. I also outline specific criteria for objectively distinguishing south-friendly collaborative models that facilitate authentic capacity building from the alternative pseudo-capacity building or outright incapacity building business models commonly practiced by de facto competitors headquartered in high-income countries (HICs).

Results: Authentic capacity building practices not only cover the full direct and indirect costs of participation by LMIC recipients, they also either embed carefully crafted benefit sharing plans into associated collaborative agreements or offset the opportunity costs or commitments to service provider contracts with correspondingly increased overhead rates. In contrast, the outright incapacity-building business models practiced by many HIC-headquartered primary recipients aim to either exclude local institutions entirely from funding opportunities or confine them indefinitely to trivial token roles. While more nuanced, pseudo-capacity building business models do support the development of LMIC organizations and investigators to levels of technical competence, they also insidiously undermine their progress towards excellence and independent competitiveness. They achieve this by subtly promoting mediocrity within African subrecipients, thus enabling HIC-headquartered primary recipients to sustain their leadership roles indefinitely.

Beyond approaches to productive engagement with genuine allies at HIC institutions, I also explain specific tactics that de facto competitors commonly deploy to seed division within and between local institutions in African LMICs and then outline effective approaches for countering them.

Conclusion: Adopting authentic capacity-building approaches can enhance the independence, competitiveness, and long-term sustainability of African research institutions.

Keywords: capacity, equity, sustainable development, institutional growth

Paper ID# 250

Title: Barriers and opportunities for community-based vector control in an emerging *An. Stephensi* Context in Marsabit County, Northern Kenya

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Background: The emergence of *An. stephensi* in the Horn of Africa threatens malaria control, particularly in arid and peri-urban settings where domestic water storage practices create suitable breeding habitats. However, evidence of community engagement in such settings remains limited.

Methods: A mixed-methods study was conducted in Saku Sub-County, Marsabit County. Quantitative data were collected from 220 households using structured questionnaires and environmental assessments (EA) of mosquito breeding sites. Qualitative data were obtained from Key opinion leaders (n=12) and eight FGDs with parents (n=40), and school-aged children (n=40). Quantitative data were analyzed descriptively, while qualitative data were analyzed thematically and integrated during interpretation.

Results: Although malaria awareness was high (93.2% correctly identified transmission; 94.1% expressed concern), awareness of *An. stephensi* was very low (3.2%). Most households reported using mosquito prevention methods (78.6%), including bednets (72.7%), but environmental management (EM) practices were limited (17.3% removal of stagnant water; 6.4% covering water storage containers). EA identified 148 larva-positive and 152 pupa positive containers, mainly: water tanks (n=136), jerrycans (n=48), and drums (n=27), with water tanks contributing to most breeding sites.

Key barriers: limited knowledge of *An. stephensi*, misconceptions, financial constraints, and competing livelihood demands. **Opportunities:** strong community willingness to engage in vector control activities, and the influential role of schools and children in behavior change.

Conclusions: Despite high malaria awareness, substantial gaps persist in knowledge and practices for controlling *An. stephensi*. Domestic water storage containers, e.g. water tanks, are key breeding sites and intervention targets. Strengthening community knowledge, promoting EM & leveraging schools and children as change agents could enhance sustainable vector control.

Keywords: *An. stephensi*; community-based vector control; environmental management; barriers; opportunities; school-based intervention

Paper ID# 127

Title: A qualitative investigation of community experiences of ITNs use among community members in the Mbalmayo Health District, Cameroon, and their implications for sustainability.

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Background: Vector control using insecticide-treated nets (ITNs) has been central to malaria control strategies. Between 2011 and 2023, over 30 million ITNs were distributed in Cameroon. Despite this, ITN use (58%) remains lower than ownership (77%). There is limited qualitative evidence on factors influencing ITN use and non-use in the Mbalmayo Health District. This study assessed community members (CM) experiences, barriers, and facilitators of ITN use and their implications for sustainability.

Methods: Qualitative research methods were used to achieve the objective set. Semi-structured interviews were conducted with a total of 12 participants of both sexes across 5 villages within two health areas (Angonfeme and Ekoumeyek), in June 2023. Data analysis was done following the thematic framework approach.

Results revealed that CM have fair knowledge about malaria, with some cultural understanding around the causes and transmission. ITNs were perceived and understood by CM as physical barriers and protection during sleep and were described as a veil offering protection against mosquitoes and other insects/animals such as snakes and scorpions. Perceived high cost of purchase of ITNs and unavailability of ITNs from mass campaigns in the region were determinants of ITN use among CM. Non-use was associated with economic, social, cultural, and programmatic factors. These factors include repurposing nets for fishing, hunting, nursing of seeds, selling of nets (0.83 USD) to buy locally made alcoholic drinks known as 'Odontol'. Poor community engagement in the distribution process, as well as net attributes such as the fabric, mesh size, and dimension of the nets, were also determinants of non-use.

Conclusion: The study highlights that ITN non-use is influenced by socioeconomic factors, access-related barriers, and net characteristics. Strengthening equitable access to ITNs, health education, community engagement, and behavior change communication, while improving net quality and dimensions, could enhance uptake and sustained use

Keywords: ITN, Malaria, Qualitative Research, Community perceptions, ITN use, ITN Non-use

Paper ID# 191

Title: Scaling entomological surveillance capacity using a Train the Trainer model for VectorCam deployment in Uganda.

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2. Vector Control Innovations, NC

Background: Accurate identification of malaria vectors is fundamental to effective entomological surveillance and targeted control interventions. However, limited entomological expertise at sub-national and community levels remains a major constraint in many endemic settings. VectorCam, an artificial intelligence-based mosquito identification tool, presents an opportunity to decentralize entomological surveillance while improving accuracy and timeliness of data.

Methods: A structured Train-the-Trainer (ToT) model is being implemented in 14 Ugandan districts. A total of 17 Vector Control Officers (VCOs) were trained as trainers using a standardized curriculum covering mosquito collection methods, mosquito identification, specimen handling, and use of the VectorCam application. The trained VCOs subsequently cascaded the training to Village Health Teams (VHTs). Performance during cascade training was assessed using a structured return demonstration checklist focusing on key competencies. Training effectiveness was assessed using pre- and post-training knowledge assessments.

Results: A total of 30 VHTs were assessed; overall mean knowledge scores increased from 54.8% to 77.3% post training, representing an average improvement of 22.4 percentage points. Key areas of improvement included mosquito identification (20.9%), specimen handling (48.7%), mosquito collection methods (17.8%), and VectorCam knowledge (10%). Field validation of the model concurs with the VectorCam-assisted identification tool, morphological and PCR-based identification methods, confirming its reliability and suitability for field operations.

Conclusion: The ToT model is an effective and scalable approach for building decentralized entomological surveillance capacity. It enabled rapid deployment of VectorCam while maintaining quality and standardization across multiple levels of the health system. This approach offers a practical pathway for integrating digital innovations into routine malaria surveillance.

Keywords: VectorCam, Vector Control Officers, Entomological surveillance, Village Health Teams, Train-the-Trainer

Paper ID# 35

Title: Community evaluation of vectrontm t500 (broflanilide) for indoor residual spraying for malaria vector control in Siaya County, Kenya.

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Background: Indoor residual spraying (IRS) remains a core malaria vector control intervention, though threatened by insecticide resistance. VECTRON™ T500 (broflanilide) represents a novel IRS product targeting GABA receptors.

Methods: A two-arm study was conducted in Bar-Olengo, Siaya County, Kenya in 2024. Twenty-five structures per arm were sprayed with either VECTRON™ T500 (100 mg a.i./m²) or Actellic™ 300CS (1 g a.i./m²), with five water-sprayed controls. Residual efficacy was assessed using the World Health Organization (WHO) wall cone bioassay. Insecticide susceptibility of wild malaria vectors was determined by WHO tube and CDC bottle assays. Residual efficacy, insecticide susceptibility, community acceptability, and adverse events were analysed with independent t-test using R version 4.4.0.

Results: VECTRON™ T500 had higher mortality than Actellic™ 300CS over six months on both wall types. Against resistant *Anopheles gambiae* s.s. Bungoma strain, VECTRON™ T500 achieved $98.73 \pm 3.51\%$ mortality (95% CI 97.95-99.51%) compared to $80.22 \pm 11.23\%$ for Actellic™ 300CS (95% CI 77.72-82.72%; $t_{78} = -10.15$, $p < 0.001$, Cohen's $d = 2.27$). For susceptible *An. gambiae* Kisumu strain, VECTRON™ T500 maintained 100% mortality versus $89.60 \pm 6.34\%$ for Actellic™ 300CS (95% CI 88.19-91.01%; $t_{78} = 10.53$, $p < 0.001$, Cohen's $d = 2.38$). Actellic™ 300CS efficacy declined below 80% after month 4, while VECTRON™ T500 remained $> 95\%$ effective throughout. For insecticide susceptibility tests, wild *An. gambiae sensu lato (s.l.)* and *An. funestus s.l.* showed 100% susceptibility to broflanilide with no cross-resistance detected. No adverse events occurred in VECTRON™ T500 versus 8% (12/150) in Actellic™ 300CS households. Community acceptance was 100% for VECTRON™ T500 versus 99.33% (149/150) for Actellic™ 300CS, though not statistically significant.

Conclusion: VECTRON™ T500 demonstrated superior residual efficacy, excellent safety profile, and high community acceptance compared to Actellic™ 300CS

Keywords: Broflanilide; Indoor residual spraying; Malaria vector control.

Paper ID# 150

Title: Assessment of knowledge, attitudes, and practices (KAP) about host and mosquito behavior during the upsurge of malaria cases in KwaZulu-Natal.

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Background: Malaria elimination efforts in South Africa are still ongoing. Community knowledge of malaria and its prevention methods is essential for successful elimination. This study aimed to assess community knowledge of malaria, mosquito behaviour, and the prevention methods employed outdoors.

Methods: The survey was conducted in KwaZulu-Natal during night mosquito collections and local case investigations. A five-question survey was administered in 36 households, including 29 participants identified through local case investigations (FOCI).

Results: Ninety-four percent of participants confirmed the presence of mosquitoes, and 48% reported being bitten while sleeping. Mosquito bites most frequently occurred between 7 and 8 pm (41%), and stagnant water bodies, particularly after rainfall, were observed (40%). The majority of participants (57%) reported using long-sleeved clothing as an outdoor prevention method.

Conclusion: Knowledge levels regarding malaria and mosquito bite prevention were satisfactory, and participants demonstrated appropriate attitudes and practices. However, there is a need to introduce less well-known prevention methods and to extend health education programs to participants lacking adequate knowledge. These measures are essential to support malaria elimination efforts in endemic districts through community involvement.

Keywords: Knowledge, malaria, prevention, mosquito

Paper ID# 233

Title: From Capacity to Impact: Women in Vector Control Accelerating Malaria & Other Vector borne Diseases Elimination in Africa

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5. Centre for Research in Infectious Diseases (CRID)

Background: Despite the progress made in controlling vector-borne diseases (VBDs) in recent years, the burden of VBDs remains significantly high in tropical and subtropical regions. The Pan-African Mosquito Control Association (PAMCA), through its Women in Vector Control (WiVC) program sought to strengthen women's participation and leadership in VBD control and elimination initiatives in Africa.

Methods: Between 2021 and 2023, PAMCA WiVC successfully hosted and co-organized various training sessions including effective communication and leadership skills, proposal and manuscript writing, and the prevention and resolution of safeguarding issues, among others.

Results: A total of 95 women from 29 countries in Africa were trained. Furthermore, the program rolled out a structured mentorship initiative, "LiftHer2," in which 42 mentees and 30 mentors from two cohorts, each lasting one year, were enrolled. To increase visibility and networking, 17 women in early, mid, and senior career stages from 11 countries in Africa were identified, recognized and awarded for their excellent work and contributions to the fight against VBDs. Ten early-career women received travel sponsorship to attend and present their research work during the 8th and 9th PAMCA annual conferences in 2022 and 2023, respectively. Monitoring and evaluation of the program indicated that several women who participated in the activities advanced in their careers, with 8 and 6 successfully completing Masters and PhDs studies respectively, while several enrolled for postgraduate studies, others secured new jobs or received promotions at their workplaces.

Conclusion: The WiVC Program has demonstrated that training, mentorship and recognition of excellence are crucial in empowering and strengthening women's leadership and highlight the value of investing in women scientists and practitioners as a strategy for strengthening Africa's capacity to prevent and control vector-borne diseases

Keywords: Women; Vector-borne diseases; PAMCA; Africa

Scientific Session 13: Vector Surveillance & Bionomics

Paper ID# 193

Title: Vector atlas: an open-access platform for consolidating and standardizing malaria vector surveillance data across Sub-Saharan Africa

Peter Gitu^{1,*}

1.icipe

Introduction: Malaria remains a major public health challenge in Sub-Saharan Africa, driven by shifting vector distributions, environmental change, and rising insecticide resistance. Control efforts require harmonized surveillance data, which are often fragmented. The Vector Atlas addresses this by providing an open-access platform to consolidate and standardize malaria vector data.

Methods: The platform integrates occurrence, bionomics, and insecticide resistance data from literature and partners. Records undergo georeferencing and taxonomic standardization. It uses a containerized architecture (Docker, Azure) with a GraphQL API and a multilingual interface optimized for low-bandwidth settings.

Results: The portal offers interactive maps and analytical tools to filter, visualize, and download datasets, including species distribution models across eleven insecticide classes. It has recorded 18,457 visits from 4,443 users in 103 countries and hosts 44,648 curated records.

Conclusions: The Vector Atlas provides scalable, open infrastructure for harmonized vector data, enabling data-driven malaria control and supporting targeted interventions.

Keywords: malaria

Paper ID# 195

Title: Divergent ecology and genetics of *Aedes aegypti* across contrasting Dengue risk regions in Kenya

Josephine Osalla^{1,*}, Gilbert Rotich¹, David Tchouassi¹

1.icipe

Background: Dengue virus risk varies across locations, yet the role of vector bionomics and population structure remains poorly described. We investigated genetic and ecological variation in *Ae. Aegypti* aligns with spatial differences in dengue risk in Kenya.

Methods: Cross-sectional surveys (2022-2023) were conducted post-rainy season in two ecologically distinct peri-urban sites: Marigat (Rift Valley; non-dengue-endemic) and Ukunda (coast; dengue-endemic). Adult abundance and oviposition were assessed using BG-Sentinel traps and ovitraps, respectively. Mosquitoes were analysed for blood meal sources, arboviruses, and mitochondrial cox-1 sequences to assess genetics and population structure.

Results: Vector indices showed contrasting patterns. Ukunda exhibited higher adult abundance than Marigat (IRR=3.21, $p<0.0001$) and 68% human blood-feeding rate, indicating greater human-vector contact and transmission potential. In contrast, Marigat showed higher egg densities (IRR=2.17, $p=0.006$) alongside a predominantly zoophilic feeding profile (71.4%), reflecting reduced human

exposure. Genetic analysis revealed high mitochondrial haplotype diversity ($Hd=0.995$) with largely site-specific haplotypes and limited mixing, consistent with restricted gene flow. Coastal populations were predominantly associated with the domestic ecotype, unlike Rift Valley populations. While no pathogenic arboviruses were detected, distinct insect-specific virus profiles were observed between sites.

Conclusion: Differences in abundance, feeding behaviour and genetic structure aligned with spatial variation in dengue risk. The mismatch between egg and adult indices highlights the limitations of single surveillance measures. The absence of detectable virus in endemic Ukunda may reflect low vector infection, underscoring need for longitudinal, multi-seasonal sampling. Integrating entomological, genetic, and ecological data can improve risk assessment and support more targeted vector control.

Keywords: *Aedes aegypti*, genetic diversity, arbovirus surveillance, dengue, insect specific viruses

Paper ID# 80

Title: Development and reproductive fitness of dengue vectors in Ghana

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Background: The invasion of *Aedes albopictus* in West Africa has heightened the risk of dengue outbreaks. We determined how the invasive *Ae. albopictus* vector could compete with native vectors *Ae. aegypti* and *Ae. vittatus* in Ghana, as *Ae. albopictus* is known to compete or sometimes outcompete native vectors when they invade countries.

Methods: Larval surveys were conducted to sample *Aedes* immatures. Emerging adults were morphologically identified. Larval life tables were conducted in cut car tyres (56cm x 15cm) to determine development time. Adult life tables were conducted using F3 mosquitoes under field conditions to determine reproductive fitness. Human blood was provided to the adult female mosquitoes daily through the arm of the first author.

Results: Development time (L1–L4) was not significantly different among the species (*Ae. aegypti*: 7.2 ± 0.84 days, *Ae. albopictus*: 7.9 ± 1.0 days, *Ae. vittatus*: 8.3 ± 1.0 days). Pupation rates were not significantly different, as was survivorship. In combined microcosms, where all three species were raised together, *Ae. Vittatus* survivorship was lower (0.76 ± 0.18) compared to *Ae. aegypti* (0.84 ± 0.21) and *Ae. albopictus* (0.82 ± 0.18). *Aedes aegypti* maintained similar reproductive fitness across seasons

whereas that of *Ae. vittatus* and *Ae. albopictus* were higher in the dry and rainy season respectively. Intrinsic growth rates among the species were similar across seasons ($p \geq 0.264$). During the dry season, *Ae. aegypti* lived the longest (83.00 ± 9.82 days), followed by *Ae. vittatus* (76.00 ± 7.21 days), and *Ae. albopictus* (68.00 ± 13.19 days). In the rainy season, *Ae. aegypti* lived the longest (109.60 ± 32.26 days), followed by *Ae. vittatus* (80.60 ± 13.01 days), whereas *Ae. albopictus* lived the shortest (78.00 ± 0.71 days).

Conclusion: This study shows that despite *Ae. albopictus* having shorter adult longevity, its comparable developmental and reproductive traits suggest that it could proliferate and compete with native vector species in Ghana.

Keywords: *Aedes albopictus*, *Aedes aegypti*, *Aedes vittatus*, Dengue fever, Reproductive fitness, Larval development

Paper ID# 173

Title: Bionomics of Major Malaria Vectors in Senegambian Border Areas in Senegal

Ndèye Aita Ndoeye^{1,*}, Moussa Diop¹, Ndèye Seny Diagne¹, Edouard G. Tine¹, El Hadji Amadou Niang¹
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Background: Malaria remains a major public health problem in Senegal, with seasonal transmission varying by area. However, the entomological determinants of transmission in border regions remain insufficiently documented. This study aimed to characterize the main entomological factors associated with malaria transmission along the Senegal-Gambia border.

Methods: Five cross-sectional surveys were conducted between July 2023 and March 2024 in four localities, including two border sites Nemataba (N) and Ndrame Ndimb (NN) and two control sites Medina Dianguette (MD) and Paoskoto (P). Adult mosquitoes were collected using human catches and pyrethrum sprays. Species of identification, blood meal analysis, and *Plasmodium* detection were carried out using PCR and ELISA techniques. Kruskal Wallis test for Biting densities.

Results: A total of 2,301 *Anopheles* mosquitoes were collected, with *An. gambiae* s.l. (60%) and *An. funestus* (35%) being the predominant species. Molecular identification showed that *An. gambiae* s.s. predominated at MD, whereas *An. arabiensis* was dominant at the other sites. All *An. funestus* specimens were identified as *An. funestus* s.s.. The highest biting rates were recorded for *An. gambiae* s.l. at MD (12.63 bites/person/night) and for *An. funestus* at P (2.88 bites/person/night). Parity rates ranged up to 60% for *An. gambiae* s.l. and 57.72% for *An. funestus*. The human blood index reached 77.1% at MD and was absent at P. Malaria Transmission was detected only at MD and P, with entomological inoculation rates of 0.0707 and 0.0726 infectious bites/person/night, respectively. No

significant differences in mean biting densities were found among the study sites ($p = 0.08$).

Conclusion: These results highlight significant spatial variability in the bionomic characteristics of malaria vectors in the Senegal-Gambia border region. They underscore the importance of continuous entomological surveillance to guide vector control strategies tailored to local contexts.

Keywords: Bionomics, Malaria vector, Senegambian, Border area

Paper ID# 61

Title: Larviciding intervention targeting malaria vectors also affects Culex mosquito distribution in the city of Yaounde, Cameroon

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2. OCEAC

Background: Although culex species are considered to be equally affected by control measures targeting malaria vectors, there is still not enough evidence of the impact of interventions such as larviciding on the distribution of these mosquito species. The present study assessed the impact of a larviciding trial targeting malaria vectors on Culex mosquito species in the city of Yaoundé, Cameroon.

Methods: A cluster randomized trial comparing 13 treated clusters and 13 untreated clusters was implemented. Data were collected at baseline and during the larviciding intervention, from March 2017 to November 2020. The microbial larvicide vectomax g was applied once every 2 weeks in the intervention areas. Adult mosquitoes were collected using CDC light traps in both intervention and non-intervention areas and compared between arms.

Results: Globally, larviciding intervention was associated with 69% reduction in aquatic habitats with culex larvae and 36.65% reduction of adult culex densities in houses. Adult culex densities were reduced both indoors (35.26%) and outdoors (42.37%). No change in the composition of culex species was recorded.

Conclusion: The study suggests a high impact of larviciding on culex mosquito species distribution. The impact of the intervention can be improved if typical culex breeding habitats, including pit latrines, are targeted.

Keywords: Larviciding, Culex, *Bacillus Thuringiensis*, *Bacillus Sphaericus*, Yaounde

Paper ID# 41

Title: Malaria vectors diversity and seasonality in sustaining disease transmission in an endemic area of Kati-Faladie, Mali.

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Background: *Anopheles (An) coluzzii*, *An. gambiae*(s.s.), *An. arabiensis* and *An. funestus* mosquitoes are the dominant vector species of *Plasmodium* parasites transmission in Mali. The vector's massive circulation is observed during the rainy season and clearly decreases during dry season with only a few mosquitoes able to survive during this season. The main objective is to assess the diversity of *Anopheles* mosquito populations during dry and rainy seasons. Furthermore, this study aimed to identify the major species sustaining continued malaria transmission across seasons. Methods:

Methods: From a cross-sectional study in malarias endemic area, mosquitoes were captured twice, the rainy and dry seasons using pyrethroid spray catches in Kati-Faladie. Collected mosquitoes were identified according to the morphological keys and molecular techniques such as PCR-RFLP (IGS regions). *Plasmodium spp* positivity in each mosquito was characterized by qPCR using parasite 18 S genes.

Results: In Kati-Faladie site, 1,082 and 1,705 mosquitoes were captured in rainy and dry seasons respectively inside the same houses. In the rainy season, 454 (42%) were anophelines and 624 (58%) culicines. During dry season, 65 (3.81%) of the captured mosquitoes were *Anopheles*, while 1,640 (96.19%) were *Culex*. Morphologically, anopheline population consisted of 100% *An. gambiae* s.l. *Anopheles* species diversity in rainy season was comprised of the sister taxa, *An. gambiae* s.s and *An. coluzzii* followed by *An. gambiae/An. coluzzii* hybrid and *An. arabiensis*. However, only *An. coluzzii* was found as vectors across rainy and dry seasons sustaining malaria transmission. *Anopheles* infection rate of *Plasmodium falciparum* was 10.5% and 3.7% for rainy and dry respectively. Conclusion: *Anopheles coluzzii* species can survive in dry season and could sustain malaria transmission. This highlights the importance of tackling *Anopheles Coluzzi* species and residual malaria transmission to eradicate the disease in rural area of Mali.

Keywords: *Anopheles*, Malaria, Kati-Faladie, seasonality, diversity.

Paper ID# 17

Title: Prevalence and associated factors of dengue virus infection in an endemic area in Tanzania.

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Background: Dengue, transmitted by *Aedes* mosquitoes, causes about 40,000 deaths globally each year, with increasing outbreaks in Tanzania, including 13 deaths reported in Dar es Salaam and Tanga in 2019. Despite high mosquito exposure (Up to 45.3% of the population in Lower Moshi tested positive for antibodies to mosquito salivary peptides), local transmission dynamics and risk factors are poorly understood. This study assessed factors associated with dengue exposure in urban and semi-urban populations of Dar es Salaam.

Methods: A cross-sectional survey included adults and children over 2 years attending outpatient and reproductive and child health clinics. Past exposure was measured with ELISA IgG, and current infection with dengue NS1 antigen test. Demographic, socio-economic, and clinical factors were collected and analyzed using logistic regression.

Results: A total of 394 patients were included (82.7% female and 17.3% male; mean age 28.2 ± 14.7 years, range 2–88). The seroprevalence of previous dengue infection based on ELISA IgG was 22.3%, while 1.8% had evidence of current infection by NS1 antigen positivity. Both NS1 and ELISA IgG positivity were significantly higher among males than females (NS1: 5.9% vs 0.9%; $p = 0.005$; IgG: 35.3% vs 19.6%; $p = 0.005$). In logistic regression, female sex was associated with lower odds of dengue exposure compared to males (aOR= 0.32; 95% CI: 0.11–0.93; $p=0.036$). Age above 40 years, participation in outdoor sports and presence garbage collection near residential area were

significantly associated with dengue infection ($P < 0.05$).

Conclusions: Dengue transmission persists in Dar es Salaam with evidence of past exposure and ongoing infection. Environmental conditions and demographic factors contribute to transmission risk. Strengthening vector control, environmental sanitation, and targeted public health interventions is essential to reduce dengue infection in urban communities.

Keywords: Dengue virus, Seroprevalence, Risk factors, Urban health, Tanzania.

Paper ID# 134

Title: Blood host preferences and competitive inter-species dynamics within an African malaria vector species complex inferred from signs of animal activity around aquatic larval habitats

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3. Sokoine University of Agriculture
4. Nyerere National Park

Background: The feeding behaviours and competitive relationships of sibling species within the *Anopheles gambiae* complex within natural ecosystems remain largely unexplored.

Methods: Aquatic habitats were surveyed for *An. gambiae* complex larvae and signs of human, livestock or wild animal activity across a gradient of natural ecosystem integrity in southern Tanzania, encompassing domesticated human settlements, a partially encroached Wildlife Management Area (WMA), and well conserved natural ecosystems within Nyerere National Park (NNP).

Results: While only *An. arabiensis* was found in fully domesticated ecosystems, its non-vector sibling species *An. quadriannulatus* occurred in conserved areas and dominated the most intact natural ecosystems. Proportions of larvae identified as *An. arabiensis* were positively associated with human and/or cattle activity and negatively associated with distance inside NNP and away from human settlements. Proportions of *An. quadriannulatus* were positively associated with activities of impala, warthog and possibly bushpig, implicating them as likely preferred blood hosts. Despite dominance of *An. quadriannulatus* in conserved areas, *An. arabiensis* was even found in absolutely intact natural environments >40km inside NNP, suggesting it can survive on blood from one or more wild mammals.

Conclusions: Such self-sustaining refuge populations of *An. arabiensis* inside conservation areas,

supported by wild blood hosts that are fundamentally beyond the reach of conventional insecticidal interventions may confound efforts to eliminate this key malaria vector. However, such refugia may also enable more effective insecticide resistance management. This new approach to indirectly identifying common blood hosts may also be applicable to diverse zoophagic mosquitoes, enabling incrimination of bridge vectors responsible for pathogen spillover from wildlife reservoirs into livestock and/or human populations.

Keywords: *Anopheles gambiae*, *Anopheles arabiensis*, *Anopheles quadriannulatus*, blood source, host choice, population dynamics

Paper ID# 123

Title: Building circular economies for health: integrating community perspectives and environmental metrics from a women-led black soldier fly farm in Coastal Kenya

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3. HERI - KENYA

Introduction: In coastal Kenya, unmanaged organic waste threatens environmental integrity, food security, and public health, intensifying the spread of diarrheal and mosquito borne diseases.

Methods: To address these interconnected challenges, Environmental Research Institute (HERI-Kenya) established an innovative women led Black Soldier Fly (BSF) farm that converts organic waste into valuable resources, creating a circular system that links waste reduction, sustainable agriculture, and climate resilience.

Results: Since its launch in January 2025, the HERI BSF farm has processed over 6,000 kg of organic waste, producing 143 kg of larvae for high protein poultry feed and 69 kg of nutrient rich frass fertilizer. Life Cycle Assessments reveal remarkably low emissions, 0.02–0.03 kg CO₂ eq per kg of waste processed, avoiding approximately 19.7 kg CO₂ eq for every 22 kg of frass produced, far below emissions from conventional disposal and agriculture. Complementing these environmental metrics, a Knowledge, Attitudes, and Practices survey (KAP) of 51 community participants revealed that 41 percent associate unmanaged waste with illnesses such as cholera and skin rashes, while 92 percent recognize BSF farming as an effective waste management strategy.

Conclusion: Women are key agents of change, underscoring the importance of gender inclusive climate adaptation. By integrating environmental data with community insights, this initiative

exemplifies a scalable, low emission, and gender equitable model for circular economies of health. Our findings demonstrate the potential of BSF in promoting circular economies of health.

Keywords: Circular Economies, Environmental Metrics, Black Soldier Fly, Community Perspectives

Scientific Session 14: Parasite tracking and Genomics

Paper ID# 229

Title: Building Sustainable Molecular Research Capacity in Burkina Faso to Enable Next-Generation Malaria Vector Control

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2. IRSS

Background: Gene drive is one of the most promising solutions for malaria eradication enabling the potential suppression or modification of mosquito populations to interrupt disease transmission. However, their successful and ethical implementation requires not only technological advances but also locally embedded scientific capacity, regulatory readiness, and research leadership in endemic regions. To address this gap, the Liverpool School of Tropical Medicine (LSTM), in partnership with the Institut de Recherche en Sciences de la Santé (IRSS) in Burkina Faso, has established a capacity-strengthening programme to develop African-led expertise in molecular entomology, genetics, and gene drive research.

Methods: Two cohorts of PhD students (8 in total) from the University of Nazi Boni participated in a structured training programme over a four-year period combining intensive laboratory training at LSTM followed by projects with research independence.

Results: With 12 months remaining, the programme has achieved significant technical and capacity milestones: Development of transgenesis platforms in *Anopheles funestus*, Molecular surveillance of gene drive target sites, Identification of novel genetic pathways for use in population suppression gene drive strategies, Investigation of sex chromosome biology in *Anopheles funestus* to inform targeted genetic interventions.

Conclusions: By combining technology development with human capital investment, this work provides a scalable model for African-led innovation in malaria control, directly aligned with global eradication goals. Importantly, it supports a shift from externally driven research to locally owned and innovative relevant solutions. This approach contributes not only to advancing gene drive technologies but also to building the scientific, regulatory, and institutional foundations, positioning institutions across Africa at the forefront of next-generation malaria interventions.

Keywords: Building Capacity, Gene Drive, Vector Control

Paper ID# 28

Title: Germline-specific transposase expression improves transgene transmission during piggyBac-mediated transformation in *Anopheles Funestus*

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3. Institut de Recherche en Science de la Sante

4. Liverpool School of Tropical Medicine

Background: Development of genetic tools for malaria vector control requires efficient and reproducible germline transformation systems. However, progress in *Anopheles funestus* has been limited by the lack of robust transformation methods, restricting functional genomics studies, and the development of genetic control strategies.

Methods: PiggyBac-mediated germline transformation was evaluated in *An. funestus* using a donor plasmid carrying a 3xP3-EYFP marker and attP docking site, co-injected with either a heat-shock promoter-driven (hsp) or germline-specific vasa-driven transposase helper plasmid. A total of 600 embryos were injected with the vasa system and 502 with the hsp system under identical conditions. Germline transformation was assessed by screening G₁ progeny for fluorescence and transgene inheritance. Estimated germline transformation rates were calculated as the number of minimum independent founders divided by the number of transient G₀ adults.

Results: Both helper systems supported successful germline transformation, and each generated a minimum of three independent founders. Characterization identified nine stable transgenic lines, indicating multiple integration events from some founder pools. The vasa-driven helper produced high transient expression and improved recovery of fluorescent G₁ progeny, whereas the hsp-driven helper yielded fewer fluorescent progeny. Estimated germline transformation rates were 7.5% and 4.7% for the vasa and hsp systems, respectively. Transgenic lines showed variable fluorescence intensity and tissue-specific expression consistent with positional effects of genomic integration.

Conclusion: Both helper systems successfully supported piggyBac-mediated germline transformation in *Anopheles funestus*. The vasa-driven helper improved recovery of fluorescent progeny and yielded a higher estimated germline transformation rate, providing a valuable platform for functional genomics and future genetic control applications

Keywords: *Anopheles funestus*, Germline transformation, piggyBac transposon, Transgenesis, Vector

control.

Paper ID# 117

Title: CRISPR-CAS9 mediated *hppd* gene knockout reveals its potential as vector control target in the malaria mosquito *Anopheles funestus*

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1. IRSS-DRO

Background: Increasing insecticide resistance in malaria vectors threatens the efficacy of current interventions. Innovative control strategies, including genetic-based approaches, are being developed to enhance and complement existing vector control efforts. Identifying novel candidate targets for genetic control represents an important step. The gene encoding 4-hydroxyphenylpyruvate dioxygenase (HPPD) is a key enzyme in the tyrosine detoxification following a blood meal in hematophagous insects. Here, we investigated the functional role of HPPD in *Anopheles funestus* through nitisinone (NTBC) chemical inhibition and CRISPR-Cas9-mediated gene knockout.

Methods: Dose-response assays were conducted on insecticide susceptible *Anopheles funestus* FANG and metabolically resistant FUMAZ strains to assess mortality following NTBC-supplemented blood meals. A GFP-marked knockout line was then generated by targeting exon 2 of HPPD using CRISPR-Cas9. Phenotypic, developmental, and reproductive parameters were evaluated to assess the fitness cost associated with the gene knockout in heterozygous and homozygous transgenic individuals.

Results: Our results revealed that *An. funestus* is susceptible to NTBC inhibition regardless of resistance profile (LC50: FANG= 1.23 μ M, FUMAZ= 0.73 μ M). HPPD gene knockout showed that homozygous females exhibited complete mortality within 24 hours following a blood meal, which was consistent with the lethal phenotype observed with NTBC-mediated chemical inhibition. However, there were no statistically significant differences in heterozygous individuals' life parameters, including fertility and longevity, compared to wildtypes, suggesting that HPPD is haplo sufficient.

Conclusion: This study provides experimental evidence that HPPD is essential for *Anopheles funestus* survival post blood meal and underscores its potential as a candidate target for innovative genetic vector control.

Keywords: HPPD, gene knockout, CRISPR-cas9, genetic control, *Anopheles*

Paper ID# 105

Title: Bridging the resistance gap: From genomic insights to the rational design of new insecticides in Kenya

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1. KEMRI

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Background: Mosquito-borne diseases like malaria and dengue remain major global health threats. Vector control is hampered by widespread insecticide resistance. This study investigated the taxonomic status and resistance profiles of *Anopheles gambiae* s.l. across Kenya and explored the rational discovery of next-generation, selective acetylcholinesterase 1 (AChE1) inhibitors designed to be potent against resistant mutants while safe for humans.

Methods: CDC bottle bioassays were conducted at diagnostic and intensity doses (1×, 2×, 5×, 10×) across five Kenyan epidemiological zones. Taxonomic status and resistance mechanisms were identified via whole-genome sequencing (WGS). Discovery efforts targeted AChE1 using phenoxyacetamides, 4-thiazolidinones, and indole derivatives designed for high selectivity for insect enzymes over human counterparts.

Results: Deltamethrin resistance was confirmed in all zones; 24-hour mortality ranged from 58.8% (Kiambu) to 90.8% (Kwale). Resistance intensity was highest in Busia (10× dose required for susceptibility), while Kirinyaga showed only 86% mortality at 5×. Alpha-cypermethrin and pirimiphos-methyl resistance were widespread, but chlorfenapyr and clothianidin achieved 100% mortality. WGS provided the first confirmed detection of *anopheles coluzzii* in Kenya (Turkana County). Genomic profiling revealed high resistance allele frequencies: *vgsc*-I995f (62%), *gste2*-i114t (64%), and the double mutant *vgsc*-v402l+i1527t (38%), suggesting a range of extension from west/central Africa. Furthermore, three compound classes achieved >100-fold selectivity for mosquito AChE1 and remained effective against the *g122s* resistance mutant in both *An. gambiae* and *Aedes aegypti*.

Conclusion: Findings highlight an urgent need for integrated resistance monitoring and the development of safer, resistance-breaking insecticides to maintain progress in malaria control.

Keywords: *Anopheles gambiae*, *An. coluzzii*, CDC bioassays, WGS, insecticide resistance, AChE1 inhibitors, *vgsc*-I995f, *gste2*-i114t, Kenya

Paper ID# 199

Title: Metagenomic insights into microbiota diversity across malaria vector species and insecticide resistance profiles in Cameroon

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Background: Mosquito-associated microbiota is increasingly recognized as important factors influencing vector competence, ecological adaptation, and insecticide resistance. However, little is known about microbiota diversity among malaria vectors in Central Africa.

Methods: This study investigated the distribution of bacterial communities associated with *Anopheles* mosquitoes collected between 2023 and 2024 from six sites across five eco-geographical regions in Cameroon using multiple sampling methods. Metagenomic analyses as described by Favia et al. (2007) were conducted to characterize microbiota profiles across mosquito species and insecticide resistance genotypes (RR, RS, SS) following *kdr* genotyping analysis.

Results: Marked variation in bacterial diversity was observed across mosquito species, sites, and genotypes. In Yaoundé, *Anopheles coluzzii* RR mosquitoes harbored more bacterial taxa (14) than RS (12) and SS (8), with *Streptococcus* and *Aeromonas* detected exclusively in RR mosquitoes. In Yangah, *An. arabiensis* SS mosquitoes showed greater diversity (23 taxa) than RS (20), whereas SS mosquitoes displayed the highest diversity in *An. pharoensis* and *An. ziemanni*. Spatial analyses identified Djohong and Yangah as sites with the highest microbiota diversity. Species-specific differences were also observed, with *An. coluzzii* generally harboring more diverse bacterial communities than other species.

Conclusion: This study provides one of the first comparative metagenomic assessments of mosquito microbiota across multiple eco-geographical regions in Cameroon. The preliminary findings reveal strong associations between microbiota composition, ecological setting, mosquito species, and insecticide resistance status. The enrichment of specific bacterial taxa in resistant mosquitoes suggests possible microbiome-related mechanisms involved in vector adaptation and resistance, highlighting the importance of integrating microbiome studies into malaria vector surveillance and

control strategies.

Keywords: Insecticide resistance, Microbiota, Mosquito, Malaria.

Paper ID# 163

Title: Standing variation in thermotolerance in the major malaria mosquitoes increases along clinal gradient of increasing aridity and is facilitated by adaptation via chromosomal inversion polymorphisms.

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Background: While ramping and static assays are often utilized to assess insects' vulnerability to temperature extremes associated with the rapidly changing climate, these approaches have not been used extensively in mosquitoes to predict their thermal limits of survival, fitness, and distribution in time and space.

Methods: Using 80 mosquitoes per population in ramping (25-45°C) and static (25-43°C) assays we compared inter- and intra-species thermotolerance of 17 populations of female malaria mosquitoes, including *An. coluzzii*, *An. gambiae* s.s. and *An. arabiensis*, collected along clinal gradient of increasing aridity spanning humid Atlantic coast (swamp) of southern Nigeria, northward through Savannah and Sahel in Nigeria and Niger Republic. We established species mean CTmax and LT50s at 80% relative humidity and interrogated the molecular basis of the mosquitoes' heat tolerance.

Results: While individuals' CTmax range between 39-47°C, interpopulation variations in thermotolerance were observed with CTmax increasing along clinal gradient, and with swamp and rainforest populations exhibiting lower mean CTmax (<43°C), while the Sahel mosquitoes exhibited marginally higher mean CTmax (up to 44°C). For static assays, 42°C was found to be the discriminating temperature, at which all populations reached their LT50s at 24h, except for the Sahel populations, with higher LT50s. The 2La inverted genotypes (2La/2La and 2La/2L+a) were strongly associated with heat survival in individual mosquitoes exhibiting CTmax of 45-47°C, and survivors of up to 43°C in static assays, regardless of ecological origin.

Conclusion: Local adaptations to hotter environments impose standing variation in thermotolerance

in African Anopheles, with 2La structural variation conferring heat tolerance advantage. These findings can inform predictive modelling about Anopheles distribution in the fast-warming world, for future planning of targeted control measures, in the face of scarce resources.

Keywords: Malaria, mosquitoes, Anopheles, climate change, heat tolerance, 2La, inversion

Paper ID# 145

Title: Therapeutic efficacy of Artemether Lumefantrine in the treatment of uncomplicated Plasmodium falciparum malaria in Msambweni Sub- County, Coastal Kenya.

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Background: Malaria remains a leading cause of morbidity in Kenya, with the Coastal region experiencing a high disease burden. Despite the World Health Organization's recommendation of Artemisinin-based Combination Therapies (ACTs), reports of partial resistance are emerging across Sub-Saharan Africa. This study evaluated the therapeutic efficacy of Artemether-lumefantrine (AL), Kenya's first-line treatment, in Msambweni, Kwale County.

Methods: A one-arm prospective therapeutic efficacy study (TES) was conducted based on the standard WHO 42-day protocol. Children aged 6 months to 14 years with microscopically confirmed uncomplicated *P. falciparum* malaria (1,000–200,000 parasites/ μ l) were enrolled. Participants received direct observed treatment of AL and were followed up for 42 days. The primary endpoints were Adequate Clinical and Parasitological Response (ACPR) at days 28 and 42

Results: Of 1,189 patients screened, 166 were enrolled (median age: 68 months; median parasitemia: 25,000/ μ l). By Day 3, 92.8% of participants had cleared their parasites, with a median clearance time of 2 days. In the Per Protocol (PP) analysis, the ACPR was 87.5% (95% CI: 82.3–93.1) at Day 28 and dropped to 81.4% (95% CI: 75.1–87.9) by Day 42. Intention-to-Treat (ITT) results were comparable, with an ACPR of 80.2% at Day 42.

Conclusion: This data provides evidence that AL efficacy in Msambweni sub-county is nearing WHO thresholds of more than 10% failure rate. The high parasite and fever clearance rates, however, indicate that Artemether lumefantrine remains a highly effective first-line treatment for uncomplicated malaria in Kenya. Although most of the parasite recurrences were driven by Late Parasitological Response, this is an indication that a subset of the population serves as a reservoir for potential malaria transmission.

Keywords: Malaria, Therapeutic Efficacy Trial, ACPR,

Paper ID# 114

Title: Genomic connectivity and adaptive Gene Flow in *Anopheles gambiae* from East and Central AfricaFekadu Gudeta^{1,*}

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Background: We characterized the genomic population structure and adaptive gene flow in *Anopheles gambiae* from western Ethiopia, Benishangul-Gumuz and Gambella and compared them with East and Central African populations.

Method: All the samples were whole-genome sequenced and analysed bioinformatically. Seventy-nine mosquito samples were passed on quality control after sequencing and genome-wide regions.

Result: The finding revealed that Ethiopian populations are internally homogenous and genetically most similar to inland East African cohorts: Uganda (western and eastern); Kenya (Busia, Kiambu, and Turkana); Tanzania (Kagera); and Nord-Ubangi in the DRC, with extremely low differentiation ($F_{st} \approx 0.003-0.011$). In contrast, coastal populations of Kenya (Kilifi) and Tanzania (Tanga) formed distinct clusters with elevated F_{st} values ($F_{st} \approx 0.05-0.07$), suggesting population bottlenecks and ecological specialisations. Ethiopian populations carry both East African (L995S) and Central African (L995F) alleles at the *Vgsc* locus, alongside variants in *Cyp6aa/p* and *Gste2*.

Discussion: Despite broad regional cohesion, dispersal in Ethiopia is constrained by ecological and geographical barriers, such as river basins, mountainous terrain, and cropland expansion. At insecticide resistance loci, allele sharing proved highly locus-specific: metabolic variants such as *Cyp6aa/p* and *Gste2* broadly mirrored genome-wide connectivity; at the same time, target-site mutations like *Vgsc*-L995F remained geographically restricted. Notably, Ethiopia emerges as a genomic “melting pot” where resistance alleles from East and Central Africa converge, creating critical zones for onwards dissemination. Western Ethiopian *An. gambiae* are genetically closer to inland East African populations than to coastal East African or Central African populations. It underscores Ethiopia’s role within the inland East-Central African continuum while highlighting localized ecological limits on connectivity.

Keywords: *Anopheles gambiae* s.s., Adaptive gene flow, genome-wide connectivity, Locus-specific allele sharing, population structure

Paper ID# 24

Title: Non-geographical population structure of malaria vector *Anopheles gambiae* and *Anopheles coluzzii* but weak structure in *Anopheles arabiensis* within Burkina Faso:

Implications for vector control and gene drive implementation

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Background: Malaria control tools are nowadays challenged by the expansion and persistence of insecticide resistance in the malaria vector along with the changes in vector behaviour. To complement and reinforce the existing control tools, innovative vector control methods, such as gene drives, are currently under development. Understanding the *Anopheles gambiae* s.l. population structure is crucial for the implementation of genetic control tools and improvement of existing control strategies. Here we investigated the genetic diversity and population structure of *Anopheles gambiae* s.l. populations from three climatic zones in Burkina Faso.

Method: mosquito specimens were collected using the pyrethroid spray capture technique. The whole genomes of *An. gambiae* s.l. were sequenced as part of the *Anopheles gambiae* 1000 Genomes Project. MalariaGEN Resource were used to analysed the data.

Results: The results revealed the absence of geographical population structure in *An. coluzzii* and *An. gambiae* s.s collected in the three climatic zones, implicating high gene flow within the country. *Anopheles arabiensis* showed a structure that separates Hauts-Bassins samples in the Soudanian zone from others *An. arabiensis* samples. The cryptic species previously identified in the country were not detected in this study. Our findings indicate also population expansion in *An. gambiae* s.l. however *An. arabiensis* populations show evidence of a smaller population size or a bottleneck.

Conclusion: The population structure of *An. gambiae* s.s and *An. coluzzii* across the country is characterized by a lack of geographical differentiation. These findings have important implications for both current vector control strategies and the potential implementation of gene-driven technologies. Indeed, the lack of geographical population structure offers the potential for rapid spread of gene drive construct. It demands also a coordinated and regional approach to manage insecticide resistance.

Keywords: Population structure, malaria vectors, gene drive, population expansion, vector control

Scientific Session 15: Novel Vector Control Tools & Product Innovation

Paper ID# 201

Title: Exploration of the potential of bacterial fermentative activity in blocking the transmission of *Plasmodium sp.*

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Background: In the context of public health issues, malaria incidence continues to increase, highlighting the need to implement innovative and effective strategies. Bacterial ferments supplementation to mosquitoes' diet could contribute to the proliferation of their intestinal microbiota in order to create competition between microorganisms, which could impact the outcome of *Plasmodium sp* infection in *Anopheles gambiae s.l.* The aim of this study was to assess the effect of probiotics and postbiotics such as *Lactobacillus sp.*, *Lactococcus sp.* and *Bifidobacterium sp.* on blocking malaria transmission.

Methods: This was a six-month experimental study conducted on laboratory *Anopheles* mosquitoes at the Institut des Sciences et Technique (INSTech). Daily doses of 3×10^{10} , 6×10^{10} , and 9×10^{10} CFU/L of bacterial suspension, corresponding to 0.05%, 0.1%, and 0.15% probiotic/postbiotic solutions, respectively, were administered via supplementation with mosquitoes sugar juice. Furthermore, after exposure to the treatment solutions, a series of experimental infections were performed. Parameters such as feeding rate and certain criteria related to vector capacity (prevalence, oocyst intensity) were evaluated. Chi-square test (χ^2), Generalized Linear mixed Model (GLM) and Cox survival analysis were used for statistical analyses.

Results: Our results showed a significant effect of treatment on the proportion of feeding mosquitoes and on adult mortality ($p < 0.001$). Furthermore, a reduction in parasite load was observed on day 16 post-infection at doses of 6×10^{10} and 9×10^{10} CFU/L, on the one hand and a lower proportion of ruptured oocysts compared to the control groups on the other hand. This fraction of fissured oocysts is negatively influenced by the total number of oocysts hosted in the mosquito stomach, especially for those that have undergone at doses of 6×10^{10} CFU/L.

Conclusion: Bacterial inocula could play a crucial role in blocking the transmission of *Plasmodium sp.*

Keywords: Probiotics, Postbiotics, Supplementation, Bacterial inocula, *Anopheles gambiae s.l.*, Blocking Malaria Transmission

Paper ID# 135

Title: Artificial blood diet drives transient fitness costs in *Anopheles stephensi* but maintains vector competence.

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Background: Large-scale research on mosquitoes as vectors usually relies on preserved vertebrate blood or blood from sedated live animals. Artificial diets like SkitoSnack offer promising long-term solutions, but their generational impact on mosquito fitness and parasite development requires a comprehensive assessment.

Methods: We transitioned *Anopheles stephensi* mosquitoes from mouse blood (MB) to SkitoSnack (SS) and assessed impacts on mosquito life history traits and vector competence at generation 0 and after several generations.

Results: Our results reveal that the initial transition from blood feeding to SS (generation F0) causes substantial fitness costs for mosquitoes. Specifically, females fed SS were 37% less likely to lay eggs, and those that did lay produced 33% fewer eggs, alongside significant drops in maternal lipids, glycogen, and total sugars reserves. These impacts extended to the next generation, with F₁ offspring showing 10% lower hatch rates and 22% lower pupation rates compared to MB-fed controls. However, following maintenance on SS for 6-10 generations, most of these fitness costs improved. By F₆ generation, mosquito survival recovered and feeding rates matched those of blood-fed controls. Furthermore, SS-reared mosquitoes make highly competent vectors, with infection prevalence, oocysts burdens and sporozoites loads matching those reared with MB. By F₁₀ generation most traits such as nutritional reserves, hatch rate, pupation rate and offspring development had fully recovered. However, despite this amelioration the clutch size in SS remained 20% less than the MB-reared mosquitoes.

In addition, there is evidence for fast adaptation to SS diet, the minor impacts on survival don't affect vector competence studies, and the clutch size might be improved with more generations of selection and potentially increasing iron levels in SS.

Conclusion: Overall, SkitoSnack is a practical, cost effective, and scalable alternative to vertebrate blood without ethical or financial constraints.

Keywords: scalable, resource-efficient alternative to vertebrate blood without the ethical or financial constraints

Paper ID# 37

Title: Spatio-temporal distribution of Aedes mosquitoes and impact of microbial larvicides: An ovitrap-based surveillance in peri-urban areas of Yaoundé, Cameroon

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Background: *Aedes* mosquitoes are primary vectors for dengue, chikungunya, and Zika.

Understanding their population dynamics is critical for predicting proliferation and optimizing control. This study characterized the spatio-temporal distribution of *Aedes* and evaluated microbial larvicide efficacy in peri-urban areas of Yaoundé, Cameroon.

Methods: A longitudinal ovitrap-based study was conducted in Nkolbisson, Yaoundé, over two phases: a 12-month pre-intervention period (June 2022-June 2023) using 100 ovitraps across 14 sites and a 6-month intervention period (July 2023-January 2024). During the intervention, baseline-monitored stations 1–50 served as controls, while stations 51–100 were treated monthly with VectoMax® G biolarvicide. Weekly collections of eggs and larvae were performed, followed by laboratory rearing and morphological identification. Species diversity, abundance, and ovitrap indices (OI) were analyzed to assess transmission risk.

Results: During pre-intervention, 51,499 mosquitoes (4 genera, 14 species) were recorded. The *Aedes* genus predominated (n=51,146), led by *Ae. albopictus* (88.14%), followed by *Ae. simpsoni* (5.97%) and *Ae. Aegypti* (5.12%). During the intervention phase, mosquito abundance was significantly lower in treated traps (2,901) compared to controls (21,226) ($p < 0.001$). *Aedes albopictus* remained dominant throughout. Oviposition peaked in April - May 2023 and November 2023, reflecting seasonal environmental drivers. While larviciding significantly reduced mosquito abundance and spatial distribution, ovitrap indices remained

high in the pre-intervention phase before reaching their lowest levels during the intervention

Conclusion: Microbial larviciding effectively suppresses *Aedes* populations under field conditions in this peri-urban setting. These findings highlight the utility of ovitraps for monitoring and the need for rigorous, targeted larval control within integrated vector management strategies.

Keywords: *Aedes*, VectoMax®G, ovitraps, Yaoundé, Cameroon

Paper ID# 256

Title: Antimalarial-treated nets: a potential novel intervention with modelled impact comparable to pyrethroid-chlorfenapyr nets

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Background: Pyrethroid (Pyr)-chlorfenapyr (CFP) insecticide-treated nets (ITNs) have mitigated reduced efficacy as pyrethroid resistance has spread across sub-Saharan Africa. Interventions with novel mechanisms of action are needed to mitigate future CFP resistance.

Methods: This was a combined laboratory and modelling study. As a proof-of-concept antimalarial-treated net (ATN), netting was coated with endochin-like quinolone-453 (ELQ-453) at 200 mg/m²; *Anopheles gambiae* rested on treated or untreated nets for ≤6 minutes at various times before or after an infectious *Plasmodium falciparum* blood meal. Oocyst and sporozoite count data, assayed by dissection up to 13 days post-infection, were fitted in RStan to characterize time-dependency of transmission-blocking probability and extrinsic incubation period (EIP) lengthening. Published field oocyst counts and efficacy decay were incorporated to represent a final product. Fitted parameter estimates calibrated transmission dynamics simulations in different settings with a custom fork of the malaria simulation R package for ATNs and a pyrethroid-combined ATN (Pyr-ATN), versus Pyr-only, Pyr-PBO and Pyr-CFP.

Results: Concurrent ATN exposure and an infectious blood meal are estimated to fully block onward transmission. Transmission-blocking probability remains >50% when ATN exposure

occurs up to 33 h [95% CrI: 30, 37] before, or 18 h [95% CrI: 10, 23] after infection. ATN exposure after infection is estimated to lengthen EIP by up to 32% [95% CrI: 23, 44], with ≥ 2 days lengthening when exposure occurs up to 8.4 days [95% CrI: 7.1, 9.5] post-infection. Across all settings, ATNs were projected to avert similar cases to Pyr-CFP ITNs, with Pyr-ATNs averting more.

Conclusions: ATNs would provide a novel mechanism of malaria control that can leverage well-established ITN distribution channels. Modelling indicates epidemiological impact could be comparable to Pyr-CFP and mitigate future CFP resistance.

Keywords: Antimalarial-treated nets; Transmission-blocking; Insecticide resistance management; Mathematical modelling; Malaria control

Paper ID# 22

Title: Evaluation of long-lasting insecticidal nets (LLIN) performance using an experimental hut trial (eht) in Chikwawa district, Malawi.

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Background: Novel indoor vector control tools involve the use of insecticides with new modes of actions and dual chemical treated nets. One of the methods for measuring the efficacy of these interventions is the use of an Experimental Hut Trial (EHT). A study was conducted to evaluate the performance of dual active nets distributed in Malawi using EHT.

Methods: Six experimental huts were enrolled and Olyset plus (OP), Permanet 2 (P2), Royal guard (RG), Interceptor 2 (IG2), Interceptor (IG1) nets and untreated nets were used to characterize nature and efficacy of pyrethroid dual bed nets co-treated with chlorfenapyr, PBO or pyriproxyfen compared to standard pyrethroid only nets in unwashed and washed EHT. Outcomes measured were mosquito density, mortality, blood feeding inhibition status, and fecundity status.

Results: In the EHT, the highest blood-feeding inhibition was recorded for the IG2 net, relative to the standard PermaNet 2.0 net (OR= 1.39-1.91, $P<0.05$). The highest 72-h mortality rate was recorded for the OP net compared to the PermaNet 2.0 net (OR=0.30, 95% CI: 0.17-0.51, $P<0.001$). In contrast, the RG registered lower odds of mortality (OR=0.42,

$P < 0.001$) as compared to other ITN and its killing efficacy declined with aging. In terms of oviposition and fecundity, none of the mosquitoes collected from huts across all net types laid any eggs.

Conclusion: Interceptor G2 nets and OP nets showed a potential to significantly improve the control of malaria-transmitting vectors as IG2 confers personal biting protection and the bed nets laced with PBO provided better mortality which suggest that this combination could be a potential insecticide resistance management tool for preventing malaria transmission in areas with high pyrethroid resistance. The pyriproxyfen net only confer mosquito killing effect when new and efficacy declines with aging.

Keywords: Malaria, *Anopheles gambiae*, Experimental hut, Bed net, Pyrethroid resistance.

Paper ID# 31

Title: Cytochrome P450 2B6 Polymorphisms and Malaria Risk in Nigerian Children: Exploring Host Genetics as a Tool for Targeted Interventions

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Background: Malaria remains a major public health challenge in sub-Saharan Africa, particularly among children under five years. In Nigeria, artemisinin-based combination therapy is the first-line treatment for *Plasmodium falciparum* malaria. However, treatment response varies among individuals, partly due to genetic variation in drug-metabolizing enzymes. Cytochrome P450 2B6 (CYP2B6), a key antimalaria drug metabolizing enzyme, exhibits genetic polymorphisms that may influence drug response and malaria susceptibility. This study investigated the frequency of common CYP2B6 variants (516G>T [rs3745274], 785A>G [rs2279343], and 64C>T [rs2279345]) and their association with malaria in a Yoruba population, highlighting their potential as markers for emerging interventions.

Methods: Two hundred malaria-positive Yoruba children were recruited and genotyped using restriction fragment length polymorphism–polymerase chain reaction (RFLP-PCR). Genotypic and allelic frequencies were calculated, linkage disequilibrium (LD), Hardy–Weinberg equilibrium (HWE) was assessed, and associations were tested under three genetic models using PLINK v1.90 and Haploview 4.2.

Results: Minor allele frequencies were 0.12 (785A>G), 0.375 (64C>T), and 0.423 (516G>T). The variants were not in LD. 785A>G and 516G>T conformed to HWE. Genotype distributions of 785A>G and 64C>T differed significantly across malaria phenotypes. Notably, 785A>G was associated with reduced malaria risk. Under dominant and additive models, 785A>G reduced the risk of uncomplicated malaria (odds ratio [OR] = 0.35; 95% confidence interval [CI]: 0.15–0.81; $p = 0.0142$) and severe malaria (OR = 0.44; 95% CI: 0.20–0.97; $p = 0.0439$) relative to asymptomatic malaria.

Conclusion: CYP2B6 785A>G may protect against malaria while influencing artemisinin metabolism. These findings highlight host genetic markers as potential tools for emerging malaria interventions and support the development of precision public health strategies.

Keywords: CYP2B6, malaria risk, SNP, Yoruba Population, Children

Paper ID# 15

Title: Genetic variation of plasmodium falciparum histidine-rich protein-2 (pfrhp2) gene and overcoming malaria diagnostic threats/challenges in Bamenda and Yaoundé, Cameroon.

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Background: Reliable malaria detection is undermined by pfrhp2 gene deletions and systemic field microscopy inaccuracies. This study evaluated the prevalence of pfrhp2 deletions and operational diagnostic challenges in Cameroon.

Methods: A cross-sectional hospital-based study screened 2,934 febrile patients presenting at clinical facilities in Bamenda (N = 2,464) and Yaoundé (N = 470) in 2024. Field microscopy (MP) performed by laboratory technicians was compared against HRP2 rapid diagnostic tests (RDTs). DNA was extracted using Chelex and validated via human glyceraldehyde-3-phosphate dehydrogenase (hsgapdh) genotyping. Molecular confirmation of Pf was conducted via nested PCR targeting the Pf18S rRNA on all discordant samples (MP-positive/RDT-negative) and a subset of low-density concordant (MP positive/RDT positive) positive samples (50-200 parasites/ μ L). Parasite DNA integrity was verified using pfglurp nested PCR prior to definitive semi-nested pfrhp2 deletion profiling. Diagnostic metrics were computed using PCR as the reference standard.

Results: Molecular screening identified 107 discordant cases (n=84 Bamenda; n=23 Yaoundé) and 200 concordant positives. Validation yielded 106 hsgapdh-positive templates. PCR confirmed that 97.59% (81/83) of discordant cases in Bamenda and 95.65% (22/23) in Yaoundé were negatives, revealing massive MP false positives (103/106). Only 3 discordant samples (2.91%) were Pf positive. One pfrhp2 deletion was confirmed in Bamenda, establishing a true deletion prevalence of 0.49% (1/205) in the parasite-positive pool by microscopy. RDTs remained reliable; sensitivity was 81.82%–

85.71% and specificity 90.48%–98.00% across sites ($P < 0.0005$).

Conclusion: Malaria control in Cameroon is threatened more by a microscopy overdiagnosis epidemic (>95 %) than by pfhrp2 deletions (0.49 %). While HRP2-RDTs remain clinically utility, diagnostic accuracy requires urgent technician refresher training, protocol adherence, and AI-integrated MP.

Keywords: Pfhrp2 deletion, diagnostic challenges, Bamenda, Yaoundé, Cameroon

Paper ID# 66

Title: A novel method for controlling adult simulium to support elimination of onchocerciasis: preliminary study

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Background: Onchocerciasis, a neglected tropical disease caused by the filarial worm *Onchocerca volvulus*, is transmitted to humans through the bites of blackflies of the genus *Simulium*. Despite multiple rounds of ivermectin treatment, transmission of onchocerciasis continues to persist. This preliminary study aims to assess the impact of “Host Decoy Traps” (HDT) on *Simulium* populations in order to accelerate the elimination of the disease.

Methods: The research was conducted in Bafia, a hyperendemic region near the Mbam River in Cameroon. The study was carried out in two phases. Phase 1 established baseline data on blackfly biting rates using the Human Landing Catch (HLC) method while testing two HDT variants: one baited with CO₂ and one without. In Phase 2, four of the more effective HDT variants were utilized as an intervention, operating for three consecutive days each month for two months, with ongoing HLC monitoring. A distance of 20 meters was maintained between the traps.

Results: Analysis revealed that CO₂-baited HDTs were significantly more effective, capturing 65.52% of *Simulium* compared to the unbaited traps. Baited HDT was used for the study. Preliminary results indicated that a total of 3,321 blackflies were collected, resulting in a monthly biting rate of 17,112 bites per person. During the intervention phase, the monthly biting rate decreases to 12,275 bites per person. The intervention also demonstrated a reduction in human landing catches, suggesting that the efficacy of the HDTs might decrease the aggressiveness of the blackflies and alter their biting

behavior

Conclusion: Overall, the interventions significantly reduced blackfly populations and transmission parameters, leading to decreased human exposure to bites. Ongoing monitoring and further research are essential for optimizing control strategies. The findings indicate that HDT shows promise in combating onchocerciasis, warranting further investigation for sustainable vector control.

Keywords: Simulium, Control, Onchocerciasis, elimination, Host Decoy Trap

Paper ID# 3

Title: Possible association of the L1014F kdr mutation with a higher prevalence and load of the Plasmodium-blocking symbiont Microsporidia MB in *Anopheles gambiae* s.l. in Benin

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Background: The present study aims to assess the association of the Plasmodium transmission-blocking endosymbiont Microsporidia MB previously identified in *Anopheles gambiae* s.l. with the carriage of the genotypes of the L1014F kdr mutation.

Methods: Adult mosquitoes were field collected using human landing catches (HLCs) across 60 villages in the Covè, Ouinhi, and Zangnanado communes of southern Benin. After morphological identification, a sub-sample of *An. gambiae* s.l. were molecularly speciated and genotyped for the L1014F kdr mutation by Polymerase Chain Reaction (PCR). Enzyme-Linked Immunosorbent Assay (ELISA) and qPCR were also used to assess infection with Plasmodium falciparum sporozoites and Microsporidia MB, respectively.

Results: The *An. gambiae* complex (N=1040) was composed of 93.7% *An. coluzzii*, 4.4% *An. gambiae* s.s., 0.2% *An. gambiae* s.s./*coluzzii* hybrids, while the rest failed to amplify. Infection prevalence with Microsporidia MB was 1.6% (95% CI: 0.7-3.3) in *An. coluzzii* and 2.2% (95% CI: 0.1-13.2) in *An. gambiae* s.s. The *P. falciparum* sporozoite rate was 2% (95% CI: 1.2-3.1, N=974) in *An. coluzzii*, and null in *An. gambiae* s.s. (N=46). None of the mosquitoes infected with Microsporidia MB were infected with *P. falciparum*. The frequency of the L1014F kdr mutation was 75.1% (95% CI: 73.1-76.9) in *An. coluzzii* and 91.3% (95% CI: 83.1-95.9) in *An. gambiae* s.s. Microsporidia MB was absent in kdr-SS mosquitoes but was present in low proportions in both kdr-RS and kdr-RR mosquitoes (1.9%, 95% CI: 0.6-5.1). The mean load of Microsporidia MB DNA was higher in kdr-RR (23.23 ng/ul, 95% CI: 18.77-28.48) compared to kdr-RS (10.13 ng/ul, 95% CI: 7.36-13.91) mosquitoes.

Conclusion: Findings of the present study suggests that a natural impairment of the Plasmodium

parasite development could occur more in the L1014F kdr resistant allele bearer mosquitoes, as they displayed a higher prevalence and load of *Microsporidia MB* than their susceptible counterparts.

Keywords: *Microsporidia MB*, *Plasmodium*, L1014F kdr mutation

Scientific Session 16: Insecticide Resistance monitoring and Management

Paper ID# 249

Title: Evidence of microbiome contribution to the escalation of pyrethroid resistance in the major malaria vectors *Anopheles gambiae s.s.* and *Anopheles funestus s.s.*

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Background: Exacerbation of pyrethroid resistance severely jeopardises the effectiveness of malaria vector control efforts. However, the mechanisms enabling the vectors to now survive exposure to very high doses of pyrethroids remain unclear.

Methods: Using High-throughput sequencing of the 16S ribosomal RNA gene coupled with antibiotic treatment, we provide evidence linking the mosquito microbiome to the escalation of pyrethroid resistance in major African malaria vectors, *Anopheles gambiae* (s.s.) and *Anopheles funestus* (s.s.).

Results: A significant difference in bacterial composition was observed in *An. gambiae* s.s. between resistant mosquitoes exposed to 1X and 10X in the diagnostic dose of permethrin, and the susceptible strains (PERMANOVA-F: 8.06; p= 0.02). The abundance of *Pseudomonas_1* (Log2FC: 4.42, p= 0.0001) and *Burkholderia_1* (Log2FC: 4.95, p= 0.001) bacteria were consistently associated with mosquitoes surviving 1X and 10X the diagnostic concentrations of permethrin, respectively, while *Serratia_2* bacteria was mostly associated with insecticide susceptibility. In the *An. funestus* s.s. strain, there was no significant difference in bacterial alpha- and beta-diversity between the FUMAZ-R (exhibiting normal deltamethrin-resistance) and FUMAZ-HR (selected for high deltamethrin-resistance). However, in FUMAZ-HR, there was an increase in the abundance of *Rahnella* (Log2FC: 15.954, p= 9.73 E-12) and *Leucobacter* (Log2FC: 7.6, p= 0.008) bacteria. Furthermore, treating resistant mosquitoes (both *Anopheles* species) with broad-spectrum bactericidal antibiotics (penicillin/streptomycin) via sugar solution increased their susceptibility to various diagnostic doses of permethrin and deltamethrin in WHO pyrethroid intensity bioassays.

Conclusion: Overall, our study emphasizes the potential role of the microbiome in the escalation of insecticide resistance in *Anopheles* mosquitoes, identifying key bacterial strains associated with insecticide resistance and susceptibility.

Keywords: Malaria, Microbiome, Pyrethroids, Resistance escalation, *An. funestus* s.s., *An. gambiae* s.s.

Paper ID# 26

Title: Insecticide resistance profiles of *Anopheles arabiensis* and relationship with *microsporidia* mb infection in two rice agroecosystems in Kenya

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Background: Insecticide resistance monitoring is central to the Global Plan for Insecticide Resistance Management in malaria vectors. This study assessed the susceptibility of *Anopheles arabiensis* from Mwea and Ahero, Kenya, to six insecticides and examined the association between resistance and *Microsporidia* MB, a symbiont known to block malaria transmission.

Methods: F₁ females were tested against permethrin, deltamethrin, alphacypermethrin, malathion, bendiocarb, and DDT using CDC bottle bioassays. Resistance intensity and synergist bioassays (with piperonyl butoxide, PBO) were conducted for pyrethroids, and *Microsporidia* MB infection was quantified via qPCR.

Results: Out of 3,120 mosquitoes tested, both populations were susceptible to bendiocarb but resistant to all pyrethroids. Mortality rates were low for alphacypermethrin, permethrin, and deltamethrin (Ahero: 0%, 4.7%, 25.7%; Mwea: 25.7%, 6.2%, 26.6%). Permethrin resistance intensity increased with concentration. Ahero remained susceptible to malathion but showed reduced DDT susceptibility (92.7%), whereas Mwea was susceptible to DDT but resistant to malathion (69.2%). PBO fully restored pyrethroid susceptibility in Mwea, indicating metabolic resistance, and partially restored permethrin susceptibility in Ahero suggesting other mechanisms. *Microsporidia* MB was detected in Ahero, with significantly higher infection density in mosquitoes surviving 2× and 5× permethrin doses compared to those that succumbed to these doses ($p = 0.002$).

Conclusion: *An. arabiensis* populations exhibited heterogeneous but high levels of insecticide resistance, particularly pyrethroids. These findings underscore the need for synergist-based interventions in resistance management. This study is the first to link *Microsporidia* MB density with insecticide resistance intensity in *An. arabiensis*, warranting further investigation into this

relationship and its implications for malaria control.

Keywords: Malaria vectors, Insecticide resistance, Irrigation, Pyrethroids, Microsporidia MB

Paper ID# 20

Title: Pesticide residues in house dust as a route of exposure and potential driver for insecticide resistance in *Anopheles* mosquitoes

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Introduction: Insecticide resistance in malaria vectors threatens the sustainability of malaria control strategies. Rural Zambian households sit at the intersection of national ITN/IRS coverage and widespread agricultural insecticide use, with limited household-level differentiation between sources. We explored whether household dust may act as a reservoir of pesticide residues from either pathway, representing a potential exposure route for *Anopheles* mosquitoes.

Methods: Soil and dust samples from 19 rural Zambian houses contained cypermethrin (0.013–2.45 µg/g), profenofos (0.001–0.086 µg/g), imidacloprid (0.00006–16.2 µg/g), fipronil (0.001–0.19 µg/g), and amitraz metabolites (1.0–647 µg/g). Bioassays used a WHO cone bioassay adapted to force soil-contact exposure, with lab-reared, non-blood-fed *An. coluzzii* females aged 2–5 days (WUR colony).

Results: LC₅₀ values were 9.69 µg/g (cypermethrin), 18.45 µg/g (profenofos), and 11.4 µg/g (fipronil), all above concentrations detected in dust, suggesting limited to no acute lethality. Sublethal effects were nevertheless observed: cypermethrin, profenofos, and imidacloprid reduced mosquito longevity at doses well below their LC₅₀, with Lowest Observed Effect Concentration (LOEC) values overlapping environmental ranges. Residue levels in several households matched or exceeded those linked to sublethal effects.

Conclusion: Chronic, low-dose exposure could impair mosquito survival and induce detoxification responses, which may contribute to resistance development under field conditions. In ongoing work, we will compare the prevalence of insecticide resistance genes across sites to test whether they are more common in areas with higher household contamination. House dust may be an overlooked driver of selection, linking agricultural and public health insecticide use to vector control. Integrating residue monitoring into resistance-management frameworks may help address this underexplored

risk.

Keywords: Malaria; *Anopheles*; Insecticide resistance; Pesticide; Mosquito

Paper ID# 253

Title: *Metarhizium pingshaense* infection reverses insecticide resistance in *Anopheles gambiae* *sensu lato* by altering gene expression and energy depletion

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Background: New tools are required to address insecticide resistance in malaria vectors to strengthen existing control strategies. The entomopathogenic fungus *Metarhizium* spp. has shown a strong ability to reduce the survival and vectorial capacity of infected mosquitoes. However, interaction with insecticide and the underlying mechanisms are still unclear. Here we aim to elucidate the molecular and biochemical mechanisms underlying this interaction.

Methods: Female *An. coluzzii* VKPER, field-collected *An. gambiae* *s.l.* and *An. gambiae* Kisumu aged from 3 to 5 days were sprayed with *Metarhizium pingshaense* S10 (1×10^7 spores/ml) or Tween 80 solution (control). Mosquito survival was monitored up to 14 days post infection. Glucose, glycogen, and lipids were quantified according to Van Handel's protocol. Gene expression including CYP6P3, CYP6Z1, GSTe2 and Defensin was quantified by RT-qPCR following exposure to deltamethrin. These experiments were repeated at 1 hour, 4 and 8 days of post-infection, with three replicates for each. Transcription and energy data were analysed using a mixed-effects linear model and survival data with Coxph model.

Results: *Metarhizium* infection significantly reduced mosquito survival. Mean glycogen concentration was $118.6 \pm 14.9 \mu\text{g/L}$ (control) vs 27.3 ± 14.9 (j4) and $39.7 \pm 14.9 \mu\text{g/L}$ (j8) in treated group, respectively, lipids concentration was 243.3 ± 19.3 vs 181.0 ± 19.3 (j4) and $200.0 \pm 19.3 \mu\text{g/L}$ (j8). Glucose concentration was similar in both groups. Compared with deltamethrin alone, a decrease in the expression of defensin -22.7% (95% CI: 5.2–40.2, $p = 0.012$), GSTe2 -34.2% (95% CI: -10.3–79.9, $p = 0.15$), CYP6Z1 -21.8% (95% CI: 4.4–39.3, $p < 0.05$), and CYP6P3 -36.3% (95% CI: 10.9–61.7, $p < 0.05$) was observed.

Conclusions: Overall, these findings suggest that *Metarhizium pingshaense* may improve chemical

insecticide efficacy by impairing mosquito fitness and reducing insecticide resistance-related gene expression.

Keywords: Malaria, Vector control, *Metarhizium spp.*, Deltamethrin, Integrated vector control

Paper ID# 107

Title: Two highly selected CYP6P4a and CYP6P4b alleles confer insecticide resistance in the major malaria vector *An. funestus* in Cameroon, undermining the effectiveness of insecticide-treated bed nets.

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Background: The rise of insecticide resistance (IR) in malaria vectors is a severe threat to control efforts. Understanding the underlying mechanisms of driving IR is key for developing sustainable interventions. Our study investigated the genomic drivers of pyrethroid resistance escalation and how two genes, Cytochrome 6P4a and 6P4b, drive IR in the malaria vector, *Anopheles funestus*, in Cameroon.

Methods: We used whole genome sequencing (WGS) on highly resistant and highly susceptible field *An. funestus* from Cameroon (2021), pyrethroid insecticide metabolism assays, and transgenic *Drosophila* fly models to characterize the genetic drivers of pyrethroid IR in this population. We further developed two DNA-based molecular diagnostic tools, which were used to track IR across several countries in Africa.

Results: The WGS analyses identified genomic signatures linked to strong IR, notably at the rp1 (chromosome 2R) locus, with the selection of a mutant allele for CYP6P4a and CYP6P4b. Recombinant enzymes from these alleles exhibited significantly greater ability (3-fold) to metabolize pyrethroids than wild-type enzymes. Transgenic flies expressing the alleles also exhibited higher resistance to pyrethroids (mortality <50%) than those expressing wild-type alleles (>80%), further confirming their role in IR. Moreover, our diagnostic tools revealed that these variants are linked to reduced bed net killing efficacy, as mosquitoes bearing the mutant alleles had significantly higher chances of surviving exposure to pyrethroid-treated bed nets. Tracking their spread revealed a rapid rise in frequency in Cameroon from 10% in 2014 to 98% in 2021. These variants were also detected across East and Central Africa.

Conclusion: Our study demonstrated an important role played by CYP6P4a and CYP6P4b in IR

escalation in *An. funestus* and introduced two DNA-based diagnostic tools for IR detection and monitoring, strengthening resistance surveillance and deployment of appropriate bed nets.

Keywords: Genetics; Insecticide resistance; Molecular diagnostic tools

Paper ID# 236

Title: Insecticide resistance pattern of *Anopheles gambiae* s.l. in urban Freetown, Sierra Leone.

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Background: Insecticide resistance in malaria vectors threatens the effectiveness of insecticide-treated nets (ITNs) and indoor residual spraying (IRS) in Sierra Leone. This study assessed insecticide resistance, species composition, and knockdown resistance (kdr) mutations in *Anopheles gambiae* s.l. populations from Freetown.

Methods: *Anopheles gambiae* s.l. larvae were collected from Portee and New England Ville Fin Freetown city, Sierra Leone between June and October 2023 and reared to adults. Female mosquitoes aged 3–5 days were tested using WHO susceptibility assays against deltamethrin and alphacypermethrin, with and without piperonyl butoxide (PBO). Susceptibility to pirimiphos-methyl, chlorfenapyr, and clothianidin was also evaluated. A subset of mosquitoes was identified to sibling species and screened for L1014F and L1014S kdr mutations.

Results: A total of 2,600 mosquitoes were tested. *Anopheles gambiae* s.s. was the predominant species (91.45%), followed by *An. coluzzii* (8.37%) and *An. arabiensis* (0.18%). High resistance to pyrethroids was observed at both sites. Deltamethrin mortality was 13% in New England and 9% in Portee, while alphacypermethrin mortality was 8% and 10%, respectively. PBO significantly increased mortality for both insecticides, indicating metabolic resistance. Mosquitoes remained fully susceptible to pirimiphos-methyl and chlorfenapyr but showed possible resistance to clothianidin. The L1014F mutation was detected at near-fixation levels, while L1014S was absent.

Conclusion: *Anopheles gambiae* s.l. populations in Freetown exhibit high pyrethroid resistance, likely driven by the widespread L1014F mutation and metabolic resistance mechanisms. Clothianidin shows possible resistance while Chlorfenapyr and pirimiphos-methyl were fully susceptible. Continued resistance monitoring is needed to guide malaria vector control. The use of PBO-based and dual-active ingredient ITNs should be sustained to support malaria control efforts in Sierra Leone.

Keywords: Malaria; *Anopheles gambiae*; insecticide resistance; kdr; Sierra Leone; pyrethroids; PBO; vector control

Paper ID# 238

Title: Long-term effects of indoor residual spraying on malaria vector populations and insecticide resistance in central Mali

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Background: Indoor residual spraying (IRS) was implemented in the Baraouéli district of Mali from 2012 to 2016, using carbamates in 2012–2013 and pirimiphos-methyl in 2014–2016. This study assessed the long-term effects of IRS on malaria vector populations and insecticide resistance.

Methods: Entomological surveys were conducted in Boidié, Kamba, and Soungoula villages before and after IRS campaigns in 2014 and 2015, and after IRS withdrawal in 2017. Indoor-resting *Anopheles gambiae s.l.* were collected by pyrethrum spray catches (PSC), while human landing catches (HLC) were performed to assess human-vector contact. WHO susceptibility bioassays were conducted using DDT, permethrin, deltamethrin, bendiocarb, and pirimiphos-methyl. Molecular analyses characterized kdr and ace-1 resistance markers.

Results: A total of 353 *Anopheles gambiae s.l.* were collected by PSC during IRS implementation (2014–2015) compared with 1,615 after IRS withdrawal in 2017, representing a 4.6-fold increase in indoor vector abundance ($\chi^2 = 371.7$, $p < 0.0001$). HLC collections increased from 106 specimens during IRS implementation to 769 after IRS withdrawal. Bioassays revealed strong resistance to DDT and pyrethroids, with mortality rates ranging from 2.7% to 14%, whereas mortality to bendiocarb ranged from 89% to 95%. Full susceptibility to pirimiphos-methyl was observed. High frequencies of kdr-resistant genotypes were detected among 325 specimens, with significant variation among villages ($\chi^2 = 13.88$, $p = 0.031$). Ace-1 resistant genotypes were rare among 329 specimens and showed no significant variation among villages ($p = 0.322$).

Conclusion: IRS substantially reduced malaria vector populations and human-vector contact. Following its withdrawal, vector abundance rebounded rapidly while resistance to DDT and pyrethroids remained high. Continuous entomological and molecular surveillance is essential to guide resistance management and sustain malaria vector control in Mali.

Keywords: *Anopheles gambiae s.l.*; Indoor Residual Spraying (IRS); Insecticide Resistance; kdr Mutation; ace-1 Mutation.

Paper ID# 255

Title: Escalating pyrethroid resistance in *Anopheles funestus* increases Plasmodium transmissionBrice Natchema Soh Fonkou^{1,*}, Magellan Tchouakui¹, Jeannette Tombi², Charles S. Wondji¹

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Background: The swift rise in pyrethroid resistance among malaria vectors poses a major challenge to malaria control. However, limited understanding of the vectorial capacity of highly resistant mosquitoes hinders predictions of how new interventions may affect malaria transmission. Further research is needed to determine how resistance escalation influences transmission dynamics.

Methods: Wild *Anopheles funestus* s.l. mosquitoes were collected from two regions of Cameroon between February and September 2021 using a Prokopack aspirator. Resistance to permethrin, deltamethrin and alphacypermethrin was assessed using WHO tube bioassays at diagnostic dose (DD), 5× DD and 10× DD. Plasmodium sporozoite infections were detected using TaqMan and nested PCR, and resistance markers were genotyped by allele-specific PCR.

Results: Mosquitoes from Mibellon exhibited intense pyrethroid resistance, with only 33% mortality at the DD and <95% mortality at 5× and 10× DD, whereas Elende populations showed lower resistance intensity. Sporozoite infection rates were high in both sites (8.8% and 6%, respectively). Mosquitoes killed by elevated doses of type II pyrethroids were significantly more infected with Plasmodium than survivors ($p < 0.05$). Moreover, mosquitoes surviving the highest deltamethrin doses showed reduced vectorial capacity compared with those surviving the 1× DD (OR=2.8; 95% CI=1.1–7.3; $p=0.041$). High infection rates also persisted among mosquitoes surviving the highest permethrin concentrations. Genotypic analysis identified the L119F-GSTe2 mutation as associated with resistance escalation and increased Plasmodium transmission, whereas homozygous-resistant 454A-CYP9K1 mosquitoes were less infected than susceptible individuals.

Conclusion: These findings highlight the urgent need for effective resistance management strategies to combat escalating pyrethroid resistance, while supporting the sustained use of type II pyrethroids, which remain effective against key Plasmodium-transmitting populations.

Keywords: *An. funestus*, resistance escalation, malaria transmission, vectorial capacity, GSTe2.

Paper ID# 99

Title: Longitudinal surveys of *Anopheles* mosquitoes in Penka-Michel, Cameroon, revealed complex malaria transmission, widespread insecticide resistance, and circulation of non-*falciparum* species

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Background: In the Western Highlands of Cameroon, particularly in Penka-Michel, malaria control remains a challenge due to microclimatic factors, vector plasticity, insecticide resistance, and the co-circulation of non-*falciparum* *Plasmodium* alongside *P. falciparum*

Methods: A 12-month entomological Survey (September 2023-August 2024) was conducted in Penka-Michel to investigate malaria transmission dynamics and insecticide resistance markers, including knockdown resistance mutations (L1014F, N1575Y) and metabolic resistance genes (G119S-Ace1, E205D-CYP6P3, L119F-GSTe2, CYP6P9a/b). Vector density and *Plasmodium* prevalence were monitored. Climate associations with vector abundance and resistance allele frequencies were analyzed using Spearman correlation and Generalized Linear Models (GLMs).

Results: Malaria transmission has depended on the coexistence of three species: *Anopheles funestus* (43.7%), *Anopheles gambiae* (42.9%), and *Anopheles ziemanni* (13.5%). The site was hyperendemic with an annual EIR of 839.5 infective bites/human/night. *Plasmodium falciparum* predominated (70.2%), yet a significant non-falciparum burden was observed (*P. malariae*, 27.5%; *P. ovale*, 22.1%). *An. funestus* was the principal driver (IR=7.8%, EIR=0.9 infective bites/human/night), with *P. falciparum* and *P. ovale curtisi* peaking in the later rainy season (November), while *An. gambiae* (IR=5.4%; EIR=0.6 ib/h/n) vectored *P. malariae* (14.5%) primarily, followed by a sustained peak in the dry season (January). Widespread insecticide resistance was observed, with resistant homozygotes detected in 70% of infected mosquito samples. We observed associations of L119F-GSTe2 mutations with *P. ovale curtisi* transmission (IRR=1.15, $p=0.03$), and L1014F-kdr with *P. malariae* (IRR=2.2, $p=0.04$).

Conclusion: These dynamics highlight a complex multi-species system in which seasonal vector efficiency and insecticide resistance sustains hyperendemicity of the often-overlooked non-falciparum malaria species.

Keywords: Malaria, Transmission, *Anopheles*, insecticide resistance, non-falciparum, Western Highland Cameroon.

Paper ID# 69

Title: Chlorfenapyr-based net Interceptor G2 reduces infection and pyrethroid resistance in *An. gambiae* from Cameroon and Uganda

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Background: Vector control has substantially reduced malaria in Africa, but intense pyrethroid resistance in *Anopheles* mosquitoes now threatens these gains. Dual active-ingredient LLINs such as Interceptor G2 (IG2), are now introduced to mitigate pyrethroid resistance.

Methods: Here, we ask whether large-scale IG2 deployment in Cameroon and Uganda can (i) restore phenotypic susceptibility, (ii) reduce *Plasmodium* infection in vectors, and (iii) drive measurable

short-term evolutionary change in resistance markers.

Results: Household surveys and net inspections showed high IG2 and other LLIN ownership (>90%) but only moderate use (<60% slept under a net the previous night), indicating that low and heterogeneous usage is now a critical barrier to impact. WHO and CDC bioassays nevertheless showed significantly higher pyrethroid mortality in *An. gambiae s.l.* at all IG2 sites 2–3 years post-deployment, indicating partial restoration of susceptibility. *Plasmodium* infection rates in field-collected mosquitoes declined modestly, consistent with improved vector control. Molecular analyses revealed no significant change in L995F-kdr and E2056D-CYP6P3 frequencies between pre- and post-IG2 periods, despite strong laboratory fitness costs, suggesting that short-term evolutionary responses at these loci are subtle. In contrast, CYP6Z1 and CYP9K1 expression declined significantly after IG2 deployment but remained above susceptible-strain levels, indicating a quantitative reduction rather than elimination of metabolic resistance. Surveys of farmers and pesticide sellers revealed extensive agricultural insecticide use, which may counteract IG2-driven selection against resistance.

Conclusion: Overall, IG2 appears to reduce resistance intensity and infection risk without rapid replacement by alternative resistance mechanisms, but realizing its long-term benefits will require integrated management of insecticide use across public-health and agricultural sectors.

Keywords: Malaria, *Anopheles gambiae*, pyrethroid resistance, chlorfenapyr, dual active ingredient nets, resistance management

Scientific Session 17: Spatial Epidemiology & Modelling

Paper ID# 181

Title: The feasibility and success of Sub-National tailoring approach for malaria prevention and control and challenges of its sustainability in Tanzania

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Background: The changing funding and political landscape are two sides of the same coin which have significant impact on health systems, service provision as well as disease prevention, control and expected outcomes. In 2015 Tanzania introduced Sub-National Tailoring to address financial scarcity and disease burden, but was officially implemented between 2020 and 2025, and led to great success in malaria reduction. This study aimed to evaluate how the country SNT processes applied the efficiency and sustainability framework for malaria control and elimination.

Methods: The study was conducted in Kigoma, Lindi, and Shinyanga Regions. Convergent parallel

mixed methods design was used to assess the performance in terms of efficiency and sustainability of SNT implementation in Tanzania. Key Informant Interviews (KIIs) were conducted among government and other implementing partners to document the evolution of SNT, its effectiveness, and sustainability. Thematic content analysis was used in data analysis.

Results: The institutionalization of SNT into the national malaria program facilitated significant improvement in quality and access to diagnostic and treatment at all levels of service provision and prevention at community level. The SNT approach facilitated the allocation of prevention and control strategies based on discovered heterogeneity in malaria transmission and led to significant reduction in malaria burden. Despite success gained, several challenges are identified such as insufficient resources due to over dependency in donor funding; local funding is lower and non-inclusion of climatic data in disease stratification.

Conclusion: Significant local investments in malaria prevention and control are urgently required to ensure key prevention and control strategies to minimize the risk of malaria rebound. Inclusion of climate information is essential to facilitate appropriate allocation of interventions in response to the transmission of risks.

Keywords: Malaria, Sub-National Tailoring, data, allocation of interventions

Paper ID# 148

Title: Building sustainable in-country spatial modelling capacity for malaria vector control: Vector Atlas' PhD support programme

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Background: Effective malaria vector control increasingly depends on high-resolution spatial models integrating entomological, environmental and intervention data. The Vector Atlas — an international partnership funded by the Gates Foundation — was established in 2022 to deliver an open-access platform of analysis-ready vector occurrence, bionomics and insecticide resistance data, and to leverage those data to generate maps supporting National Malaria Control Programme (NMCP) decision-making. Such outputs are central to NMCPs, but the analytical expertise to develop them has typically remained concentrated outside Africa. At an early partnership event, representatives from 16 African countries identified strong demand for in-country capacity to maximise the use of vector surveillance data through spatial analysis. In response, we designed a structured doctoral programme targeting candidates already working with partner NMCPs.

Methods: The programme supports local enrolment and co-supervision of candidates pursuing

research objectives co-developed with NMCPs. Vector Atlas provides close supervision, networking and an adaptive curriculum spanning model-based thinking, spatial modelling and reproducible research workflows, delivered through hands-on mentorship, training intensives and exchange visits. Critically, the cohort supports each other to build and consolidate their skills.

Results: Candidates were recruited across four countries, with a second recruitment phase under way. Each student combines deep familiarity with the Vector Atlas database with sustained engagement with NMCPs and their data, developing tailored responses to continental and country-specific problems — for example, sub-national insecticide resistance and vector distribution maps.

Conclusion: Embedding doctoral training of the next generation of applied spatial modellers supports sustained African leadership and development of leading-edge models and maps for improved malaria vector control.

Keywords: Capacity building, modelling, Sustainability

Paper ID# 119

Title: A new spatial modelling framework for mapping the effectiveness of vector control

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Background: Mass distribution of indoor vector control has drastically reduced the burden of malaria, but this strategy is running out of steam. Outdoor-biting secondary and invasive vectors and rising insecticide resistance reduce intervention impact while vector control budgets are shrinking. Securing the impact of vector control over the coming decades requires local targeting of varied vector control measures to maximise overall impact for a given budget.

Methods: I present a spatial modelling framework for fine-scale mapping of the local effectiveness of vector control interventions at reducing transmission. Combining spatial and statistical models of vector biology (distributions, bionomics, insecticide resistance), simple models of intervention effects on vectors, and user-provided spatial vector control scenarios, the framework maps reductions in vectorial capacity. Vector control decision-makers can then compare the impact on transmission of alternative spatial mixes of vector control interventions, accounting for how vector biology affects their impact.

Results: By synthesizing varied and complex vector biology data into a single measure of impact, the framework supports vector control decision-makers to compare their own scenarios. This also

provides an intuitive link to established mechanistic models that evaluate impact of disease burden.

Conclusion: The framework can be used to model any mix of vector-control interventions. Minimum requirements are sufficient data to map vector densities and species composition, knowledge of species-specific biting rates and behaviours, and understanding of how each intervention impacts vector biting and survival. I demonstrate the framework by applying it to an example of malaria vector control in Africa, leveraging the Vector Atlas database, spatial models, and stakeholder engagement. The resulting district-level maps quantify how effectively single-AI and dual-AI nets could reduce transmission.

Keywords: Mapping; Spatial; Modelling; Malaria

Paper ID# 242

Title: Modeling predictors of malaria Incidence in two epidemiologically distinct low to moderate and high transmission regions of Ethiopia

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Background: Malaria, a parasitic disease transmitted primarily by female *Anopheles* mosquitoes, continues to pose a significant threat to public health, particularly in tropical and subtropical regions. Ethiopia is facing significant health challenges due to malaria, with 75% of the landmass endemic to malaria and around 69% of the population residing in these areas facing the risk of infection, where periodic outbreaks contribute up to 20% of deaths among children under the age of five. The objective of this study was to predict malaria incidence in low to moderate and high transmission regions of Ethiopia.

Methods: The study used weekly aggregated clinical and meteorological data collected from the Oromia and Gambella regions of Ethiopia from January 2014 to December 2023. We employed Random Forest (RF), Extreme Gradient Boosting (XGBoost), Light Gradient Boosting Machine (LGBM), and Deep Neural Networks (DNN) machine learning models to forecast malaria incidence by analyzing ten years of data involving malaria cases and climatic data.

Results: The findings of the study revealed that XGBoost and RF were found to be more accurate in predicting malaria incidence compared to DNN and LGBM. Additionally, the findings also suggested that a one-month lagged carry-on effect, and a three-month rolling (moving average) improved the predictive accuracy of the models. Malaria-positive ratio, location, temperature, seasonality, humidity, and rainfall were the features that determined malaria incidence in the study regions.

Conclusions: Machine learning models enhance decision-making and resource allocations, improve

health outcomes, and influence disease prognosis and prediction, making them a versatile tool in the healthcare system. The findings of this study can help programs generate early warning signals and take timely and effective preventive measures to control the spread of malaria, accelerating the ongoing global efforts towards malaria elimination.

Keywords: Malaria incidence, Machine learning models, lagging, rolling, climatic features, Ethiopia

Paper ID# 55

Title: Modelling the impact of ivermectin-based optimal strategies on malaria control: the role of formulation, coverage, and mosquitocidal efficacy timing

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Background: Despite wide use of insecticidal nets and indoor spraying, residual malaria transmission persists due to insecticide resistance and mosquito behaviours like early and outdoor biting. Ivermectin (IVM) can kill mosquitoes after blood feeding, regardless of the timing or location of the bite. However, oral IVM's short efficacy duration and required frequent dosing limits epidemiological impact. Using mosquitocidal efficacy data from a long-acting injectable IVM formulation (BEPO® technology), we modelled its effect on malaria transmission, comparing it with oral regimens evaluated in the fields.

Methods: We developed an original mathematical model incorporating IVM's pharmacodynamic persistence and stratifying humans by age and sex. Three regimens were evaluated: (i) monthly oral IVM at $3 \times 300 \mu\text{g/kg}$ for 4 months, (ii) monthly oral IVM at $1 \times 400 \mu\text{g/kg}$ for 3 months, and (iii) long-acting BEPO® injection at 0.6 or 1.0 mg/kg. The model includes post-exposure effects on mosquitoes, and the target population excludes women of childbearing age or pregnant women, and children under 15 kg. Mosquitocidal efficacy data were derived from published human oral studies and from preclinical studies in livestock (cattle) for injectable formulations.

Results: Campaigns delivering ivermectin are projected to lower clinical prevalence, with slightly greater benefits in Burkina Faso-like seasonal settings when aligned with the transmission peak. Under perennial transmission and 50–90% target population coverage, oral regimens reduced total cases (all ages) by 7–11%, 9–14%, and 24–38% over one year, depending on the regimen and the

data source. A single long-acting injectable IVM campaign achieved 16–29%, rising to 33–57%, 48–74%, and 59–78% with two, three, and four campaigns, respectively.

Conclusion: Long-acting injectable ivermectin offers increased and sustained efficacy and simpler delivery to tackle residual malaria transmission. Phase 1 trials are timely and warranted.

Keywords: Malaria, Ivermectin, Formulation, Mosquitocidal efficacy, Structured model.

Paper ID# 190

Title: Potential impacts of supplementing next generation long-lasting insecticidal nets with household-scale micro-mosaic deployment of indoor residual spraying with insecticides upon rates of incipient resistance trait emergence and selection

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Background: Prolonged use of few insecticide classes available for long-lasting insecticidal nets and indoor residual spraying (IRS) has driven widespread resistance of malaria vector mosquitoes to this limited arsenal of active ingredients. However, recent innovations like next-generation LLINs (NG-LLINs) containing two complementary insecticides and new insecticide classes for IRS offer new opportunities for pre-emptive resistance management by deploying more diversified actives as mixtures, combinations, rotations or mosaics.

Methods: Here, a deterministic model of mosquito foraging behaviour was formulated to predict the probabilities of successful feeding, deterrence or mortality across repeated feeding attempts in scenarios with different combinations of NG-LLINs and/or IRS micro-mosaics with varying levels of insecticide diversification at the household scale.

Results: The primary outcome was the probability that a single F_0 mosquito carrying a novel resistance trait to a new IRS insecticide successfully feeds, survives and reproduces, thereby establishing those traits within the population. The secondary outcome was the selection coefficient governing the spread of such novel resistance traits from the F_1 generation onwards. For indoor

human-biting vectors like *An. funestus*, combining NG-LLINs with two IRS micro mosaics may delay resistance emergence to about 2 to 2.5-fold, due to direct mortality by NG-LLINs, but gains were limited by outdoor-feeding and adding insecticides beyond two is not expected to provide additional benefits. Once resistance becomes established in F_1 , selection coefficients remain high regardless of intervention mix. For Zoophagic vectors like *An. arabiensis*, these interventions offer little resistance management benefits.

Conclusion: Exclusively indoor-focused vector control strategies may not satisfactorily slow insecticide resistance emergence and spread, so new outdoor protection measures that close these coverage gaps with complementary insecticides will be needed.

Keywords: Resistance, Micro-mosaics, Mathematical Model

Paper ID# 67

Title: Genetic allee effect: exploiting the fate of small populations to contain invasive vectors

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Background: The recent invasion of the Asian malaria vector *Anopheles stephensi* into Africa poses a significant and growing threat to malaria transmission, driven primarily by its distinct ecological and behavioural adaptations that set it apart from native African vectors. However, in the early stages of biological invasion, small founding populations are often inherently vulnerable to several demographic limitations that can give rise to Allee effects (decrease population growth under low density). Although strong Allee effect is relatively uncommon in many species, emerging genetic technologies offer the possibility of deliberately engineering similar effects using genetic load.

Methods: We developed a stochastic individual-based model (IBM) of metapopulation networks, that integrates both the population dynamics and genetics of an invasive species and later parameterized it to simulate the life history and population dynamics of *An. stephensi*. Using this framework, we evaluated whether introducing genetic load can generate sufficiently strong density-dependent feedback to limit establishment and spatial spread across the network.

Results: Simulations demonstrated that introducing genetic load into an invasive population produced demographic bottlenecks consistent with Allee effect, particularly during the colonization of new patches. Increasing genetic load intensity progressively delayed establishment, reduced spatial spread, and at sufficiently high loads, frequently drove local populations to extinction.

Conclusion: These findings suggest that genetic load-induced Allee effects represent a promising strategy for exploiting the inherent vulnerabilities of low-density populations. Our results advance

the growing evidence base for integrating genetic technologies, such as gene drives, into vector control and management frameworks.

Keywords: Malaria, *Anopheles stephensi*, Allee effect, biological invasion, Genetic load, Individual-based model

Paper ID# 184

Title: Mathematical modeling of gene drive replacement under environmental constraints: The influence of density-dependent larval competition.

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Background: Gene Drive technology offers a promising approach for malaria control by genetically modifying mosquito populations. However, translating these tools to the field requires understanding how ecological factors like limited resources and mosquito life history influence success. This study develops a biologically grounded model to assess how density-dependent larval competition affects invasion and fixation of a CRISPR-based homing gene drive.

Methods: Our model tracks male and female mosquitoes through larval and adult stages, simulating resource competition that limits population growth. We incorporate key biological mechanisms: sex-specific survival and reproduction, fitness costs of the drive, and biased inheritance from homing. Stability and sensitivity analyses identified critical factors determining whether the drive is established in a wild population.

Results: Our analysis reveals a significant "invasion barrier": a minimum number of drive-carrying mosquitoes must be released to initiate successful spread. Below this threshold, the drive fails. This barrier is critically determined by homing efficiency and fitness costs. Crucially, including larval competition and life stages substantially raised this barrier and lowered final drive frequency versus simpler models. The most influential parameters were homing efficiency and adult female survival costs.

Conclusion: Our findings demonstrate that ecological complexity is essential for accurate predictions. We provide actionable release thresholds needed to overcome ecological barriers. Failure to account for environmental constraints like larval competition could lead to unsuccessful field trials, highlighting the need for robust release strategies and caution when interpreting simpler model results.

Keywords: Gene drive; CRISPR-Cas9; homing; stage-structured model; density-dependent larval competition; next-generation matrix; bifurc

Paper ID# 207

Title: Insights of antiplasmodial potentials of the secondary metabolites from *Cycicodiscus gabunensis*: virtual screening, drug-likeness and molecular dockingNgo Hanna Joelle^{1,*}

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Background: Despite all efforts to eliminate malaria, it remains a life-threatening disease. There is an urgent need to develop new antimalarial potentials with novel modes of action. Secondary metabolites from *Cylicodiscus gabunensis*, a medicinal plant, have shown a broad spectrum of activities. This study therefore investigated the antimalarial potentials of the secondary metabolites from *Cylicodiscus gabunensis*.

Methods: Virtual screening using databases enabled the identification of several classes of compounds: polyphenols, triterpenes, saponins, and gallate esters. The in-silico prediction of antimalarial activity was carried out through molecular docking on the target proteins 1me6 and 4DPD. Furthermore, the evaluation of pharmacokinetic parameters performed using the SwissADME and ADMETlab 3.0.

Results: The results revealed favorable binding energies for chlorogenic acid (–12.317 kcal/mol) and ellagic acid (–10.874 kcal/mol) against 1me6, as well as maslinic acid (–11.077 kcal/mol) and araliasaponin I (–10.983 kcal/mol) against 4DPD. These values, lower than –10 kcal/mol, suggest strong inhibitory interactions with the studied targets. Gallate esters (butyl gallate and octyl gallate), along with caffeic acid, exhibited a more balanced pharmacokinetic profile, characterized by good, predicted permeability, satisfactory free fraction, and limited toxicity. In contrast, certain bulky saponins, despite their excellent docking scores, showed limitations in terms of oral bioavailability.

Conclusion: The integration of docking results and ADMET predictions thus highlight promising candidates, particularly gallate esters and caffeic acid for their favorable pharmacokinetic balance, as well as chlorogenic acid and maslinic acid for their strong structural affinity toward the protein targets. These findings provide a rational basis for further experimental studies to confirm the antimalarial potential of compounds derived from *Cylicodiscus gabunensis*.

Keywords: *Cylicodiscus gabunensis*; antimalarial; in silico; molecular docking; drug-likeness.

Scientific Session 18: Vector Surveillance & Bionomics

Paper ID# 54

Title: Study of species composition revealed an unexpected presence of *Anopheles coluzzii* in a Southern area of Mozambique

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Background: Four members of the *Anopheles gambiae* complex are known to occur in Mozambique: *An. gambiae sensu stricto* (s.s.), *An. arabiensis* and *An. merus*, which are involved to varying degrees in malaria transmission, and the non-malaria vector *An. quadriannulatus*, each exhibiting different geographical distribution and behavior characteristics. This work aimed to study species composition within members of *Anopheles gambiae* complex and *Anopheles funestus* group in Maputo province, an area targeted for malaria elimination.

Methods: Mosquito were collected during 2020 to 2024, in sentinel sites of National Malaria Control Program in all 8 districts of Maputo province using standard entomological collection techniques such as Human Landing Catches (HLC), Pyrethrum Spray Catches (PSC), CDC Light Traps (CDC LT) and Window Exit Traps (WET). Species were initially identified morphologically and subsequently members of *Anopheles gambiae* complex and *Anopheles funestus* group identified by Polymerase Chain Reaction (PCR) methods.

Results: During 2021, three *Anopheles coluzzii* specimens (1.66%), from Boane, Manhiça and Matola, were identified out of 181 *An. gambiae* complex specimens. This constitutes the first reporting of *An. coluzzii* in Mozambique and in the southernmost region of Africa. However, analyses conducted in collection of 2022 to 2024 did not detect this species and only confirmed that *An. merus* and *An. funestus* s.s. are the main members of *An. gambiae* complex and *An. funestus* group, respectively.

Conclusion: *Anopheles coluzzii*, initially found in West Africa, extended its distribution beyond this region, including East Africa, but has not been reported in the southern regions of Africa. The

presence of *An. coluzzii* in the southern areas of Mozambique was an important but unexpected finding. Further work is recommended on the distribution of the members of this complex, sequencing the samples to confirm the species as well as vector incrimination in various locations in the country and region.

Keywords: *Anopheles coluzzii*, infection rates, southern Mozambique

Paper ID# 23

Title: Seasonal comparison of *Anopheles* mosquito abundance in malaria endemic districts across Northern, Central and Southern Malawi, July 2023-January 2025.

Shupikai Kambiring'oma^{1,*}

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Background: Routine monitoring of vector species composition, abundance, dynamics, feeding pattern, and host preference is the base to determine when, what, and how control should be implemented. A study was conducted to investigate the seasonal abundance of *An. gambiae* and *An. funestus* mosquitoes across Northern, Central and Southern malaria endemic districts in Malawi.

Methods: A longitudinal entomological survey was carried out from July 2023 to January 2025 with monthly mosquito collections. Mosquitoes were sampled using the Pyrethrum Spray Catch (PSC) method and CDC Light Traps (CDC-LT). Mosquitoes were identified morphologically to their species complex level and a subset of *Anopheles gambiae sensu lato* (s.l.) specimens were further confirmed by diagnostic Polymerase Chain Reaction (PCR) to their species level. Data was recorded and analyzed using Microsoft Excel and R software.

Results: *Anopheles* densities were higher in the dry seasons (77%) as compared to the wet seasons, and the dominance was statistically significant. Mosquitoes collected in lake shore districts with higher temperatures mostly accounted for the statistics. Overall, 63 541 mosquitoes, including 43 257 *An. funestus* and 20 284 *An. gambiae*, were collected in all seasons. *Anopheles funestus* s.l. was the predominant taxon (68%). Out of 7438 specimens successfully screened with a diagnostic PCR, 6193 were *An. funestus* s.l. mosquitoes and 1245 were *An. gambiae* s.l. From the 1245 *An. gambiae* s.l. samples, 1212 were confirmed as *An. Arabiensis* and 33 as *An. gambiae* s.s. Molecular species level identification was not done for *An. funestus* s.l. group.

Conclusion: High *anopheles* mosquito density during the dry season collections calls for urgent response when planning for malaria control interventions especially prior to dry seasons. Indoor interventions such as IRS and ITN are recommended as they target the predominant *Anopheles funestus* in Malawi.

Keywords: Malaria, *Anopheles gambiae*, *Anopheles funestus*, abundance, seasonal variation

Paper ID# 273

Title: The Entomology for Impact Initiative: reimagining vector surveillance as decision-driven intelligence in an era of reduced financing

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Background: Entomological surveillance underpins evidence-based vector control, yet the withdrawal of major donor financing threatens the sustainability of national programmes. This demands a shift away from costly, comprehensive monitoring toward strategic surveillance that is explicitly designed to inform programmatic decisions at a substantially lower cost.

Methods: The Entomology for Impact Initiative (EII) reframes surveillance around four core programmatic decisions: which vector control tool to deploy, where, when, and whether it worked. Anchored in the WHO 2025 Malaria Surveillance, Monitoring and Evaluation Manual, EII developed a decision-support tool mapping programmatic questions, indicators and sampling methods to each decision. These were operationalized through costing tools to strengthen national funding proposals.

Results: EII has supported country-tailored surveillance plans and budget models supporting Global Fund Grant Cycle 8 applications across several countries. Outputs include a practitioner's quick guide, hybrid fixed-and-rotating surveillance architectures, and multi-scenario costing tools enabling ministries to weigh strategic trade-offs. These demonstrate that surveillance can be substantially streamlined while preserving the information needed for tool selection, resistance management, and outbreak response.

Conclusion: EII offers a transferable model for transitioning from activity-driven monitoring to decision-driven entomological intelligence. By linking each indicator to a defensible decision and cost, the approach equips national programmes to sustain effective vector surveillance amid constrained financings.

Keywords: Vector control decision-making, entomological surveillance, sustainable financing, insecticide resistance,

Paper ID# 92

Title: Leveraging Community Health Promoters for enhanced malaria vector surveillance: Lessons from Kenya site of the AnoSTEP Project

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Background: The invasion of *Anopheles stephensi* in sub-Saharan Africa threatens malaria control efforts, yet routine surveillance systems have limited geographic coverage and sampling frequency to track invasive vectors effectively. The Kenya site of the AnoSTEP Afrika Project integrated Community Health Promoters (CHPs) into decentralized vector monitoring while examining behavioral and environmental factors associated with *An. stephensi* establishment and spread.

Methods: A surveillance network was established across 60 sites in 21 Kenyan counties. CHPs were recruited through NMCP networks and trained in larval sampling, habitat identification, and electronic data capture. Larval surveillance was conducted bi-weekly within a 2 km radius of each site. Structured community and household observations documented water-use, storage, waste disposal, and environmental conditions influencing mosquito breeding. Comparison of positive and negative sites enabled assessment of behavioral and environmental factors associated with vector presence. Quality assurance included continuous supervision and molecular specimen identification.

Results: Between August 2025 and March 2026, the CHP-led network completed 6,578 larval habitat surveys. *Anopheles stephensi* was detected in 52% (31/60) of sites across 10 counties, including new detections in Baringo, Tana River, Kilifi, and Kitui counties, contributing to a more comprehensive understanding of its geographic distribution.

Conclusion: Integrating CHPs into malaria vector surveillance was operationally feasible, enabling broad geographic coverage, frequent sampling, and longitudinal monitoring across multiple counties. This community-based approach demonstrates the potential of locally embedded health workers to strengthen surveillance for invasive malaria vectors while generating complementary evidence on behavioral and environmental factors associated with vector establishment and spread

Keywords: *Anopheles stephensi*, invasive species, community-led surveillance, Community Health

Promoters, larval source management, Kenya

Paper ID# 98

Title: Patterns of human expose to malaria vectors and malaria transmission in central and southeastern Senegal

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1. UCAD

Background: Malaria remains a major public health problem in many African countries, including Senegal, where 429,369 malaria cases and 314 related deaths were recorded in 2024. Most of the transmission is insured by *Anopheles gambiae s.l.* and *Anopheles funestus* during the rainy and the beginning of dry season. Efficacy and evaluation of interventions against malaria vectors requires a proficient of how gaps in protection manifest. This study was conducted to determine the bionomics of *An. gambiae s.l.* and the effect of human behavior on malaria transmission.

Method: The study was conducted from July 2023 to March 2024 in Passy, Koar and Bandafassi. *Anopheles* mosquitoes were sampled using Human Landing Catches and Pyrethrum Spray Catches, and human behavior was recorded on field sheets. Infection status, and species molecular identification were determined using Enzyme-Linked Immunosorbent Assay and Polymerase Chain Reaction techniques, respectively.

Results: A total of 619 *An. gambiae s.l.* were collected during the entomological survey. Molecular identification using PCR revealed the presence of *An. arabiensis* 66.68%, *An. coluzzii* 16.11%, *An. gambiae* with 15.11%. Hybrids (*An. gambiae/An. coluzzii*) accounted for 1.66%, which were obtained only from Koar. The entomological inoculation rates were 0.103 and 0.167 infected bites per person per night in Bandafassi and Koar, respectively, and transmission was not detected in Passy. High proportions of protection gaps were recorded outdoors with 68%, 41%, and 39% in Passy, Koar and Bandafassi, respectively. While indoors, protection gaps were 54% at Bandafassi, 29% at Koar and 12% at Passy.

Conclusion: This work has shown that *Anopheles* were mostly nocturnal, with bites occurring between dusk and dawn and pronounced at the extremes. This biting behaviour could increase the risk of transmission, as people tend to use bed nets during the second half of the night and get exposed during the morning.

Keywords: Bionomics, *Anopheles gambiae s.l.*, human behavior, transmission, malaria, Senegal.

Paper ID# 147

Title: Integrated entomological surveillance and predictive modelling to identify high-risk malaria transmission areas in current four elimination Counties in Kenya.

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Background: Malaria transmission in Kenya varies geographically and is influenced by vector ecology, climate variability, and human-vector interactions. This study employed a longitudinal integrated entomological surveillance and predictive modelling to assess mosquito vector distribution, malaria risk, and resurgence patterns in four malaria elimination counties in Kenya: Kirinyaga, Nyandarua, Nyeri, and Laikipia.

Methods: Adult mosquitoes were collected using pyrethrum spray catches, hand catches, and light traps, followed by morphological and molecular identification. Sporozoite infection and host blood meal sources were determined using ELISA. Small Area Estimation (SAE) combined with Random Forest machine learning was used to identify malaria resurgence hotspots and priority intervention areas at sub-county level. Multivariable regression assessed predictors of malaria transmission ($p < 0.001$).

Results: A total of 2,563 mosquitoes were collected. *An. Gambia* accounted for 99.73% of the mosquito population. All sporozoite-positive mosquitoes ($n=25$) were detected exclusively in Kirinyaga County. Blood meal analysis revealed human-vector interaction (7.49%), while malaria incidence peaked in 2018 among children under five years. The SAE model revealed marked spatial heterogeneity across the four counties, with Kirinyaga recording the highest resurgence risk scores, particularly in Kirinyaga Central sub-county and random Forest analysis also identified Laikipia as a priority area. Temperature and precipitation were significantly associated with malaria incidence ($p < 0.001$). The predictive model highlighted localized hotspots that may not be detectable through routine surveillance alone.

Conclusion: Integrating entomological, environmental, and epidemiological data improved hotspot detection and supported evidence-based targeting surveillance and vector control interventions. The modelling approach successfully identified areas at greatest risk of malaria resurgence, hence proper decision-making.

Keywords: Malaria, predictive modelling, mosquitoes

Paper ID# 151

Title: *Wolbachia* restricts midgut cell-to-cell viral spread without impairing initial DENV Infection

Godfrey Indinda^{1,*}

1.The Connecticut Agricultural Expe

Background: *Wolbachia* is an obligate intracellular bacterial symbiont that protects mosquitoes against arboviruses such as Dengue, Zika, West Nile, and Chikungunya though the efficacy can vary depending on the system used to study virus blocking (natural vs trans infection), strains of *Wolbachia*, host species, cell line vs insect host. The mechanism(s) of inhibition remain unresolved; the protective phenotype likely stems from a combination of resource competition, host immune priming, metabolic alterations, and strain-specific factors. It remains unclear whether this blocking occurs at the initial viral cellular entry or during cell-to-cell spread.

Methods: By studying DENV-2 in the *Aedes aegypti* midgut at early time points (18 hours post viral infection), we discovered that while the bacteria do not block the initiation of viral infection, they effectively restrict viral midgut dissemination.

Results: Our comparison revealed a hierarchy of protection: wMel provides the most robust restriction and clearing by day 7 post infection compared to wAlbB.

Conclusion: This suggests that *Wolbachia* blocking phenotype is mediated by viral spread restriction rather than acting as a barrier to viral entry.

Keywords: *Wolbachia*; arbovirus; DENV; protective phenotype; *Aedes aegypti*

Paper ID# 138

Title: Understanding *Aedes aegypti* mosquito ecology to reduce dengue transmission in Tanzania

Frank Tenywa^{1,*}, Silvan Haelg², Makame Haji³, Ummi A. Kibondo³, Pie Muller², Daniel Musellem³, Jason Moore³, Jane Machange³, Oswald Dogan³, Iddi H. Mapipi³, Yeromin Mlacha³, Johnson K. Swai³, Christian Lengeler², Sarah J. Moore³

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Background: In the past half-century, dengue has increased by 30-fold. Climate change and

intercontinental trade are driving the spread of the disease. The financial capital of Tanzania, Dar es Salaam, is now experiencing dengue outbreaks nearly every year. Therefore, this study intended to determine the primary characteristics and dengue transmission risk of *Aedes aegypti* mosquitoes in the Ilala, Kinondoni, and Temeke districts of Dar es Salaam city.

Method: A two-year longitudinal survey was conducted monthly in 240 houses to sample *Aedes aegypti* mosquitoes using four mosquito sampling methods: i) mosquito dipper, ii) Prokopack aspiration, iii) Ovitrap iv) Biogent Sentinel trap. The collected *Aedes aegypti* mosquitoes were pooled into 10 individuals and tested for DENV1-4 serotypes using qPCR. Field larvae were reared to F1 and tested for phenotypic resistance to public health used insecticides using the WHO tube tests and genotypic resistance profile using qPCR.

Results: In total, 83,530 mosquitoes were collected and 7.3% (n=6070) were *Aedes aegypti*. Temeke district accounted for 51.5% (n=3129) of all collected *Ae. aegypti* mosquitoes followed by Ilala 25.9% (n=1573) and Kinondoni 22.5% (n=1368). 4030 mosquito pools of 10 individuals per pool were obtained, 168, 103, and 132 pools from Temeke, Ilala, and Kinondoni districts respectively. Temeke and Kinondoni districts were positive for DENV-2 serotype, with Temeke district demonstrating higher infection rate (11.9). *Aedes aegypti* from all three districts showed resistance to pyrethroid and organochlorine (<20% mortality) and were susceptible to carbamate. Also, mosquitoes from all districts showed F1534C mutations.

Conclusion: In Dar es Salaam City, Temeke district is at high risk of the Dengue outbreak due to high *Aedes aegypti* mosquito density and dengue infection rate. Carbamate is a suitable insecticide class for *Aedes aegypti* control that we recommend being used in fumigation and space spray in the city.

Keywords: DENV; dengue fever; traps; blood feeding; longitudinal survey; *Aedes aegypti*; Mosquito ecology; Insecticide resistance

Paper ID# 192

Title: Adulticidal activities and synergistic effects of *Citrus aurantiifolia* peels and *Hyptis spicigera* leaves essential oils against *Anopheles gambiae* s.l. (Diptera: Culicidae)

Damas Dainone Ignore^{1,*}

1. PAMCA

Background: Research on new plant-based insecticides meets the need for an alternative to address mosquito resistance to synthetic insecticides. This study assessed the adulticidal activity and synergistic effects of essential oils (EOs) from *Citrus aurantiifolia* peels and *Hyptis spicigera* leaves on female adults of *Anopheles gambiae* s.l.

Methods: The extraction yields were on the order of 0.17 and 0.11%, respectively, for *C. aurantiifolia* and *H. Spicigera* EOs obtained by hydro distillation. The phytochemical composition of the EOs was analysed by Gas Chromatography coupled with Mass Spectrometry (GC-MS). GC-MS revealed that the essential oils of *C. aurantiifolia* and *H. spicigera* contained high amounts of monoterpene compounds (100% and 87.14%, respectively). Adulticidal activity was assessed using WHO and CDC bottle bioassays at concentrations of 2.5, 5, 7.5, and 10 mg/ml/btl.

Results: The EOs of both plants caused significant concentration dependent Knock down and adulticidal activities. Individually, *H. spicigera* EOs had more adulticidal effects (LC50 = 4.42 mg/ml/btl) than did *C. aurantiifolia* EOs (LC50 = 6.79 mg/ml/btl). An EO mixture 25%Ca + 75%Hs from *C. aurantiifolia* and *H. spicigera* had synergistic effects (CI = 142.84; SF = 1.42) on female *Anopheles gambiae* adults.

Conclusion: Combinations of the two plant EOs considerably optimize their insecticidal effectiveness.

Keywords: Malaria; *Anopheles gambiae*; essential oils; adulticidal; synergistic effects

Paper ID# 230

Title: Chikungunya and Dengue in mosquitoes during the 2025 Mombasa outbreak

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1. KEMRI - Wellcome Trust Research Programme

2. KEMRI Wellcome Trust

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Background: Arboviral diseases remain a major public health concern along the Kenyan coast, with recurrent outbreaks of dengue and chikungunya. In 2025, a chikungunya outbreak was reported in Mombasa; however, arboviruses circulating in mosquito vectors during this period remain under-characterized. This study investigated mosquito-borne viruses using an individual-based, vector-focused approach.

Methods: Mosquitoes were collected and morphologically identified, then preserved in TRIzol and processed individually, avoiding pooled analysis. Viral detection was performed using PCR followed by sequencing, with additional metagenomic analysis conducted using the CZID platform.

Results: A total of 48 mosquitoes were analysed, comprising *Aedes aegypti* (n=42), *Culex quinquefasciatus* (n=5), and *Luzia tigripes* (n=1). Arboviral screening identified chikungunya, dengue, and West Nile viruses in mosquito populations, indicating their involvement in the 2025 outbreak.

Metagenomic profiling revealed insect-specific viruses associated with *Aedes* and *Culex*, alongside bacterial endosymbionts such as *Wolbachia pipientis* and *Asaia*, and the avian malaria parasite *Plasmodium relictum* detected exclusively in *Culex* mosquitoes. Individual mosquito preservation with minimal freeze–thaw improved arbovirus detection.

Conclusion: These findings demonstrate co-circulation of chikungunya and dengue viruses in mosquito vectors during the 2025 Mombasa outbreak and highlight the value of individual-based vector surveillance.

Keywords: Dengue, Chikungunya, *Aedes*, Metavirome, Outbreak, Mombasa

Paper ID# 140

Title: Prevalence, seasonality, microbiome associations, and *Plasmodium falciparum* Co-infection patterns of *microsporidia MB* in malaria vectors of Coastal Kenya

Caroline Wanjiku ^{1,*}

KEMRI-Wellcome Trust Research Programme

Background: Sustained malaria control is increasingly threatened by widespread insecticide resistance and vector behavioural adaptations that reduce the effectiveness of conventional interventions. Microbial symbionts such as *Microsporidia MB* (MMB) have emerged as promising complementary tools due to their *Plasmodium falciparum* transmission-blocking potential. However, important gaps remain regarding MMB distribution, microbiome associations, and interactions with malaria parasites.

Methods: Indoor and outdoor CDC light-trap collections were conducted during three seasonal surveys in two villages of Kwale County, Kenya. A total of 1,396 randomly selected anophelines were dissected into gonads, midguts, and cephalothoraxes. Gonads and midguts were screened for MMB using PCR targeting the 18S rRNA gene. Cephalothoraxes were used for MALDI-TOF MS species identification, PCR-based *P. falciparum* sporozoite detection and species confirmation of a 10% subsample. Bacterial 16S rRNA sequencing using Oxford Nanopore Technology was performed on all MMB-positive specimens and corresponding negatives for microbiome profiling.

Results: Overall MMB prevalence was low (4.7%) and varied across villages, seasons, and species groups. Infections were detected in members of both *An. gambiae* and *An. funestus* groups. MMB localized to ovarian and midgut tissues, with gravid females showing higher odds of infection. Distinct bacterial community profiles were observed between MMB-infected and uninfected mosquitoes, including enrichment of specific taxa in infected individuals. One MMB–*P. falciparum* co-infection was detected in *An. rivulorum*.

Conclusions: MMB occurs naturally in malaria vectors from coastal Kenya at low prevalence and appears associated with tissue-specific microbiome restructuring, particularly in ovarian tissues. Detection of MMB-*P. falciparum* co-infection suggests that transmission-blocking efficiency may vary across vector species and warrant further investigation.

Keywords: Endosymbionts, malaria vectors, *Microsporidia*, *Plasmodium falciparum*, Transmission blocking

List of Poster Abstracts

Indoor Residual Spraying & Insecticide Resistance

Paper ID# 182

Title: Limits effects of entomopathogenic fungus local strain S26 of *Metarhizium pingshaense* on vectorial competence of *An. gambiae s.s* in malaria transmission in Southwestern Burkina Faso

Souro Millogo^{1,2,*}

1. IRSS

2. Centre MURAZ

Background: Biological control using microorganisms to fight malaria vectors is a promising tool with insecticide resistance in endemic areas. However, the potential effects of entomopathogenic fungus on mosquito's life story traits (vectorial competence and survival) and *Plasmodium* development are well unknown. This study aimed to evaluate the effects of local entomopathogenic strain *Metarhizium pingshaense*S26 in *An. gambiae s.s* on vectorial competence and survival in malaria transmission endemic area.

Methods: Females *An. gambiae s.s* mosquitos were fed firstly to *P. falciparum* gametocytes through Direct Feeding Membrane Assay (DFMA) technique and secondly were exposed to local strain S26 of *Metarhizium pingshaense* at concentration 107 conidia/ml under laminar flow hood to assess the impact of this entomopathogenic fungi on *Anopheles* vectorial competence (oocysts and sporozoite stages) and survival in an endemic area like Burkina Faso.

Results: Our findings showed that entomopathogenic fungus MetèS26 reduced significantly mosquito survival in *An. gambiae s.s* infected to *P. falciparum* gametocytes ($p < 2e-16$). At 107conidia/ml in *An. gambiae s.s*, local strain Met_S26 had no effect on oocysts prevalence ($p=0,86$ et $p=0,61$, respectively at 7 day and 14-day post-infection) of *P. falciparum* and its intensity ($p=0,62$ et $p=0,20$, respectively at 7th et 14th day post-infection).

Conclusion: Our study paves the road to understand the effect of entomopathogenic fungus strain on

malaria transmission and life story traits such as survival. Further studies are needed to understand the molecular and immunological mechanisms of tripartite interactions between Plasmodium, Metarhizium, and mosquito in an integrated vector management.

Keywords: *P. falciparum*, *An. gambiae* s. s, entomopathogenic fungus, *Metarhizium pingshaense*, vectorial competence, survival, malaria,

Paper ID# 167

Title: Sovrenta 15wp: potential game changer in malaria vector control against *Anopheles arabiensis* in Chiredzi, Zimbabwe

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1. National Institute of Health Research

2. Chiredzi district hospital

Background: Indoor residual spraying (IRS) remains a cornerstone of malaria control in Zimbabwe. This study evaluated the residual efficacy of Sovrenta 15WP against *Anopheles arabiensis* and wild-collected *An. gambiae* s.l. compared with Insecticide B under experimental hut conditions

Methods: The study was conducted at The De Beers Research Laboratory, Chiredzi, Zimbabwe, from June 2025 to May 2026. Sovrenta 15WP, Insecticide B, and water control were applied to experimental huts, each with painted, brick, mud, and cement wall surfaces, using a randomized allocation design (three huts per treatment, giving a total of 9 huts). Monthly WHO cone bioassays were performed for 12 months using laboratory-reared *An. arabiensis* and wild-collected *An. gambiae* s.l., with mortality recorded 72 hours post-exposure. Shapiro Wilk tests assessed normality. Insecticide performance was compared using t-tests and Wilcoxon rank-sum tests, while one-way and two-way ANOVA evaluated wall surface and wall surface × insecticide effects.

Results: Mean mortality remained high throughout the study (>96% for both species). For *An. arabiensis*, mean mortality was 99.20% for Sovrenta 15WP and 99.75% for Insecticide B (mean difference -0.55%; 95% CI: -2.37 to 1.27; p=0.526; Cohen's d=-0.266). For *An. gambiae* s.l., mean mortality was 96.68% and 96.56%, respectively (mean difference 0.13%; 95% CI: -3.65 to 3.91; p=0.944; Cohen's d=0.029). No significant differences were observed between insecticides on any wall surface (all p>0.05), and no wall surface-insecticide interaction was detected (p=0.848; $\eta^2=0.0043$). Mortality remained ≥80% on all wall surfaces throughout the 12-month period.

Conclusion: Sovrenta 15WP demonstrated residual efficacy comparable to Insecticide B against *An. arabiensis* and *An. gambiae* s.l. for 12 months under experimental hut conditions. Findings support its

potential inclusion in IRM on the basis of residual effect only

Keywords: IRS. Sovrenta 15WP, *An. arabiensis*, *An. gambiae s.l.*, IRM, residual, 12 months, IVM, malaria vector control

Paper ID# 257

Title: Impact of metabolic pyrethroid-resistance genes (CYP6P4a and CYP6P4b) in *Anopheles funestus* on the efficacy of chlorfenapyr-based bed nets (Interceptor G2 and PermaNet Dual)

Riccardo Feudjio thiomela^{1,*}, Derrick Foffie¹, Manuela Tchatchoua¹, Metissa Djondji¹, Raoul Tazokong¹, Charles Wondji¹

1. Centre for Research in Infectious Diseases

Background: The increasing spread of insecticide resistance in malaria vectors, particularly pyrethroids, threatens current malaria control efforts and highlights the need for innovation. The development of molecular markers of insecticide resistance and the deployment of new-generation nets (NGN), such as Interceptor G2 (IG2) and PermaNet Dual (PD), which combine pyrethroids (targeting VGSC) and chlorfenapyr (disrupting ATP production), are key tools for sustaining progress toward malaria elimination. This study assessed the impact of two recently established pyrethroid resistance markers in *Anopheles funestus*, CYP6P4a-H169R and CYP6P4b-I288N, on the performance of NGN.

Methods: Insecticide resistance profiles of a field population (Elende) and a hybrid strain (Elende x Fang) of *An. Funestus* were determined using WHO tube and bottle bioassays. The efficacy of IG2 and PD was then evaluated using experimental hut trials in comparison with PBO-based nets (PermaNet 3.0) and pyrethroid-only net (PermaNet 2.0 (P2.0)). Mosquitoes were genotyped using allele-specific PCR to investigate associations between CYP6P4a/b markers and bed net performance.

Results: Field population showed high-intensity resistance to pyrethroids but remained susceptible to chlorfenapyr. IG2 and PD achieved high mortality rates (92.5% and 94%, respectively ($P > 0.05$)), but both were significantly more effective than P3.0 (68.3%) and P2.0 (23.9%) ($P < 0.0001$). For CYP6P4a, homozygous resistant and heterozygous mosquitoes were respectively 11 and 6 times more likely to survive exposure to P2.0 than homozygotes susceptible ($P < 0.0001$). Similar results were observed for the CYP6P4. On the contrary, neither CYP6P4a nor CYP6P4b was associated with survival after exposure to IG2 or PD, confirming the strong performance of chlorfenapyr-based nets.

Conclusion: Despite high pyrethroid resistance in this population, NGN remains highly effective, regardless of CYP6P4a/b resistance genotypes. Their deployment should be prioritized in NMCP

Keywords: *Anopheles funestus*, Pyrethroid resistance, chlorfenapyr, new-generation net, CYP6P4a-

H169R and CYP6P4b-I288N

Paper ID# 155

Title: Are new insecticide-treated nets consistent in killing resistant mosquitoes?Olukayode Odufuwa^{1,*}, Sarah Moore^{1,2}

1. Ifakara Health Institute

2. London School of Hygiene and Tropical Medicine, and Swiss Tropical and Public Health Institute

Background: Widespread pyrethroid resistance led to a new generation of insecticide-treated nets (ITNs) containing chlorfenapyr and pyrethroid-piperonyl butoxide. Ensuring ITNs' performance consistency is critical. This study assesses variability in bioefficacy between the positive control Interceptor G2 (IG2) and Olyset Plus (OLP), and explores correlations among chemical content, resistance profiles, and bioefficacy during quality checks before regeneration time (RT) and in experimental hut trials (EHT).

Methods: A retrospective analysis of studies from the Ifakara Health Institute was conducted. Pooled mosquito mortality estimates for IG2 and OLP nets were calculated using random-effects meta-analysis for inter-study heterogeneity. Data from tunnel and cone bioassays against resistant *Anopheles arabiensis* and susceptible *An. gambiae*, were analysed: unwashed before RT, unwashed before EHT, and 20x-washed before EHT. Linear regressions assessed the relationships among mortality, resistance profiles, and whole-chemical content retention.

Results: Significant variability occurred across datasets. IG2 72-hour tunnel mortality ranged: 59%–97% (unwashed/RT), 42%–56% (unwashed/EHT) and 31%–53% (20x-washed/EHT). OLP 24-hour cone mortality ranged: 72%–100% (unwashed/RT), 18%–51% (unwashed/EHT), and 11%–37% (20x-washed/EHT). Mortality did not correlate with resistance profiles; however, EHT mortality significantly correlated with pyrethroid retention in IG2 nets (P-value=0.0001). Cone unreliably assessed the IG2 pyrethroid component, with susceptible strain mortality varying widely from 23%–84%.

Conclusion: Despite consistent environmental conditions, substantial variability exists, driven by ITN sources and production date. We recommend establishing acceptable performance ranges for positive controls, avoiding ITNs manufactured over two years before testing, and mandating resistance monitoring with mosquito wing length measurements to ensure data reproducibility.

Keywords: ITN, variability, dual-active ingredient, Interceptor G2, Olyset Plus, malaria, mosquito, Tanzania

Paper ID# 160

Title: The before and after method (bam): a chemical approach to determining insecticide regeneration time in pyrethroid-chlorfenapyr ITNs.Olukayode Odufuwa^{1,*}, Aidi Lugenge², Alphonse Assenga², Sarah Smoore^{1,2,3}

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3. Swiss Tropical and Public Health Institute

Background: Artificial ageing through washing is critical for evaluating the chemical and biological durability of insecticide-treated nets (ITNs). However, determining the precise regeneration time (RT), the period required for insecticide to replenish on the net surface after three laboratory washing, is essential to reduce variability in bioassays and ensure realistic testing. This study aimed to estimate the RT for both coated and incorporated pyrethroid-chlorfenapyr ITNs using a standardised insecticide measure of surface concentration.

Methods: A "Before and After Method" (BAM) was employed to assess Interceptor® G2 (coated) and ProNet Duo (incorporated) ITNs. Surface concentration was calculated by comparing chemical assays of net sections before and after a standardised soap wash. Bioefficacy was simultaneously evaluated using tunnel tests with pyrethroid-resistant *Anopheles arabiensis* across multiple regeneration intervals ranging from 3 hours to 40 days after three washes.

Results: Chemical analysis indicated a regeneration time of one day for chlorfenapyr, alphacypermethrin, and bifenthrin across both net types. These results were consistent with bioefficacy data, which also showed a one-day RT in tunnel tests. While chemical data exhibited lower variability than bioassays, no significant correlation was found between surface insecticide concentration and mosquito mortality, suggesting a functional bio-efficacy plateau within the tested range.

Conclusion: The BAM successfully predicted a one-day regeneration time for both incorporated and coated pyrethroid-chlorfenapyr ITNs. This method provides a stable alternative for determining RT, supporting more accurate and standardised artificial ageing protocols for next-generation ITNs.

Keywords: BAM, *Anopheles*, chlorfenapyr, Interceptor G2, ProNet Duo, ITNs, Tanzania

Paper ID# 198

Title: The Ifakara Ambient Chamber Test (I-ACT) for evaluation of Indoor Residual Sprays: A Non-Inferiority Test of Sylando® 240SC and Sumi Shield® 50WG

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2. BASF SE, Professional & Specialty Solutions, Public Health

3. BASF Corporation, Professional & Specialty Solutions, Public Health Global Development

Background: New insecticides for indoor residual spraying (IRS) are being developed to manage resistance. Chlorfenapyr (Sylando® 240SC), a pro-insecticide, is metabolized by active mosquitoes into the toxic metabolite tralopyril. This mode of action requires adapted “free flying” bioassays (because chlorfenapyr is converted to its toxic metabolite tralopyril when mosquitoes are metabolically active).

Methods: A miniature-experimental hut (MEH) assay was developed within the Ifakara Ambient Chamber Test (I-ACT) with a rabbit as a host to measure residual efficacy under controlled conditions. Sylando® 240SC was compared with Sumi Shield® 50WG (clothianidin) for 12-month residual efficacy against malaria and arbovirus vectors. Residual activity was assessed on mud, wood and concrete with two huts per substrate treated with Sylando® 240SC, one with Sumi Shield® 50WG, and one with untreated control. Five replicates of 20 mosquitoes per strain (malaria vectors: pyrethroid-susceptible *Anopheles gambiae* and-resistant *An. arabiensis* and *An. funestus*; culicines *Aedes aegypti* and *Culex quinquefasciatus*) were exposed overnight at one-week post spraying and monthly thereafter. Multivariable mixed-effect logistic regression with binomial errors and log link function assessed non-inferiority with a 7% margin on mosquito mortality as the primary outcome for malaria vectors.

Results: Both products induced delayed mortality, with higher effects on malaria vectors than culicines. Across all substrates and malaria species combined over the full 12 months of observation, Sylando® 240SC was non-inferior to Sumi Shield® 50WG on mortality measured at 72 h (76% vs. 67%, OR = 0.86, 95% CI: 0.77–0.97) and 168 h (89% vs. 82%, OR = 0.74, 95% CI: 0.63–0.87).

Conclusion: Sylando® 240SC performed comparably to Sumi Shield® 50WG, supporting its use as an IRS additional option. The new I-ACT mini-experimental-hut assay provides a practical tool for evaluating pro-insecticides.

Keywords: Sylando; chlorfenapyr; Sumi Shield; clothianidin; Ifakara Ambient Chamber Test (I-ACT); insecticide; bioassay; indoor residual

Paper ID# 174

Title: Spatial colocation analysis of mosquito species across selected communities from Isoko, Delta State, Nigeria.

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1. University of Port Harcourt

Background: Mosquitoes are found in environments which support their survival. Spatial analysis can reveal the association between environmental attributes and mosquitoes. However, spatial associations which can reveal local associations between species have been rarely explored in understanding the associations of mosquitoes' species presence across places. This study measured the local pattern of spatial association among Malaria, Filariasis and Yellow Fever vectors from eleven communities in Delta State, Nigeria.

Method: Field surveys were conducted across the settlements in the study area from June - December 2023 from 160 instances. Locations were recorded; samples collected and identified morphologically. Local colocation quotients (LCLQ) were computed to determine the spatial heterogeneity and association pattern of larva stages of four mosquito genera (*Anopheles*, *Aedes*, *Culex* and *Mansonia*) collected. Significant LCLQ values were those >1 , and the higher values denote higher associations and patterns.

Results: The results showed four patterns of paired association among the mosquito species across the communities sampled which are *Culex- Anopheles*, *Culex- Aedes*, *Culex- Mansonia* and *Anopheles- Aedes*. Significant colocation ($p<0.05$) was found in 14 instances, across the patterns between *Culex - Anopheles* in one location, *Culex - Aedes* in three locations, *Culex - Mansonia* in one location, *Anopheles - Aedes* in two locations while a significant isolated pattern was seen in one location.

Discussion: Outcomes of the spatial analysis demonstrate that vectors species in the study area had significantly strong spatial association, but the degree of the association was dependent on the physical condition and preference of the habitats, denoting common environmental characteristics responsible for vector survival and disease transmission. A wide-scale analysis of different regions is required to establish this finding and incorporate it into vector surveillance and control studies.

Keywords: Colocation analysis, Disease, Isoko, Spatial association, Vectors.

Paper ID# 180

Title: Molecular characterization, transgenerational transmission and sexual auto-dissemination within *Anopheles* mosquitoes of the malaria parasite transmission blocking *Microsporidia Sp* MB in Burkina Faso

Souro Millogo^{1,2,*}

1. IRSS

2. Centre MURAZ

Background: Biological control of malaria vectors using endosymbiotic microorganisms is a promising tool in the context of insecticide resistance. Our study assed to evaluate molecular characterization, transgenerational transmission and sexual auto-dissemination within *Anopheles* Mosquitoes of the Malaria Parasite Transmission Blocking *Microsporidia Sp* MB in Burkina Faso.

Methods: An entomological study was carried out to collect engorged females *Anopheles* resting inside human dwellings, focusing on engorged female mosquitoes, specifically *An. gambiae s.l.* These females were induced to lay eggs individually, resulting in the establishment of colonies of both MB-carrying and MB-negative mosquitoes for three generations. Crossbreeding between MB-infected males and MB-uninfected females was performed. PCR analyses identified the molecular species of *An. gambiae s.l.* and confirmed the presence of *Microsporidia sp.* MB in the samples. Additionally, sporozoites were detected in field *An. Coluzzi* through molecular analysis.

Results: Our findings showed that MB prevalence was significantly higher in *An. coluzzii* than in *An. gambiae s.s.* Furthermore, uninfected virgin female mosquitoes had a lower rate of MB sexual transmission compared to males. In *An. gambiae s.s.*, there was no significant vertical transmission between F2 and F3 in each mosquito strain, while transgenerational transmission was significantly higher in *An. gambiae s.s.* than in *An. coluzzii*. Additionally, 73% of field *An. coluzzii* mosquitoes tested positive for *Microsporidia sp. MB*, indicating a negative correlation between *Microsporidia sp. MB* and *P. falciparum*.

Conclusions: Our findings showed that *Microsporidia sp. MB* could be a promising biological tool to reduce malaria transmission. However, further research is required to understand the interactions between mosquitoes, *Microsporidia sp. MB*, and *Plasmodium* before large-scale implementation

Keywords: *P. falciparum*, *Microsporidia sp. MB*, endosymbiotic microorganisms, *An. gambiae s.l.*, Sexual auto-dissemination, transgeneration

Paper ID# 165

Title: The invisible factor behind insecticide loss in Olyset® netsJilly Mseti^{1,*}

1. Ifakara Health Institute

Background: Insecticide-treated nets (ITNs) are a frontline defense against malaria, but their contribution depends on the chemicals they carry. Over time, these insecticides can evaporate, leaving families vulnerable. This study tracks the 'invisible loss' of protection in Olyset® nets, evaluating the net's ability to retain bio efficacy and how well the nets kill mosquitoes over eight months.

Methodology: To test the nets' ability to retain bioefficacy, we hung unwashed and laboratory-washed Olyset® nets in an experimental hut at the Ifakara Health Institute in Tanzania. We then tracked how effectively the nets killed mosquitoes over eight months. Using standardised WHO tests, we challenged the nets against two groups: resistant (hard-to-kill) *Anopheles arabiensis* and susceptible (easier-to-kill) *An. gambiae*.

Results: Cone Bioassays: Against resistant *An. arabiensis*, 24-hour mortality fell from 100% at baseline to 32% by month four. Susceptible *An. gambiae* mortality also declined, dropping from 100% to 48.7% (washed) and 79.3% (unwashed). Tunnel Tests: Mortality for resistant mosquitoes dropped from 82% to below 50% in month four. However, the nets remained highly effective against susceptible mosquitoes, maintaining >90% mortality through eight months.

Conclusion: Insecticide levels deplete significantly over time due to evaporation rather than washing, as both net types performed similarly. This identifies evaporation as a critical factor in reduced ITN efficacy, particularly against resistant mosquito populations. Future net designs must prioritize better retention of active ingredients to ensure long-term malaria protection.

Keywords: Cone bioassay, tunnel test, bio efficacy, evaporative loss, net aging

Paper ID# 8

Title: The effect of repeated washing of the royal guard, interceptor g1 and g2 nets on survival of *Anopheles* mosquitoes in Chikwawa district; MalawiJudith Banda^{1,*}

1. Lilongwe University of Agriculture and Natural Resources

Background: Long-lasting insecticidal nets (LLINs) are a key malaria control tool that protects users from infectious mosquito bites. The World Health Organization (WHO) recommends that LLINs maintain their insecticidal effectiveness after repeated washing throughout their operational lifespan. WHO durability assessments evaluate whether nets retain adequate bio efficacy after up to 20

standardized washes, with acceptable performance defined as $\geq 80\%$ mosquito mortality after 24 hours or $\geq 95\%$ knockdown after 60 minutes in bioassays. New-generation dual active ingredient LLINs, including Interceptor® G2 (IG2) and Royal Guard® (RG), have been developed to improve control of insecticide-resistant malaria vectors. However, evidence of their wash resistance compared with conventional LLINs remains limited. This study evaluated the wash durability of IG2 and RG relative to Interceptor® G1 and an untreated control net.

Methods: The LLINs were washed 20 times using WHO standard soap and dried in a shed while considering the regeneration time of each net. WHO cone bioassays were conducted using 2-3 days *An. gambiae* Kisumu and *An. gambiae* s.l. A total of 1,400 mosquitoes were exposed to all nets for 3 minutes. Knockdown was observed from 5 minutes to 60 minutes. Final mortality was observed from 24hrs to 72 hrs for each net.

Results: High mortality ($>80\%$) of mosquitoes was observed across the washes for all the three treated nets and test mosquitoes. Time to knock down increased with number of washes for IG1. There was a significant difference in knock down mortality for *An. gambiae* s.l between untreated vs RG (95% CI -98.26 to -92.54, $p < 0.001$). The difference was not significant in IG1 and IG2 (95% CI -5.737 to 2.137, $p = 0.6317$).

Conclusion: Repeated washing of Interceptor IG2 and Royal guard nets did not affect the efficacy of these nets which shows that the distribution of these nets in Malawi have a positive impact in reducing malaria vectors.

Keywords: *Anopheles*, net washing, survival, mortality

Paper ID# 261

Title: High insecticide resistance and loss of net physical integrity: A big challenge for vector control in Cameroon

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Background: Long-lasting insecticidal nets (LLINs) remain one of the most widespread and impactful malaria prevention and control in Africa. Unfortunately, the continued effectiveness of these interventions is threatened by the spread of pyrethroid resistance in most endemic settings. This study was conducted to investigate major factors influencing the physical integrity and bio-efficacy of nets in Yaoundé.

Methods: From 2024 to 2025, a cross-sectional survey was conducted across 188 randomly selected households in 15 study sites to assess the physical integrity and bio-efficacy of nets as well as the factors associated with net utilization. The WHO cone assay was used to assess the bioefficacy of nets. Holes in LLINs were counted and classified into four sizes, and net integrity was determined using the WHO-recommended PHI. To identify the factors affecting net physical integrity, univariate negative binomial mixed regression models were used, while multivariate mixed logistic regression models were used to identify the factors affecting net bio-efficacy.

Results: A total loss of bio-efficacy and an extremely high loss of physical integrity of nets were observed in Yaoundé. High insecticide resistance against field *An. gambiaes.l.* mosquitoes were observed, with mortality rates ranging between 0% and 42.19%. Nearly all LLINs assessed had holes and over 25% of these nets were in « torn condition». The most common types of holes were size 1, and the majority of these holes were on the front side of the net. Many factors were found to strongly correlate with the reported loss of effectiveness and physical integrity of nets.

Conclusions: National malaria control programs should raise public awareness on the appropriate handling, best practices and maintenance of nets. New approaches and active system of insecticide resistance monitoring urgently need to be implemented to slow down the spread of insecticide resistance and strengthen vector control and eradicate malaria

Keywords: LLINs, Physical integrity, Bio-efficacy, *Anopheles gambiae*, Yaoundé, Cameroon

Paper ID# 46

Title: The evaluation of the SumiOne™ spatial emanators against wild *Anopheles funestus* in experimental huts in Siaya, Western Kenya

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Background: Spatial Emanators (SEs) are a promising vector control approach that could supplement existing malaria control tools.

Methods: SumiOne™ SE efficacy was evaluated indoors in six experimental huts over 24 nights using human landing catches (HLCs) and aspiration. Collections were conducted in two 12-night phases, alternating between HLC and aspiration every six nights. Outcomes included reductions in human landing rates, density, exophily, and blood feeding inhibition.

Results: *Anopheles funestus* sl. was the predominant species (n=1679;82.2%), followed by *An. gambiae* sl. (n=340; 16.6%). SumiOne™ SE significantly reduced indoor and outdoor densities of *An. funestus* with 63% protective effect indoors (IRR = 0.37, 95% CI: 0.20-0.69, p = 0.0087) while there was a 44% reduction outdoor although this was not statistically significant (IRR = 0.56, 95% CI: 0.31-1.00, p = 0.0702). Overall *An. funestus* density (indoor and outdoor combined) was reduced by 58% (IRR=0.42, 95% CI: 0.22-0.79; p=0.0222). The rate of exophily of *An. funestus* exiting was 34% (95% CI: 27%-42%) in the intervention huts compared to 2% (95% CI: 1%-4%) in the control huts (p<0.0001). Blood feeding inhibition for *An. funestus* was 46% with 41% (95% CI: 36%-51%) of the collected mosquitoes being blood fed in the intervention huts compared to 81% (95% CI: 76-86) blood fed in the control huts, (p<0.0001).

Conclusion: These findings support SumiOne™ SE's potential as a complementary vector control tool alongside existing core interventions such as insecticide-treated nets and indoor residual spraying, particularly in settings where additional protection against malaria vectors is needed. Given the recent WHO conditional recommendation for SEs, the demonstrated efficacy of SumiOne™ SE contributes important evidence for expanding the portfolio of available SE products, which will be critical for ensuring sustainable supply, fostering market competition, and supporting innovation as SEs are scaled up.

Keywords: Spatial emanators, *Anopheles funestus*, SumiOne™ SE

Insecticide Resistance and Monitoring

Paper ID# 234

Title: Site-specific bio-efficacy of Interceptor G2 and Royal Guard against highly pyrethroid-resistant *Anopheles gambiae* s.l. in experimental hut trials in southwestern Burkina Faso.

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Background: Insecticide-treated nets (ITNs) had lowered malaria cases and deaths by 68% in endemic regions of Burkina Faso by 2015, but today, the challenge of insecticide resistance requires novel ITN treatments.

Methods: This study assessed the effectiveness of dual active ingredient ITNs, Interceptor G2 and Royal Guard against highly resistant (< 10% mortality rate to alpha-cypermethrin 0.05%) *Anopheles gambiae s.l.* in experimental hut trials in Tannounyan region, Burkina Faso. Following World Health Organisation 2013 guidelines, two sets of six, west African type huts were located at two sentinel sites (Tiefora and Tengrela) at a distance of 40 km from each other.

Results: Among 22,234 mosquitoes collected over three years, 66.6% were *An. gambiae s.l.* with *Anopheles coluzzii* and *An. gambiae s.s.*, dominant in abundance at Tengrela and Tiefora respectively. Unwashed Interceptor G2 ITNs induced the highest mosquito mortality rates, 57% and 34% as 72-hour mortality in Tiefora and Tengrela respectively; mortality rates were higher for *An. gambiae* than *An. coluzzii* and significantly higher in both sites compared to standard ITNs. Net washing or aging reduced the efficacy of both Interceptor G2 and Royal Guard. Only unwashed Royal Guard nets reduced blood-feeding success compared to standard ITNs. Follow up on the sublethal effects of the different arms showed Royal Guard ITNs drastically reduced *Anopheles gambiae s.l.* offspring numbers compared to other net treatments.

Conclusions: Our study suggests that dual-ingredient net impacts vary with local vector ecology, emphasizing the need for targeted strategies of deployment and monitoring.

Keywords: *Anopheles gambiae s.l.*, Interceptor G2, Royal Guard, experimental hut, Burkina Faso, insecticide resistance, sublethal effect

Paper ID# 143

Title: Cytochrome p450-mediated pyrethroid resistance in *Anopheles mosquitoes*: A review of diversity and regional distribution in AfricaKemi Adetunji^{1,*}*1. Nigerian Institute of Medical Research*

Background: Pyrethroid resistance in *Anopheles* mosquitoes is primarily driven by metabolic resistance and poses a significant threat to malaria control and elimination efforts in Africa. Cytochrome P450 (CYP450) enzymes play a key role in the detoxification of pyrethroid insecticides, reducing the effectiveness of vector control interventions, and contributing to sustained malaria transmission. Despite the importance of CYP450-mediated resistance, information on molecular markers suitable for resistance surveillance remains limited.

Methods: We explored PubMed and Google Scholar with the keyword's metabolic resistance, pyrethroid resistance, CYP450 in *Anopheles*, resistance in *Anopheles*, and insecticide resistance. A total of 128 records were retrieved. Following the exclusion of 55 duplicates, 3 conference proceedings, 18 studies involving Asian *Anopheles* populations, and 2 studies on non-*Anopheles* species, 50 studies met the eligibility criteria and were included in the final analysis.

Results: The review revealed that *Anopheles gambiae* populations in West Africa frequently utilize CYP6Z2 for pyrethroid metabolism. CYP325A3 was consistently expressed in both *Anopheles gambiae* and *Anopheles funestus* across West, East, and Southern Africa, suggesting possible evolutionary conservation. However, CYP325A3 expression was lower in West African *Anopheles gambiae* populations than in *Anopheles funestus* populations from East and Southern Africa. Additionally, CYP6Z3 was consistently detected in *Anopheles gambiae* populations inhabiting similar eco-climatic regions.

Conclusion: Overall, this review demonstrates the broad distribution and variable expression of CYP450 genes across Africa, indicating that metabolic resistance is subject to environmental factors. The recurrent detection of CYP6Z2, CYP6Z3, and CYP325A3 highlights their potential as candidate molecular markers for resistance surveillance and management in malaria vector control programmes.

Keywords: Pyrethroid, Insecticide resistance, Cytochrome P450, Vector control, Metabolic protein, Efficacy, Malaria, *Anopheles*

Paper ID# 159

Title: Effects of the diet of the mosquito *Anopheles gambiae* on its resistance to deltamethrinKhadidiatou Cissé-Niambélé^{1,*}, Jacob C Koella¹, Benjamin Koudou Guibéhi²1. *University of Neuchâtel*

CSRS

Background: While many aspects of the genetic basis of mosquito resistance to insecticides are understood, the degree to which this resistance is affected by environmental parameters such as diet remains unclear. Therefore, two experiments were performed to evaluate how the diet of *Anopheles gambiae*, that is its sugar and blood meals, influences its resistance to deltamethrin.

Methods: The first experiment focused on sugar meals taken from different plants and on the time between the blood meal and the exposure to the insecticide. Mosquitoes had continuous access to *Tevethia nerifolia*, *Ixora coccinea* or *Mandalium coromandelianum* as sugar meals, and half of them received a blood meal. After 15–18 h (i.e., at a time when digestive genes are upregulated) or 60–63 h (i.e., after digestion). They were then exposed to 0.5% deltamethrin for one hour and measured the proportion of mosquitoes that were knocked down during the exposure and that died within the next 24 h. The second experiment examined how the sugar-meal (consisting of the same three plants) interacted with the age at blood feeding. Mosquitoes were blood-fed or left unfed four or 11 days after emergence and exposed to the insecticide 1 day later.

Results: In the first experiment, the plant species had no effect on the rates of mortality or knock-down. If the mosquitoes were exposed earlier, blood-feds were 22.7% less likely to die and 10.0% less likely to be knocked down than unfed, but if they were exposed later, blood-feeding increased mortality by 8.7% and knock-down by 14.0%. In the second experiment, neither the plant nor its interactions with blood meal or age affected mortality, but younger mosquitoes had lower mortality (60.7%) than older ones (66.4%), independently of their blood-meal.

Conclusion: These results underline the complex role of the mosquitoes' diet in response to insecticides.

Keywords: Nectar meal, Blood meal, Insecticide resistance, Mosquitoes, deltamethrin, *Anopheles gambiae*

Paper ID# 157

Title: Susceptibility profile of *Anopheles arabiensis* populations in urban areas of Keur Massar and Rufisque in Dakar, Senegal

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Background: Given the increasing complexity of malaria in urban areas, linked, amongst other things, to population growth, sanitation issues and climate change on the one hand, and peri-urban agriculture and other polluting activities on the other, close monitoring of resistance evolution is required. This study aimed to characterize insecticide susceptibility profile and resistance mechanisms in *An. arabiensis* populations.

Methods: The sampling was carried out by collecting pre-imago stages in Keur Massar and Rufisque. The adult females (3-5-day-old) were subjected to susceptibility tests using WHO protocol. Molecular identification of *An. gambiae* s.l. and detection of Kdr and Ace-1 mutations were characterized using PCR.

Results: A total of 1,115 samples were tested from Keur Massar (575) and Rufisque (540). *Anopheles arabiensis* was the exclusive species found in both districts. The results showed resistance to pyrethroids, with mortality rates ranging from 24.8% to 84%. The populations tested were susceptible to pirimiphos-methyl in all study sites. However, resistance to bendiocarb was observed at Keur Massar (67.7%). The L1014S and L1014F mutations were detected in both areas. The findings indicated that individuals carrying the double mutation (1014F and 1014S) were more abundant, with allele frequencies of 57% in Keur Massar and 50% in Rufisque. The 1014S allele was significantly more common in both areas compared with the 1014F allele ($p < 0.05$). Furthermore, the G119S mutation was detected only in the heterozygous state. The frequencies of the 119S resistance alleles were 9.1% and 26.2% at Keur Massar and Rufisque respectively.

Conclusion: Overall, this study reveals widespread resistance to pyrethroids and to bendiocarb limited to Keur Massar, as well as a susceptibility to pirimiphos-methyl in both locations among populations of *An. arabiensis*. Lack of significant association between Kdr mutations and phenotypic resistance was observed.

Keywords: *An. arabiensis*, insecticides, susceptibility, resistance, Kdr, Ace-1, Keur Massar & Rufisque

Paper ID# 13

Title: KDR mutations and pyrethroid resistance undermine control of *Anopheles gambiae* s.l in Osun state, Nigeria.

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Background: The scourge of insecticide resistance by *Anopheles* mosquitoes remains a public health menace globally. This study evaluates the resistance status of adult female *Anopheles gambiae* s.l to pyrethroids (permethrin, deltamethrin and alpha-cypermethrin), organophosphate (pirimiphosmethyl) insecticides and knockdown resistant (kdr) gene detection in Osun State, Nigeria where pyrethroids are commonly employed.

Methods: Larval sampling was done between 0700hr and 1100hrs weekly between January and December 2022. Collected larvae were reared to adult stage in the Department of Animal and Environmental Biology laboratory of Osun State University, Osogbo, Nigeria and then identified morphologically using morphological keys. Insecticide bioassay was conducted with Permethrin (0.75%), deltamethrin (0.05%), alpha-cypermethrin (0.05%), and pirimiphosmethyl (0.25%) using WHO tube assay. The mosquitoes were subjected to molecular analysis to detect the kdr gene.

Results: Pirimiphosmethyl had a higher knockdown (KD60) and mortality than the pyrethroids tested ($p < 0.05$). There was also no resistance to Pirimiphosmethyl across the study areas. There was resistance to the pyrethroids tested with a mortality of 90-97%, indicating possible resistance. However, Ila showed confirmed resistance to Permethrin, Ejigbo to Alpha-Cypermethrin, and Deltamethrin, with % mortality of 86%, 60%, and 40%, respectively ($p < 0.05$). In addition, the kdr gene was detected across the study areas.

Conclusion: The present study reveals the insecticidal efficacy of pirimiphosmethyl against female *Anopheles gambiae* s.l and the inefficacy of pyrethroids. Thus, the need to intensify efforts on *Anopheles* insecticide resistance surveillance through the use of pirimiphosmethyl in indoor residual spray (IRS) and frequently interchanging the pyrethroid type used in insecticide-treated nets (ITNs). Synergist can be tested in further studies.

Keywords: Insecticide resistance; *Anopheles*; knockdown

Paper ID# 106

Title: Identification of novel gene cluster potentially associated with insecticide resistance in *Anopheles gambiae* s.l.

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Background: Despite the increasing emergence of insecticide resistance, insecticide-based interventions remain the primary method for malaria vector control in Africa. To maintain the effectiveness of these interventions, continuous monitoring and identification of novel resistance mechanisms is essential. This study investigated potential new insecticide resistance genes in the *Anopheles gambiae* complex.

Methods: Whole-genome sequencing data from 1,908 mosquitoes of the *Anopheles gambiae* complex available through the Anopheles gambiae 1000 Genomes Project were analyzed. Using Google Colab and Python programming language, genome-wide scans for positive selection, genetic variation analyses, and population structure analyses were performed to identify and characterize candidate resistance genes.

Results: Strong signatures of positive selection were detected in a chromosome 2L region containing an aldehyde oxidase gene cluster (AGAP006220, AGAP006221, AGAP006224, AGAP006225, and AGAP006226). Numerous single nucleotide polymorphisms (SNPs) were identified, including 569, 691, 1433, 978, and 811 non-synonymous SNPs in AGAP006220, AGAP006221, AGAP006224, AGAP006225, and AGAP006226, respectively, with some variants reaching fixation. Copy number variations (CNVs), including deletions and amplifications, were also detected at low frequencies (<12%). Population structure analyses revealed adaptive and geographic gene flow between *An. gambiae* and *An. coluzzii*, indicating the potential spread of putative resistance-associated variants across populations.

Conclusions: The co-occurrence of strong positive selection and high-frequency functional variants in genes encoding detoxification enzymes provides genomic evidence that aldehyde oxidases may contribute to insecticide resistance in *Anopheles gambiae* s.l. These findings highlight the value of genomic surveillance for identifying novel resistance markers and informing evidence-based vector control strategies.

Keywords: malaria, *An. gambiae* s.l., insecticide resistance, aldehyde oxidase, genomic surveillance

Paper ID# 104

Title: Metabolic insecticide resistance shapes biting behavior and malaria transmission intensity in *Anopheles funestus* from southern Cameroon

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Background: The rapid spread of insecticide resistance in African malaria vectors threatens the effectiveness of pyrethroid-based interventions. While resistance reduces insecticide-induced mortality, its impact on malaria transmission remains poorly understood. We investigated whether metabolic resistance modifies key components of vectorial capacity in natural populations of *An. funestus* in forested Cameroon.

Methods: Cross-sectional entomological surveys were conducted in three rural localities using human landing catches and indoor electric aspirations. Insecticide susceptibility and LLIN bio-efficacy were assessed following WHO protocols. Mosquito parity, *Plasmodium* infection (oocyst and sporozoite stage), resistance markers (L119F-GSTe2 and G454A-CYP9K1), and gene expression levels were analyzed. Associations between resistance and biting behavior, parity, infection, and entomological inoculation rates (EIR) were analyzed statistically.

Results: *Anopheles funestus* exhibited moderate to high pyrethroid resistance (mortality: 7.5–84.4%), mainly driven by cytochrome P450 detoxification, as susceptibility was restored after PBO exposure. Standard and dual-AI LLINs showed low efficacy (mortality: 0–34.9% and <80%, respectively), whereas PBO-based nets remained effective (≥80%). Resistance genotypes were not associated with oocyst infection (χ^2 : 0.12–3.35; $p > 0.1$) but showed site-specific effects on sporozoite infection. Resistant mosquitoes were more likely to be parous, bite indoors ($p < 0.05$), exhibit prolonged nocturnal activity, and sustain higher indoor EIR, indicating enhanced transmission potential.

Conclusion: Cytochrome P450-mediated resistance in *An. funestus* undermines LLIN efficacy and is associated with behavioral and survival traits that sustain malaria transmission. These findings underscore the need for integrated control strategies targeting both physiological resistance and behavioral adaptation while supporting the continued use of PBO-based nets.

Keywords: Metabolic resistance, biting behavior, *An. funestus*, Malaria transmission, Cameroon

Paper ID# 115

Title: Xeno surveillance of *Plasmodium falciparum* antimalarial drugs resistance in Bama, Burkina Faso.

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Background: Resistance to nearly all antimalarial compounds remains a major obstacle to malaria control. Strengthening surveillance systems is therefore essential for monitoring the spread of resistance and guiding health policies. In this context, Xeno surveillance emerges as an innovative and complementary tool. This study evaluated the potential of Xeno surveillance for monitoring antimalarial resistance in Bama (Burkina Faso).

Methods: Blood-fed mosquitoes and dried blood spots (DBS) were collected from 110 households and from patients with symptomatic malaria at Bama health facility during two cross-sectional surveys (rainy season _2018 and dry season _2019). Parasite DNA was extracted using the Kingfisher method, and the pfcr, pfcpp, pfcppmp, and pfcspp genes were genotyped using HRM (pfcr) and AmpSeq (pfcpp, pfcppmp, and pfcspp) techniques to determine allelic mutation frequency and the multiplicity of infection (MOI), respectively.

Results: The allelic frequencies of the PfCRT-K76T mutation, adjusted by MOI, were higher ($p < 0.05$) during both surveys in mosquitoes (40% and 77%) than in humans (29% and 23%). Furthermore, the average MOI was significantly higher ($p < 0.05$) during the rainy season survey (1.88 in mosquitoes; 3.64 in humans) compared to the dry seasons.

Conclusion: These findings suggest that mosquito blood meals can accurately reflect mutation frequencies, particularly those with low prevalence, thereby highlighting the potential of Xeno surveillance as a suitable surveillance tool.

Keywords: Xeno surveillance, *Plasmodium falciparum*, MOI, Burkina Faso

Paper ID# 196

Title: Investigating the contribution of ATP-Binding Cassette (ABC) transporters to insecticide resistance in a major African malaria vector: *Anopheles funestus* s.s.

Murielle Wondji^{1,*}

1. *CRID*

Background: Vector control remains central to malaria prevention, but increasing insecticide resistance in *Anopheles* mosquitoes threatens the effectiveness of existing vector-control tools. While enzymes for Phase I metabolism, such as cytochrome P450s and Phase II, such as UGTs, are well characterized, the contribution of Phase III ABC transporters to resistance remains poorly understood. Here, we investigated the contribution of ABC transporters to alpha-cypermethrin resistance in a major malaria vector, *Anopheles funestus* in Cameroon.

Methods: We used natural populations of *An. funestus* s.s. collected from Elende, Cameroon. Pyrethroid susceptibility profile was assessed using WHO tube bioassays, followed by larval and adult synergist assays with the ABC transporter inhibitor, verapamil, in combination with the insecticide. RNA-Seq-based transcriptional profiling of alphacypermethrin-exposed *An. funestus* s.s. was performed, and a candidate for ABC transporter was functionally validated using RNA interference.

Results: Verapamil pre-exposure partially restored susceptibility, with a significant increase of mortality from 40–70% in standard assays with deltamethrin, alpha-cypermethrin, and permethrin, to 50-90% after exposure. Assays were performed in larvae and adults. RNA-Seq identified several ABC transporters potentially associated with pyrethroid resistance, with ABCA (AFUN019220) being the most over-expressed ABC in exposed versus susceptible (9-fold vs FANG), together with canonical detoxification genes such as Cyp6P9a (23-fold) and Cyp6P9b (10-fold). RNAi-mediated knockdown of ABCA (AFUN019220) significantly increased mortality from 9% to 27% after alpha-cypermethrin exposure compared with GFP-injected controls.

Conclusion: Taken together, these findings support a role for ABC transporters, particularly ABCA (AFUN019220), in pyrethroid resistance in field populations of *An. funestus* s.s., underscoring the need to consider these genes when designing resistance control and management strategies.

Keywords: *Anopheles funestus*; insecticide resistance; pyrethroids; ABC transporters; ABCA(AFUN019220); RNA-Seq; RNAi

Paper ID# 186

Title: Larvicidal activity and molecular interactions of *Furoquinoline* alkaloids from *Araliopsis Soyauxii* with wild-type and g119s mutant acetylcholinesterase of the malaria vector

Anopheles gambiae

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Background: The use of synthetic insecticides has led to target-site mutations such as G119S in acetylcholinesterase, which is a major threat in *Anopheles gambiae* mosquitoes' control. To obtain alternative sources of novel bio-friendly insecticides, our study investigated the larvicidal activity and molecular interactions of four alkaloids isolated from *Araliopsis soyauxii* (Rutaceae) Nkolbisine, Tecleaverdoornine, Kokusaginine, and Flindersiamine against insecticide-susceptible and resistant *An. gambiae* populations.

Methods: The alkaloids of the *A. soyauxii* were obtained from stem barks using column chromatography and characterized by NMR spectroscopy. Using WHO larvicidal bioassays protocol, the susceptible Kisumu strain and field collected strains of *An. gambiae* populations characterized as carrying G119S Ace-1 mutation were exposed to the purified alkaloids with temephos control in distilled water. Molecular interactions analysis was conducted via Molecular docking and MM-GBSA analysis.

Results: Nkolbisine was the most potent, with LC₅₀ values of 51.63 mg/L in the Kisumu strain and 60.12 mg/L in the field strain at 24 h. Tecleaverdoornine was also very active, and Kokusaginine and Flindersiamine followed. Our docking results revealed that Nkolbisine and Tecleaverdoornine had a positive binding affinity to wild-type as well as mutant AChE, with docking of scores -8.94 and -7.75 kcal/mol (wild-type) and -9.25 and -7.90 kcal/mol (mutant), respectively. Interactions such as hydrogen bonding with catalytic residues (GLU448, SER283) and π - π stacking were conserved in aromatic residues (TYR493, TRP441). MM-GBSA analysis, showed that Nkolbisine (-46.27 to -29.39 kcal/mol) interacts favorably with both enzymes.

Conclusion: Hence, Nkolbisine and Tecleaverdoornine are promising larvicidal candidates active against both susceptible and resistant populations of *An. gambiae*.

Keywords: acetylcholinesterase G119S mutation; *Anopheles gambiae*; furoquinoline alkaloids; insecticide resistance; larvicidal activity

Paper ID# 200

Title: Nationwide surveillance of insecticide resistance in *Anopheles gambiae* s.l. across Burkina Faso: uniform pyrethroid failure, high-intensity resistance, and widespread CYP450-mediated metabolic mechanisms

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1. *IRSS*2. *UJKZ*3. *UNB*4. *UCAD*5. *SP*6. *Palu*7. *CHAI*

Background: Insecticide resistance in *Anopheles gambiae* s.l. threatens pyrethroid-based malaria vector control across sub-Saharan Africa. Comprehensive resistance data are urgently needed to guide evidence-based decisions in Burkina Faso, one of the highest malaria burden countries in the region.

Methods: WHO tube bioassays were conducted at 26 sentinel sites across three eco-climatic zones during the 2024 transmission season using deltamethrin, permethrin, malathion, bendiocarb and pirimiphos-methyl. Resistance intensity, PBO synergist assays, species identification and kdr-West (L1014F), kdr-East (L1014S), and Ace-1 (G119S) genotyping were conducted on 473 mosquitoes from 15 sites.

Results: Confirmed pyrethroid resistance was detected at all 26 sites (deltamethrin 18.5%, permethrin 19.2%), with no significant zonal variation ($P > 0.05$). Resistance intensity was high at Kaya (RR = 18.7) and moderate at Ouagadougou (RR = 7.1). Malathion and pirimiphos-methyl retained near-complete efficacy (>99%); confirmed bendiocarb resistance was restricted to Diébougou (89.1%, $P = 0.013$). PBO pre-exposure restored susceptibility at 15 of 16 tested combinations ($P < 0.05$), confirming widespread CYP450-mediated metabolic resistance. The kdr-W allele frequency was not correlated with deltamethrin mortality ($\rho = -0.275$, $P = 0.301$). Species composition differed significantly across zones ($\chi^2 = 64.94$, $P < 0.001$).

Conclusions: *Anopheles gambiae* s.l. in Burkina Faso displays severe, uniform, multi-mechanistic

pyrethroid resistance combining near-fixed *kdr* mutations with CYP450-mediated metabolic resistance. Organophosphates retain efficacy and should be protected through IRS rotation. PBO-reversible metabolic resistance supports priority deployment of PBO-pyrethroid LLINs across all zones.

Keywords. *Anopheles gambiae s.l.*; pyrethroid resistance; *kdr* L1014F; CYP450; PBO synergist; resistance intensity; Burkina Faso.

Paper ID# 130

Title: Phenotypic insecticide resistance and *kdr* mutation profiles in *Aedes aegypti* in Mauritania

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Background: *Aedes aegypti* mosquitoes are present in Nouakchott, where dengue has been endemic since 2014. To assess their resistance to insecticides, eggs were collected in August 2024 from twelve sites spread across five neighborhoods.

Methods: Adult females and first-generation (F1) larvae were used in the bioassays. Adults were exposed to adulticides permethrin, deltamethrin, bendiocarb, and malathion at discriminating doses, while larvae were exposed to seven concentrations of *Bacillus thuringiensis israelensis* (Bti) and temephos in accordance with WHO protocols.

Results: The results reveal high resistance in adults to all insecticides evaluated. Low mortality was observed for all insecticides tested: very low for malathion (5.6%), low for permethrin (18.5%) and deltamethrin (32.6%), and moderate for bendiocarb (64.3%), indicating strong resistance, particularly to organophosphates and pyrethroids. In contrast, the larvae remained susceptible to Bti (LD50 < 50 µg/L) and temephos (LD50 = 6.8 ± 0.7 µg/L). The *kdr* mutations were detected by PCR and sequencing and revealed three *kdr* mutations associated with pyrethroid resistance: S989P, V1016G, and F1534C. The tri-locus genotypes SP/VG/FC are significantly associated with survival to pyrethroids, and PP/GG/FF with resistance to deltamethrin. In Mauritania, there is no vector control program.

Conclusion: These results underscore the urgent need to implement an integrated pest management program that combines the use of biological larvicides, environmental management, and public awareness campaigns.

Keywords: *Aedes aegypti*; arbovirus; Bti; insecticide resistance; kdr; larvicides; temephos; pyrethroids; Mauritania

Paper ID# 30

Title: A survey of aedes mosquito bionomics, insecticide susceptibility and Sero-epidemiology of dengue in the Lake zone, Tanzania

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Background: *Aedes* borne arboviruses like dengue, Chikungunya, yellow fever, and Zika are an increasing global health threat, driven by unplanned urbanization and the spread of artificial mosquito breeding sites. Tanzania has seen repeated dengue outbreaks, with Dar es Salaam as a persistent hotspot. However, arbovirus surveillance remains limited in other regions like the Lake Zone.

Methods: This study investigated *Aedes* mosquito bionomics, insecticide susceptibility, and human dengue sero-epidemiology in urban, semi-urban, and rural areas of Mwanza, Tanzania. A cross-sectional survey was conducted in November 2023 across nine communities with varying urbanization levels. Data collection focused on adult and larval mosquito density, breeding site types, water quality, insecticide resistance, and dengue virus presence in mosquitoes. Human dengue exposure was assessed using rapid diagnostic tests and ELISA on a random sample of hospital attendees from entomological sampling sites.

Results: In total, 180 houses and 503 containers were inspected, revealing 973 immature *Aedes aegypti*, mostly from discarded containers and used tires. The container index peaked in urban areas (57.4%). Rapid tests showed 5% of participants had recent/current dengue infection, while ELISA IgG indicated 40% had prior exposure. Catalytic modeling estimated 10% annual dengue exposure in the population. Spatial analysis revealed heterogeneity in mosquito indices and human exposure. Population density was the main driver of adult mosquito abundance and dengue virus exposure.

Conclusion: These findings confirm active dengue transmission in Tanzania's Lake Zone and highlight the need for sustained surveillance in densely populated areas to prevent future outbreaks.

Keywords: Arboviruses; urbanization; Dengue transmission

Paper ID# 245

Title: The I236M-CYP6P4 mutation confers high fitness costs and increase susceptibility to chlorfenapyr-based nets in the malaria vector *Anopheles gambiae* from Uganda

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Background: Metabolic resistance is widespread in *Anopheles gambiae* malaria vectors, and is largely driven by overexpression and/or mutation of detoxification enzymes such as cytochrome P450. However, the fitness costs of these mechanisms and the impact of different long-lasting insecticidal nets (LLINs) remain poorly understood for this vector.

Methods: This study evaluated the impact of the CYP6P4-I236M resistance mutation on LLIN's efficacy and life-history traits of *Anopheles gambiae* s.l. from Uganda.

Results: It was found that the mutation was strongly linked to higher survival rates in homozygous resistant (RR) mosquitoes than homozygous susceptible (SS) conspecifics (OR = 7.4, 95% CI 2.7–21.2, P = 0.001) exposed to pyrethroid-only nets (PermaNet 2.0). A similarly strong association was found for pyrethroid-PBO nets (PermaNet 3.0) (OR = 9.0, 95% CI 3.5–21.5, P < 0.0001), indicating that CYP6P4-I236M reduces the effectiveness of both conventional and PBO-based LLINs. In contrast, the mutation showed a weaker negative association with survival on new-generation chlorfenapyr-based nets, notably PermaNet Dual (OR = 2.9, 95% CI 1.3–6.3, P = 0.007). Fitness assays showed important biological costs in the Mayugex Kisumu F2 strain, with the CYP6P4-I236M mutation associated with slower larval development and shorter adult lifespan, causing the resistant allele to decline over generations despite the heterozygote advantage observed for fecundity and egg viability. In a field-derived resistant Mayugex (Uganda) colony maintained without additional selection over 20 generations, the mutation remained fixed and resistance high, despite decreased CYP6P4 expression,

suggesting the involvement of compensatory mechanisms.

Conclusions: Overall, these findings show that fitness costs can drive resistance reversal when selection pressure is removed early, supporting the use of mixture or rotation strategies, especially with chlorfenapyr-based nets, to manage resistance more effectively.

Keywords: Metabolic resistance, Pyrethroids, Chlorfenapyr, *Anopheles gambiae*, Fitness cost, resistance management

Paper ID# 263

Title: Rapid evolution of insecticide resistance and patterns of pesticides usage in agriculture in the city of Yaoundé, Cameroon

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Background: The practice of agriculture in urban settings contributes to the rapid expansion of insecticide resistance in malaria vectors. However, there is still not enough information on pesticide usage in most urban settings. The present study aims to assess the evolution of *Anopheles gambiae* (s.l.) population susceptibility to insecticides and patterns of pesticide usage in agriculture in the city of Yaounde, Cameroon.

Methods: WHO susceptibility tests and synergist PBO bioassays were conducted on adult *An. gambiae* (s.l.) mosquitoes aged 3 to 5 days emerging from larvae collected from the field. Seven insecticides (deltamethrin, permethrin, DDT, bendiocarb, propoxur, fenitrothion and malathion) were evaluated. The presence of target site mutation conferring knockdown (kdr) resistance was investigated using TaqMan assay, and mosquito species were identified using SINE-PCR. Surveys on 81 retailers and 232 farmers were conducted to assess general knowledge and practices regarding agricultural pesticide usage.

Results: High resistance intensity to pyrethroids was observed with a high frequency of the kdr allele 1014F and low frequency of the kdr 1014S allele. The level of susceptibility of *An. gambiae* (s.l.) to pyrethroids and carbamates was found to decrease with time (from > 34% in 2022 to < 23% in 2024

for deltamethrin and permethrin and from 97% in 2022 to < 86% in 2024 for bendiocarb). Both *An. gambiae* (s.s.) and *An. Coluzzi* were recorded. Over 150 pesticides and fertilizers were sold by retailers for agricultural purposes in the city of Yaounde. Poor practices including extensive and inappropriate application of pesticides as well as poor management of perished pesticides and empty pesticide containers were also documented

Conclusions: The study indicated rapid evolution of insecticide resistance and uncontrolled usage of pesticides by farmers in agriculture. There is an urgent need to address these gaps to improve the management of insecticide resistance

Keywords: Vector control, *Anopheles gambiae*, Insecticide resistance, Pesticide management, Yaounde, Cameroon

Paper ID# 77

Title: The epidemiological impact of pyrethroid resistance on malaria burden in the Democratic Republic of the Congo: a mathematical modelling study

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Background: Malaria control in the Democratic Republic of the Congo (DRC) is increasingly threatened by pyrethroid resistance in malaria vectors, but its impact on the effectiveness of insecticide-treated nets (ITNs) remains uncertain.

Methods: Discriminating-dose bioassay data collected between 2009 and 2021 were obtained from the WHO Malaria Threats Map and used to characterise temporal changes in phenotypic pyrethroid resistance. Information on the timing, location and type of nets distributed during mass campaigns was extracted from Programme National de Lutte contre le Paludisme reports. These data were incorporated into a mechanistic malaria transmission model calibrated to national malaria cases and deaths. Observed intervention histories were compared with counterfactual scenarios without increasing resistance and without pyrethroid-PBO nets.

Results: The spread of pyrethroid resistance was estimated to have caused 33.6 million additional malaria cases (95% CrI: 31.5–37.0 million) and 6.08 thousand additional deaths (95% CrI: 3.18–7.29 thousand) between 2009 and 2024, compared with a scenario in which resistance did not increase. The introduction of pyrethroid-PBO nets from 2019 averted an estimated 5.73 million additional cases (95% CrI: 3.43–7.82 million) and 11.4 thousand deaths (95% CrI: 6.62–15.6 thousand) relative to continued use of pyrethroid-only nets.

Conclusion: Pyrethroid resistance substantially reduced the public-health benefit of pyrethroid-only

ITNs in the DRC. Pyrethroid-PBO nets partly restored this protection, supporting continued resistance surveillance and targeted deployment of more effective ITNs.

Keywords: Pyrethroid resistance; malaria transmission; mathematical modelling; insecticide-treated nets; PBO nets.

Paper ID# 225

Title: Effects of an artificial blood-based diet on the adaptive value and susceptibility to *Plasmodium falciparum* in *Anopheles* mosquitoes from Burkina Faso

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Background: New strategies for malaria control are based on laboratory experiments. These tests use mosquitoes, yet in insectariums, the production of mosquitoes requires the use of animal blood. However, this practice faces ethical issues. To find alternative solutions, this study aims to evaluate the competence of three species of mosquitoes maintained in the insectarium with artificial blood.

Methods: Two generations of female mosquitoes (F3 and F6) including *An. coluzzii*, *An. gambiae*, and *gambiae*-Kisumu strain aged 5 days previously fed with artificial blood and rabbit blood were respectively infected with two parasitic isolates (440gam/μl and 144gam/μl) by the direct membrane feeding method. Seven days after infection, the females were dissected for oocyst counting.

Results: For this experiment, the treatment had no effect on the prevalence of oocysts in the three species in F3 (LRT X21 = 0.01; P = 0.90), however in F6 for all species combined, there was a significant effect (LRT X21 = 23.32; P < 0.001). Regarding oocyst intensity, there was no significant interaction between treatment and species in F3 (LRT X22 = 3.01; P = 0.22) and F6 (LRT X22 = 1.91; P = 0.38).

Conclusion: In general, artificial blood did not impact the vector competence of mosquitoes. Therefore, artificial blood could truly be an alternative in the production of mosquitoes in the insectarium, as it promotes susceptibility to *Plasmodium falciparum* infection in *Anopheles*.

Keywords: Artificial blood, Vector competence, *Plasmodium falciparum*, Parasitic isolates

Paper ID# 109

Title: Environmental contaminants drive insecticide resistance in *Anopheles* Mosquitoes in Ghana

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Background: Insecticide-based interventions such as indoor residual spraying (IRS) and long-lasting insecticide nets (LLINs) have significantly reduced malaria transmission globally; however, their sustainability is increasingly threatened by insecticide resistance. While insecticide and pesticide use are known drivers of resistance, the role of environmental contaminants remains underexplored.

Methods: This study investigated the impact of environmental contaminants on insecticide resistance by sampling *Anopheles* larvae from six environmentally contaminated sites (petroleum spill, mining, and industrial areas). Insecticide susceptibility status of *Anopheles gambiae* s.l was done using WHO susceptibility bioassay and bottle assay. Heavy metals and pesticide residues in larval habitats were quantified using Inductively Coupled Plasma–Mass Spectrometry (ICP-MS) and Gas Chromatography-Mass Spectrometry (GC-MS), respectively.

Results: WHO bioassays revealed resistance to clothianidin (MR = 54-80%), chlorfenapyr (MR = 80-84%), and high-intensity pyrethroid resistance across all sites, with pirimiphos-methyl resistance detected in a mining site. Multiple kdr mutations (0.12-0.98) and a high Ace-1 allele frequency (0.62) were observed. Chemical analyses detected heavy metals and chemical residues, including manganese (0.22-0.98 ppm), zinc (0.04-0.50 ppm), clothianidin (LOQ = 0.054), and atrazine (LOQ = 0.13-0.31). A significant association between heavy metals and insecticide resistance was observed ($P = 0.04$). *Anopheles coluzzii* (n = 40/240, 81.7%) was the dominant species, *An. gambiae* s.s. (7.5%), *An. arabiensis* (7.1%) and hybrid (3.8%) ($\chi^2 = 36.9$, df = 12, $P < 0.001$).

Conclusion: These findings provide evidence that environmental contaminants are significantly associated with insecticide resistance in *Anopheles gambiae* s.l., highlighting the need for enhanced surveillance and resistance management strategies for effective malaria vector control.

Keywords: Heavy metals, Chemical residue, Insecticide resistance, novel kdr mutation

Paper ID# 169

Title: One-year efficacy of SC Johnson guardian™ spatial repellent against wild pyrethroid-resistant *Anopheles arabiensis* in Tanzania

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Background: Spatial repellents (SRs) disrupt mosquito behaviors to reduce human-vector contact. A clinical trial of Mosquito Shield™ (month-long SR) demonstrated malaria protective efficacy in Kenya. However, longer-lasting products are needed for malaria control programs. This study evaluated the 12-month entomological efficacy of Guardian™ (a longer-duration SR) and compared its performance to Mosquito Shield™ against wild pyrethroid-resistant *Anopheles arabiensis*.

Methods: Experimental hut trials were conducted in Tanzania. Guardian™ was evaluated over 12 months using two methods: 1) a feeding experiment measuring blood-feeding and 24-hour mortality (16 huts, 8 nights/month), and 2) a human landing catch (HLC) experiment measuring landings (32 volunteers/night). Midway, an independent 32-day trial compared Guardian™ to Mosquito Shield™. The primary endpoint was the number of blood-fed *An. arabiensis*. Secondary endpoints included proportion blood-fed and 24-hour mortality. Mixed effects negative binomial and logistic regression models were used.

Results: Over 12 months, Guardian™ reduced blood-feeding by 82.7% (95% CI: 78.5%-86.1%) and landing by 65.1% (95% CI: 59.4%-70.0%) compared to controls. Guardian™ induced 20.1% mortality in pyrethroid-resistant mosquitoes. For the primary comparative endpoint, Guardian™ was superior to Mosquito Shield™ in reducing the number of blood-fed mosquitoes (rate ratio = 0.60, 95% CI: 0.40-0.89, $P=0.012$). No statistical difference was observed between the two products for proportion of blood-fed or induced mortality.

Conclusions: Guardian™ demonstrated strong, long-term efficacy against pyrethroid-resistant malaria vectors and offers greater protective benefit than Mosquito Shield™, supporting its potential use in malaria control programs.

Keywords: Spatial repellent, transfluthrin, *Anopheles arabiensis*, pyrethroid resistance, experimental hut trial, malaria vector control

Paper ID# 101

Title: Insecticide resistance status and heat shock protein expression in *Anopheles gambiae* s.l in highland and lowland sites in Ghana

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Background: Globally, the control of malaria is undermined by insecticide resistance in vector populations. In Ghana, vector control largely relies on long-lasting insecticidal nets and indoor residual spraying, yet their effectiveness is threatened by rising resistance in malaria vectors. Limited data exist on how environmental factors, including altitude and varied resistance mechanisms, influence resistance in the vectors. This study examined the genotypic, phenotypic and metabolic resistance profiles alongside heat shock protein (HSP) expression in *Anopheles gambiae* s.l. in selected highland and lowland sites in Ghana.

Methods: Larvae were collected from a highland site (Abetifi) and lowland sites (Ada, Tema) and reared to adults. Female *An. gambiae* s.l. were exposed to permethrin 0.75%, deltamethrin 0.05% and pirimiphos-methyl 0.25%. Mortality was recorded after 24 hours. Target-site mutations (L1014F/S, G119S, N1575Y) were detected using PCR; metabolic resistance was assessed using metabolic enzyme assays and HSPs (70, 83, and 90) expression quantified using RT-qPCR.

Results: Bioassays revealed high resistance to permethrin and deltamethrin with mortalities ranging from 13.8% -35% across all sites. Pirimiphos-methyl resistance was only observed in Abetifi (65%). High L1014F mutation was detected across sites (0.75 to 0.98). β -esterase activity in mosquitoes from Abetifi was reduced compared to the Kisumu strain (fold change = 0.81) (95% CI: 0.23–0.29; $p < 0.0001$). Monooxygenase activity was significantly elevated across sites ($P < 0.05$). Significant overexpression of HSP83 [exposed (4.59 to 7.01) vs unexposed (3.91 to 6.37) and HSP90 [exposed (0.26 to 4.53) vs unexposed (0.02 to 2.35)] were observed in malaria vectors.

Conclusion: *Anopheles gambiae* s.l. showed intense pyrethroid resistance across sites, driven by target-site mutations, elevated monooxygenase and GST activity, and increased HSP83 and HSP90 expression, threatening vector control effectiveness.

Keywords: Insecticide resistance, *Anopheles gambiae* s.l., kdr mutation, metabolic resistance, Heat Shock Proteins

Paper ID# 206

Title: Relationship between *Wolbachia wanga* infection and insecticide resistance in *Anopheles coluzzii*: phenotypic and genotypic evidence from Burkina Faso

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Background: The interactions between *Wolbachia* and insecticides represent a key issue in entomology due to their combined effects on *Anopheles* biology and resistance evolution. Indeed, *Wolbachia* influences essential mosquito traits including physiology, immunity, and longevity while

insecticides exert strong selective pressure. Therefore, assessing their reciprocal effects is critical to optimize Wolbachia-based control strategies and improve sustainable malaria control programs. This study thus investigated the relationship between wAnga infection and phenotypic/genotypic insecticide resistance in *Anopheles coluzzii*.

Methods: Susceptibility of 433 wild-caught *Anopheles coluzzii* to selected pyrethroid and organophosphate insecticides was assessed using WHO tube bioassay. Subsequently molecular analyses were performed including species identification within *Anopheles gambiae* complex using Short Interspersed Elements 200X PCR, detection of wAnga infection by Nested PCR targeting 16SrRNA gene and genotyping of L1014F as well as G119S mutations using respectively Allele-specific and Restriction Fragment Length Polymorphism PCR.

Results: The overall prevalence of wanga infection was 32.10% and mortality rates were 8.73% following pyrethroids exposure and 100% for organophosphates with no significant association between wAnga infection and bioassay mortality (Mantel–Haenszel test: $p = 0.8974$). Moreover, L1014F genotypes frequencies were 8.01% RR, 14.28% RS and 5.92% SS in wAnga-positive versus 18.12% RR, 41.81% RS and 11.85% SS in negative. For G119S, genotypes consisted of 3.75% RS, 58.75% SS in wAnga-positive and 37.5% SS in negative. Finally, no association was observed between wAnga infection and the distribution of L1014F (χ^2 test: $p = 0.4765$) or G119S (Fisher exact test: $p = 0.288$) genotypes.

Conclusion: No association was observed between wAnga infection and insecticide resistance, suggesting no impact of resistance on Wolbachia-based biological control strategies.

Keywords: *Anopheles*, wAnga, bioassay, phenotypic/genotypic resistance, biological control

Paper ID# 205

Title: Larvicidal activity of green silver Nanoparticles from *Moringa oleifera* on insecticide-resistant *Anopheles coluzzii*, in Burkina Faso

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6. DRCO

Background: The increasing resistance of malaria vectors to conventional insecticides necessitates the development of environmentally friendly, sustainable control methods. Therefore, studies on biosynthesized nanoparticles have shown promising results with larvicidal, and adulticidal activities. Our study evaluated the larvicidal activity of *Moringa oleifera* silver nanoparticles against an insecticide-resistant strain of *Anopheles coluzzii*, in Burkina Faso.

Methods: Larvicidal bioassays were conducted according to modified WHO guidelines using third-instar larvae of an insecticide-resistant strain of *Anopheles coluzzii*. Larvae were exposed to *Moringa oleifera* crude extract and silver nanoparticles at concentrations of 20, 30, and 40 ppm. For each concentration, three replicates of 26 larvae were tested, and the experiment was repeated twice. A negative control consisting of deionized water was included in the triplicate. Larval mortality was recorded every 24 h for 72 h post-exposure.

Results: Larval mortality was significantly affected by concentration and treatment type ($p < 0.001$), with no significant interaction between these factors. Silver nanoparticles were consistently more effective than the *Moringa oleifera* crude extract at all concentrations and exposure times ($p < 0.0001$). After 72 h, nanoparticle-induced mortality approached 90%, whereas the crude extract produced less than 20% mortality. Probit analysis at 24h confirmed the higher potency of nanoparticles ($LC_{50} = 4.88 \pm 1.81$ ppm; $LC_{90} = 70.88 \pm 1.39$ ppm) compared with the crude extract ($LC_{50} = 339.8 \pm 3.31$ ppm; $LC_{90} = 16068.38 \pm 21.55$ ppm).

Conclusions: These results demonstrate the significant larvicidal potential of *M. oleifera* based green silver nanoparticles, suggesting their possible use as an environmentally friendly and sustainable alternative to chemical larvicides in vector control programs.

Keywords: *Moringa oleifera*, silver nanoparticles, biosynthesis, mosquito, larvicide

Paper ID# 72

Title: Temporal and geo-ecological patterns of malaria and *Plasmodium falciparum* antimalarial resistance in Cameroon, 2019-2021 and 2025

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Background: Malaria distribution across geo-ecological zones in Cameroon remains spatial heterogenous with persistent localized hotspots. This has been attributed to geo-ecological difference, transmission intensity and parasite genetics, while rapid proliferation of antimalarial

resistance undermines control, prevention and treatment measures. The prevalence of malaria, hotspot and distribution of molecular markers of antimalarials resistance (Pfcrt, Pfdhfr, Pfdhps, Pfk13 and Pfmdr1) were assessed.

Method: This was a cross-sectional community and clinical survey involving 10,207 participants recruited from 2019 to 2021 and 2025 with 5817 and 4390 participants respectively across randomly selected 50 health facilities in Cameroon. Malaria parasite was determined using rapid diagnostic test (mRDT) and real time polymerase chain reaction (qPCR)-VarATS for *Plasmodium falciparum* detection after DNA extraction from dry blood spots (DBS) using Chelex100. About 1,242 *P. falciparum* isolates were sequenced using MAD4HatTeR protocol. Genetic Report Card Genetic Report Card –User Guide and visualization using R statistical package.

Results: Among the 10,207 individuals screened, malaria prevalence in 2025 was 26.3% (823/3281) by mRDT and 50.3% (2025/4031) by qPCR-VarATS. For the 2019-2021 survey, prevalence was 23.7% (1292/5458) by mRDT and 58.8% (1947/3313). Molecular surveillance of 2019-2021 shows high frequency of Pfcrt sensitive CVMNK (81.4%) and 33.2% SP-(CIRNI-SGKAA)-quadruple mutations. About 43.9% Y184F mutation and 36.7% Pfmdr-NFD haplotypes were observed with <5% rare K13 mutant alleles. Isolates form a dense central cluster showing a level of genetic homogeneity, ancestry sharing, and high gene flow with Tiko indicating a transmission hub.

Conclusion: Malaria remains disproportionately high across zones in Cameroon. The widespread 184F mutation and NFD haplotypes underscore ongoing Lumefantrine selection with an increase re-emergence of Pfcrt-K76 wild type alleles.

Keywords: Malaria, Antimalarial, Drug Resistance

Paper ID# 75

Title: Pyrethroid Resistance Patterns in *Anopheles gambiae* and Implications for Vector Control in Rwanda

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Background: Evidence-based vector control interventions depend on understanding the distribution and mechanisms of insecticide resistance in malaria vectors. This study assessed the status of insecticide resistance in *Anopheles gambiae* to pyrethroids, permethrin, deltamethrin, and alphacypermethrin across 18 sites in Rwanda, representing key malaria transmission strata.

Methods: Larvae were collected from October 2022 to April 2023 using the dipping method, reared to adulthood, and tested using WHO standard bioassays. Susceptibility profiles were analysed with

chi-square tests to compare mortality rates. The level of significance was set at $P < 0.05$. To calculate the 95% CI, we used the sample mean, standard deviation, and sample size to determine the critical value from the t-distribution corresponding to 95% confidence. These bounds indicate the range within which the true knockdown rate is likely to fall with 95% confidence.

Results: There was a high resistance to permethrin in various sites, including 42% Gashora, 48% Mubuga, 69% Rwaza, and 70% Kirarambogo. Pre-exposure to PBO only partially restored susceptibility, with mortality between 70 and 80% at resistant sites. In Kigali city, mortality with alphacypermethrin was 94%, and with PBO, it failed to restore susceptibility, suggesting the involvement of resistance mechanisms beyond those inhibited by PBO. Overall, the evidence indicates that metabolic mechanisms play a major role in pyrethroid resistance, though target-site mutations, like *kdr*, cannot be ruled out. The reliance on phenotypic data without molecular confirmation remains a limitation, underscoring the need for molecular assays to identify resistance-associated genetic markers.

Conclusions: This study provides baseline data on the resistance status of *An. gambiae* in Rwanda and highlights the urgent need to integrate molecular tools into routine surveillance to guide more effective vector control strategies.

Keywords: insecticide resistance, *Anopheles gambiae*, pyrethroid resistance, molecular tools

Paper ID# 69

Title: Chlorfenapyr-based net Interceptor G2 reduces infection and pyrethroid resistance in *An. gambiae* from Cameroon and Uganda

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Background: Vector control has substantially reduced malaria in Africa, but intense pyrethroid resistance in *Anopheles* mosquitoes now threatens these gains.

Methods: Dual active-ingredient LLINs such as Interceptor G2 (IG2) are now introduced to mitigate pyrethroid resistance. Here, we ask whether large-scale IG2 deployment in Cameroon and Uganda can (i) restore phenotypic susceptibility, (ii) reduce *Plasmodium* infection in vectors, and (iii) drive measurable short-term evolutionary change in resistance markers.

Results: Household surveys and net inspections showed high IG2 and other LLIN ownership (>90%) but only moderate use (<60% slept under a net the previous night), indicating that low and heterogeneous usage is now a critical barrier to impact. WHO and CDC bioassays nevertheless showed significantly higher pyrethroid mortality in *An. gambiae* s.l. at all IG2 sites 2–3 years post-deployment, indicating partial restoration of susceptibility. *Plasmodium* infection rates in field-collected mosquitoes declined modestly, consistent with improved vector control. Molecular analyses revealed no significant change in L995F-kdr and E2056D-CYP6P3 frequencies between pre- and post-IG2 periods, despite strong laboratory fitness costs, suggesting that short-term evolutionary responses at these loci are subtle. In contrast, CYP6Z1 and CYP9K1 expression declined significantly after IG2 deployment but remained above susceptible-strain levels, indicating a quantitative reduction rather than elimination of metabolic resistance. Surveys of farmers and pesticide sellers revealed extensive agricultural insecticide use, which may counteract IG2-driven selection against resistance.

Conclusion: Overall, IG2 appears to reduce resistance intensity and infection risk without rapid replacement by alternative resistance mechanisms, but realizing its long-term benefits will require integrated management of insecticide use across public-health and agricultural sectors.

Keywords: Malaria,

Vector Surveillance & Bionomics

Paper ID# 213

Title: Updating *Anopheles funestus* group members in Burkina Faso: species distribution and contribution to malaria transmission.

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Background: The *Anopheles funestus* group and the *Anopheles gambiae* complex are among the most efficient malaria vectors in Africa, thriving in a variety of environments and well adapted to semi-permanent and permanent water bodies. This study investigated the spatial distribution of the *An. funestus* group and its potential contribution to malaria transmission in Burkina Faso.

Methods: An entomological survey was conducted from October to December 2022 across 67 sites within the ecological zones of Burkina Faso. *An. funestus* was detected in 22 sites. Mosquitoes were collected using pyrethrum spray catches (PSC) and identified at the species group level using morphological keys. Polymerase chain reaction (PCR) was used for species identification within the *An. funestus* group, blood meal source determination, and *Plasmodium falciparum* detection.

Results: A total of 617 members of the *An. funestus* group (45 males and 572 females) were collected across eight regions of Burkina Faso. *Anopheles funestus* s.s. was the predominant species, accounting for 95% (589/617) of specimens identified. Most *An. funestus* s.s. were found in the Hauts-Bassins (30%) and Sud-Ouest (55%) regions. Hybrids between *An. rivulorum* and *An. rivulorum*-like represented 3.57% (22/617) of specimens. Blood meal analysis showed that 64.3% of identified blood meals originated from animal hosts. *Plasmodium falciparum* infection was detected in 5.76% (33/572) of tested females.

Conclusions: This study updates the distribution of the *An. funestus* group in Burkina Faso and highlights its potential role in malaria transmission. The findings support strengthened surveillance of indoor-resting malaria vectors and the inclusion of *An. funestus* in the development of innovative vector control strategies.

Keywords: *Anopheles funestus*; *Plasmodium* infection; Blood source; Burkina Faso; Distribution.

Paper ID# 210

Title: Fungal microbiota of vector mosquitoes: synthesis of current knowledge and perspectives for biocontrol.

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Background: Vector-borne diseases represent a major public health concern, particularly in tropical regions. Vector control is mainly based on insecticides, whose intensive use leads to resistance and environmental impacts. Therefore, alternative approaches are needed. The fungal microbiota of mosquitoes represents a promising avenue for the development of innovative biocontrol strategies.

Methods: This systematic review, conducted in accordance with PRISMA guidelines, analyzed studies on the fungal microbiota of mosquitoes of the genera *Aedes*, *Anopheles*, and *Culex*, using two databases (PubMed and Google Scholar). Study quality was assessed using the Joanna Briggs Institute (JBI) tool. The analysis focused on fungal diversity according to mosquito species, the geographical distribution

of studies, identification approaches, developmental stages, mosquito organs, and the anti-vectorial potential of the identified fungi

Results: Out of 7,458 identified records, 32 studies were included. These studies were mainly conducted in the United States, Brazil, France, Italy, and Kenya, with low representation from Africa and Asia. The main fungal phyla identified was Ascomycota, Basidiomycota, and *Microsporidia mycota*, including yeasts, filamentous fungi, and an obligated intracellular fungus. Several fungal genera were isolated, with a predominance in *Aedes*, followed by *Culex* and then *Anopheles*. Identification approaches were mostly molecular, sometimes complemented by culture-based methods. Fungal species were isolated at different developmental stages and from various organs, particularly the gut and reproductive organs. Several studies reported biological effects, including inhibition of larval development and a reduction in vector competence.

Conclusion: Mosquitoes harbor a diverse fungal microbiome that remains largely unexplored but holds great potential for innovative vector control strategies.

Keywords: *Anopheles spp*, *Aedes spp*, *Culex spp*, Fungal microbiota, Vector control

Paper ID# 212

Title: Spatial distribution and biodiversity of *Anopheles* mosquito species across climatic zones in Burkina Faso: Implications for malaria vector control

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Background: Malaria transmission in sub-Saharan Africa is mainly driven by the *Anopheles gambiae* complex and *Anopheles funestus*, whose distribution varies across ecological settings. Secondary species occur at lower densities but may contribute to transmission depending on local conditions. Assessing *Anopheles* biodiversity using indices such as species richness, Shannon, and Simpson is essential to characterize their diversity and relative abundance. This study investigated the biodiversity and spatial distribution of *Anopheles* species across the three climatic zones of Burkina Faso.

Methods: Indoor resting mosquitoes were collected in 67 health districts across 13 regions using pyrethroid spray catches. Specimens were morphologically identified, and a subset of *Anopheles gambiae* sensu lato collected from 33 districts was analyzed by PCR to identify sibling species.

Biodiversity was assessed using species richness, Shannon, and Simpson indices.

Results: A total of 30,521 *Anopheles* mosquitoes were collected. *Anopheles gambiae* sensu lato predominated (94.4%), with highest abundance in the Sudano-Sahelian zone. Other species, including *Anopheles rufipes*, *Anopheles funestus*, and *Anopheles pharoensis*, were less frequent. Abundance peaked in October. Biodiversity showed a gradient from humid southern to arid northern zones, with higher diversity in the Sudanian zone. Molecular analysis revealed significant variation in sibling species distribution, with *Anopheles coluzzii* predominant in Sahelian and Sudano-Sahelian zones, while *Anopheles gambiae* sensu stricto dominated in the Sudanian zone.

Conclusions: Marked spatial variation in *Anopheles* composition was observed across Burkina Faso. These findings highlight the importance of vector biodiversity for malaria transmission and support locally adapted vector control strategies

Keywords: *Anopheles* species, Biodiversity indices, climatic zones, Malaria, Vector control strategies, Burkina Faso.

Paper ID# 226

Title: Adaptative dependence on saline water in *An. gambiae* s.s mosquitoes from coastal Kenya

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Background: Saltwater tolerance plays an important role in the epidemiology of mosquito-borne diseases, particularly in coastal regions where saline aquatic habitats are expected to increase as a result of sea-level rise associated with global warming. This environmental change may favor the proliferation of salt-tolerant mosquito species and potentially alter local disease transmission dynamics. However, aside from *Anopheles merus*, the salinity tolerance profiles of other malaria vector species occurring along the Kenyan coast remain poorly understood. This study was conducted to evaluate the effect of salinity on the development of an insectary-reared *Anopheles gambiae* sensu stricto strain originating from coastal Kenya.

Methods: First-instar larvae of *An. gambiae* s.s were reared under standard insectary conditions using four larval water treatments: groundwater alone, deionized water alone, and groundwater and deionized water both supplemented with 0.25% (w/v) sodium chloride. Developmental performance was assessed by measuring time to pupation and the wing length of emerging adults as a proxy for body size.

Results and Discussion: Regardless of the type of water, addition of sodium chloride resulted in a significant reduction of the time to and resulted in larger sized mosquitoes.

Conclusion: Salinity appears to play an important role in the development of coastal strains of *Anopheles gambiae* s.s. Under insectary conditions, incorporation of low salt concentrations into standard larval rearing protocols may improve the maintenance and productivity of these strains. However, further investigations involving wild-caught *An. gambiae* populations and other major malaria vector species from the region are needed to better characterize salinity tolerance and its biological and ecological significance.

Keyword: Sea level, *An. gambiae* s.s

Paper ID# 208

Title: Characterization of the microbiota of *Anopheles coluzzii* infected with Microsporidia MB

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1. IRSS

2. DRO

Introduction: *Microsporidia MB* is a naturally occurring endosymbiont associated with mosquitoes of the *Anopheles gambiae* complex and is known for its ability to block *Plasmodium* development in the host. However, the mechanisms underlying this effect remain poorly understood and may be linked to interactions with the mosquito bacterial microbiota. This study aimed to characterize cultivable bacteria associated with *Anopheles coluzzii* mosquitoes infected (MB+) and uninfected (MB-) with *Microsporidia MB*.

Methods: Cultivable bacteria were isolated on LB medium from 3-5-day-old adult *Anopheles Coluzzi* mosquitoes infected (MB+) and uninfected (MB-), reared at the IRSS insectary. Infection status was confirmed by PCR. Genomic DNA from purified isolates was extracted using the 2% CTAB method. The V3-V4 region of the 16S rRNA gene was amplified and sequenced using Sanger sequencing. Results: A total of 60 bacterial colonies were isolated. Five species were identified: *Elizabethkingia anopheles*, *Cedecea selenitireducens*, *Cedecea lapagei*, *Chryseobacterium rhizoplanae* and *Serratia surfactantfaciens*. *Elizabethkingia anopheles* was dominant (58.3%), followed by *Cedecea* spp. (16.6% each). MB+ mosquitoes showed higher bacterial richness (5 species) than MB- mosquitoes (3 species). *Chryseobacterium rhizoplanae* and *Serratia surfactantfaciens* were found only in MB+ mosquitoes.

Conclusion: This study highlights an association between *Microsporidia MB* infection and cultivable bacterial composition in *Anopheles coluzzii*. The higher richness observed in MB+ mosquitoes

suggests potential interactions between this endosymbiont and the microbiota. Further high-throughput sequencing studies are needed to better understand these interactions.

Keywords: Malaria, *Microsporidia* MB, Microbiota, *Anopheles coluzzii* and Vector competence

Paper ID# 133

Title: Comparison of trapping efficacy of modified Ovillanta, modified Gravid *Aedes* Trap (GAT), Biogent GAT and BG sentinel for monitoring *Aedes aegypti* in Tanzania

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1.Ifakara Health Institute

Background: *Aedes* mosquito surveillance is essential for guiding effective arbovirus control strategies. However, the gold-standard BG-Sentinel (BGS) trap is expensive and requires electricity, limiting large-scale use in resource-constrained settings. This study evaluated the trapping efficacy of alternative locally made, low-cost oviposition-based traps (Ovillanta and Gravid *Aedes* Traps, GAT) compared to BioGents GAT (BG-GAT) and BGS for monitoring adult *Aedes aegypti* densities.

Methods: An outdoor field evaluation was conducted in Bagamoyo, Tanzania, from October to December 2025 using a 6 × 6 Latin square design over 72 days. Six trapping methods were assessed: modified Ovillanta with yeast, modified Ovillanta without yeast, BG-GAT with yeast, one modified GAT (1MoGAT) with yeast, four MoGATs with yeast, and the BGS with BG-lure. Traps operated for 24 hours, and the collected mosquitoes were morphologically identified. Trapping efficacy was compared using mixed-effects, negative binomial regression, and Bland–Altman analysis.

Results: The modified Ovillanta with yeast captured the highest number of female *Ae. aegypti* (n = 468) among oviposition-based traps and performed comparably to the BGS trap (n = 497; IRR = 1.03; 95% CI: 0.76–1.41; p = 0.828), with a Bland–Altman means difference of 0.403 (limits –17.292 to 17.292). Its performance decreased by 30% without yeast (n = 321; IRR = 0.69; 95% CI: 0.51–0.95; p = 0.023). Compared to the yeast-baited Ovillanta, BG-GAT captured significantly fewer mosquitoes (n = 95; IRR = 0.19; 95% CI: 0.13–0.27; p < 0.001), as did 1MoGAT (n = 31; IRR = 0.06; 95% CI: 0.04–0.10; p < 0.001) and 4MoGAT (n = 35; IRR = 0.07; 95% CI: 0.04–0.11; p < 0.001).

Conclusion: The yeast-baited modified Ovillanta demonstrated efficacy comparable to BGS and significantly higher than GAT-based designs, indicating it is a scalable, cost-effective, and battery-free tool for monitoring adult *Ae. aegypti* in resource-limited settings.

Keywords: *Aedes aegypti*; Mosquito traps; Vector control, Ovillanta; Bioagent-Sentinel; Gravid *Aedes* Trap; Locally modified Gravid *Aedes*

Paper ID# 96

Title: Effect of *Guiera senegalensis* leaf extracts on the gut bacterial flora of *Anopheles gambiae* complex mosquitoes.

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Background: Malaria remains a major public health concern in Sub-saharan Africa. Where control efforts are increasingly challenged by resistance to insecticides and antimalarial drugs.

Paratransgenesis which targets the bacterial flora to block *Plasmodium* transmission, represents a promising alternative strategy. However, this approach may be affected by the widespread use of medicinal local plants with antibacterial properties.

Methodology: We assessed the effect of *Guiera senegalensis*, a medicinal plant, on the gut bacterial flora of *Anopheles gambiae* complex mosquitoes. Extracts dissolved in DMSO were mixed with human blood from gametocyte carriers at set concentrations and given through blood meals. qPCR targeting 16S rRNA genes of families (Eubacteriaceae, Enterobacteriaceae, Flavobacteriaceae) and genera (*Asaia*, *Pantoea*) was performed.

Results: Quantitative PCR analysis revealed high prevalence of *Asaia* (58.7%) and Flavobacteriaceae (56.5%), followed by *Pantoea* (42.4%) and Enterobacteriaceae (35.9%). Ct value distributions indicate sustainable variability in bacterial loads. No statistically significant differences were observed between treated and control groups for Enterobacteriaceae and Flavobacteriaceae. Similarly, *Asaia* and *Pantoea* loads showed a non-significant increase in Ct values in treated mosquitoes, suggesting a trend toward reduced bacterial abundance. Overall, *Guiera senegalensis* did not significantly alter bacterial loads but exhibited a subtle, non-significant modulatory effect on specific taxa.

Conclusion: These findings suggest that *Guiera senegalensis* has a limited but potentially selective impact on the gut bacterial flora of *Anopheles gambiae* complex mosquitos. Observed trends, particularly for *Asaia*, may have biological implications for bacterial flora-based vector control strategies. Given its widespread use in traditional medicine, further investigations are necessary to clarify its potential effects on Paratransgenesis approaches.

Keywords: Medicinal plants, mosquito bacteria, malaria transmission, *An. gambiae* complex.

Paper ID# 146

Title: Impact of artemether–lumefantrine treatment, circadian rhythm, and serum replacement on the infectiousness of wild *Plasmodium falciparum* gametocytes to *Anopheles gambiae sensu stricto* mosquitoes

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Background: Asymptomatic gametocytemia carriers are scarce but serve as key reservoirs for *Plasmodium falciparum* gametocytes. For evaluation of transmission-blocking interventions (TBIs) gametocytemic individuals are essential. Many factors such as artemether–lumefantrine (AL) treatment, mosquito feeding time (day vs. night), and serum replacement may influence mosquito infectiousness through direct membrane feeding assay (DMFA). This study aimed at optimizing DMFA as the method of mosquito feeding through assessing the following 1) artemether–lumefantrine treatment 2) mosquito feeding time and 3) serum replacement on gametocyte infectiousness to mosquitoes in a low malaria transmission setting

Methods: Six gametocytemic carriers were found to be eligible, from whom 4 mL of venous blood was drawn. This blood was given to female *Anopheles gambiae sensu stricto* (s.s.) mosquitoes via DMFA under controlled conditions. Oocyst prevalence and intensity were determined on fed mosquitoes: 1) 9 days post-AL treatment, 2) for day feeds versus night feeds, and 3) with and without serum replacement.

Results: Mosquito infection rates declined post-AL treatment, with significantly fewer mosquitoes infected [odds ratio (OR) = 0.20, 95% confidence interval (CI): 0.13–0.31, $p = 0.001$] compared to day 0. Feeding during the dark cycle time did not significantly affect mosquito infection rates (OR = 0.77, 95% CI: 0.53–1.12, $p = 0.175$). Lastly, compared to whole blood, serum replacement increased infection rates (OR = 1.73, 95% CI: 1.33–2.25, $p = 0.001$).

Conclusion: To obtain robust results, we confirm that DMFA should be conducted using blood from gametocytemic carriers without a recent history of AL treatment, using serum replacement to enhance infection success. In this setting, assays could be conducted outside of the mosquitoes' dark cycle without affecting results.

Keywords: Artemether Lumefantrine, Oocyst, Prevalence, *Plasmodium falciparum*, gametocytes, Circadian rhythm, *Anopheles gambiae*

Paper ID# 139

Title: Persistence of residual *Anopheles gambiae* populations associated with frontier human settlements and nocturnal livelihood-related activities at the fringes of a large conservation area in southern Tanzania

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Background: Following the rapid scale-up of long-lasting insecticidal nets (LLINs) in 2008 across the Kilombero Valley of southern Tanzania, *Anopheles gambiae* Giles, a highly efficient and human-specialized malaria vector, essentially disappeared within two years and has rarely been detected since. However, an ecological study of its sibling species within the *An. gambiae* complex, namely *An. arabiensis* Patton and *An. Quadriannulatus*, Theobald, conducted across an interface between human settlements and conserved wilderness, detected sparse, highly focal populations of *An. gambiae*.

Methods: A total of 4,704 *An. gambiae* complex specimens were collected across a heterogeneous landscape and identified to sibling species level using polymerase chain reaction. Spatial distribution was examined across settlement types, and Poisson regression models were used to compare capture rates. Mean standing population sizes were conservatively estimated using established ecological assumptions.

Results: Only 10 specimens were identified as *An. gambiae* s.s. Seven were captured at three fishing camps within a Wildlife Management Area (WMA), while none were found in five established villages or in the national park. Two were detected in scattered farming settlements and one in a near-natural area close to small transient homesteads. Capture rates at fishing camps were higher than in peripheral settlements (RR [95% CI] = 0.088 [0.011, 0.695], P = 0.021) and natural areas (RR [95% CI] = 0.043 [0.003, 0.495], P = 0.012). Estimated mean standing populations ranged from 26 to 41 females per fishing camp.

Conclusion: The absence of *An. gambiae* from areas without resident humans aligns with its anthropophagic nature. Residual populations in frontier communities appear linked to nocturnal livelihood activities that limit LLIN use. These focal refugia may allow persistence under partial insecticide pressure, but their sparse distribution suggests targeted interventions could eliminate them.

Keywords: Gonotrophic cycle, Ecological refugia, Mosquito surveillance, Ecological niche, Outdoor exposure

Paper ID# 136

Title: Exploring near-infrared spectroscopy ability to determine the species of *Anopheles gambiae sensu lato* from different environmental conditions in Burkina Faso

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Background: Near-infrared spectroscopy (NIRS) has shown ability to identify *Anopheles* species with moderate to high accuracy, but its validation requires evaluating its performance under varying environmental conditions that may affect mosquito cuticle properties and measurement accuracy. This study investigated the influence of environmental conditions on NIRS accuracy to determine *Anopheles gambiae sensu lato* (s.l.) species.

Methods: Environmental conditions of three important seasonal periods in Burkina Faso covering the onset, the peak and the end of the rainy season were mimicked in the laboratory using incubators. Emerged *An. gambiae* and *An. coluzzii* from laboratory colonies were reared in each period using temperature and relative humidity for predicting mosquito species by NIRS. Wild *An. gambiae* s.l. were caught during the 3 different periods described above and analyzed by NIRS to predict *Anopheles* species. All data analysis was performed using a binomial logistic regression model. NIRS discriminated between laboratory-reared *Anopheles* with 83% of accuracy independently of any environmental condition (84%). A similar trend was found in wild-caught *Anopheles*. NIRS accuracies varied slightly in laboratory *Anopheles* (77–85%) and more strongly in their field counterparts (67–84%).

Results: In both cases, models developed from the season of interest were more accurate than models trained with insectary conditions or from a different period of the year, indicating temperature and humidity can impact NIRS accuracy. Models derived from laboratory mosquitoes reared under fluctuating environmental conditions predicted field-derived mosquito species with a low accuracy (59%). NIRS was able to determine *An. gambiae* s.l. species under different environmental conditions with modest accuracy. Models trained using wild mosquitoes from one season could predict species in wild mosquitoes from a different season, though with slightly lower accuracy.

Conclusion: NIRS showed moderate accuracy in identifying *An. gambiae* s.l. species, with

performance significantly affected by seasonal and environmental conditions. Models developed using mosquitoes from the same season were the most accurate, while laboratory-based models performed poorly on field mosquitoes. These findings suggest that season-specific and field-derived calibration models are essential for improving the accuracy and reliability of NIRS in malaria vector surveillance.

Keywords: Near infrared spectroscopy, *Anopheles species*, Environmental conditions, Temperature, Relative humidity

Paper ID# 170

Title: Mapping of malaria vectors in Kasai-Central Province, Democratic Republic of Congo to support subnational tailoring of vector control

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Background: Sub-national tailoring of malaria vector control requires geographically detailed data that capture local variation in the distribution of vectors. Such data remain scarce in DRC, where the NMCP sentinel surveillance network is limited to a single site per province. In Kasai-Central, the sentinel site, Mikalayi covers 26 health zones, leaving most areas entomologically uncharacterized. To address this data gap, a community-based *Anopheles* collection was established to generate geographically representative entomological data through province-wide vector surveillance.

Methods: Between April 2025 and March 2026, indoor *Anopheles* mosquitoes were collected across 26 health zones, to characterize spatial and seasonal variation in malaria vector populations. Twenty-five households were surveyed monthly in a village from each sentinel health area (total of 650 households). Mosquitoes were collected early in the morning (5:00-9:00) using mouth aspiration conducted by trained community health workers, morphologically identified by professional entomologists to complex/species level using standard taxonomic keys, and stored for future molecular analysis.

Results: A total of 10,150 *Anopheles* were collected from 650 fixed households monitored monthly over 12-month period (7,800 household visits), corresponding to an average of 1.3 *Anopheles* per

household visit with substantial variation across health zones. The dominant vectors were the *An. gambiae* complex and *An. funestus* group, with a few secondary vectors being collected. These preliminary findings confirm the presence of key vectors across all 26 health zones and their heterogeneity. Full results, including genetic screening for insecticide resistance markers, are expected by the end of 2026.

Conclusion: This project developed a simple cost-effective method to fill the gap in the data required for generating the analysis needed to support sub-national tailoring of vector control.

Keywords: *Anopheles* surveillance; sub-national tailoring; Kasai-Central; entomological data.

Paper ID# 124

Title: Entomological Drivers of Malaria Transmission in Northern Mozambique: Evidence from a High-Burden Mining Setting

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Background: Nampula Province accounts for 54% of Mozambique's malaria burden, with mining areas such as Moma and Larde of particular concern due to rapid population growth and environmental changes from extractive activities. This study characterizes vector ecology in a highly endemic setting, highlighting key entomological indicators and gaps in community protection.

Methods: Mosquito collections were conducted using: i) human-baited tent traps, ii) window exit traps, iii) pyrethrum spray catches, and iv) larval collections. These were complemented by direct observations of human behavior, recording indoor and outdoor presence, and ITN use during collection nights. Insecticide resistance in *An. gambiae* s.l. was assessed using the standard WHO tube test procedure, in which adult female mosquitoes, were exposed to insecticide-treated papers for 60 minutes and mortality was recorded after a 24-hour.

Results: *An. gambiae* s.l. was predominant (n=215), followed by *An. funestus* s.l. (n=27) and *An. tenebrosus* (n=24). Biting was mainly nocturnal, peaking indoors (18:00-22:00) and outdoors (22:00-04:00), increasing exposure in the evening and late night. Resting behavior varied: *An. gambiae* s.l. and *An. tenebrosus* were mainly endophilic, while *An. funestus* s.l. was more exophilic. High resistance to deltamethrin was observed (39% mortality). Pre-exposure to PBO restored mortality to 100%, suggesting that metabolic resistance mechanisms were primarily responsible for the observed resistance. Behavioral data revealed exposure gaps: 62% of human-vector contact occurred outdoors,

beyond ITN protection.

Conclusions: Malaria transmission in Nampula's mining belt is sustained by multiple vector species, with *An. gambiae s.l.* and *An. funestus s.l.* as primary vectors and *An. tenebrosus* as a potential secondary contributor. Outdoor biting and metabolic resistance threaten ITN and IRS effectiveness, underscoring the need for complementary control strategies targeting outdoor exposure.

Keywords: Vector ecology; Human behavior; Insecticide resistance; Outdoor transmission; Malaria vector control; Mining communities

Paper ID# 223

Title: Performance and comparative evaluation of a Novel diagnostic assay, Novaplex™ malaria assay kit.

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1. KEMRI

Background: Accurate malaria diagnosis and species identification are critical for tailored treatment and surveillance. This study evaluated the performance of the Novaplex™ Malaria Assay against routine microscopy, rapid diagnostic tests (RDTs), and quantitative PCR (qPCR) as the reference standard.

Methods: Whole blood samples from 142 suspected malaria cases in Matayos, Kenya, were analyzed using microscopy, RDTs, Novaplex™, and qPCR. Sensitivity, specificity, positive predictive value (PPV), negative predictive value (NPV), accuracy, and Cohen's kappa (κ) agreement were calculated. Results: Novaplex™ outperformed microscopy and RDTs in sensitivity, accuracy, and NPV, matching qPCR closely in species identification. Compared to qPCR, Novaplex™ achieved 95.5% sensitivity and 87.5% specificity, while microscopy and RDTs achieved lower sensitivities of 63.7% and 61.5%, respectively. Novaplex™ demonstrated a 99.2% PPV and 53.9% NPV, whereas microscopy and RDTs showed much lower NPVs (12.5% and 11.9%). Overall accuracy for Novaplex™ was 95.1% with substantial qPCR agreement ($\kappa = 0.642$ [0.398–0.885]). Conversely, microscopy and RDT accuracies were 65.5% and 63.4%, showing only slight qPCR agreement ($\kappa = 0.148$ and $\kappa = 0.136$).

Conclusion: The Novaplex™ Malaria Assay demonstrated superior diagnostic performance to microscopy and RDTs, with accuracy comparable to qPCR. It holds strong potential as a reliable tool, though further field evaluations are required to assess its feasibility and cost-effectiveness in resource-limited settings.

Keywords: Novaplex, *Plasmodium* species, qPCR

Paper ID# 87

Title: Individual-level and geospatial factors influencing malaria risk in Kwale County, Kenya

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Background: Perennial malaria transmission in Kenya's coastal region undermines tailored interventions, with Kwale County remaining a high-burden area. We assessed the influence of individual and geospatial factors on malaria risk among children using data from a phase III trial of ivermectin mass drug administration.

Methods: A total of 1,232 children aged 5–15 years were enrolled from 42 clusters in Ramisi and Pongwe Kikoneni wards and followed monthly over six visits. *Plasmodium falciparum* infection was tested at enrolment and at follow-up using rapid diagnostic tests. Spatial covariates were derived from satellite data. Multilevel logistic regression with nested random intercepts accounted for clustering at the cluster and household level. Predictors were first assessed using univariable models, followed by two multivariable approaches: (i) stepwise selection with liberal inclusion criteria ($p \leq 0.20$) and backward elimination guided by confounding assessment and epidemiological plausibility, and (ii) penalized variable selection using elastic net regression.

Results: The stepwise model demonstrated superior fit based on lower AIC and BIC values. Overall, 75.7% ($n = 1001$) of children reported sleeping under a bed net the previous night, and 60.3% ($n = 363$) lived in homes constructed with mud or palm walls. Bed net use (aOR: 0.47, 95% CI: 0.35–0.62), greater distance from wetland marshes (aOR: 0.42, 95% CI: 0.28–0.64), and rainfall (lag 0) (aOR: 0.26, 95% CI: 0.11–0.62) were associated with reduced odds of Pf infection. In contrast, lagged rainfall (lag 2) (aOR: 1.15, 95% CI: 1.01–1.31) and longer travel time to the nearest health facility (aOR: 1.57, 95% CI: 1.12–2.19) were associated with increased malaria risk. Malaria risk in Kwale County is influenced by a combination of individual and household-level factors.

Conclusion: Incorporating these determinants into spatially targeted and context-specific malaria control strategies could reduce transmission.

Keywords: GLMM, *plasmodium falciparum*, malaria, risk, RDT, LLIN, Kenya, school-aged, rainfall, temperature

Paper ID# 211

Title: Density-dependent inhibition of *Plasmodium falciparum* sporogonic development by *Microsporidia* MB in *Anopheles* mosquitoes from Burkina Faso

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Introduction: The emergence of insecticide resistance in malaria vectors highlights the need for complementary transmission-blocking strategies. *Microsporidia* MB (MB), a naturally occurring symbiont of *Anopheles* mosquitoes, has shown promise in reducing *Plasmodium* development.

Methodology: We established a stable MB-infected laboratory colony and experimentally challenged mosquitoes with *Plasmodium falciparum*. Mosquitoes were dissected at day 7 post-infection to assess oocyst prevalence and intensity, and at day 14 to evaluate sporozoite-stage infections. Infection outcomes were compared between MB-infected (MB+) and uninfected (MB-) mosquitoes.

Results: MB infection significantly reduced parasite development at both stages. At day 7, oocyst prevalence decreased from 90% in MB- mosquitoes to 19% in MB+ mosquitoes ($p = 6 \times 10^{-49}$), corresponding to a transmission-blocking activity (TBA) of 79%. Mean oocyst intensity was also reduced from 8.7 to 1.6 oocysts per female, representing a transmission-reducing activity (TRA) of 82%. High-density MB infections achieved up to 96% TBA and 91% TRA. Day 14 dissections further revealed markedly reduced sporozoite prevalence in MB+ mosquitoes, indicating sustained inhibition throughout sporogonic development.

Conclusion: These findings support *Microsporidia* MB as a promising symbiont-based tool for malaria control.

Keywords: *Microsporidia* MB; *Plasmodium falciparum*; *Anopheles* mosquitoes; symbiont-based control; transmission-blocking

Paper ID# 85

Title: Assessing the abundance distribution of schistosome vector snails across Henga valley, Mzimba, Malawi

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Background: Schistosomiasis is a parasitic disease transmitted by fresh water snails. As one of the diseases transmitted by snails, more than 90% of the cases are in Africa Prevalence of

Schistosomiasis in Malawi stands at 40-50%. The battle to eliminate this disease through MDA has been unsuccessful in the past years in some regions including Malawi, WHO has recommended new strategies for global schistosomiasis control emphasize targeting the freshwater vector snails for schistosomiasis, hence a need for the research in Malawi. The research aimed to map species distribution, abundance and infection rate of schistosome vector snails in the Northern part of Mzimba.

Methodology: A total of eight sites were surveyed for the presence of snails; sampling was done using handpicking and scooping methods. Schistosoma snails were identified. A proportion of sampled snails were screened for cercaria. Vegetation cover, physico-chemical parameters were recorded at each site

Results: A total of 2790 snails were collected, the only intermediate host for Schistosoma parasite that was found at the sampled site was *Bullinus globosus* which was also dominant in terms of abundance, *Lymnea natalensis* and *Bellamia mornard* were other species which were collected and their relative abundance were 69.21%, 21.65% and 9.14% respectively. The highest number of snails were recorded at Lombo dam, which represents 84.41% of the whole population. The infection rate of snails was 8.75%. Depth was the only physico chemical parameter which had significant correlation with schistosome snail abundance ($r = 0.74$).

Conclusion: presence of schistosome intermediate vector snail species from the *Bulinus* genus which were shedding cercaria, can establish a potential schistosomiasis health risk to communities surrounding these water bodies since there is high number of people from this area who uses the water for domestic purposes. Hence, it is important to control the snails to prevent transmission of disease.

Keywords: Schistosomiasis, snails, and vectors.

Paper ID# 91

Title: Integrating MALDI-TOF MS and molecular detection of *Plasmodium* sporozoites into routine national malaria vector surveillance in Kenya

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Background: Effective malaria control relies on accurate identification of vector species and their infection status. Conventional microscopy and serological methods are labour intensive and limit high-throughput surveillance. We report findings from a collaboration with the National Malaria Control Programme (NMCP) integrating MALDI-TOF MS for mosquito species identification and PCR-

based *Plasmodium* sporozoite detection into routine surveillance in Kenya.

Methods: Mosquitoes were collected from four NMCP sentinel sites (Migori, Kirinyaga, Kilifi, Kwale) in 2025 using CDC light traps, Human Landing Catch, and Prokopack aspiration. Specimens were morphologically identified and analysed using MALDI-TOF MS for species identification. Species composition was analysed descriptively by site and complex. *Plasmodium falciparum* infection was assessed using PCR targeting the 18S rRNA gene.

Results: A total of 392 *Anopheles* mosquitoes were analysed. The *An. gambiae* complex predominated (55.9%), followed by the *An. funestus* complex (39.3%), with other species at 4.8%. Within the *An. gambiae* complex, *An. arabiensis* (131) and *An. gambiae* s.s. (80) were dominant, while *An. funestus* s.s. (89) and *An. rivulorum* (64) dominated the *An. funestus* complex. Kirinyaga contributed most samples (42.3%), followed by Kwale (28.1%), Kilifi (19.1%), and Migori (10.5%). MALDI-TOF MS enabled rapid identification. No *P. falciparum* sporozoites were detected.

Conclusion: Integrating MALDI-TOF MS into NMCP workflows provides a rapid, accurate, and scalable approach for vector identification. The absence of sporozoite infection suggests low transmission during sampling, seasonal variation, or effective interventions. Variation in species composition across sites highlights the need for location-specific vector control strategies and supports data-driven malaria surveillance.

Keywords: MALDI-TOF MS, PCR, malaria vectors, *Anopheles*, sporozoites, surveillance, NMCP, DHIS2

Paper ID# 70

Title: Species Composition and Distribution of Anopheles Mosquito Vectors in Zanzibar, Insights from Routine Entomological Surveillance (2015–2025)

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1. Zanzibar Malaria Elimination Program - Ministry of Health

2. TEMT- Swiss TPH

3. MEZA Project

Background: Malaria transmission depends on the composition, distribution, and behavior of *Anopheles* vectors. Understanding local vector species is essential for effective control. This study assessed the species composition and distribution of *Anopheles* mosquitoes in Zanzibar, focusing on key vectors sustaining transmission.

Methods: A longitudinal entomological surveillance study was conducted from 2015 to 2025 across 11 sentinel sites in Unguja and Pemba. Adult mosquitoes were collected using Human Landing

Catches (HLC), Prokopack aspirators, and Pit Traps. Two houses per site were used for HLC, five for Prokopack, and two pits. HLC was conducted indoors and outdoors from 18:00–06:00, while Prokopack and pit collections were done in the morning. Mosquitoes were identified morphologically, and all female *Anopheles* were analyzed using PCR for species confirmation.

Results: *Anopheles arabiensis* was the dominant species, accounting for 86.3% in Unguja and 88% in Pemba. Other species included *An. gambiae* s.s (4.12%), *An. rivulorum* (3.24%), *An. Merus* (0.9%), and *An. rufipes* (0.8%), with others at very low levels. These findings indicate ecological diversity and potential for residual transmission, especially outdoors. Notably, *An. gambiae* s.s showed an increasing trend in Unguja, suggesting the risk of indoor transmission.

Conclusion: Malaria transmission in Zanzibar is mainly driven by *An. arabiensis*, whose behavior limits indoor interventions. The increasing presence of *An. gambiae* s.s highlights the need for continuous surveillance and adaptive control strategies. PCR-based identification remains essential for guiding vector control and elimination efforts.

Keywords: Vector Surveillance and *Anopheles Arabiensis*

Paper ID# 204

Title: *Wickerhamomyces* spp. in *Anopheles gambiae* s.l. mosquitoes: a symbiotic yeast for malaria control in Burkina Faso.

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Background: One of the strategies for vector control is biological control, which can use symbiotic microorganisms, including fungi. The genus *Wickerhamomyces*, a budding yeast belonging to the phylum Ascomycota and the family Wickerhamomycetaceae, whose natural habitats include plants, soil, fermented fruits, and flowers, is found in the midgut and reproductive organs of mosquitoes. Previous studies have demonstrated a protective effect of a strain of this yeast against certain entomopathogenic microorganisms in *Anopheles stephensi*, highlighting its potential for vector control. The objective of this study is to isolate and identify the genus *Wickerhamomyces* in wild mosquitoes of the *Anopheles gambiae* complex in western Burkina Faso.

Methods: Mosquitoes collected from three areas of Bobo-Dioulasso in western Burkina Faso (Dioulassoba, Vallée du Kou, and Soumouso) in November 2024 were first identified

morphologically. Their different organs were then dissected, homogenized in PBS, and cultured on Sabouraud Chloramphenicol agar. Molecular biology techniques enabled the identification of the yeast *Wickerhamomyces* directly from organ pools and from colonies. R software analyses used GLM and McNemar's test to assess *Wickerhamomyces*, $P < 0.05$ significant.

Results: The overall prevalence of *Wickerhamomyces* in *Anopheles gambiae* s.l. mosquitoes were 17.24% (95% CI: 17.77–24.17). This prevalence varied significantly according to the collection site (p -value = $5.48e-08$), the *Anopheles gambiae* species (p -value = $5.84e-04$), and the developmental stage of the mosquitoes (p -value = $1.71e-11$). However, it was similar across all organs. Four mosquitoes (two *Anopheles arabiensis* and two *Anopheles coluzzii*) were co-infected with *Wickerhamomyces* and *Plasmodium falciparum*.

Conclusion: This study reports the prevalence of the genus *Wickerhamomyces* in wild mosquitoes of the *Anopheles gambiae* complex, highlighting the need to investigate its potential for malaria control in Burkina Faso.

Keywords: *Anopheles gambiae*, Malaria, *Wickerhamomyces*, Burkina Faso

Paper ID# 209

Title: Molecular diversity of parasites and bacteria with profiling of pathogen derived metabolites in tsetse preferred hosts

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Background: Tsetse flies (*Glossina spp.*) remain pivotal vectors of trypanosomes and other pathogens affecting wildlife and domestic animals across sub-Saharan Africa. Understanding host–vector–pathogen interactions are essential for sustainable disease control. This study investigates parasite and bacterial diversity in tsetse-preferred wildlife hosts, alongside profiling pathogen-derived metabolites circulating in host blood.

Methods: Protozoan parasites and helminths will be detected using 18S rRNA sequencing and PCR assays, while bacterial communities will be characterized through 16S rRNA sequencing. Parallel metabolomic profiling will identify pathogen-derived compounds, offering insights into their physiological impact on hosts and potential roles in modulating tsetse feeding behavior and parasite survival.

Results: By integrating parasitological, microbiological, and metabolomic approaches, this research establishes a transdisciplinary framework for decoding host–pathogen–vector dynamics. Preliminary findings emphasize ecological and biochemical cues that shape vector competence, highlighting how microbial and metabolic signals influence transmission cycles. Final analyses are scheduled for July 2026.

Conclusion: The anticipated outcomes will enhance surveillance of parasite and bacterial diversity in wildlife reservoirs and inform community-based tsetse control strategies. Beyond veterinary and public health applications, the study underscores the value of molecular and metabolomic profiling in designing innovative, locally grounded, and globally relevant approaches to vector-borne disease management

Keywords: Tsetse, Parasites, Bacteria, Metabolomics, Vector Competence

Paper ID# 202

Title: Mosquito biodiversity based on different trapping methods for mosquito surveillance in Burkina Faso

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Background: Mosquito surveillance is essential for assessing the emergence or controlling vector-borne diseases. However, its effectiveness depends in part on the performance of collection methods. Here, we evaluated the performance of mosquito collection methods to better guide vector monitoring strategies.

Methods: The study was performed in a semi-urban and periphery sites in Diébougou, in Burkina Faso. Four trap types including the Tent, BG-Sentinel, Double net and CDC light were used for eight days of mosquito collection. A trap rotation system across four sampling points per site was carried out, with the same exposure frequencies for each trap. Collected mosquitoes were morphologically identified to determine the genera, sex and female gonotrophic status per trap/site. The R software was used for statistical analysis.

Results: Overall, 561 mosquitoes were collected, including 57.9% (325/561) females. The distribution by genus was 58.6% *Culex spp*, 20.5% *Anopheles*, 16.0% *Mansonia* and 4.8% *Aedes*. The Tent trap was more effective across all species (60.2%) and the collection site. The BG-Sentinel trap

and the Double net trap performed worse, with similar frequencies (9.6% and 9.3%). No differences were found in the distribution of gonotrophic status per trap. However, the Tent trap and CDC light trap collected more unfed female mosquitoes, at about 45.0% and 33.3%, respectively.

Conclusion: Our results did not show an optimal collection method overall. However, the Tent trap has shown good efficacy for quantitative mosquito monitoring. In contrast, the BG-Sentinel trap and Double net trap seem to be more efficient for species diversity sampling. Thus, combining collection methods could improve mosquito surveillance and support targeted vector control.

Keywords: *Anopheles*, *Aedes*, *Culex*, *Mansonia*, Mosquito surveillance

Paper ID# 38

Title: Assessment of the larval ecology of *Aedes* mosquitoes and arbovirus transmission risk in four mid-sized cities of southern Cameroon

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2. *OCEAC*

3. *Organization of Coordination for the Control of Endemic Diseases in Central Africa*

Background: Vector-based surveillance is crucial for monitoring arboviral diseases such as dengue, chikungunya, yellow fever, and Zika. In Cameroon, data on the distribution and bionomics of *Aedes* species in medium-sized cities within the equatorial forest region are limited. This study assessed the distribution, larval habitats, and bionomics of immature *Aedes* stages across four mid-sized cities of southern Cameroon.

Methods: Larval surveys were conducted from March 2022 to March 2023 in Bertoua, Kribi, Sangmelima, and Abong-Mbang. Three surveys were carried out per season (rainy/dry) at each study site, systematically inspecting selected households. Water-holding containers were inspected using the dipping method and collected immatures stages were reared to adults for morphological identification. Entomological indices estimated arboviral transmission risk, and species co-occurrence in larval habitats was recorded. A generalized linear model was used to compare abundance and distribution among sites, seasons, and breeding sites.

Results: From 758 larval habitats inspected including used tires, tanks, breeze blocks, plastic and metal containers, 3,820 mosquitoes belonging to four genera and 11 species emerged dominated by *Aedes albopictus* (71.7%) and *Aedes aegypti* (27.2%), peaking in the rainy season (81.3%). Tires and plastic containers were the most common larval habitats. Bertoua and Kribi exhibited the highest transmission risks, with House, Container, and Breteau indices reaching 76%, 57.69%, and 150 in

Bertoua, and 62%, 50.44%, and 114 in Kribi. GLM confirmed larval abundance varied significantly across localities, seasons, and breeding sites ($P < 0.0001$).

Conclusion: Regular vector-based surveillance is vital to reduce arboviral transmission risk in Cameroon, especially during the rainy season around discarded tires and plastic containers near dwellings. Findings from Kribi and Bertoua emphasize the need to strengthen integrated vector management.

Keywords: arboviral diseases, *Aedes aegypti*, *Aedes albopictus*, southern, Cameroon

Paper ID# 39

Title: Mathematical modelling as a decision-support tool for infectious disease control

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Background: Infectious diseases remain a major public health challenge, particularly in low- and middle-income countries where limited resources require efficient and evidence-based control strategies. Mathematical modeling has become an essential tool for understanding disease transmission and informing intervention planning.

Methods: This study explores the use of mathematical modelling as a decision-support tool by integrating epidemiological parameters, transmission dynamics, and intervention scenarios within simulation-based frameworks. Different control strategies were assessed through scenario analysis to evaluate their potential impact under varying epidemiological conditions.

Results: The modelling approach demonstrates how simulation can support the comparison of intervention strategies, estimate their potential effectiveness, and identify optimal approaches based on impact, feasibility, and cost considerations. Results highlight the usefulness of modelling in high-transmission settings, where it enables exploration of multiple scenarios and supports evidence-based prioritization of control measures.

Conclusion: Mathematical modeling provides a robust framework for analyzing disease dynamics and guiding public health decision-making. By enabling scenario exploration and prediction, it supports the design of more effective and targeted intervention strategies. Strengthening interdisciplinary collaboration between modelling, epidemiology, and data analysis is essential to enhance its impact on infectious disease control.

Keywords: Mathematical modelling, Infectious diseases, Epidemiology, Disease transmission, Decision support systems.

Paper ID# 44

Title: PfTIP Secretion and Immune Modulation in *Plasmodium falciparum*.Christiane Donkeu^{1,2,*}1. *University of Yaounde*2. *Centre Pasteur Cameroon*

Background: The *Plasmodium falciparum* T-cell immunomodulatory protein homolog, PfTIP, is a novel invasion-related protein thought to play additional roles in modulating host immune responses. This study aimed to examine the cellular localization and secretion patterns of PfTIP in both laboratory-cultured parasites and naturally infected individuals. The research tested how plasma levels of the protein are associated with host immune responses and parasite survival.

Methods: The study utilized immunofluorescence microscopy and enzyme-linked immunosorbent assays (ELISA) to characterize PfTIP expression across asexual parasite stages. Researchers analyzed plasma from naturally infected individuals to measure protein levels, anti-PfTIP antibodies, and cytokines such as TNF- α , IL-10, and the chemokine MIP-1. Additionally, in vitro parasite growth inhibition assays were performed using rabbit antibodies targeted against an immunodominant peptide of the PfTIP protein.

Results: PfTIP is expressed in all major asexual forms and exported in a stage-dependent manner to the host erythrocyte surface, predominantly during schizont development. High plasma levels of naturally induced anti-PfTIP antibodies strongly associated with submicroscopic carriage or the absence of parasites in peripheral blood. Furthermore, rabbit antibodies to PfTIP significantly reduced parasite growth in vitro. A strong negative correlation was observed between PfTIP plasma levels and MIP-1, indicating potential modulation of vascular activation. TNF- α /IL-10 ratios remained balanced regardless of individual parasitemia or PfTIP levels.

Conclusion: These findings suggest that PfTIP plays a dual role in facilitating host cell invasion and suppressing host inflammatory responses. By modulating the immune environment in favor of parasite survival, PfTIP represents a significant factor in *P. falciparum* pathogenesis and a potential target for malaria reduction strategies.

Keywords: *Plasmodium falciparum*; T-cell immunomodulatory protein homologue; host cell invasion; anti-inflammatory activity.

Paper ID# 254

Title: Mapping the distribution of invertebrate non target organism in three villages in western Burkina Faso prior the implementation of genetic control tool against malaria vectors

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4. *Imperial*

Background: Mosquito control programs are challenged by mosquito-borne diseases such as malaria, insecticide resistance, and environmental impact on non-target organisms. To address this situation, Target Malaria consortium is in the process of developing a genetic tool that will control malaria mosquitoes *Anopheles* and that may have little or no impact on non-target organisms. A census or mapping of all non-target organisms in the breeding sites is therefore necessary at this time at our study sites. The objective of our study is to obtain information on the presence of non-target organisms sharing the same larval habitat and, where possible, their ecological relationships with the target mosquito species.

Methods: Larval habitats sampling was conducted during our monthly field surveys started in 2017 and is still ongoing at our Souroukoudingan and Bana sites in western Burkina. Sampling consisted of collecting with a sieve any living organism from about twenty larval habitats and keeping them in 90% alcohol. Identification (Jean-Luc Gattolliat) then allowed us to determine the order and family of each invertebrate collected.

Results: After identification, results showed that the different larval habitats sampled were composed of several orders and families at all sites. The Holometabole Coleoptera order and Dytiscidae family were the most represented while the Paurometabole Odonata order and Anisoptera Libellulidae family were the least represented at both sites.

Conclusion: These results could constitute a mapping of all non-target organisms existing on our sites currently and could inform us on a probable impact of the use of genetic control

Keywords: Non-target, organism, genetic, control, Order

Paper ID# 252

Title: Mosquito population and dynamics in Webuye, Western Kenya

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Background: Malaria remains a major public health problem globally, especially in children under 5 years, with approximately 282 million cases and about 610,000 deaths in 2024, most occurring in Sub-Saharan Africa. Understanding vector species composition and physiological status is essential for informing malaria control interventions. This study aimed to characterize mosquito populations across four cohort study sites (Kinesamo, Maruti, Nangili, and Sitabicha) in Webuye, Western Kenya.

Methodology: Indoor resting mosquitoes were collected weekly from 75 cohort households between Feb 2024 and Feb 2025 using the Prokopack aspiration. Female *Anopheles* mosquitoes were sorted by abdominal status and identified morphologically and genetically. Also, blood-fed and half-gravid females were screened for sporozoite infection using qPCR. To assess changes in mosquito population dynamics following piperonyl butoxide (PBO) net deployment, collections were categorized into pre-PBO (before 30 June 2024) and post-PBO (from July 2024) periods.

Results: A total of 1,631 female *Anopheles* mosquitoes were collected across the four villages. Maruti had the highest proportion 656 (40.2%), followed by Kinesamo 436 (26.7%), Nangili 365 (22.4%), and Sitabicha 174 (10.7%). *An. gambiae* s.l. was the most prevalent, 1,027 (63%), followed by *An. funestus* at 32%. Out of 1,631, 864 (53%) were blood-fed, while 414 (25.4%) were gravid. A total of 1,407 (86.3%) mosquitoes were collected before PBO net distribution and 224 (13.7%) after distribution. Among *An. gambiae*, 934 (90.9%) were collected pre-PBO and 93 (9.1%) post-PBO, while *An. funestus* mosquitoes comprised 426 (80.7%) and 102 (19.3%), respectively. A total of 62 (5.8%) mosquitoes tested positive for sporozoites.

Conclusion: Despite ITN deployment, heterogeneity in vector populations highlights the need for continued entomological surveillance to inform malaria control interventions in Western Kenya.

Keywords: Malaria, *Anopheles* mosquitoes, vector surveillance, sporozoite infection, PBO nets

Paper ID# 18

Title: Characterizing Anopheles Species and their host preferences in Nkhotakota, Malawi

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Background: Nkhotakota District in Malawi continues to report high malaria cases despite ongoing control interventions like ITNs, IRS, and IPTp. Two main mosquito species *Anopheles funestus* s.s and *Anopheles gambiae* s.l are responsible for transmitting malaria in Malawi. However, limited data exists regarding the blood-feeding behavior of these mosquitoes. This study investigates the feeding patterns of the Anopheles mosquitoes in Nkhotakota district.

Methods: A total of 400 Adult female *Anopheles* mosquitoes were sampled from Vwawa and Ngalauka, through pyrethrum spray catches. Samples were identified morphologically and preserved. DNA extraction and PCR analysis determine species and blood meal sources. Amplified products were visualized via agarose gel electrophoresis, and host identity was confirmed by comparing band sizes against reference controls

Results: Human-derived feeds were predominant, with 159 (91.0%), with 91.3% and 95.1% for An. funestus and An. gambiae respectively. Livestock feeds accounted for just 16 (9.0%), including (cow (40.0%), Goat (4.8%), Pig (1.0%)) from Ngalauka and a record of (cow (40.0%), Goat (1.6%), Pig (3.3%)) from Vwawa. An. funestus feeding behavior for Vwawa and Ngalauka showed a significant bias toward human feeding ($p=1.895 \times 10^{-12}$ and $p=2.2 \times 10^{-16}$ respectively).

Conclusion: Mosquitoes showed a strong preference for human hosts in both sites, indicating elevated human-mosquito contact and sustained malaria transmission risk.

Keywords: Anthrophilic, Zoophilic, Human blood Index, *Anopheles*, Host preference

Paper ID# 14

Title: High prevalence and risk factors associated with asymptomatic malaria among children (5-14) years in Nkwen village Northwest region Cameroon

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2. The University of Bamenda

Background: Asymptomatic malaria is a significant silent threat to malaria control and eradication due to their contribution to the persistence of malaria transmission. This study aimed to investigate

prevalence and risk factors associated with asymptomatic malaria infections among children in Nkwen Village, Northwest Region of Cameroon.

Methods: The study was a community-based cross-sectional study conducted between June-December 2022. Structured, closed-ended, pre-tested questionnaires were administered to obtain information. Patients' temperature was measured using an infrared forehead digital thermometer. Consented participants (5-14) years without any observed signs and symptoms, suggestive of malaria were included in the study. Asymptomatic malaria was detected and quantified by microscopy and polymerase chain reaction.

Results: Out of 246 apparently healthy children examined, the prevalence of asymptomatic malaria (all *P. falciparum*) was 65.9% (162/246) and 59.3% (146/246) by PCR and Microscopy respectively. Considering both diagnostic methods, the prevalence of asymptomatic malaria was higher in females (67.7 % and 62.2%) than males (63.9% and 56.3%) by PCR and microscopy respectively. Vector-based interventions, including insecticide-treated bed net and indoor residual spray, were found to have significant impacts on asymptomatic malaria infections, with non-users of these measures carrying much higher risks of infection. In addition, individuals living in poorly constructed households (open eaves) or with a family history of malaria were more prone to asymptomatic infections.

Conclusions: The high prevalence of asymptomatic malaria detected in this study is a big challenge and can be a threat to the present malaria control programme. Both individual- and household-level risk factors were identified. Thus, it should be considered in assessing and reorganizing more effective malaria elimination strategies to achieve the desired goal of malaria control.

Keywords: Asymptomatic malaria, risk factors, children

Paper ID# 241

Title: Malaria vector biting patterns and human nocturnal behaviour: risk assessment in Manchene Village, Nchelenge district, Zambia

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Background: Malaria remains a significant public health concern in Zambia, with Nchelenge District experiencing persistent transmission despite high coverage of long-lasting insecticidal nets (LLINs) and indoor residual spraying (IRS). This study assessed the relationship between malaria vector biting patterns and human nocturnal behaviour in Manchene Village to identify periods of elevated exposure risk.

Methods: A cross-sectional design was employed, integrating entomological surveillance with direct observations of human night-time activities. CDC light traps were deployed indoors and outdoors in all 30 households from 18:00 to 06:00 hours, while observers recorded outdoor activities, sleeping patterns, and bed net use. Mosquitoes were identified morphologically to species level, and data were analysed using descriptive statistics, Chi-square tests, ANOVA, and logistic regression in SPSS version 25 at $p < 0.05$ level of statistical significance.

Results: A total of 2,160 mosquitoes were collected, with *Anopheles funestus s.l* accounting for 99.0%, followed by *An. ziemani nambiensi* (0.7%) and *An. gambiae s.l* (0.3%). Vector activity was recorded throughout the night, peaking between 22:00 and 02:00 hours. Observations indicated that most residents remained outdoors between 18:00 and 21:00 hours, Logistic regression confirmed that collection time significantly predicted the likelihood of being bitten ($p < 0.001$), while being under a net was not statistically significant ($p = 1.000$), suggesting potential gaps in usage or insecticide resistance.

Conclusion: The study concludes that malaria exposure in Manchene Village is driven by the temporal overlap of peak vector activity and unprotected human behaviour. Effective malaria control in such settings requires behaviour-focused strategies that complement LLINs and IRS, including early evening protection, outdoor vector control tools, and targeted community health education.

Keywords: Malaria vector, human nocturnal behaviour, biting patterns, exposure

Paper ID# 246

Paper Title: Choosing Mosquito Pool Sizes: How Many Mosquitoes Make a Good Pool?

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1. *University of Glasgow*

Background: Vector surveillance is essential for monitoring malaria and other vector-borne diseases (VBDs). How captured mosquitoes are analyzed, particularly whether and how they are grouped into pooled samples, underpins key estimates of infection rates. However, the methodological basis for selecting mosquito pool sizes remains poorly defined, and the implications of variable pool sizes for interpreting infection rates are not clearly articulated. This study aims to (i) characterise and compare mosquito pooling strategies across VBD surveillance contexts, (ii) identify factors influencing pool size selection, and (iii) understand researchers' experiences.

Methods: A mixed-methods design was employed. A structured literature review systematically identified studies reporting mosquito pool sizes across malaria, arbovirus, and onchocerciasis surveillance, with data analyzed using generalized linear models to assess variation across diseases.

In parallel, semi-structured interviews with 31 vector surveillance researchers were conducted and analyzed thematically to explore decision-making processes and constraints.

Results: Pooling strategies were frequently unreported. Where reported, pool sizes varied widely across diseases, with no consistent relationship to collection size. Arbovirus surveillance showed extreme variability (2 to >4000), while malaria (5–10) and onchocerciasis (50–100) were more standardised. Justifications were rarely provided. Interviews indicated that decisions are seldom statistically optimised, instead reflecting operational constraints such as capacity, cost, norms, and expert judgement.

Conclusion: These findings suggest that pool size is a context-dependent operational choice rather than an optimised parameter, introducing uncertainty in how infection rate estimates are generated and compared across settings. A key gap remains: the impact of pool size on estimates is not well understood, and guidance is lacking, particularly in heterogeneous transmission settings.

Keywords: Arbovirus, vector, surveillance

Paper ID# 36

Title: Influence of different host blood-meal sources on the reproductive outcomes in *Anopheles gambiae*: enhancing fecundity in a mass rearing environment

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Background: Blood-meal source identification is important for mass rearing of *An. gambiae*. We investigated feeding success, reproduction performance and survivorship of *An. gambiae* fed on five host blood meals compared to human blood meal.

Methods: The study was conducted in 2022 at KEMRI, Kisumu. Three-days-old female *An. gambiae* mosquitoes were fed on Pig, cow, goat, chicken, sheep, and human blood meals. Gravid mosquitoes laid eggs and resultative larvae and adults monitored for survivorship. Feeding success and eggs laying was analyzed using two-way Analysis of Variance (ANOVA). Survivorship was analyzed using Kaplan Meier survivor analysis.

Results: Human blood meal (Mean = 125.25 ± 3.86) had the highest feeding success with no statistically significant difference with pig blood meal ($t(6) = 0.453$, $p = 0.666$). The highest

proportion of females that laid eggs were from human blood meal (Mean = 36.50 ± 2.08) followed by chicken blood meals (Mean = 27.50 ± 5.44) and then pig blood meal (Mean = 26.25 ± 2.87). The mean number of eggs laid per mosquito was highest in human blood meal (111.65 ± 5.74) followed by pig blood meal (100.46 ± 6.36). High hatchability in human-blood ($88.35 \pm 5.61\%$) with no significant difference with pig blood-meal $t(38) = 0.52857$, $p = 0.60017$. High pupation percentage in pig blood meal (Mean = 83.50 ± 4.79) and goat blood meal for the shortest pupation time (9.79 ± 0.41 days). Larval survival rate was highest in pig blood meal (Mean = 0.57 ± 0.11) and adult survival rate in human blood meal (Mean = 0.73 ± 0.04) with no significant difference with the pig blood-meal $t(113) = 1.0810$, $p = 0.2819$. Pig blood meal (56 days) demonstrated the longest survival period, close to human blood meal (57 days).

Conclusion: Pig blood meal was an excellent alternative to human blood meal. Pig blood-meal adoption may reduce dependence on human blood, facilitating scalable, ethical, and sustainable mosquito production for malaria control research.

Keywords: Blood meal, mass rearing, *An. gambiae*

Paper ID# 240

Title: Investigating the natural presence of *Wolbachia* and microsporidia in *An. gambiae* in four Cameroonian villages

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3. NIAID

Background: Endosymbiotic microorganisms such as *Wolbachia* and *Microsporidia* are increasingly recognized for their potential role in mosquito biology and pathogen transmission. This study assessed the prevalence of *Wolbachia*, *Microsporidia*, and *Plasmodium* in *Anopheles gambiae* mosquitoes collected from four locations in Cameroon.

Methods: A total of 94 *Anopheles gambiae* mosquitoes were collected in Belabo, Essé, Kékem, and Yangha. Genomic DNA was extracted using the Hotshot method. *Plasmodium* infection and *Microsporidia* were detected by qPCR using the *Microsporidia* MB strain primers, followed by gel electrophoresis for *Wolbachia* detection. Infection frequencies were calculated and compared across different study sites.

Results: Of the 94 mosquitoes analyzed, *Wolbachia* was detected in 23 specimens, representing an

overall prevalence of 24.5%. Infection rates varied by site, with Belabo having the highest proportion of positive mosquitoes (12/18; 66.7%), followed by Essé (4/30; 13.3%), Kékem (4/16; 25.0%), and Yangha (3/30; 10.0%). *Microsporidia* were detected in 44 of the 93 successfully tested mosquitoes (47.3%), representing the most frequently observed microorganism. In contrast, *Plasmodium* infection was low, with only 2 positive mosquitoes out of 93 analyzed (2.2%), with the infected specimens coming from Belabo and Kékem. These results reveal significant variation in the prevalence of endosymbionts among the study sites and highlight a low prevalence of malaria parasites in the mosquito populations examined.

Conclusion: Natural infections with *Wolbachia* and *Microsporidia* are present in *Anopheles gambiae* populations in Cameroon, with *Microsporidia* showing a particularly high prevalence. The low frequency of *Plasmodium* infection suggests that there is limited circulation of the parasite in the vectors sampled during the study period.

Keywords: *An. gambiae*, *Wolbachia*, *microsporidia*, *Plasmodium*, Belabo, Essé, Kékem, and Yangha

Paper ID# 7

Title: Distribution of adult *Anopheles* mosquitoes in low and high malaria transmission areas in Malawi (Chikwawa and Balaka districts)

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Background: Entomological surveys provide essential data on composition, density, and malaria incidence rates which help to establish the link between mosquito populations and malaria transmission intensity. However, there is limited data on mosquito distribution in relation to transmission intensity, which hinders the effectiveness of control strategies. This study assessed the distribution of adult *Anopheles* mosquitoes in Chikwawa and Balaka districts

Methods: Adult Mosquito sampling was carried out once per month during the dry season and rainy season using CDC light traps from July, 2023- June 2024. Ten houses were sampled for one night at each site. The trap was placed at the end of bed where the legs point at 1m from the floor. Mosquito species were identified using morphological keys, density calculated, and monthly malaria cases data were obtained from health facilities located near each mosquito collection site.

Results: 455 adult female *Anopheles* mosquitoes were collected from four sites in the two districts. Most were *An. gambiae* (85.9%) and *An. funestus* (13.4%), with few *An. tenebrosus* and *An. costani*. Kabota and Balaka had the highest mosquito counts (45.9%), followed by Ntwana, Chikwawa (34.1%). Seasonally, Ntwana, Chikwawa had more mosquitoes in the dry season, while Kabota, Balaka

peaked in the rainy season. Malaria incidence rate reflected these seasonal trends Chikwawa had the highest rate in Ntwana (32.4 per 1000) in the dry season, Nyamphota peaked in the rainy season (31.1 per 1000), while Chimdikiti in Balaka district consistently recorded the lowest malaria incidence rates. Overall, across both seasons, Nyamphota showed a high malaria incidence rate despite lower mosquito density.

Conclusion: *Anopheles gambiae* was the dominant mosquito species among all *Anopheles* mosquitoes, and malaria cases were affected by site and season. These findings highlight the need for targeted control interventions in high-risk areas during peak transmission periods.

Keywords: *Anopheles*, density, malaria incidence

Paper ID# 177

Title: Understudied vectors with outdoor-biting behaviour evade indoor-based interventions with potential to sustain residual malaria transmission in a pre-elimination setting of Choma district, Southern Zambia.

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1. *Macha research trust*

Background: Despite primary vector reductions (*An. gambiaes.s.*, *An. arabiensis*) via IRS and ITNs, residual malaria persists in Choma, Zambia. Understudied species (*An. squamosus*, *An. rufipes*, *An. pretoriensis*, *An. coustani*) exhibit exophilic/exophagic behaviors, evading current indoor interventions. We analyzed four studies (2015-2022) to assess their role in persistent transmission.

Methods: Adult *Anopheles* collected using CDC light traps indoors, outdoors near human areas and near animal enclosures. Larval surveys across 295 water bodies (2022-2023). Blood meal analysis and CSP-ELISA for *Plasmodium falciparum* (2015-2023).

Results: Outdoor traps (porch, animal pen) captured greater species diversity and higher densities than indoor traps, with most species year-round outdoors; *An. arabiensis* absent in dry season. Direct indoor vs. outdoor comparison showed outdoor traps consistently caught more mosquitoes, indicating outdoor biting. Sporozoite positive mosquitoes (2015-2019) included *An. arabiensis* and understudied *An. coustani*, *An. squamosus*, *An. rufipes*; none detected 2020-2023. Blood meals: *An. arabiensis* highly anthropophilic (47%). Understudied species predominantly zoophilic but showed opportunistic human feeding (*An. squamosus* 4.7%, *An. rufipes/pretoriensis* 2.3%, *An. coustani* 6.1%). Streams/rivers dominated larval habitats (55%); alkaline (pH>8) and clear water (77%) predicted larval presence.

Conclusion: Understudied species were predominantly captured outdoors, with outdoor traps

recorded higher densities and diversity than indoor collections, confirming preferential outdoor biting thus evading indoor based interventions ITNs/IRS. Their sporozoite positivity and opportunistic human feeding, despite zoophilia, indicate potential to sustain residual transmission, supporting outdoor targeted control.

Keywords: Understudied vectors, *anopheles*, Malaria

Paper ID# 188

Title: Indoor residual spraying of distinct insecticide formulations in a household-scale micro-mosaic format: Feasibility and effectiveness for malaria vector control in rural Zambia

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Background: Zambia recently adopted mosaic application patterns as an insecticide deployment strategy for managing resistance in malaria vector populations. While macro-mosaic applications of indoor residual spraying (IRS), a commonly used supplement to long-lasting insecticidal nets (LLINs), vary the active ingredients used from one village to the next, micro-mosaics vary between households. Herein, two different IRS formulations in a household level micro-mosaic was piloted in south-eastern Zambia nested within a village scale macro-mosaic, enabling comparison of their individual effects on residual mosquito densities and species composition.

Methods: Nine health facility catchment areas in Luangwa district were assigned one of three IRS regimes: (I) DDT applied to all houses, (II) Clothianidin–deltamethrin mixture (CD) applied to all houses, OR (III) Micro mosaic where DDT and CD were alternated between adjacent houses. Generalized linear mixed effects models were used to analyze captured mosquito counts, comparing residual populations of primary and secondary malaria vectors by group, complex, and species levels.

Results: Over 1620 trap nights, the numbers of primary and secondary malaria vectors captured were generally very low, confounding precise estimation of mean densities or comparisons with satisfactory statistical power. Nevertheless, the densities of all *Anopheles* species identified were

approximately comparable across all IRS regimes ($p \geq 0.1420$), and no differences were observed between regimes regarding species composition of the *Anopheles funestus* group ($p \geq 0.072$) or *Anopheles gambiae* complex ($p \geq 0.1410$).

Conclusion: Household-level micro-mosaic applications of distinct IRS formulations may be just as immediately effective over the short term as conventional macro-mosaic deployments of each formulation separately in different villages, potentially offering a useful additional option for mitigating against resistance evolution over the long term.

Keywords: Resistance, Mosquitoes, Micro-mosaics, Macro-mosaics

Paper ID# 12

Title: Mosquito feeding assays according to standardized procedure in children from the sub-prefectures of Maferinyah and Kaback, Guinea

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Background: Malaria remains a significant public health challenge, particularly in sub-Saharan Africa, where innovative solutions such as the Transmission Blocking Vaccine (TBV) hold promise for interrupting malaria transmission. Recent advancements in malaria vaccines, notably the R21 and RTS, S vaccines, have been developed for young children. However, to enhance protection for all vulnerable populations, additional complementary control measures are crucial. In this regard, Guinea has joined Mali and other sub-Saharan nations in undertaking specialized evaluations, including the Direct Skin Feeding (DSF) test, to accurately assess the efficacy of new malaria vaccines targeting the mosquito vector.

Methods: This study was a comprehensive three-month cross-sectional analytical project, structured into three research rounds between May and July 2025. A total of 500 participants aged 5 to 18 were recruited — 400 from Kaback and 100 from Maferinyah. Each participant underwent a blood smear and rapid diagnostic test during monthly visits, and all were subjected to the DSF for a duration of 15 minutes, monitoring any adverse events at 24 and 48 hours.

Results: Results demonstrated no adverse events throughout the study duration. The mosquito engorgement rates were recorded at 93.77%, 90.84%, and 96% for rounds one, two, and three, respectively. Survival rates varied between rounds, with 57% in the first round and 67% in the subsequent rounds. Importantly, positive oocysts were identified solely in the third round, at a rate of 1.3%.

Conclusion: The findings bolster the viability of the DSF test as a reliable surrogate for measuring the

efficacy of the TBV in forthcoming field trials in Maferinyah, contributing significantly to efforts aimed at malaria elimination.

Keywords: Direct Skin Feeding, Guinea, Maferinyah, Malaria, Transmission Blocking Vaccine

Paper ID# 21

Title: Estimating the entomological inoculation rate of *Plasmodium falciparum* transmitted by *Anopheles funestus* and *Anopheles gambiae* in Chelokoto and Chilungo villages in Salima district.

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¹

1. LUANAR

Background: Malaria remains a major health concern in Africa, with Malawi being heavily affected. Despite a decline in cases, the disease still threatens communities, especially children under five. *An. funestus* and *An. gambiae* are the primary malaria vectors in the country. Salima district reports high malaria cases despite a relatively lower mosquito population. This study aimed to compare the abundance, sporozoite infection rates, and estimate entomological inoculation rates of *An. funestus* and *An. gambiae* in two villages in Salima District

Method: Mosquitoes were collected from Chilungo and Chelokoto villages in Salima District using CDC-Light Traps over a five-month period August - December 2024. Mosquitoes were identified morphologically while *An. gambiae* complex under molecular identification. Specimens were labeled and analyzed at LUANAR's Biotech Lab using ELISA to detect *Plasmodium falciparum* sporozoites.

Results: A total of 288 *Anopheles* mosquitoes were collected from both sites where 263 *An. funestus* (91.3%) and 25 *An. gambiae* (8.7%). Sporozoite of *An. gambiae* (n=10) in Chilungo had sporozoite rate of 10% (1/10) and EIR of 1.43, while *An. funestus* (n=153) showed 3.9% (6/153) and EIR of 8.57. At Chelokoto, *An. gambiae* (n=15) had 6.7% (1/15) and EIR OF 1.43, while *An. funestus* (n=110) with 7.3% (8/110) and EIR of 11.42. Fisher's Exact Tests indicated no significant differences in sporozoite positivity between species, while Chi-square tests confirmed that higher EIR values for *An. funestus* were driven by its greater abundance rather than higher infection rates.

Conclusion: These results demonstrate that *An. funestus* appears to be a dominant malaria vector in Salima District. Its consistently higher EIR across both sites suggests elevated transmission risk and underscores the importance of targeted control measures focused on this species which are use of long-lasting treated nets and Indoor Residual Spraying as is an indoor biter, while monitoring *An. gambiae*

Keywords: Malaria, *Anopheles funestus*, Entomological Inoculation Rate, *Plasmodium falciparum*.

Paper ID# 183

Title: Environmental characteristics of *Aedes aegypti* larval habitats in Nouakchott, Mauritania

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Background: In Nouakchott, *Aedes aegypti* represents a major public health concern and is responsible for dengue epidemics. Identifying the factors that influence the distribution and productivity of breeding sites is crucial for designing effective control strategies. Physicochemical parameters were measured, and larvae were collected using the standard dipping method, in which a standard dipper was used to sample water from containers. A total of 294 observations were carried out during the study, corresponding to the total number of visits to water collection sites across the different surveyed habitats.

Methods: Larval positivity and abundance were modeled using logistic and negative binomial regressions, respectively.

Results: Depth, distance from the habitat, type of water source, and sun exposure were statistically significant and independently associated with the presence of *Ae. aegypti* larvae in water samples (aOR = 5.18, 95% CI [1.66–16.18], p-value = 0.005; aOR = 0.00, 95% CI [0.00–0.02], p-value < 0.001; aOR = 252.88, 95% CI [4.05–15,786.84], p-value = 0.009, and aOR = 0.04, 95% CI [0.01–0.26], p-value < 0.001, respectively). *Aedes aegypti* breeding sites were primarily artificial, temporary, located near dwellings, and shaded. Plastic water containers, wells, and barrels were the most common breeding sites. Larval abundance decreased with increasing pH (aOR = 0.50, 95% CI [0.33–0.75], p = 0.001) and surface area (aOR = 0.48, 95% CI [0.27–0.87], p = 0.016).

Conclusion: *Ae. aegypti* in the study area are multi-resistant to adulticides and dengue has been endemic epidemic since 2014; therefore, vector control should prioritize eliminating or treating peridomestic water containers, especially plastic tanks and barrels, and using biological larvicides for small, shaded breeding sites.

Keywords: *Aedes aegypti*; arbovirus; breeding sites; larvae; Mauritania; Nouakchott

Paper ID# 189

Title: Outdoor biting dominance of *Anopheles arabiensis* and structural limits of indoor vector control in a low-sustained malaria transmission setting of Choma, Southern Zambia.

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Background: Residual malaria transmission persists in Choma District, Southern Zambia, despite ongoing vector control interventions. Previous studies suggested that some transmission may occur outdoors, with potentially understudied vector species contributing to exposure. This study characterized *Anopheles* species composition, indoor–outdoor biting behavior, and human behavior-adjusted exposure.

Methods: Monthly indoor and outdoor mosquito collections were conducted from February–December 2024 in 12 randomly selected households across three zones using CDC light traps and human landing catches (HLC) (18:00–06:00), with nine collection rounds per zone. *Anopheles* mosquitoes were morphologically identified to species level and screened for *P. falciparum* by ELISA. Human behavioral observations informed behavior-adjusted biting rate estimates, and negative binomial regression identified key determinants of mosquito abundance.

Results: A total of 1,558 female *Anopheles* representing 11 species were collected. *An. arabiensis* dominated human landing catches (98.1%), with 80% captured outdoors, confirming exophagic behavior. Outdoor biting peaked at 21:00 (3.70 bites/person/hour; outdoor: indoor ratio 4.4:1). No sporozoite-positive specimens were detected. At peak biting (20:00), 42.3% of participants were outdoors and unprotected. Despite near-universal ITN use (99.8%), outdoor-awake exposure (39.2%) was comparable to ITN-prevented exposure (38.3%), highlighting a significant outdoor transmission gap. Seasonality was the strongest predictor of abundance.

Conclusion: *An. arabiensis* exhibited predominantly outdoor, early-evening biting, coinciding with peak community exposure before bed net use. The near equivalence of outdoor-awake and ITN-prevented exposure represents a structural gap that indoor interventions cannot address. Multi-species surveillance and outdoor vector control strategies are essential for malaria elimination in the Choma District.

Keywords: *Anopheles arabiensis*, outdoor biting, residual malaria transmission, exposure, adjusted-human behavior, Insecticide-treated

Vector & Parasite Genomics

Paper ID# 52

Title: Spatial and temporal signatures of genomic insecticide resistance markers in the *Anopheles arabiensis* mosquito malaria vector from Ethiopia

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Background: Insecticide resistance in *Anopheles* mosquitoes threatens the effectiveness of insecticide-treated nets (ITNs) and indoor residual spraying (IRS) in Ethiopia. Genomic analysis is essential to identify both known and novel molecular markers of resistance and to inform management strategies.

Methods: We investigated insecticide resistance genes using whole-genome sequencing in *Anopheles arabiensis* sampled across multiple Ethiopian regions. Genetic markers linked to target-site substitutions, metabolic resistance, and copy number variants (CNVs) were analyzed, and signals of selection were examined across chromosomes.

Results: Resistance markers showed marked geographic and temporal variability. The Vgsc-L995F substitution in the voltage-gated sodium channel gene was highly prevalent in northern Ethiopia but less common elsewhere. Western Ethiopia exhibited metabolic resistance, with elevated CNV frequencies at the cytochrome P450 cluster Cyp6aa/p and the carboxylesterase Coeae2-7g. In the Central Rift Valley, marker frequencies were generally lower, though CNVs at Gste2 and Cyp9k1 were frequent. Seasonal shifts were observed, including increasing frequencies of Vgsc-L995F and several cytochrome P450 variants during the major transmission season, with patterns varying by location. Selection scans revealed signals on chromosome 2L centered on the Coejhe1-5e genes in Werkamba, and additional signals on chromosome 3L (~20 Mb) near detoxification-related genes, including

those associated with the ubiquitin-proteasome system in Asossa.

Conclusions: Molecular insecticide resistance in *An. arabiensis* likely arises from a complex interplay of malaria interventions, agricultural practices, human behavior, and vector ecology. Integrating genomic surveillance into entomological monitoring is critical for strengthening resistance management, and further investigation of lesser-known adaptive mechanisms could have significant consequences for vector control.

Keywords: *Anopheles arabiensis*, target site resistance, metabolic resistance, insecticide resistance, malaria mosquito vector

Paper ID# 62

Title: Molecular Xenomonitoring for assessing malaria parasite prevalence as a proxy to human cases and vector blood-feeding patterns in South Ethiopia

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Background: Understanding mosquito blood-meal sources and parasite transmission dynamics is essential for effective malaria control. This study investigated *Plasmodium* prevalence in mosquito abdomens and salivary glands, along with blood-meal origins, in five malaria-endemic villages in southern Ethiopia.

Methods: Adult *Anopheles* mosquitoes were collected monthly using indoor and outdoor CDC light traps and pyrethrum spray catches (PSCs) from 10 randomly selected households per method. Sampling was conducted six times at three-month intervals between April 2022 and August 2023. Blood-fed mosquito abdomens were analyzed for *Plasmodium* parasites and host origin using nested polymerase chain reaction (PCR). Heads and thoraces were tested for *P. falciparum*, *P. vivax*-210, and *P. vivax*-247 circumsporozoite proteins (CSPs) using enzyme-linked immunosorbent assay (ELISA).

Results: A total of 1,593 female *Anopheles* mosquitoes were collected, of which 98% were *An. gambiae* s.l. PCR analysis of 510 blood-fed abdomens detected *Plasmodium* infection in 18.1% (92/510). *P. falciparum* was most prevalent (9.4%), followed by *P. vivax* (4.2%), while mixed infections accounted for 4.5%. ELISA-based CSP rates were 0.25% (4/1,593) for *P. falciparum* and 0.44% (7/1,593) for *P. vivax*-210, with no mixed infections detected. Among blood-fed mosquitoes,

84% (427/510) had identifiable vertebrate hosts. Humans were the dominant source (64%), followed by goats (55.3%) and cattle (12%). Single-host feeding occurred in 21% (human), 7.5% (goat), and 5% (cattle), while multiple-host feeding (up to four hosts) was also observed. Human blood indices were 65% (indoor CDC traps), 62% (PSC), and 52% (outdoor CDC traps).

Conclusions: The findings reveal frequent mosquito contact with infected hosts and diverse feeding behavior, sustaining malaria transmission risk. Integrated control strategies targeting both indoor and outdoor biting vectors are necessary to effectively reduce transmission.

Keywords: *Plasmodium* infections, Blood meal sources, southern Ethiopia

Paper ID# 51

Title: Genome-wide sequence analysis of malaria vectors reveals genetically isolated *Anopheles coluzzii* populations along the slopes of Mount Cameroon

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Background: *Anopheles gambiae* complex is a major vector for the transmission of malaria parasites and other disease-causing pathogens. Unravelling the population structure of this vector could reveal crucial insights into parasite transmission dynamics and evolutionary adaptations that are vital for disease control and elimination.

Method: This study explored WGS data of 276 *An. gambiae* complex collected between 2019 and 2020 in six communities across the altitudinal gradient of Mount Cameroon and sequenced samples from Burkina Faso. These samples were sequenced at Sanger institute (as part of the MalariaGEN Vector Observatory Project) to determine the population structure of this complex. The siblings of this complex were assigned into taxa based on their known AIMs. A set of 100,000 neutral SNPs were selected for population structure and differential analysis using PCA, Fst, Admixture, IBD and population dynamics analysis within Cameroon's cohorts together with sequenced samples from Burkina Faso.

Results: Ninety-three (93), 178, and 4 of the vectors were identified as *An. coluzzii*, *An. gambiae*, and *An. melas* respectively while one was unassigned. Population structure revealed two subpopulations of *An. Coluzzi i* (referred to as *An. coluzzii* A and B), from the same locality (Missellele), indicating divergence despite probable sympatry, with the *An. coluzzii* B ancestrally closer to those from Burkina Faso. However, the *An. coluzzii* A sub-population was most differentiated from all other *An. coluzzii* populations, strongly driven by variants on the X and 2L chromosomes, suggesting local reproductive isolation and ecological adaptation.

Conclusion: These genetic divergence and recent expansion of all species in all populations, call for further genomic surveillance to support locally tailored vector control and malaria elimination efforts. Thus, failure to account for this cryptic diversity may result in mismatched interventions and sustained transmission

Keywords: Malaria, *Anopheles coluzzii*, population Biology, speciation

Paper ID# 120

Title: Metabolomic profiling of insecticide resistance in *Anopheles* Mosquitoes

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Background: The rapid escalation of insecticide resistance in *Anopheles* vectors remains a primary obstacle to malaria elimination across Africa. While genomic and proteomic markers have provided deep insights into resistance mechanisms, they often fail to capture the dynamic, functional changes occurring at the physiological level. Metabolomics, the comprehensive study of small-molecule metabolites, offers a high-resolution lens into the actual biochemical phenotype of resistant mosquitoes. This study aims to characterize the metabolic shifts associated with pyrethroid resistance in *Anopheles* populations. By comparing susceptible and resistant strains, we seek to identify specific metabolic pathways, such as those involved in antioxidant defense and energy metabolism, that are rerouted to facilitate survival under chemical pressure.

Method: A phenotypic bioassay (per WHO guidelines) was performed on field-collected mosquitoes from Ogun State and Lagos. Resistant samples (3-5) per group were quenched with methanol, and metabolites were extracted using a modified Bligh-Dyer method. Utilizing advanced analytical platforms, including two-dimensional gas chromatography-time-of-flight mass spectrometry, we will perform non-targeted metabolic profiling on mosquito tissues.

Results: Preliminary findings suggest that resistant mosquitoes exhibit distinct metabolic signatures. Identifying these metabolic fingerprints provides a dual advantage: it offers a new suite of biomarkers for real-time resistance monitoring in the field and highlights novel biochemical targets for the next generation of synergists.

Conclusion: By integrating metabolomics into vector surveillance, this research moves beyond traditional mapping to understand the functional biology of resistance. This approach is critical for developing data-driven vector management strategies tailored to the evolving biochemical landscapes

of African malaria vectors.

Keywords: Metabolomics, Insecticide resistance, *Anopheles*, Functional phenotype Vector control

Paper ID# 118

Title: Genomic insights into the spread and evolution of insecticide resistance variants in *Anopheles gambiae* s.l. from Burkina Faso

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Background: The intensive use of insecticide-based control tools has led to the rapid evolution of resistant phenotypes in malaria vector populations. Understanding the evolutionary processes underlying these resistances is essential to inform the development and deployment of effective control interventions. This study investigated the geographical spread and the genetic background of insecticide resistance variants in *Anopheles gambiae* s.l. in Burkina Faso.

Methods: The genomes of *An. gambiae* mosquitoes collected in 2022 from 8 sites in Burkina Faso were sequenced as part of the Ag1000G Project. The genomic data were analyzed using a wide range of genomic analysis methods.

Results: The study identified five pyrethroid-resistant mutations (995F, 995S, 402L(g>t, c), 1527T and 1570Y) at high frequencies. Six diploidy groups were identified, including novel combinations of the resistance-associated alleles (995F, 402L(g>t, c) and 1527T), which formed new genotypes within *An. coluzzii* populations. New resistance genotypes, not associated with 995F, were observed in *An. coluzzii*, probably due to recombination and gene flow events. Interestingly, strong linkage disequilibrium ($r^2=0.821$) was observed between 1527T and 402L(g>t) compared to 1527T and 402L(g>c). The PCA revealed three clusters of *An. coluzzii* populations, driven by 995F, 402L(g>t, c) and 1527T. Other insecticide resistance associated variants such as copy number variations and SNPs in the Ace1 gene (ace1-G280S), cytochrome P450s, esterases and glutathione S-transferases were identified at high frequencies in the same mosquito populations, indicating the intensity and diversity of resistance mechanisms in the country.

Conclusion: The study underscores the extent and spreads of insecticide resistance variants in Burkina Faso. It highlights the importance of genomic surveillance of malaria vectors to monitor and detect new resistance variants and to understand the evolutionary processes in vector populations.

Keywords: insecticide, resistance, genomics, *An. gambiae s.l.*, malaria

Paper ID# 214

Title: Prevalence of hrp2 and hrp3 gene deletions and characterization of their flanking regions in *Plasmodium falciparum* isolates from human blood and malaria vectors from Busia County.

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Background: Clinical diagnosis of malaria in Kenya is performed mainly using Rapid Diagnostic Tests (RDTs), with the most common type being the HRP-based RDT. The emergence of *P. falciparum* parasites with deletions in the pfhrp2 and pfhrp3 genes threatens the sensitivity of these tests, leading to false-negative results. This study investigated the prevalence, temporal trends, and genetic characteristics of pfhrp2 and pfhrp3 gene deletions in *P. falciparum* isolates from both human and mosquito vectors collected in Busia County, Western Kenya, in 2016 and 2023.

Methods: Genomic DNA of *P. falciparum* extracted from 10 human dried blood spots and 10 *Anopheles gambiae* complex mosquitoes underwent PCR assays to detect pfhrp2 and pfhrp3 gene deletions. Oxford Nanopore sequencing was deployed and data analyzed to characterize structural deletions and sequence variations.

Results: Of the 10 *P. falciparum* isolates from DBS, 40% (4/10) of samples demonstrated hrp2-negative but hrp3-positive genotypes. Vector analysis revealed that 30% (3/10) of samples were positive for *P. falciparum*. Within this subset, discordant gene patterns were observed, with 33.3% (1/3) of sporozoite-positive samples exhibiting hrp3-negative but hrp2-positive profiles. Descriptive statistics highlighted variability in the hrp2/hrp3 gene presence between human and mosquito-derived samples. Inferential analysis using chi-square testing indicated no statistically significant association between host type and gene deletion patterns ($p > 0.05$), likely due to the limited sample size. Findings from this study provide critical evidence on the prevalence and evolution of pfhrp2/3 gene deletions in a high-burden setting.

Conclusion: The results will inform national diagnostic policy, support enhanced molecular surveillance, and contribute to the optimization of malaria control strategies in endemic regions.

Keywords: pfhrp3 gene deletions, pfhrp2 gene deletions, HRP-based RDTs, pfhrp2 flanking gene regions, pfhrp3 flanking gene regions

Paper ID# 221

Title: Genomic surveillance of insecticide resistance in Zambia among malaria vectors.

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Background: Insecticide-based vector control has played a significant role in reducing the malaria disease burden. However, the widespread use of vector control has been associated with an increase in insecticide resistance posing a threat to the current vector control tools. This current study aims to assess the genetic basis of insecticide resistance of *Anopheles gambiae* and *Anopheles funestus* in Zambia.

Methods: Whole Genome Sequencing was implemented on mosquito specimens from Nchelenge, Ndola, and Katete (2016-2021). Population structure analysis utilized the NJT, PCA and Fst analyses whereas genetic diversity analyses utilized nucleotide diversity, Watterson's theta and Tajima's D. SNP/CNVs screens were performed across known insecticide resistance loci; GWSS were performed to identify novel signals of positive selection.

Results: Population structure analysis revealed restricted gene flow for *An. gambiae* between Copperbelt and Luapula populations (Fst=0.005). Luapula populations showed higher diversity and more negative Tajima's D values. High SNP frequency of the Vgsc-L995F variant was recorded in *An. gambiae* populations; Cyp6aa1 and Cyp6aa2 frequencies were higher in Copperbelt. In *An. funestus*, rdl was fixed and Cyp6-P450 CNV frequency was >65%. *Anopheles gambiae* showed more selection signals (vgsc, rdl, Ace-1, Gste2, Cyp6-P450s, cyp6m2 and Coeae2g-7g) compared to *An. funestus* (rdl, cyp6-P450s and Cyp9k1).

Conclusion: Our findings imply that *An. gambiae* populations are more impacted by resistance than *An. funestus*. Interestingly, we observed restricted gene flow between Copperbelt and Luapula in *An. gambiae* populations but not in *An. funestus* populations. Furthermore, the frequency of insecticide resistance markers was higher in Copperbelt than Luapula. This work highlights the need for continuous genomic monitoring of vector populations to support targeted and evidence-based vector control programme.

Keywords: Genomic surveillance, malaria vectors, Zambia

Climate, Environment & Vector Ecology

Paper ID# 251

Title: Efficacy of permethrin/chrysanthemum- and icaridin-impregnated textiles in preventing Chrysops silacea and Chrysops dimidiata bites in a loiasis-endemic region: a single-blind randomized controlled trial

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Background: Loiasis is an Afrotropical vector-borne disease caused by *Loa loa*, transmitted by *Chrysops dimidiata* and *C. silacea*. Nearly 42 million live in moderate to high transmission areas, and over 23 million people are infected. There are no established control tools to reduce transmission risk. Whereas skin and textile repellents prevent bites from other arthropods, data on protective efficacy against *Chrysops* remains scarce. Therefore, we decided to conduct a randomized controlled clinical trial evaluating the efficacy of two textile-impregnated repellents alone and combined with two previously tested skin-applied repellents against *Chrysops* bites in a hyperendemic loiasis region in Gabon.

Methods: Commercial arthropod textile repellents (icaridin, permethrin/Chrysanthemum) alone and in combination with one active skin repellent (citriodiol or DEET) or an inactive control were applied on randomly assigned volunteers. The number of blood meal attempts by *Chrysops* flies or the frequency and duration of *Chrysops* landings on clothing and skin were primary and secondary endpoints, respectively.

Results: Permethrin/Chrysanthemum-treated clothing significantly reduced both blood meal attempts and skin resting time by (55%, $p=0.02$), whereas the effect of icaridin-treated textiles was not significant. The highest efficacy in reducing blood meal attempts and skin resting time was achieved by the combination of textile and active skin repellents. Indirect comparisons revealed that permethrin/Chrysanthemum + citriodiol offered the highest efficacy, with reductions by 93% and

90%, $p < 0.001$ respectively), followed by permethrin/Chrysanthemum + DEET (86% and 84%, $p < 0.001$ respectively). However, no single repellent or combination thereof succeeded in reducing the number of landings on treated skin or treated clothing.

Conclusion: Studies showed that the combination of textile applied and skin-applied repellents is the best option to reduce exposure to infective bites.

Keywords: Arthropod repellent, permethrin/Chrysanthemum, icaridin, DEET, *Citriodiol*, *Chrysops*, deer fly, loiasis, Gabon, *Loa loa*

Emerging & Invasive Vectors

Paper ID# 6

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Background: In Zimbabwe, malaria is primarily transmitted by *An. arabiensis*, *An. gambiae* s.s. and *An. funestus* s.s. In 2018, Hwedza District transitioned to malaria elimination phase after the Zimbabwe Ministry of Health and Child Care, and partners distributed 36,044 deltamethrin ITNs to 4,658 households in five targeted wards to achieve 100% ITN net access. Subsequently, Hwedza recorded 737 malaria cases in 2019 of which 147 were locally transmitted cases, 118 in 2021 with 74 locals, 105 in 2022 with 44 locals, and 64 in 2023 with 23 locals, showing an 11-fold reduction in cases and a six-fold reduction in local transmission.

Methodology: To conduct surveillance against the residual transmission, from August – November 2023, 102 larval and 268 adult mosquitoes were collected around Garaba, Chikurumadziwa, Makarara, and Zvidhuri health centers in the district.

Results: Of the 370 mosquitoes morphologically identified and confirmed by PCR, 22.4% were *An. gambiae* complex spp, comprising *An. arabiensis* (7.8% of the total samples), *An. quadriannulatus* (9.5%), *An. rufipes* (19.4%), *An. coustani* (18%), *An. pretoriensis* (13.5%), *An. demeilloni* (8.9%), *An. funestus* s.l. (6.8%) among others, and 4% of the total samples remained unidentified. Pf-ELISA showed that none of the adult-collected mosquitoes were infected. IR tests against deltamethrin were conducted on the larval-collected adult specimens, among which 18 (28%) were *An. arabiensis*. These 18 were tested for Kdr and ACE-1 resistance mutations by PCR and exhibited susceptible alleles. Ultimately, this study showed a 7.8% relative abundance of *An. arabiensis* after a period of scarcity (median 1.2%) from 2019–2022. None of *An. arabiensis* captured as adults (11), among which five were caught outdoors, was found to be sporozoite-infected.

Conclusion: However, as an efficient malaria vector in Zimbabwe, *An. arabiensis* needs monitoring

because its escalating abundance amid residual cases may threaten the malaria elimination status of Hwedza.

Keywords: *An. arabiensis*, malaria, elimination

Policy, Advocacy & Health Systems

Paper ID# 34

Title: Determinants of household investigation coverage among malaria cases reported in Zanzibar's malaria surveillance system

Abstract

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Background: Since 2012, Zanzibar has implemented a Case-based Malaria Surveillance System that enables health facilities to notify all confirmed malaria cases within 24 hours of diagnosis, facilitating timely household case investigations and response. Household investigations aim to identify the sources and factors that sustain transmission. However, the coverage of household investigations for malaria cases remains challenging; the average of all notified cases that underwent household investigation from 2022 to 2024 is 71%. The study aimed to assess the determinants of household malaria case investigation coverage in Zanzibar.

Methods: An analytical cross-sectional design was employed to analyze 29,897 malaria cases reported in the surveillance system from 2022 to 2024, using STATA software version 14. Descriptive statistics were used to analyze socio-demographic characteristics, while Binary logistic regression estimated Adjusted Odds Ratios (AOR) and 95% confidence intervals (CI) for case investigation completeness.

Results: Of all malaria cases, 22,854 (76.4%) underwent household investigation. The analysis showed that districts reporting a high number of malaria cases had 0.67 times lower odds of complete household investigations (AOR = 0.67; 95% CI: 0.617-0.735, P< 0.001). Furthermore, an association was found between household investigation of malaria cases and the completeness of patient information provided at health facilities including the name of a notable person from the

village (AOR = 2.02; 95% CI: 1.69–2.42; $P < 0.001$) and the mobile contact of the patient (AOR = 2.62; 95% CI: 2.33–2.96; $P < 0.001$). Conversely, cases reported beyond 24 hours after diagnosis were less likely to be investigated at the household level compared to those reported within 24 hours (AOR = 0.67; 95% CI: 0.61–0.73, $P < 0.001$).

Conclusion: The findings highlight that timely case notification and the provision of complete patient information at health facilities are key determinants of household investigation coverage.

Keywords: Malaria, Surveillance, Zanzibar

Surveillance Data Systems & Digital Platforms

Paper ID# 113

Title: The Vector Atlas database: An open access resource for African malaria vector data to support evidence-based vector control.

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Background: Malaria remains a leading global vector-borne disease, with a high burden of cases and deaths occurring in Africa and requires a competent mosquito to carry the *Plasmodium sp.* parasite from host to host. Although vector control interventions substantially reduce transmission, their effectiveness is challenged by limited knowledge of local vector composition, behaviour and ecology, as well as growing insecticide resistance (IR) to the main classes of insecticides used in their control.

Methods: To address these gaps, the Vector Atlas (VA) provides evidence-based spatial models and maps to support vector control decision making. Underlying our maps and supporting our models is the Vector Atlas Database (VADB), consolidating analysis-ready data for vector control decision making. The VADB integrates historic datasets on vector occurrence, bionomics and IR with newly abstracted published data for dominant and secondary vector species. Data extraction follows a standardized protocol and structured template. Data records contain mandatory georeferenced location information, time period and species identity, alongside supplemental fields describing collection methods, environmental and community context, IR and behavioural/bionomic metrics relevant for disease transmission. A three-tier quality assurance process is applied to ensure data consistency and geospatial accuracy.

Results: The VADB is hosted via the VA platform (vectoratlas.icipe.org) and holds data abstracted from >3000 published sources resulting in >50000 data rows. Data are georeferenced to point or polygon spatial resolution and can be visualized, filtered and downloaded via an interactive map.

Conclusion: These data support a suite of vector-focused maps (species suitability, abundance, IR)

and provide an evidence-based resource for researchers, public health practitioners, and policymakers to assist their decision-making for targeted and adaptive vector control interventions.

Keywords: Vector, Mosquito, Occurrence, Bionomics, Insecticide Resistance, Vector Control, Database, Open access, Africa, Malaria

Predictive Modelling & Spatial Epidemiology

Paper ID# 125

Title: Optimizing insecticide deployment strategies to delay quantitative resistance in mosquito populations

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3. *IRD*

4. *EPT*

Background: The large-scale use of insecticides remains a cornerstone of malaria vector control, but its long-term effectiveness is undermined by the evolution of quantitative insecticide resistance (qIR) in mosquito populations.

Methodology: We develop and analyze a mathematical model to identify optimal deployment strategies for two insecticides that differ only in their relative efficacy against target mosquito populations. Resistance is represented as a continuous phenotypic trait influencing mosquito fecundity and mortality, and the model accounts for successive deployment periods.

Results: Our results show that when mutational variance is high, the optimal strategy is to deploy the most effective insecticide at full coverage, regardless of its relative efficacy or pre-deployment exposure history. By contrast, when mutational variance is low, optimal deployment requires a transient reduction in coverage during early periods, with a threshold effect driven by both relative efficacy and initial exposure rates. Crucially, we find that, under the hypothesis, the first insecticide is ineffective against mosquitoes; simultaneous use of both insecticides is rarely optimal. Instead, sequential deployment—using one insecticide until resistance reaches a critical threshold, followed by optimal use of the second—delays resistance evolution and improves long-term control.

Conclusion: These findings provide a theoretical foundation for adaptive qIR management strategies aimed at prolonging the effectiveness of insecticides in malaria vector control.

Keywords: Nonlinear dynamical systems · Structured mathematical model · Quantitative insecticide resistance · Optimal control strategies

Paper ID# 168

Title: Reimagining Mosquito Control in Africa through Climate Data and Bayesian Spatio Temporal Modelling

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Background: Mosquito-borne diseases remain a major public health challenge in Africa, with transmission increasingly influenced by climate variability, environmental change, and evolving vector dynamics. Weak integration of surveillance data and limited predictive tools constrain effective vector control strategies.

Methods: This study develops a Bayesian spatio temporal modelling framework that integrates climate indicators, environmental variables, and vector surveillance data at the county level in Kenya. The model incorporates spatial dependence, temporal trends, and space time interactions while accounting for uncertainty and missing data. Climate sensitive covariates, including rainfall variability and temperature anomalies are used to explain vector distribution and disease risk patterns.

Results: Findings show strong spatial heterogeneity and temporal variation in vector dynamics, with climate variables significantly associated with increased vector proliferation and disease risk. The model identifies high risk hotspots and generates probabilistic risk maps that improve early warning capabilities. Compared to conventional approaches, the framework provides more robust predictions and captures localized outbreaks more effectively.

Conclusion: Integrating climate data with advanced Bayesian modelling enhances vector surveillance and supports targeted Integrated Vector Management. This approach provides actionable insights for policy and strengthens data driven decision making for mosquito control in Africa under changing environmental conditions

Keywords: Bayesian modelling, vector surveillance, climate variability, mosquito control, spatial analysis, IVM

Paper ID# 64

Title: Do modelling approaches matter more than data in estimating public health impact? A malaria transmission dynamic modelling study.

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Background: ITNs remain a cornerstone of malaria control, yet uncertainty persists regarding how well different modelling approaches reproduce real-world epidemiological outcomes, particularly

when informed by artificially versus naturally aged net data. Multiple modelling frameworks were evaluated against site-specific data from cluster randomized trials conducted in Benin and Tanzania.

Methodology: Three approaches were compared: site-specific estimates derived in this study, a meta-analysis-based model, and Model 9. Performance was assessed across pyrethroid-only, pyrethroid-piperonyl butoxide (PBO), and pyrethroid-pyrrole nets over time horizons up to 30–36 months, focusing on agreement with observed prevalence and incidence and the ability to reproduce relative reductions in malaria burden.

Results: All approaches reproduced the overall ranking of intervention effectiveness, with pyrethroid-pyrrole nets achieving the greatest reductions, followed by pyrethroid-PBO nets and pyrethroid-only nets. However, substantial variation was observed in quantitative agreement. In Tanzania, Model 9 most closely aligned with observed prevalence, whereas the other approaches consistently overestimated values. In Benin, Model 9 and the meta-analysis produced comparable estimates across time points, while the site-specific approach showed systematic overestimation. For incidence, all models overpredicted burden, although Model 9 reduced error by approximately 40–70% relative to the meta-analysis. Observed reductions relative to pyrethroid-only nets were also most accurately reproduced by Model 9.

Conclusion: These findings highlight that, although general trends and intervention rankings can be captured across modelling frameworks, important differences remain in quantitative accuracy. Improvements in model structure and calibration appear more critical than increasing data complexity, and the added value of incorporating naturally aged net data for epidemiological prediction may be context dependent.

Keywords: Malaria, ITNs, Modelling, Resistance, Effectiveness

Paper ID# 243

Title: Modelling the influence of the duration of effectiveness and time taken to implement vector control interventions for vector-borne diseases.

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Background: Implementing vector control interventions against infectious diseases is operationally challenging, with delivery and population uptake taking considerable time within a community. The slow mass drug administration (MDA) of the endectocide, ivermectin, may have contributed to the lower epidemiological impact against malaria observed in recent cluster-randomised controlled trials, but evidence supporting this hypothesis is lacking. It is unclear whether interventions with short but effective durations of entomological impact are more impactful than those killing the same number of mosquitoes but over a longer period.

Methods: Transmission dynamics mathematical models can be used to explore how different implementation periods could influence disease control. We use a simple vector-borne disease compartmental model to explore the epidemiological impact of killing the same number of mosquitoes over 10, 30 or 90 days. We then adapt the existing Imperial malaria transmission model and simulate fast and slow deployments of an effective endectocide MDA campaign in different seasonal settings.

Results: Our simple model suggests that for different mosquito-killing periods, the total number of cases averted is similar, but the observable impact may depend on when efficacy is assessed. The Imperial model suggests that for perennial and seasonal settings and for a given coverage, slow MDA deployments avert slightly more clinical malaria cases than fast synchronized distributions. The benefits of the intervention depend on how well-timed a deployment is relative to the transmission season peak, with the efficacy of an ivermectin-like endectocide MDA being up to approximately 42% lower if started late.

Conclusions: The work indicates that the duration of MDA campaigns is unlikely to drive major differences in the effectiveness of short-lived endectocides and showcases how transmission dynamics models can be used to support the interpretation of epidemiological trials.

Keywords: vector control, endectocides, logistics, deployment

Novel Vector Control Tools & Product Innovation

Paper ID# 88

Title: Attractive resting and feeding lure (ATREFEEL) as a potential complementary tool against malaria transmission

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Background: Malaria elimination in Kenya will remain an unachievable goal without new complementary vector control tools. Attractive resting and feeding lures (ATREFEELs) are designed to exploit the sugar feeding behaviour of mosquitoes by luring them to rest and ingest a poisoned sugar solution. This study evaluated the baseline performance of four ATREFEEL prototypes to identify a lead prototype and inform further design modifications.

Methods: Evaporation was determined by tracking daily weight loss of four prototypes containing 250 ml sucrose from February to June 2025 in Pwani University. Their attractiveness to mosquitoes and non-target species was assessed by monitoring double-sided sticky traps in prototypes with and without the 5 mm insect-exclusion grid. Their attractiveness to malaria vectors was assessed in a semi-field system using lab-reared *Anopheles gambiae* s.s. Data were analyzed using mixed effects and count-based regression models.

Results: Prototype IV had a significantly higher evaporation rate than other prototypes (GMR = 2.08; 95% CI [1.18 – 3.67]). Prototype IV and III attracted a higher number of mosquitoes outdoors than I and II. Grid presence had a negligible effect on mosquito visit but reduced non-target species entry by 51% (IRR = 0.49; 95% CI [0.36 – 0.65]). In the semi-field system, prototype IV attracted 13 times higher *An. gambiae* s.s. to rest and three times higher to feed than prototype I. Prototype III attracted about six times higher *An. gambiae* s.s. to rest and 30% higher to feed compared to prototype II.

Conclusion: Prototype IV and III outperformed I and II in attracting wild mosquitoes outdoors and lab-reared malaria vectors in the semi-field system. We, therefore, recommend further optimization of these two best performing prototypes and exploration of different dispensing materials to stabilize evaporation.

Keywords: Malaria, vector control, ATREFEEL, *Anopheles gambiae* s.s., non-target species

Paper ID# 179

Title: The current status of *Plasmodium falciparum* chloroquine resistance transporter gene (K76T) and *Plasmodium falciparum* multi-drug resistance gene 1 (N86Y) in Cameroon

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Background: Malaria due to *Plasmodium falciparum* remains one of the most infectious diseases in the world. Resistance to most available antimalarial drugs has been the major challenge in managing the disease. There is therefore the need for novel antimalarial drugs to circumvent the current drug resistance and pre-empt future resistance. After chloroquine withdrawal and reduced drug pressure,

parasite sensitivity may return, raising interest in reintroducing abandoned antimalarial. This study assessed prevalence of *P. falciparum* chloroquine resistance transporter gene (pfcr1 K76T) and multidrug resistance gene 1 (pfmdr1 N86Y) mutations in Buea, South West Region, Cameroon.

Methods: A cross-sectional study which recruited 155 consented participants aged from 6 months to 75years, excluding individuals with chronic illnesses. 1mL of venous blood was collected for parasitemia assessment by microscopy and molecular analysis. Parasite genomic DNA was extracted by the Chelex-PBS method. Species were differentiated using nested PCR targeting the 18S rRNA with species-specific primers, and drug resistance was assessed by amplifying the pfcr1 K76T and pfmdr1 N86Y regions followed by allele-specific restriction analysis (ASRA).

Results: Of 155 samples, 153 (98.7%) were *P. falciparum* mono-infection and 2 (1.3%) *P. ovale*. *P. malariae* and *P. vivax* were not detected. 56.1% were afebrile. Febrile individuals had higher mean parasitaemia than afebrile individuals (3,980 vs 2,984 parasites/uL, $p < 0.001$). Parasitaemia was independent of sex and age. Chloroquine-sensitive genotypes had a prevalence of 37.3% for pfcr1 K76 and 55.6% for pfmdr1 N86.

Conclusion: Data show gradual return of chloroquine-sensitive *P. falciparum* genotypes after chloroquine withdrawal in Cameroon with resistance levels still substantial: 62.7% for pfcr1 76T and 44.4% for pfmdr1 86Y.

Keywords: Polymorphic, *Plasmodium Falciparum* Pfcrt (K76T), pfmdr 1 (N86Y), Drug Resistant Genes

Paper ID# 203

Title: Contribution to the understanding of the supplementation of a probiotic candidate on the biology of *Anopheles gambiae*.l: Case of *Akkermansia muciniphila*

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Background: The diet of mosquitoes (adults and larvae) is an essential and indispensable component of their biology. The use of bacterial organisms such as *Akkermansia muciniphila* to modify the availability of this energy could therefore have an impact on their metabolism. The objective of this study was to evaluate the effect of *Akkermansia muciniphila* supplementation on the life cycle of *Anopheles gambiae* s.l.

Methods: This was an experimental study of laboratory *Anopheles* mosquitoes at the Institut des

Sciences et Technique (INSTech), subdivided into three groups. The concentration of the solutions administered to the mosquitoes was 10^7 CFU/mL of *Akkermansia muciniphila* bacterial suspension. Three administration regimens were used: The first administration involved all three groups of mosquitoes. For the second administration, only groups 2 and 3 received a second dose. Finally, for the last administration, only group 3 was exposed to the bacterium of interest. Parameters such as mortality, insemination status, feeding rate, fecundity, and fertility were evaluated. A chi-square test (χ^2), a generalized linear mixed model (GLM) and a Cox survival analysis were used to evaluate the effect of treatments on feeding rate, reproductive parameters, and survival respectively.

Results: The results showed a significant effect of the treatments, especially on the mosquitoes in group 3 ($p < 0.001$). Indeed, for these groups, a reduction in mosquito lifespan as well as a significant impact on fecundity (egg laying) and fertility (viable larvae) were observed. Indeed, these groups had a 39% ($p < 0.001$) risk of dying compared to the other groups. Furthermore, a negative effect on the proportion of eggs and larvae from these treated groups was also observed.

Conclusion: These results suggest that *Akkermansia muciniphila* could be used as a sustainable alternative in the fight against malaria-carrying mosquitoes.

Keywords: *Akkermansia muciniphila*, Supplementation, *Anopheles gambiae* s.l., Malaria, Innovative Control

Paper ID# 158

Title: External validation of the Ifakara Ambient Chamber test for evaluating the bio efficacy of chlorfenapyr and pyrethroid insecticide-treated nets in varied settings: a comparative study in Bagamoyo and Kilimanjaro.

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Background: Malaria control in Sub-Saharan Africa relies heavily on insecticide-treated nets (ITNs), yet increasing pyrethroid resistance threatens their effectiveness. The Ifakara Ambient Chamber Test (IACT) is a semi-field bioassay designed to mimic natural mosquito-human interactions and provide more realistic efficacy estimates than conventional laboratory methods. However, its performance across different ecological settings has not been externally validated. This study aims to evaluate the reliability and reproducibility of the IACT in two ecologically distinct settings in Tanzania.

Methods: An 11×11 Latin square design is being implemented at two sites: Ifakara Health Institute-Bagamoyo and KCMC University-Pamverc in Moshi. Eleven adult male volunteers per site rotate nightly across chambers and nets to ensure balanced exposure. Unwashed and 20× washed ITNs are tested against two mosquito strains: pyrethroid-resistant *Anopheles gambiae* muleba-kis and susceptible *Anopheles gambiae* s.s. Kisumu. Each night, 20 mosquitoes per strain are released per chamber. Outcomes include mosquito mortality at 24, 48, and 72 hours and blood-feeding success. Temperature and humidity are continuously monitored. Data are analyzed using descriptive statistics and mixed-effects logistic regression models.

Results: Study is ongoing, with results expected by August 2026. The results of the external validation will be presented, and their implications for assay validation will be discussed.

Conclusion: This ongoing study aims to validate the i-act as a reliable, reproducible tool for assessing its efficacy in varied environmental contexts. The findings will potentially support the broader adoption of the i-act in vector control programs and inform future developments in malaria prevention strategies.

Keywords: Ifakara Ambient Chamber Test, Insecticide-Treated Nets, *Anopheles gambiae*, Chlorfenapyr, Bio-Efficacy, External Validation

Paper ID# 19

Title: Field evaluation of the efficacy, residual activity and acceptability of Sovrenta® 15WP against malaria vectors in Adjumani district, West Nile, Uganda

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Background: Vector control remains a key strategy for reducing disease transmission, with IRS considered the most cost-effective intervention in malaria high burden areas. Developing and evaluating new molecules with different modes of action is fundamental to insecticide Resistance Management. Here, we evaluated the effectiveness and the residuality of Sovrenta®15WP, a novel

formulation for Indoor Residual Spraying recently prequalified by WHO. Additional information on acceptability of Sovrenta® 15WP by the community was collected.

Methods: This mixed method study had a Sovrenta®15WP and Actellic®300CS arm and a total of 30 houses per arm. Standard WHO bioassays were conducted on representative wall surface types with both *Anopheles gambiae* Kisumu strain and wild *An. gambiae s.l* for 12 months. Qualitative assessments included 64 key Informant Interviews and 9 Focus Group Discussions to generate specific information related to the acceptability of Sovrenta® 15WP insecticide as a new product by the community in Adjumani.

Results: The results from this study indicate that there was no significant difference in mortalities of *Anopheles gambiae* Kisumu strain mosquitoes on the 3 wall surfaces sprayed with Sovrenta 15WP (CI:95%, p=0.75711) and Actellic 300CS (CI:95%, p=0.26309). Similarly, there was no significant difference between mean mortalities of Sovrenta 15WP and Actellic 300CS for *Anopheles gambiae* Kisumu strain over 10 months (CI: 95%, p=0.416168). There was a significantly higher acceptance of Sovrenta due to its odorless and non-staining properties.

Conclusion: In conclusion, Actellic® 300 CS and Sovrenta® 15WP induced >80% mortality of susceptible *Anopheles gambiae* Kisumu strain for the tested 12 months and wild *An. gambiae s.l* for the tested 10 months on plastered, brick and mud & wattle wall surfaces. Sovrenta® 15WP's performed as well as Actellic® 300 CS, the current front-line insecticide, and would be an excellent alternate choice for IRS in Uganda.

Keywords: Isoxazoline, Isocycloseram, active ingredient, Indoor Residual Spraying

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Title: Toxicity of ivermectin to bed bugs (*Cimex hemipterus*) and risk factors associated with infestation in Kwale County, coastal Kenya.

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Background: Bed bugs (*Cimex spp.*) are obligate ectoparasites causing discomfort and psychosocial distress in human dwellings. Growing insecticide resistance necessitates alternative control strategies. This study evaluated the toxicity of ivermectin on *Cimex hemipterus*, the predominant bed

bug species in Africa, and identified household-level risk factors for infestation in Kwale County, Coastal Kenya.

Methods: A cross-sectional survey of 2,393 households assessed self-reported infestations and socioeconomic characteristics. Bed bugs collected from 40 infested households were exposed to blood meals spiked with ivermectin at five concentrations (11 ng/ml, 21 ng/ml, 43 ng/ml, 64 ng/ml, and 85 ng/ml), reflecting serum levels following a 400 mcg/kg oral dose. Mortality and fecundity were monitored over 14 days and analyzed using Cox proportional hazard models, Kaplan-Meier survival analyses, and probit regression.

Results: Infestation prevalence was 40%, strongly associated with lower socioeconomic status and mud-walled, thatched-roof housing. Higher ivermectin concentrations (43, 64, and 85 ng/ml) induced over 90% mortality within three days post-feeding, and sublethal doses completely suppressed egg-laying.

Conclusion: These findings suggest that ivermectin, delivered through mass drug administration campaigns, could serve as a viable component of integrated bed bug control. Field evaluations across diverse settings are warranted to define optimal dosing intervals for infestation elimination.

Keywords: Ivermectin; endectocides; *Cimex spp*; *Cimex hemipterus*.; bed bugs; built environment; Kwale; Kenya.

