3rd global Genetic Biocontrol Congress

3rd Global Congress on Genetic Biocontrol Technologies

Congress theme

"Advancing responsible genetic biocontrol innovations to improve animal and public health, strengthen vector control, and protect ecosystems."

Dates

March 15–18, 2027

Venue

Radisson Blu Hotel, Nairobi,Kenya

Organized by

African Genetic Biocontrol Consortium

African Genetic Biocontrol Consortium

Build | Inform | Expand

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Willy Tonui, PhD, EBS,

Founder and Chairman, African Genetic Biocontrol Consortium

Genetic biocontrol is an approach for controlling or eliminating specific organisms that threaten public health, food security and biodiversity that uses genetic variants (natural, induced or transgenic) of the target species as the controlling agents to affect the target species in ways that reduce its undesirable impacts. Robust transgenic and genome editing technologies are fueling expanding research and development of genetic platforms and systems for combating pathogen and parasite-transmitting mosquitoes, plants and insects that reduce food security, and invasive species that are destroying biodiversity.

This unique Congress will focus exclusively on the topic of genetic biocontrol and will serve to encourage cooperation, collaboration, communication, and new and exciting science at a time when new technologies such as gene drive and Wolbachia-induced cytoplasmic incompatibility are being developed.

This Congress will bring together researchers investigating genetic systems with potential applications to genetic biocontrol with technology developers and those implementing genetic biocontrol strategies to share knowledge, foster new research, compare lessons-learned and develop best practices.

This Congress will feature discovery research along with technology development and ongoing operational experiences of those moving existing technologies to the field. The Congress will bring those working on insects, plants, fish, mammals, and other organisms together. This is an opportunity to bring researchers, developers, and practitioners together so that future genetic biocontrol activities will take place within a community with shared interests and values.

OVERVIEW

THE CONGRESS

ABOUT THE AFRICAN GENETIC BIOCONTROL CONSORTIUM

The African Genetic Biocontrol Consortium (the Consortium) was established as an agreement among member organizations committed to the mission and goals to contribute to expanding African self-determination of the course of research, development, and use of genetic biocontrol approaches for controlling and eliminating malaria and other vector-borne diseases in Africa.

The Consortium was officially launched on November 30, 2020 by not-for-profit member organizations based in Africa that included the Africa One Health Network (AfOHNet), Africa Biological Safety Association (AfBSA), The Multilateral Initiative on Malaria (MIM), Network of African Science Academies (NASAC), Pan-African Mosquito Control Association (PAMCA) and the GeneConvene Global Collaborative (GeneConvene).The member organizations of the Consortium are regionally represented non-governmental professional or similar organizations representing disciplines such as biomedical research, biotechnology, entomology, vector control, public health, animal sciences, biosafety, ecology, environmental sciences, social sciences, and public engagement who are interested in genetic biocontrol technologies.

The Consortium is guided by a vision that seeks to build an informed local leadership to support decision-making on the utility of genetic biocontrol technologies for public health and requirements for their development in Africa. This will be achieved through a mission that aims to expand African self-determination of the course of research, development, and use of genetic biocontrol approaches for public health. To fulfil this mission the Consortium will provide a platform for interaction among African experts and institutions to enhance opportunities for technical capacity strengthening, knowledge exchange and deliberation about the challenges and opportunities of genetic biocontrol technologies for public health, which will amplify African influence on their development and provide critical input for decision-making by product developers, policy makers, and other stakeholders.

The approach of the Consortium is to provide the member organizations to conduct activities individually and/or jointly under the Consortium brand. It is expected that the Consortium will use its collective leverage to attract funding for activities and to inform other stakeholders. To achieve the desired impact, the Consortium will adhere to a set of core values in planning and executing its mission. These include teamwork, collaboration, power of negotiation, complementarity and strengths, continual improvement, transparency, and accountability.

ABOUT THE 3rd GLOBAL CONGRESS ON NEW EMERGING GENETIC BIOCONTROL TECHNOLOGIES

The Consortium is delighted to host the 3rd Global Congress on Genetic Biocontrol Technologies in Nairobi, Kenya in March 15 to 18, 2027. The aim of the Congress is to bring together experts from around the world to share learnings across diverse disciplines related to genetic biocontrol technologies in a 4-day event.

This Congress promises to be an engaging and stimulating event. Attendees interested in genetic biocontrol drawn from a broad spectrum of vector biologists, biosafety, and biosecurity, pharmaceutical, biotechnology research, development and clinical organizations are expected to attend. The conference draws national and international attendees from academic, commercial, research, non-governmental, and governmental sectors. It is a great opportunity to showcase your products to a broad audience of professionals.

EXHIBITION OPPORTUNITIES

The Congress offers you exposure to the many delegates of the conference and the opportunity to showcase your products and services to a global pool of customers. The exhibition area has been designed to provide the best possible promotional opportunities for participating companies. The exhibition will provide delegates and exhibitors with excellent opportunities to network and will be placed on the beautiful and spacious foyer of the hotel outside the conference rooms.

Who Should Exhibit?

Anyone who supplies, manufactures, provides services or products used in biomedical research, biosafety and biosecurity, the media fraternity and training institutions should exhibit.

When and Where

The 3rd Global Congress on Genetic Biocontrol Technologies, organized by the African Genetic Biocontrol Consortium will be held from March 15-18, 2027 at the Radisson Blu Hotel, Nairobi, Kenya.

Exhibition Schedule

The exhibition will be open from 8:00am – 6:00pm daily from March 15-18, 2027. Exhibitors will set up their booths from March 15, 2027.

Setpup & Removal

Exhibitors will be required to remove their displays on March 18, 2027.

BOARD OF DIRECTORS

MEMBERS OF THE AFRICAN GENETIC BIOCONTROL CONSORTIUM BOARD OF DIRECTORS

6 BOARD MEMBERS



Willy Tonui, PhD, EBS

Founder and Chairman, AGBC

https://tinyurl.com/2hvam3b5



Moses Kiptui

Honorary Treasurer

https://tinyurl.com/5n8bryp6



Esther Kioko

Honorary Secretary

https://tinyurl.com/2r689tdt



Dorrington Ogoyi

Member

https://tinyurl.com/3tthnp8j



Robert Karanja

Member

https://tinyurl.com/2sxxt9w6



Christopher Oyier

Member

https://tinyurl.com/zxaauhzy

CONGRESS PROGRAMME

SCIENTIFIC PROGRAMME COMMITTEE

The role of this subcommittee will be to determine the theme of the annual congress; develop and release the Call for Proposals; review all submissions; and define the schedule.

Members of the Scientific Programme Committee include:

22 COMMITTEE MEMBERS



Charles Mbogo,
Chair, Scientific Program Committee
https://tinyurl.com/mt5tmd4a



Etienne Bilgo
Vice Chair, Scientific Program Committee
https://tinyurl.com/34fsbudb



Joseph Odongo
Member
https://tinyurl.com/3a57uwnf



Vibha Ahuja
Member
https://tinyurl.com/mutvada4



Thato Mogapi
Member
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Martin Bundi
Member
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Charles Quaye
Chair of the Biorisk Management Committee, Noguchi Memorial Institute for Medical Research, Ghana
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Givemore Munhenga
Member
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Simon Kipngeno Langat,
OGW, OAP, ACIARB Member
https://tinyurl.com/tanap4up



Moussa Savadogo
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Agnes Yemisi Asagbra
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Misheck Mulumba
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Jacqueline Kado
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Gloria Ogbaki
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Ama Kudom-Agyemang,
Member
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Sandra Lombe
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Lakamy Sylla, PhD
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Rajka Fritsch
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Jewelna Akorli
Member
https://tinyurl.com/4jesnfvz



Amelie Wamba
Member
https://tinyurl.com/tswxumk8

CONGRESS SECRETARIAT

8 SECRETARIAT MEMBERS



Rosalia Omungo,
Chief Executive Officer, AGBC
https://tinyurl.com/5by2uu2z



Raphael Jilani Mwalimu
Senior Technical, Innovation and Quality Assurance Manager
https://tinyurl.com/3rpe69wr



Bennie Kibet Rotich
Technical, Innovations, Partnerships and Quality Assurance Asst. Manager
https://tinyurl.com/56sh36hu



Benard Lesalon Letoluo
Senior Officer Finance and Administration
https://tinyurl.com/2xpydtmj



Andrew Kipkoech,
Senior Manager - Digital and Data Management
https://tinyurl.com/4vzas4c6



Kipkorir Evans,
Finance Manager
https://tinyurl.com/3n4fxyyj



Sang Roselyne
Senior Manager, Strategy Planning and Monitoring
https://tinyurl.com/2pwsw3hp



Abigail Chelangat
Corporate Administrative Assistant
https://tinyurl.com/5ckb98ux

3RD GLOBAL CONGRESS PROGRAMME

High-Impact Congress Breakfast Sessions

Theme:

To provide dynamic morning exchanges and high-impact breakfast sessions that inspire transformative ideas, advance breakthrough genetic biocontrol, and mobilize global action.

Participants:

Speakers, Session Chairpersons, early-career researchers, regulators, and invited stakeholder representatives to participate.

High-impact Congress Breakfast Session - one and a half hours (7:30 am - 9:00 am)

Day 1

Welcome, orientation, and global networking breakfast

Introduce the 3rd Congress objectives, participation arrangements, and expected outcomes, followed by structured networking across countries, disciplines, and stakeholder groups. Session Co-Chairs Prof Charles Mbogo and Dr Etienne Bilgo

Day 2

Technical expert roundtables

Run parallel, facilitated discussions on priority themes and science on genetic and non-genetic biocontrol science, biosafety and risk assessment, regulation and governance, ethics, public engagement, implementation, and capacity strengthening. Session Co-Chairs - Dr Moussa Savadogo and Dr Thato Mogapi

Day 3

Stakeholder and regional consultation

Organize mixed tables representing researchers, regulators, policymakers, funders, industry, civil society, communities, and regional networks. Ask each table to identify major opportunities, concerns, evidence gaps, and collaboration needs. Session Co-Chairs Dr Jackie Kado and Dr Gloria Ogbaki.

Day 4

Commitments and action-planning forum

Convert congress discussions into practical next steps. Participants should identify joint initiatives, policy or research priorities, responsible organisations, indicative timelines, and follow-up mechanisms. Session Co-Chairs Dr Misheck Mulumba and Dr Agnes Asagbra.

DAY 1: MONDAY MARCH 15, 2027		
TIME	**ACTIVITIES**	
07:00 - 09:00	**REGISTRATION**	
07:30 - 09:00	**HIGH-IMPACT CONGRESS BREAKFAST SESSIONS**	**VENUE: MAIN HALL KILIMANJARO**
OPENING CEREMONY AND KEYNOTE ADDRESS **SESSION CHAIRPERSON: PROF CHARLES MBOGO**		**VENUE: MAIN HALL KILIMANJARO**
9:00 - 10:00	Welcome Remarks: **Rosalia Omungo**, Chief Executive Officer, African Genetic Biocontrol Consortium **Willy Tonui PhD**, Founder and Chairman, African Genetic Biocontrol Consortium **Michael Santos** PhD, Senior Vice President, Science Partnerships, Foundation for the National Institutes of Health **Mark Whittaker**, Senior Research Manager, Infectious Disease, WellCome Trust **Prof. Shaukat Abdulrazak**, Principal Secretary for Science, Research and Innovation, State Department for Science, Research and Innovation, Office of the Prime Cabinet Secretary, Republic of Kenya. Chief Guest: **H.E. Dr. Hon. Musalia Mudavadi, E.G.H.** (TBC), Prime Cabinet Secretary & Cabinet Secretary for Foreign and Diaspora Affairs ***Congress Keynote address:*** TBC **Title: Shaping the Future of Genetic Biocontrol Technologies: Precision Science, Responsible Innovation, and Global Impact** Presenter name: The keynote explores how advanced genetic technologies can precisely manage harmful pests and disease vectors. It emphasizes that scientific advancement must be supported by robust safety evaluation, ethical oversight, transparent governance, and meaningful public engagement. It also outlines the potential worldwide benefits of genetic biocontrol for human health, agriculture, biodiversity, and sustainable development, and urges scientists, policymakers, communities, and partners to work together to turn its promise into safe, inclusive, trusted solutions that save lives, improve food security, conserve biodiversity, and support a sustainable future.	
10:00 -10:30	**PHOTO SESSION, HEALTH BREAK**	
	PLENARY SESSION 1: REIMAGINING AFRICA'S HEALTH FUTURE THROUGH GENETIC BIOCONTROL **SESSION CHAIRPERSON: ETIENNE BILGO**	**VENUE: MAIN HALL KILIMANJARO**
10:30 - 11:00	*This session will convene senior government, regulatory and institutional leaders from selected African countries to advance coordinated policy action. The objective is to establish a shared understanding among senior officials of disease-control challenges, evidence on emerging vector-control tools and governance issues requiring leadership decisions.* ***Session Keynote:*** **Title:** Vector borne diseases, trends, current interventions and emerging biocontrol options – **Dr. Lauren Carrington**, Vector, Disease Control, Elimination and Eradication unit Malaria and Neglected Tropical Diseases department, World Health Organization The speaker will provide an overview of the evaluation of vector-release strategies for vector control, including genetically modified mosquitoes, *Wolbachia*-based population replacement, and sterile insect techniques. She will describe how WHO is examining the available evidence through systematic reviews, benefit–harm assessment, contextual analysis, and guideline development. The speaker will further emphasize that, notwithstanding their technical distinctions, these approaches encounter common challenges related to evidence generation, governance, community engagement, biosafety, monitoring, and implementation, thereby offering opportunities for cross-learning across disease-control disciplines.	
11:00 - 11:30	Q&A	

11:30 -13:00	***Regional leadership roundtable:*** Regional and country policy and legal readiness (High level ministry and country leaders from African countries). *The roundtable discussions will stress-test their countries' policy and legal readiness; explore how innovative genetic biocontrol tools can be integrated into national plans, health security priorities, and African Union commitments; identify key policy, legal, and institutional gaps across participating countries; and agree on opportunities for regional cooperation.* **Participating Countries**: High-level representatives from the governments of Burkina Faso, Djibouti, Ghana, Nigeria, Kenya, Mali, Senegal, South Africa, Tanzania, and Uganda. **Global/ Regional Organizations:** AUDA-NEPAD, Africa CDC, EASTECO, ECOWAS	
11:00 - 17:50	**Genetic Biocontrol for Vector Control: A Two-Day Introductory Workshop**	KILIMANJARO HALL B
13:00 -14:00	Lunch Break	
PLENARY SESSION 2: GLOBAL ADVANCES IN GENETIC BIOCONTROL APPLICATIONS-REGULATORY READINESS **SESSION CHAIRPERSONS: MOUSSA SAVADOGO & THATO MOGAPI**		VENUE: MAIN HALL KILIMANJARO
14:00- 16:00	*This session will convene regulatory leaders from health, Agriculture, biosafety, science, technology, and environment from African countries to review policy progress. This session aims to define clear, proportionate, science-based pathways for contained research, field trials, risk and ethics reviews, cross-border consultation, and post-release monitoring in participating countries.* ***Session Keynote:*** **Title: Evaluation and regulation of *Aedes aegypti* mosquitoes infected with the Wolbachia bacterium: Anvisa's (Brazil) experience and learned lessons** **Christiane Maia**, ANVISA, Brazil" ***Regulatory roundtable 2:*** Regulatory readiness (Head of agencies- Health, biosafety and environment). *During roundtable discussions, participants from health, biosafety and environmental agencies will identify key regulatory laws, guidelines, and gaps across participating countries and agree on opportunities for regional cooperation.* **Participating Agencies:** **Health** (NMCPS from Kenya, Uganda, Tanzania, Ghana, Nigeria, Djibouti); **Biosafety** (Djibouti, Kenya, Tanzania, Burkina Faso, Ghana, Nigeria, Zambia). **Biotechnology** (NABDA-Nigeria, UNCST-Uganda) **Environment** (Kenya, Uganda, Tanzania, Burkina Faso, South Africa, Nigeria)	
16:00- 16:30	**Health Break**	
16:00 - 17:00	Q&A, discussions and recommendations.	
DAY 1 ENDS		

DAY 2: TUESDAY MARCH 16, 2027

07:30 - 09:00	**REGISTRATION**	
07:30 - 09:00	**HIGH-IMPACT CONGRESS BREAKFAST SESSIONS**	VENUE: MAIN HALL KILIMANJARO
09:00 - 18: 00	**Genetic Biocontrol for Vector Control: A Two-Day Introductory Workshop**	VENUE: KILIMANJARO HALL B
PLENARY SESSION3: GLOBAL ADVANCES IN GENETIC BIOCONTROL APPLICATIONS- INSTITUTIONAL READINESS AND RESEARCH CAPACITY **SESSION CHAIRPERSON: AGNES ASAGBRA**		**VENUE: MAIN HALL KILIMANJARO**
9:00- 10:00	*This session will convene institutional leaders from African countries to assess research capacity and readiness. It will evaluate whether regulators, biosafety and ethics bodies, laboratories, entomological surveillance systems, modelling, and data analysis have the capacity to approve genetic biocontrol applications and products.* **Introductory presentation: Givemore Munhenga:** More than a decade of feasibility research on the Sterile Insect Technique for *Anopheles arabiensis* in South Africa: progress, challenges, and future directions. ***Institutional roundtable 4:*** Institutional readiness (Heads of research *from key research* institutions) *will define principles for transparent risk assessment, public participation, and community engagement, and agree on opportunities for regional cooperation.* **Participating institutions:** • **Kenya:** KEMRI, ICIPE, KALRO, ILRI • **Tanzania:** NIMR, IHI • **Ghana:** Noguchi Medical Research • **South Africa:** NICD • **Mali:** ACEME • **Uganda:** UVRI, NARO • **Burkina Faso:** IRSS • **Nigeria:** Nigeria Institute of Medical Research (NIMR) • **Senegal:** Pasteur Institute	
10:00-10:30	Q&A	
10:30 -11:00	Health Break	
11:00- 13:00	***Breakout Sessions (Regulatory, Research and Capacity, engagement and communication, financing)****:* *Senior government, regulatory, and institutional leaders from selected African countries will work in expert groups to assess policy, regulatory, research, and institutional readiness for genetic biocontrol. They will evaluate the capacity of regulators, biosafety and ethics bodies, laboratories, entomological surveillance systems, modelling, and data analysis to support approval of applications and products across Africa and recommend practical steps to close gaps and strengthen capacity.* *All participants (country, Regulatory and Institutional representatives, funders) will participate*	
13:00-14:00	Lunch Break	
14:00-15:30	Plenary negotiation of the leadership communiqué and action matrix (all)	
15:30- 16:00	Health Break	
15:30-17:00	Plenary negotiation of the leadership communiqué and action matrix and next steps (all)	
DAY 2 ENDS		

DAY 3: WEDNESDAY MARCH 17, 2027

07:30 - 09:00	**High-Impact Congress Breakfast Sessions**	**VENUE: MAIN HALL KILIMANJARO**
PLENARY SESSION 4: ADVANCES TOWARD DEPLOYMENT OF GENETIC BIOCONTROL TECHNOLOGIES **SESSION CHAIRPERSON: VIBHA AHUJA**		**VENUE: MAIN HALL 1B KILIMANJARO**
9:00 - 10:15	The plenary session will provide an update on progress made towards the deployment of both genetic and non-genetic biocontrol vectors and their impacts. **Christie Linonge Etombi**: From readiness to scale: defining pathways for Wolbachia-based dengue control in Africa **Perran Ross**: Lessons for genetic biocontrol from Wolbachia release programs in mosquitoes in Australia **Fredros Okumu**: Prospects of *An. gambiae*-based gene drives in east and southern Africa. **Thabo Mashatola:** From genetic sexing to field release: An integrated, quality-assured production and deployment platform for *Anopheles arabiensis* within the South African sterile insect technique (SIT) programme. **Bernard Bett**: Evaluating the potential impact of genetic biocontrol of Aedes mosquitoes on dengue transmission in the Horn of Africa.	
10:15 - 10:30	Q&A	

10:30 -11:00	HEALTH BREAK
PLENARY SESSION 5: CONSIDERATIONS FOR IMPLEMENTING GENETIC BIOCONTROL **SESSION CHAIRPERSON: JEWELNA AKORLI**	
11:00 - 12:30	This plenary session will focus on regulatory and operational challenges, regulatory-optimized bridge technologies toward gene drives, and approaches for evaluating the potential impacts, risks and benefits of genetic biocontrol technologies. **Andrew Hammond**: Beyond proof of concept: achieving deployable genetic control in Africa **Nikolay Kandul**: NextGenSIT: A Regulatory-Optimized Bridge Technology Toward Gene Drives. **Priyadarshani Somasekaran**: CRISPR-Cas9-mediated disruption of *Dicer-1* in *Anopheles gambiae*: Preliminary progress towards understanding the role of the miRNA pathway **Achaz-Achim Agolinou**: A CRISPR-Cas9 system targeting female reproduction in *An. funestus* for genetic control **Saberé O. G. Yemien**: CRISPR-Cas9-based gene drive targeting the blood metabolism gene HPPD in the malaria mosquito *Anopheles funestus* **GANSANE Adama:** Burkina Faso National IVM platform: What's the future following the premature termination of Target Malaria project? **Rufus Ebegba:** Challenges of Acceptance of Biotechnology and Emerging Biotechnology in Africa and Solutions
12:30 -13:00	Q&A
13:00-14:00	LUNCH BREAK
13:00-14:00	POSTERS
	Agapitus Kato: Exploring Microsporidia for Mosquito Biological Control: 18S rRNA-Based Detection in *Anopheles gambiae* and *Anopheles arabiensis* in Uganda
	Néstor Rivas: Preparing Annobón Island for population modification: household mapping, vector characterization and a baseline malaria indicator survey, Equatorial Guinea
14:00- 18:00	**WORKSHOP ON ARTIFICIAL INTELLIGENCE AND CAPACITY STRENGTHENING FOR GENETIC BIOCONTROL DECISION-MAKING PROCESSES** — **MAIN HALL 1A KILIMANJARO** **SESSION CHAIRPERSON: Justin Overcash**
BREAK OUT SESSION 6A: EXPLORATION, LABORATORY DETECTION AND CHARACTERIZATION OF ENDOSYMBIONTS IN NATURAL MOSQUITO POPULATIONS **SESSION CHAIRPERSON: BERNARD BETT**	
14:00- 17:00	This session explores mosquito-associated bacteria, fungi, and microsporidia and their potential use in innovative, sustainable malaria vector control. **Carine Létitia Traoré**: Characterization of the cultivable bacterial microbiota associated with *Anopheles coluzzii* mosquitoes infected with Microsporidia MB **Aïcha Fatimata SODRE**: *Wickerhamomyces* spp. in *Anopheles gambiae s.l.*: Prevalence, Tissue Distribution and Potential for Innovative Mosquito Biocontrol in Burkina Faso
	Haoua Traoré: Attractive sugar bait-mediated dissemination of symbiotic Serratia sp. in Anopheles for biological control of malaria Transmission **Thomas Onchuru**: Harnessing a naturally occurring mosquito symbiont to block malaria transmission **Phocas Mazimpaka**: Prevalence of *Microsporidia MB* Symbiont and Malaria Transmission Blocker in Sibling Species of *Anopheles gambiae* s.l. in Rwanda **Agapitus Kato**: Exploring the Mosquito Microbiome for Biological Control: Putative Endosymbionts of *Anopheles gambiae* and *Anopheles arabiensis* in Uganda **Diallo Ibrahim**: Development of transgenic cytoplasmic incompatibility based on *w*AnD *cif* genes in *Anopheles gambiae* G3 **Jewelna Akorli**: Natural dynamics of *Serratia marcescens* and *Enterobacter cloacae* in the *Anopheles gambiae* midgut: implications for paratransgenic malaria control **Blandine Ouédraogo**: Generation and characterisation of genetically modified *Anopheles funestus* mosquitoes expressing antimicrobial peptides **Jeremy Herren**: Advances in the development of a Microsporidia MB endosymbiont-based Plasmodium transmission-blocking strategy

BREAK OUT SESSION 6 B: GLOBAL ADVANCES IN GENE DRIVE APPLICATIONS **SESSION CHAIRPERSON: MASSOUROUDINI AKOUDJIN**	
14:00- 17:00	**Dean Goodman**: Gene drives that target malaria parasites rather than malaria vectors to control disease. **Jackson Champer**: Progress in *Anopheles stephensi* gene drives and modeling **Wolfgang Richard Mukabana**: Using gene drive mosquitoes to eliminate malaria in the western equatorial coast of Central Africa. **Jeremy BOUYER**: Environmental Monitoring of Genetic Control in the African Region: the example of *Aedes albopictus* in Reunion Island. **Daniel Sano:** Pan-African Genomic Conservation of *Plasmodium falciparum* Transmission-Stage Antigens to Inform Engineered Vector Biocontrol Strategies **Philippos Papathanos**: Engineered sex-ratio distorters for mosquito control **Ebrima SM Kolley**: A sex-specifically spliced intron confers male-biased expression on a bisexually expressed transgene in *Anopheles gambiae* **Fatuma Matwewe**: Assessment of Male Mating Competitiveness of Genetically Modified MMCP *Anopheles gambiae* against Wild-type Males under Laboratory Conditions **Stellah A. Chumbe**: Establishment of Sex-Linked Transgenic Lines In *Anopheles Funestus* **Lee Lamdan**: Spermatogenic context controls outcomes of engineered sex distortion in malaria mosquitoes **Boubacar Tembely**: Targeting the X chromosome to develop genetic tools for the control of Malaria vectors
19:00- 21:00	CONGRESS DINNER AND SCICOM AWARD CEREMONY
DAY 3 ENDS	

DAY 4: THURSDAY MARCH 18, 2027		
07:30 - 09:00	**REGISTRATION**	
9:00- 13:00: WORKSHOP 3 (TBC) MAIN HALL 1A KILIMANJARO		
PLENARY 7: AI AND SCIENCE COMMUNICATION IN AFRICA **SESSION CHAIRPERSON: JACKIE KADO**		**VENUE: MAIN HALL KILIMANJARO**
9:00 - 10:30	**Amelie Wamba**: Communicating Genetic Biocontrol Technologies in Africa: Building Public Understanding, Trust, and Informed Engagement **Milliam Murigi**: AI and the Future of Science Communication: Is Artificial Intelligence transforming science communication or disrupting it? **Odongo Oduor Joseph**: Machine Learning Enabled Detection and Quantification of Psychographic Narratives Associated with GMO Myths **Gloria Ogbaki**: Trust Before Technology: Risk Communication Lessons from Nigeria's Biosafety Experience for Gene Drive Governance **Ama Kudom-Agyemang**: PGRRI's Farmer and Community Engagement Model: A Communication Blueprint for Emerging Agricultural Technologies	
10:30-11:00	HEALTH BREAK	
11:00-13:00	SCICOM WORKSHOP: From Science to Society: Communicating Evidence, Risk and Innovation	KILIMANJARO HALL A
SESSION 8A: BIORISK MANAGEMENT AND GENETIC BIOCONTROL: BIOSAFETY ASSESSMENT AND RISK-MANAGEMENT MEASURES FOR GENETIC BIOCONTROL PRODUCTS		
11:00-13:00	**FOSTER, Geraldine Marie**: Quality Assurance Mechanisms for the assessment of the production of Modified Mosquito Products – a pilot by the World Health Organization prequalification unit **Agha Ukpai Agha:** Building Unified Biosafety and Biosecurity Governance for Advanced Vector Engineering in Africa: A Regulator Perspective. **Massouroudini Akoudjin**: Risk Assessment of the Release of Genetically Modified Male-Biased Mosquitoes (Ac(PMB)1) in a Village in Western Burkina Faso. **Nditange Shigwedha**: A Risk-Pathway Framework for Biosafety Preparedness for Gene-Drive Mosquito Technologies in Namibia **Nathaniel Frimpong Boateng:** Strengthening Biorisk Management for Emerging Genetic Biocontrol Technologies: Lessons from a High-Containment Laboratory Assessment in Ghana. **Moussa Savadogo:** Myths, misperceptions, risk perceptions versus scientific risk assessment in decision-making for genetics-based vector control in Africa	

	Joel O. Odero: Potential of VectorGrid-Africa mosquito observatories as a platform for monitoring genetically modified mosquitoes and their environmental effects **Misheck Mulumba**: Governance Structures for One Health Initiatives in Africa: A Comparative Analysis	
SESSION 8B: CAPACITY BUILDING AND BIORISK ASSESSMENT - STRENGTHENING CAPACITY FOR GENETIC BIOCONTROL RESEARCH, REGULATION, AND IMPLEMENTATION **SESSION CHAIRPERSON: RAJKA FRITSCH**		
11:00-13:00	**Samba Diarra**: Awareness and perceptions of concerns on genetically modified mosquitoes in malaria control in Mali: The need for socially and culturally legitimate governance **Hamidou Maiga**: From laboratory capacity to environmental readiness: building African systems for innovative mosquito control technologies in Burkina Faso **Amadou Guindo**: From Capacity Building to African-Led Innovation: ACEME Establishes Genetic Engineering Capability for Malaria Vector Research in Mali **Vincenzo Di Donato**: Strengthening end-to-end genome editing capacity for genetic biocontrol in Africa **Hamady Sissoko**: Cyberbiosecurity Readiness in Biomedical Research Centers in Mali: A Cross-Sectional Study from Point G (2025) ***Martin Bundi:*** Readiness for Emerging Genetic Biocontrol Technologies: An Institutional Readiness Profile for KEMRI **Charles M. Mbogo**: Building African Capacity for Mosquito Control and Elimination Through PAMCA Networks: Integrating Conventional Approaches and Emerging Technologies	
13:00 - 14:00	LUNCH BREAK	
14:00 - 18:00	**SCICOM WORKSHOP SESSION 2:** From Science to Society: Communicating Evidence, Risk and Innovation	**KILIMANJARO HALL A**
PLENARY SESSION 9: **Animal biotechnology: Genome**-editing technologies and their application in animal breeding, covering CRISPR, base and prime editing, multiplex editing, trait validation, off-target assessment, and integration of validated traits into breeding programmes. ***SESSION CHAIRPERSON: Vibha Ahuja***		**VENUE: MAIN HALL KILIMANJARO**
14:00-15:00	**Takaaki Matsuki**: Genome Editing of Egg Allergens: Development of Hypoallergenic Layer Chickens via Platinum TALEN technology **Naresh L. Selokar**: Genome-Editing Technologies for Productive, Healthy and Climate-Resilient Tropical Livestock	
PLENARY SESSION 10: Advances in Emerging Biotechnology Tools for Genetic Biocontrol: Genetic biocontrol applications for disease vectors, agricultural pests, invasive species, and animal reservoirs within a One Health framework ***SESSION CHAIRPERSON: Royden Saah***		**VENUE: MAIN HALL KILIMANJARO**
15:00-16:00	**Stephanie Gamez**: Deploying Sterile Insect Technologies for Precision Crop Protection **Marc Schetelig**: Advancing Next-Generation Precision Technologies for Invasive Insect Control **R. Asokan**: CRISPR/Cas Mediated Genome Editing, A Novel Tool in the Area-wide Insect Pest Management: Potentials and Prospects from India Perspective **Daouda Tandé Barro**: Optimizing the flight propensity as an easy quality control test for mass-reared tsetse fly *Glossina brevipalpis* **Fidelia Oluomachi Ivoke**: From Vector Genomes to Genetic Biocontrol Decisions: Harnessing Artificial Intelligence for Next-Generation Surveillance in Africa	
16:00 - 16:30	**CLOSING CEREMONY**	

WORKSHOPS

Genetic Biocontrol for Vector Control: A Two-Day Introductory Workshop

Abstract

Vector-borne diseases continue to impose substantial public-health and socioeconomic burdens. Meanwhile, insecticide resistance, shifting vector ecology, urbanisation, climate variability, and operational constraints are reducing the effectiveness of conventional control tools. Genetic biocontrol is a potential approach that is currently gaining traction as a complementary tool within integrated vector management. Advances in next-generation sequencing, molecular biology, and gene-editing technologies such as CRISPR-Cas9 have enabled the development of genetic-based systems designed either as vector-population suppression approaches or as population replacement with manipulated mosquitoes with reduced capacity to transmit diseases.

This workshop introduces the principles and practical applications of genetic biocontrol for vector control, focusing on mosquito vectors of malaria, dengue and other mosquito-borne diseases. It examines self-sustaining strategies, including gene-drive systems, Wolbachia-based population replacement, alongside self-limiting genetic strategies, including the sterile insect technique (SIT), and dominant lethal approaches and Wolbachia-based population suppression. These approaches are compared in terms of their mechanisms of action, intended outcomes, benefits, limitations, and technological readiness. Participants will move from foundational concepts in vector biology, ecology, surveillance, and disease transmission to the mechanisms, evidence, potential benefits, limitations, and appropriate use of each technology.

Through case studies and facilitated exercises, participants will explore how genetic biocontrol could complement existing tools such as insecticide-treated nets, indoor residual spraying, larval source management, environmental management, and community-based control. The workshop will also address biosafety and risk assessment, regulatory pathways, ethics, community and stakeholder engagement, monitoring and evaluation, resistance management, and phased testing for responsible deployment. By the end, participants will be able to assess where genetic biocontrol could add value to integrated vector management programmes and identify context-specific priorities for research, policy development, capacity strengthening, and potential piloting in Africa.

Learning Objectives

At the end of the workshop, participants will be able to:

- Explain the core principles and terminology of genetic biocontrol for vector control.
- Compare self-limiting products (e.g., sterile insect technique, Wolbachia-based population suppression, and dominant lethal approaches) with self-sustaining products (e.g., gene drive systems designed to spread through target populations and Wolbachia-based population replacement), focusing on their mechanism, intended outcome, benefits, limitations, and technological and regulatory readiness. Assess where genetic biocontrol could complement established measures within an integrated vector management programme.
- Identify the evidence and decision criteria required for phased testing and responsible deployment.
- Evaluate key biosafety, ecological, ethical, regulatory, resistance-management, and community-engagement considerations.
- Develop context-specific priorities for research, policy, capacity strengthening, monitoring and evaluation, and potential piloting in Africa.

Two-Day Workshop Programme

Participants will leave equipped to make evidence-informed decisions, develop country-specific action plans, and assess readiness for responsible implementation.

Day 1: Understanding genetic biocontrol; Foundations, Technologies and Applications **Theme: From basic concepts to understanding the different technology approaches**		
Time	**Session**	**Presenter**
11:00 - 11:30	Registration and networking	AGBC Secretariat
11:30 - 12:00	Welcome, objectives, expectations, and pre-workshop assessment	Moderator: Etienne Bilgo
12:00 - 13:00	Session 1: Vector-borne diseases in Africa: burden and challenges in conventional vector control.	Presentation – Lakamy Sylla / Etienne Bilgo

	This session reviews Africa's vector-borne disease burden, transmission trends, control challenges, and capacity gaps, highlighting the need for complementary approaches such as genetic biocontrol.	
13:00 - 14:00	Lunch Break	
14:00 - 15.00	Session 2: Introduction to genetic biocontrol: Concepts, terminology and intervention pathways. *This session introduces genetic biocontrol principles and compares suppression, modification, self-limiting, and self-sustaining approaches. It outlines gene drive, Wolbachia, and self-limiting systems, their role in integrated vector management, and the phased pathway from laboratory testing to possible deployment, including biosafety, regulation, ethics, engagement, and monitoring.*	Joel Odera
15:00 - 15:30	Q & A	
15:30 - 16:00	Tea Break	
15:30 - 16:15	Session 3: Understanding the technologies: genetic modification, inheritance, population suppression and population modification Session 4: Gene-drive systems: Principles, mechanisms, applications and current evidence - Case Study	Elijah Juma Elijah Juma
16:15 -17: 30	Session 5: Wolbachia-based interventions: population replacement and suppression Session 6: Self-limiting genetic systems: Principles, Approaches, and applications. Session 7: Comparing genetic biocontrol approaches: mechanisms, potential benefits, limitations, and development status	Jewelna Akorli Givemore Munhenga
17:30-17.50	Group Discussions	All
DAY 1 ENDS		

Day 2: Responsible development, governance, and application in Africa understanding the technologies to responsible research, evaluation, and potential application		**Theme: From**
9:00 - 9:30	Day 1 Recap	
9.30 -10:00	Session 8: Scientific evidence and development pathways: from laboratory research to potential field application Comparing the three approaches: benefits, limitations and readiness	Facilitated exercise
10:00 - 10:30	Session 9: Biosafety, environmental risk assessment and ecological considerations	Presentation / TBC
10:30- 11:00	Tea Break	
11:00–11:30	Session 10: Regulatory framework, institutional responsibilities, and regional considerations in Africa.	Panel discussion
11:30-12:00	Session 11: Ethics, equity and responsible innovation	Simon Langat
12:00 – 12.30	Session 12: Community and stakeholder engagement	Case study -TBN
12:30 - 13:00	Group discussions and Q& A	
13:00- 14:00	Lunch Break	
14: 00 - 15: 00	Session 13: Planning phased testing: laboratory studies to possible deployment Session 14: African experiences, research capacity, infrastructure and opportunities for collaboration	Presentation – Jonathan Case studies: Mali (Likamy), Tanzania (Dickson) and Burkina Faso (Etienne)
15:00–15:40	Session 15: Monitoring, evaluation and post-release surveillance	Group exercise
15:40–16:10	Session 16: Integrating genetic biocontrol with established vector-control measures	Scenario exercise
16.10 –16:20	Tea Break	
16:20–17:20	Session 17: Country/team planning: priorities for research, policy, capacity and piloting	Breakout groups
17.20 –17:40	Group presentations and peer feedback	Plenary
17:40–18:00	Post-workshop assessment, commitments and closing	Plenary
WORKSHOP ENDS		

Proposed Outputs

- Comparative assessment of gene drive, Wolbachia and self-limiting systems including SIT
- Draft country or institutional action plans
- Priority research, policy and capacity-strengthening needs
- Preliminary stakeholder and regulatory pathway maps
- Agreed next steps for responsible evaluation or possible piloting

Case study 1: Evaluating a Gene-Drive System for Malaria Control

A rural region in sub-Saharan Africa continues to experience high malaria transmission despite widespread use of insecticide-treated nets and indoor residual spraying. Entomological surveillance identifies a locally dominant *Anopheles* mosquito species, with increasing insecticide resistance and persistent outdoor biting.

Researchers propose evaluating a CRISPR-based gene-drive mosquito designed to spread an inherited trait that reduces female fertility, with the aim of suppressing the target vector population. Laboratory studies indicate high drive inheritance but also identify possible fitness costs and low-frequency resistant alleles. Mosquito movement across neighbouring districts and an international border is possible.

Before any field release, decision-makers must consider ecological risk, molecular resistance, geographic spread, regulatory approval, community acceptance, regional consultation, monitoring capacity, and integration with existing malaria-control measures.

Group Task

Participants should determine whether the programme is ready to progress beyond contained laboratory studies and identify the evidence required for the next testing phase.

Discussion Questions

1. What additional laboratory and contained-field evidence is required?
2. How could resistant alleles affect the drive's effectiveness?
3. What ecological effects should the risk assessment examine?
4. How should mosquito movement and possible cross-border spread be addressed?
5. Which communities, institutions, and neighbouring authorities should participate?
6. What regulatory and ethical approvals would be required?
7. Which indicators should be monitored before and after any release?
8. What criteria should trigger progression, modification, pause, or termination?
9. How should the intervention complement existing malaria-control tools?
10. What uncertainties should be communicated to affected communities?

Expected Learning Points

- Gene drives may spread beyond the initial release site and therefore require regional coordination.
- Resistance, fitness costs, and local population genetics can affect performance.
- Decisions should follow phased testing with predefined evidence requirements.
- Biosafety, ethics, regulation, and community engagement are integral to readiness.
- Existing malaria-control measures should continue unless evidence supports modification.

Case Study 2: *Wolbachia*-Based Population Replacement and Suppression

A coastal African city is experiencing recurrent dengue outbreaks despite routine larval-source management and community clean-up campaigns. Surveillance identifies *Aedes aegypti* as the principal vector. Local authorities are considering *Wolbachia*-based interventions but must decide between **population replacement** and **population suppression**.

Under the **replacement approach**, authorities would release male and female mosquitoes carrying a suitable *Wolbachia* strain. Through maternal transmission and cytoplasmic incompatibility, *Wolbachia* could spread through the local mosquito population and reduce its ability to transmit dengue.

Under the **suppression approach**, only *Wolbachia*-infected males would be released repeatedly. When they mate with local females, the resulting eggs would fail to develop, temporarily reducing the mosquito population. This approach requires reliable sex separation and sustained releases.

Before deciding, programme leaders must assess baseline mosquito density, seasonal patterns, population movement, community acceptance, regulatory requirements, production capacity, release costs, and monitoring arrangements. They must also determine whether the intervention should complement existing vector-control measures.

Discussion Questions

1. Which approach—replacement or suppression—is more appropriate, and why?
2. What baseline entomological and epidemiological data are required?
3. How do cytoplasmic incompatibility and maternal transmission affect each approach?
4. What operational risks could arise from accidental female release?
5. Which stakeholders should participate in planning and decision-making?
6. What indicators should be monitored before, during, and after releases?
7. How should you communicate uncertainty, benefits, and risks to communities?
8. Under what conditions should releases be paused, modified, or stopped

Workshop on Artificial Intelligence and Capacity Strengthening for Genetic Biocontrol Decision-Making

A four-hour workshop during the 3rd Global Congress on Genetic Biocontrol March 15-18, 2027

Course organizer: Justin Overcash, FNIH

Purpose.

African biosafety regulators, risk assessors, developers, and programme managers are already encountering artificial intelligence tools, often without institutional guidance on verification, confidentiality, data sovereignty, or accountability. This practical workshop will build foundational understanding, introduce the GeneConvene Academy, and help participants develop a shared approach to the responsible use of AI in genetic biocontrol decision-making.

Audience.

Staff of national and regional biosafety authorities, risk assessors, Institutional Biosafety Committee members, developers, and programme managers involved in genetic biocontrol governance or decision-making.

Learning outcomes

At the end of the workshop, participants will be able to:

- Explain how generative AI produces outputs, how to better use frontier models for scientific work, and why those outputs require verification.
- Develop and apply a practical verification step to AI-assisted biosafety tasks.
- Identify information that should not be entered into public AI systems.
- Compare potential AI uses in dossier triage, literature search and problem formulation, and community communication.
- Sign up for and utilize the GeneConvene Academy.

Workshop Agenda

This four-hour agenda combines concise expert input, practical application, peer exchange, and action planning. The workshop will run from 14:00 to 18:00 hrs on on Day 3, 17/03/2027.

Four-Hour Workshop Agenda

Time	Session	Activity and output
14:00–14:15	**Welcome, objectives, and baseline**	Introductions, objectives, expectations, and baseline poll.
14:15–15:15	**AI basics and responsible use**	Core concepts and confident errors; guided exercise with a simulated or redacted regulatory artifact; error-hunt and debrief.
15:15-15:30	**Spotting AI errors**	**Output**: Hands-on practice spotting common AI errors
15:30–15:45	**Break**	Refreshments and informal exchange.
15:45–16:30	**AI in biosafety workflows**	Four short examples: dossier triage, literature search and problem formulation, and community communication; moderated discussion. **Output**: Applications, opportunities and risks, and minimum controls.
16:30–17:00	**GeneConvene Academy**	Academy introduction, Biosafety Technical Series 7 demonstration, and course review. **Output**: Know how to use the GeneConvene Academy.

17:00–17:40	**Future thinking**	Presentation on the Future of AI and Risk assessment; groups map how AI could be used to enhance decision-making and classify AI support as plausible, premature, or human-led. Output: Insight into future use cases for AI in Biotech Risk Assessment and reflection on current feasibility.
17:40–18:00	**Share-back and close**	Group highlights, post-poll, commitments, and next steps. **Output**: Evaluation and cohort interest.

Delivery approach

The workshop will combine short presentations, a guided demonstration, facilitated discussion, small-group work, and individual reflection. Participants will be seated at round tables where support group work, with approximately five to eight people per group.

Facilitation team:

Dr Overcash will serve as lead speaker. Additional workflow speakers and table facilitators will be confirmed based on expertise in biosafety regulation, risk assessment, community engagement, and responsible AI use. The lead facilitator will manage time, transitions, debriefs, and the integration of outputs.

Preparation and materials

- A simulated or fully redacted regulatory artifact for the practical exercise.
- A deliberately flawed AI-generated response for the error-hunt.
- Regulatory decision-mapping templates and markers.
- GeneConvene Academy access instructions.
- A projector, stable internet access, and an offline backup of all demonstrations.
- Pre- and post-workshop poll questions and participant commitment cards.

Workshop outputs

- A one-page AI error identification sheet.
- An individual GeneConvene Academy learning pathway.
- A simplified regulatory decision map from each group, identifying one plausible AI use, one premature use, and one decision that should remain under human judgment.
- A record of participant commitments and institutional questions.
- An invitation to join a follow-on learning cohort.

Evaluation and follow-up

A brief pre- and post-workshop poll will measure changes in participants' confidence in explaining AI limitations, verifying outputs, and protecting sensitive information. The facilitation team will also review the quality of group outputs and collect participants' intended practices and follow-up questions.

Within two weeks, the organizers will circulate the workshop materials, consolidated guardrails, anonymized themes from the regulatory maps, links to selected Academy pathways, and details of the follow-on learning cohort.

SCICOM WORKSHOP

From Science to Society: Communicating Evidence, Risk and Innovation

Workshop Abstract

Scientific advances increasingly shape public health, food systems, the environment, technology and everyday life. Yet research quality alone does not determine the value of scientific evidence. How evidence, risk, and innovation are communicated strongly influences how different audiences understand, discuss, and trust them.

This workshop explores practical approaches to communicating complex scientific issues clearly, accurately and responsibly. It examines how scientists, researchers, regulators, and communication professionals can translate technical evidence into messages that matter to policymakers, the media, and the wider public, while preserving scientific accuracy and communicating uncertainty appropriately.

The workshop also addresses the communication challenges that surround emerging and potentially controversial technologies, misinformation, public concern, and risk perception. A dedicated session brings scientists and science journalists together, and through case studies, group discussions, simulations and practical exercises, participants will develop and test messages for different audiences and channels.

The aim is to move beyond the simple dissemination of research findings towards purposeful, audience-centered communication that strengthens understanding, supports informed dialogue and builds confidence in science and evidence-based decision-making.

Programme

Time	Session	Approach
11:00 – 11:15	Registration and networking	–
11:15 – 11:30	Opening and workshop orientation	Welcome, objectives, expectations and participant introductions
11:30 – 12:00	**Session 1**: Why Communicating Science Matters	Opening exercise (explain your research to a stranger), brief presentation and facilitated discussion
12:00-13:00	**Session 2**: From Scientific Evidence to Public Understanding: Knowing Your Audience	Presentation, case studies and interactive exercise
13:00 – 13:40	**Lunch break**	
13:40 – 14:40	**Session 3:** Communicating Risk, Uncertainty, Misinformation and Public Trust	Case studies and group discussion
14:40- 14:55	**Session 4**: The 3-Minute Science Challenge	Team exercise, presentations and feedback
14:55 – 15:15	**Session 5**: Science Meets the Newsroom (special session for science journalists)	Journalist panel, mock press briefing and feedback
15:15 – 15:35	**Session 6**: Your Communication Action Plan	Individual or group exercise
15:35 – 16:00	**Closing session**: key lessons, commitments and evaluation	Reflection and presentation of certificates

Signature Activity: The 3-Minute Science Challenge

Teams receive a complex scientific topic drawn from the Congress themes and prepare a message for three audiences. Each team then delivers the version for one audience, drawn at random, so every team prepares for all three and is tested on one:

Policymaker: 60 seconds

Journalist: 90 seconds

General public: 3 Minutes

Participants receive feedback on clarity, accuracy, relevance, simplicity, credibility, audience appropriateness, and the communication of uncertainty.

Special Session: Science Meets the Newsroom

Session 5 brings science journalists into the room alongside the scientists, regulators and communicators attending the workshop. It runs in three parts:

Journalist panel:

how journalists find, test and frame science stories, what they need from scientists, and what makes a source difficult to use

Mock press briefing:

participants brief the journalists on a contested scientific topic and field their questions, including difficult and skeptical ones

Journalist feedback:

participants are assessed on clarity, accuracy, credibility and how well they communicated uncertainty

Ground rules for on-the-record and off-the-record conversation are agreed at the start of the session.

Expected Outcomes

At the end of the workshop, participants will be able to:

- Explain why communication is an essential part of scientific practice
- Identify and respond to the needs of different audiences
- Translate technical evidence into accessible language
- Communicate risk, uncertainty and controversial issues responsibly
- Recognize and address misinformation and misconceptions
- Engage confidently with journalists, including in difficult interviews
- Leave with a simple communication plan for their own project, institution or area of work: audience, three key messages, channels and one risk to manage

ABSTRACTS

3RD GLOBAL CONGRESS ABSRACTS

01 High-Level Leaders Forum: Reimagining Africa's Health Future with Genetic Biocontrol

Willy Tonui, African Genetic Biocontrol Consortium

Vector-borne diseases remain a major public-health burden in Africa, compounded by insecticide resistance, changing vector behaviour, climate-related transmission risks, limited financing and cross-border ecological threats. In response, this one-day high-level forum will convene senior government, regulatory, scientific and institutional leaders from nine African countries, together with regional and technical partners, to advance coordinated, country-led action against malaria and other vector-borne diseases. Participants will consider how innovative genetic biocontrol approaches, including genetically modified mosquitoes, gene-drive research, gene editing and related biological strategies can responsibly complement existing interventions through sound research, regulation, financing and communication. The forum will promote transparent governance, rigorous science and meaningful public engagement to strengthen policy coherence, regulatory preparedness and evidence-based decision-making across Africa. Strategic discussions will address policy alignment, science-based regulation, regional cooperation, research and institutional capacity, public trust, ethical oversight, sustainable financing and long-term monitoring. Expected outputs include an endorsed leadership communiqué, a nine-country action matrix with focal points and measurable milestones, a regional coordination mechanism, targeted capacity-building packages, and a financing and partnership roadmap. By aligning scientific innovation with political leadership, the forum will strengthen national readiness, advance responsible regional cooperation and support the public-interest governance of innovative vector-control tools.

02 Vector borne diseases, trends, current interventions and emerging biocontrol options

Dr. Lauren Carrington, Vector, Disease Control, Elimination and Eradication unit Malaria and Neglected Tropical Diseases department, World Health Organization

Vector-release strategies represent an increasingly important frontier in vector control, spanning both population-replacement and population-suppression approaches. These innovations include genetically modified mosquitoes and non-genetic methods based on symbiont-induced reproductive manipulation or irradiation-induced sterility. Although the technologies differ in their mechanisms, intended effects and regulatory classification, they share the deliberate release of modified or altered vectors and raise comparable questions for public health decision-making.

Available evidence supporting these differing approaches is at different stages of maturity. *Wolbachia* population replacement has been evaluated through large-scale field studies and is increasingly implemented against *Aedes*-borne diseases, leading to generation of epidemiological and operational evidence. Genetically modified mosquito technologies encompass diverse suppression and replacement approaches targeting malaria and *Aedes*-borne diseases, but epidemiological evidence remains limited.

This presentation will describe WHO's process for the evaluation and appraisal of the current evidence base, potentially informing recommendations for the respective interventions. It will outline the common evidence-to-recommendation pathway applied across vector-control interventions: systematic evidence synthesis; assessment of benefits, harms and contextual considerations; evidence-to-decision deliberation; and recommendation development through WHO's integrated Vector Control Guideline Development Group. Related operational guidance will also be elaborated.

Despite their differences, these fields face shared challenges in evidence generation, implementation and governance, creating considerable scope for reciprocal learning. Experience from *Wolbachia* evaluation and deployment may inform genetically modified approaches, while methods and perspectives from malaria-focused research may offer lessons for arbovirus control. Cross-dialogue could also strengthen approaches to environmental and ecological assessment, biosafety, spread and persistence, community engagement, monitoring and longer-term oversight. While differentiated assessment remains necessary, their evidence, governance and implementation frameworks need not develop in isolation.

03 Beyond proof of concept: Achieving deployable genetic control in Africa

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Genetic control is a species-specific approach to suppress or modify harmful insect populations through the release of engineered insects. Approaches can be self-limiting, designed to disappear over time, or self-sustaining, using gene drives that can spread from a small release and act area-wide. Proof of concept is well advanced in malaria and arbovirus vectors, with first field releases in preparation. Whether these technologies are adopted will depend on socio-political ownership as much as on the science. This discussion will address some of the technical and operational obstacles facing a first field release and subsequent implementation at scale: durability against resistance, long-term forecasting, containment and reversibility, and production and delivery at national scale.

Our research at Biocentis addresses some of the regulatory and operational challenges that could slow the implementation of genetic control in Africa. Suppression systems are self-extinguishing by construction, so maintaining the strains takes skilled, high-technology work at every generation, and mass-producing them for safe release is harder still. To this end we have developed READY (Rearing-Enabled, Activated on DeploYment), which could hold diverse suppression systems, including gene drive, as stable homozygous strains — to simplify production at scale, ensure male-only release, and prevent breakdown or resistance during rearing.

Finally, we are closing the gap that has kept self-limiting control out of elimination campaigns: existing technologies can reach elimination, but only at costs that are unaffordable where the disease burden is greatest. Our 2GEN technology amplifies suppression while remaining contained, so a release can drive a population to elimination in the urban settings that dominate arbovirus transmission. Gene drive alone is not predicted to eradicate malaria, so elimination will need several technologies together, and a contained system released sooner can both prepare the path for an area-wide release and supplement it thereafter.

04 Characterization of the cultivable bacterial microbiota associated with Anopheles coluzzii mosquitoes infected with Microsporidia MB

Carine Létitia Traoré [1,3,] Issiaka Saré[1,2,] Etienne Bilgo [1,2]

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[3]Université Nazi Boni (UNB), Bobo-Dioulasso, Burkina Faso.

Background: Microsporidia MB is a symbiont naturally present in mosquitoes of the *Anopheles gambiae* complex. This microorganism is capable of blocking plasmodium transmission, making it a promising candidate for the development of new malaria control strategies. Despite this growing interest, the interactions between Microsporidia MB and its host's bacterial microbiota remain poorly understood. The objective of this study was to characterize the cultivable bacterial microbiota associated with Microsporidia MB-infected (MB+) Anopheles coluzzii and to compare MB-uninfected (MB–) *Anopheles coluzzii*.

Methods: Culturable bacteria were isolated on Luria-Bertani (LB) medium from 16 biological pools, comprising eight MB+ pools and eight MB– pools, with each pool consisting of four mosquitoes. Genomic DNA was extracted from purified bacterial isolates using the 2% CTAB extraction method. A partial region of the 16S rRNA gene was amplified using universal bacterial primers, and the resulting PCR products were sequenced using the Sanger method to determine their taxonomic identity. Pool-level bacterial richness, Shannon diversity, and community composition based on Jaccard dissimilarity were compared between MB+ and MB– groups.

Results: A total of 60 bacterial colonies were selected for sequencing, of which 43 yielded sequences that passed quality control and could be reliably assigned to a bacterial taxon. Sequence analysis identified ten bacterial taxa. Elizabethkingia anophelis was the most frequently recovered taxon, representing 19 of the 43 identified isolates (44.2%), followed by Cedecea sp. (18.6%), Cedecea neteri (14.0%), and Ralstonia pickettii (7.0%). E. anophelis was recovered from both MB+ and

MB− pools. MB+ pools yielded nine bacterial taxa compared

with five in MB− pools, and showed descriptively higher mean richness (2.38 vs. 1.25 taxa per pool) and Shannon diversity (0.636 vs. 0.390), although neither difference was statistically significant (P = 0.360 and P = 0.537, respectively). Jaccard-based community analysis also showed no significant difference in cultivable bacterial community composition according to MB infection status (PERMANOVA, P = 0.378).

Conclusion: These results provide a culture-based view of the bacterial microbiota associated with Microsporidia MB infection and highlight the need for larger, culture-independent and functional studies to investigate MB–microbiota interactions.

05 A CRISPR-Cas9 system targeting female reproduction in *An. funestus* for genetic control

Achaz-Achim Agolinou [1,2], Nicole Page [2], Zachary Stavrou-Down [2], Oliver Gilles Yemien [1,2], Holly Humphrey [2], Alessandra Lanfrancotti [2], Ashley Hall [2], Nabasnogo Odette Zongo [1,2], Honorine Kaboré [1,2], Gregoire Sawadogo [1,2], Nouhoun Traoré [1], Kientega Mahamadi [1], Hamidou Maïga [1], Tony Nolan [2], Abdoulaye Diabaté[1]

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Background: Gene drive strategies that target genes essential for female fertility represent a promising approach for the control of malaria vector populations. In particular, disrupting loci involved in oogenesis, such as *Nudel*, may enable effective population suppression while limiting fitness impacts on males, thereby improving the specificity and sustainability of genetic interventions. In this context, the present study aims to develop a gene knockout of the *Nudel* ortholog in *Anopheles funestus*, assess its effects on key life-history traits, and establish a multiplex gene drive line targeting this locus.

Methods: Orthology and synteny analyses were used to identify the *Nudel* ortholog in *Anopheles funestus*, followed by gRNA design targeting a conserved locus. A *Nudel* KO line was generated using CRISPR-Cas9 system. Phenotypic assays quantified egg production, larval output, and hatching rate across genotypes. Segregation analysis assessed KO inheritance patterns, and longevity assays compared survival among homozygous, heterozygous, and wild-type adults. A multiplex gene-drive construct was subsequently integrated at the *Nudel* locus to generate the gene drive line.

Results: The *Nudel* ortholog corresponds to AFUN009733 in the FUMOZ reference, updated to AFUN2_001325 in the GABON-1 genome. Loss-of-function alleles severely impaired egg production, larval output, and hatching rate in homozygous KO females, whereas heterozygous females and males overall showed no significant differences relative to wild-type. Genotype proportions of the KO line followed Mendelian expectations, and adult longevity did not differ among genotypes. A gene-drive line targeting *Nudel* was successfully established with a transmission rate of 65% for the paternal line and 83% for the maternal line.

Conclusion: These findings identify *Nudel* as a haplosufficient female fertility gene in *An. funestus* and provide validated knockout and gene drive resources for further development of *Nudel* based population suppression strategies.

06 Pan-African Genomic Conservation of *Plasmodium falciparum* Transmission-Stage Antigens to Inform Engineered Vector Biocontrol Strategies

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Genetic biocontrol strategies for malaria require parasite targets that are conserved across geographically diverse populations. In this study, evaluated five *Plasmodium falciparum* transmission-stage antigens CSP, Pfs25, Pfs48/45, Pfs230 and TRAP to prioritise candidates for future engineered vector-based transmission-blocking strategies. MalariaGEN Pf8 was the primary dataset. After sample quality control, retention of one representative sample per Pf8 case identifier, and balancing to a maximum of 30 samples per country, we analysed 596 samples from 21 countries and four African population groups. A recent-period sensitivity cohort comprised 394 samples from 14 countries (2015–2022). PASS biallelic coding SNPs with high genotype callability were extracted from identical 3D7 coding-sequence coordinates. Nucleotide diversity (π), amino-acid conservation, Shannon entropy, Tajima's D and geographic differentiation (FST) were quantified and integrated into a Biocontrol Target Suitability Index (BTSI). Independently, 63 SRA run-labelled datasets from Equatorial Guinea, Zambia,

Malawi and Eritrea were processed against the same PlasmoDB-54 3D7 reference, jointly genotyped, depth-masked (DP≥3), quality-filtered (QUAL≥30) and assessed for whole-CDS callability.

Pfs25 showed the strongest Pf8 conservation profile (π=4.1×10−5; 98.2% overall amino-acid conservation; 100% conservation for common amino-acid variants; mean FST=0.018; BTSI=0.997). Pfs230 ranked second (BTSI=0.670), followed by CSP (0.543), TRAP (0.505) and Pfs48/45 (0.501). Independent SRA validation supported Pfs25 conservation: only two globally callable variants were detected, filtered π was 8.45×10−5 and maximum pooled alternate-allele frequency was 1.8%. Whole-CDS callability for Pfs25 was 88.2% in Equatorial Guinea, 100% in Zambia and 92.7% in Malawi. Pfs230 remained comparatively conserved in well-covered Zambia and Malawi cohorts, whereas CSP and TRAP were more diverse.

Pfs25 emerged as the strongest candidate for future transmission-blocking genetic biocontrol investigation, with Pfs230 as a secondary target. Population-genomic validation can therefore strengthen target selection before advancing geographically scalable engineered vector-control strategies.

Keywords: Plasmodium *falciparum*; genetic biocontrol; Pfs25; Pfs230; population genomics; transmission blocking

07 Gene drives that target malaria parasites rather than malaria vectors to control disease

Author: Dean Goodman

Malaria is on the rise. Existing tools are failing to control disease, and annual deaths exceed 0.6 million. Gene drives offer the capacity to repress or eradicate problem pathogens like the malaria parasite[1]. Thus far, gene drives to control malaria have all focused on the vector rather than the parasite itself. But do gene drives work in malaria parasites, and are they safe? We are building and testing a variety of gene drives in Plasmodium species that infect humans, monkeys, and rodents. Our gene drives aim to reverse drug resistance, ameliorate malaria-in-pregnancy, prevent spillover of P. knowlesi from monkeys into humans, restore the efficacy of rapid diagnostic tests (RDTs), and collapse transmission of deadly falciparum malaria.

Deploying gene drive parasites entails considerable safety, ethical, social, and compliance considerations. We have been funded for world-first, in-human safety and efficacy trials of a homing, sex biasing *P. falciparum* gene drive. Exploration of ethics, economics, social licence, and regulatory frameworks for a field trial of our gene drive in a malaria endemic region are also built into our project. Our team thus has the first chance to assess the utility and acceptability of a new tool to control malaria. Importantly, this tool proposes release of a GMO pathogen, so the path to deployment is not simple.

We will present our progress-to-date in building and testing malaria parasite gene drives. I will also weigh the pros and cons of these powerful and innovative tools to modify pathogen populations.

[1] Wilde, M-L et al. (2025) Novel techniques for disrupting malaria transmission. Trends in Parasitology 41: 657-9

08 Drugging mosquitoes rather than people with antimalarials

Author: Geoff McFadden

Abstract

Malaria parasites have become resistant to almost all antimalarials. Resistance is virtually inevitable because we drug select a huge number of parasites—about one quintillion. We are trialling an alternative approach whereby we drug the mosquitoes not the people. Malaria parasites go through a population bottle neck in mosquitoes, with an infected mosquito having about 1 trillion-fold less parasites than an infected person. Mosquitoes drink nectar and sugars daily; only females blood feed and then only when they need to lay eggs. We fed Anopheles stephensi mosquitoes a new antimalarial known as T111 in their sugar water. A single feed of T111, ~5 picomoles, completely blocked the production of malaria parasite sporozoites in our mosquitoes. The drug feed could occur either prior to infection or during infection of the mosquitoes and was still effective. The T111 sugar solution remained active against mosquito parasites at 27°C for 1 month. We were also able to freeze-dry the mix of T111 and sucrose onto small squares of fabric and reconstitute the mix with water up to 1 year later, when it still abrogated malaria infection of mosquitoes. We envision drugging mosquitoes with antimalarial sugar baits as a cheap, simple solution to deploy in dwellings to reduce transmission. Drugging mosquitoes has the distinct advantage that it prevents disease rather than treats disease. Drugging mosquitoes can also 'repurpose' potent antimalarials that failed, for some reason, to succeed as viable drugs.

09 Wickerhamomyces spp. in *Anopheles gambiae* s.l.: Prevalence, Tissue Distribution and Potential for Innovative Mosquito Biocontrol 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 field-caught mosquitoes *Anopheles gambiae* complex in western in Burkina Faso.

Methods: Mosquitoes collected from three areas of Bobo-Dioulasso in western Burkina Faso (Dioulassoba, Vallée du Kou, and Soumousso) 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 Pearson's chi- squared test or Fischer's exact to assess *Wickerhamomyces*, the significance threshold was set at $P < 0.05$

Results: The overall prevalence of *Wickerhamomyces* in *Anopheles gambiae* s.l. mosquitoes was 17.1%. This prevalence varied significantly according to the collection site (p-value = 6.62

$\times 10^{-8}$), the *Anopheles gambiae* species (p-value = 7.594×10^{-9}), the developmental stage of the mosquitoes (p-value < 0.001), the sex of mosquitoes (p-value = 0.027) and the physiological status of female mosquitoes (p-value < 0.001). However, it was similar across all organs. Four mosquitoes (two *Anopheles arabiensis* and two *Anopheles coluzzii*) were co-infection of *Wickerhamomyces* and *Plasmodium falciparum*.

Conclusion: This study reports the prevalence of the genus *Wickerhamomyces* in field-caught mosquitoes of the *Anopheles gambiae* complex, highlighting the need to investigate its potential for malaria control in Burkina Faso.

Keywords: *Anopheles gambiae* s.l, Malaria, *Wickerhamomyces*, *Plasmodium* infection B, Burkina Faso

10 Attractive sugar bait-mediated dissemination of symbiotic Serratia sp. in Anopheles for biological control of malaria Transmission

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Symbiotic bacteria associated with Anopheles mosquitoes, such as Serratia, can inhibit Plasmodium development and thus represent promising biological control agents for reducing malaria transmission. However, disseminating Serratia effectively throughout wild mosquito populations remains a major challenge for field implementation of this strategy. Here, we investigated the feeding preferences of *Anopheles coluzzii* for natural fruit juices, their capacity to promote Serratia gut colonization, and their effects on mosquito fitness. Adult *An. coluzzii* were offered banana, watermelon, papaya, and glucose juice in a large cage, and feeding preferences were determined by recapturing mosquitoes and examining gut contents. Serratia gut colonization was then quantified for each sugar source. The two most attractive juices were combined into a cocktail, and mosquito preference for this cocktail, glucose, and honey was assessed, along with effects on survival, fecundity, and fertility. Banana juice was the most attractive source (35.9%), followed by watermelon juice (15.7%), yet watermelon-fed mosquitoes showed the highest Serratia colonization (1.8×10^7 CFU/midgut). Among artificial

sugar sources, honey was preferred over glucose. Mosquitoes fed the fruit cocktail showed markedly reduced survival, with a median survival time (LT50) of 3 days. Notably, Serratia presence did not alter feeding preferences for any tested sugar source. These findings identify natural fruit juices as promising means for disseminating Serratia in wild mosquito populations. Future work should characterize the microbial communities naturally present in these juices to clarify their interactions with Serratia, Plasmodium, and the mosquito host, supporting the development of symbiont-based malaria control strategies.

Keywords: Enterobacteriaceae, attractive sugar, microbiota

11 CRISPR-Cas9-mediated disruption of Dicer-1 in *Anopheles gambiae*: Preliminary progress towards understanding the role of the miRNA pathway

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Background: MicroRNAs (miRNAs) are important post-transcriptional regulators of gene expression and contribute to diverse biological processes in mosquitoes, including development, reproduction, and immunity. *Dicer-1* is a key enzyme in the miRNA biogenesis pathway, and its functional contribution to these processes in *Anopheles gambiae* remains poorly understood. Characterizing the consequences of *Dicer-1* disruption may provide insights into mosquito biology and identify mechanisms that could be relevant to future genetic control strategies. The objective of this study was to initiate the generation, and validation of a *Dicer-1* disrupted mosquito line for downstream functional analyses.

Methods: CRISPR-Cas9-mediated genome editing was used to target the *Dicer-1* locus in *An. gambiae*. Guide RNA (gRNA) was designed to target a selected region of *Dicer-1* in silico. A CRISPR helper plasmid incorporating the gRNA expression cassette, Cas9, and a selection marker, together with a donor plasmid containing left and right homology arms flanking the targeted region and a marker gene, were designed and constructed. Following validation of plasmid constructs, CRISPR-Cas9 editing reagents were introduced into *An. gambiae* embryos through microinjection. Surviving individuals were screened for fluorescence to identify individuals expressing the introduced marker.

Results: A total of 1,980 *An. gambiae* embryos were microinjected, yielding a 13.64% hatch rate (n=270), of which 6.67% (n=18) were transiently fluorescent individuals. Of these, 11 survived to adulthood (3 males, 8 females). Transiently fluorescent adults were outcrossed to wild-type *An. gambiae*, and the resulting progeny were screened to assess potential

germline transmission. To date, a total of 2,481 progeny derived from these transient crosses have been screened for the presence of the transgenic marker.

Conclusion: Microinjection, screening, and successive genetic crosses are ongoing to generate a stable *Dicer-1* knockout line. Establishment of this line will provide a platform to investigate the role of *Dicer-1*-mediated miRNA regulation in *An. gambiae* development, reproduction, survival, and fitness, contributing to a better understanding of the miRNA pathway and its potential relevance to future genetic control strategies.

Keywords: *Anopheles gambiae*, *Dicer-1*, microRNA, CRISPR-Cas9, genetic control

12 NextGenSIT: A Regulatory-Optimized Bridge Technology Toward Gene Drives

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Mosquito numbers and mosquito-borne disease cases have surged in recent years, driven by rising insecticide resistance, a warming climate, and the spread of invasive mosquitoes. These trends are especially pronounced in Africa, where malaria is now spreading into urban environments via Anopheles stephensi. This growing public health challenge has renewed interest in novel genetic approaches such as gene drives. While suppression gene drives are expected to spread and suppress a targeted Anopheles species after just a few releases, their self-propagating nature makes regulatory approval contentious, requiring a multi-country framework.

At Synvect, we have developed two biosafe-by-design genetic control tools for Anopheles gambiae and Anopheles stephensi elimination: NextGenSIT and SEPARATOR. NextGenSIT combines the safety of traditional Sterile Insect Technique (SIT) with the precision of CRISPR gene knockouts. It uses two GM strains – one expressing Cas9, the other guide RNAs – to produce NextGenSIT eggs that develop hands-free into sex-sorted, sterilized males. SEPARATOR enables high-throughput, high-precision sex-sorting of early mosquito larvae and permanently marks mosquitoes with inert, harmless fluorescent proteins.

We argue that NextGenSIT can serve as a regulatory-optimized bridge technology toward gene drives. It uses the same CRISPR components as CRISPR-based gene drives, yet remains fully contained, offering the safety profile of traditional SIT with a regulatory pathway at the single-country level. Open-field trials of NextGenSIT will pave the way for gene drives by building community acceptance, local production capacity and expertise, and regulatory precedent for CRISPR-based mosquito control. Once gene drives are ready for open-field trials, SEPARATOR can then be deployed to scale production and sex-sort male-only releases of suppression gene drives.

13 Targeting the X chromosome to develop genetic tools for the control of Malaria vectors

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Vector-borne diseases cause enormous damage, with over 700 million cases worldwide. Transmitted by mosquitoes of the Anopheles genus, malaria kills more than 600,000 people a year. To tackle the problem, several vector control strategies have been implemented or proposed, including the use of genetic control. Previous studies have shown that germline specific cleavage of the X chromosome during male meiosis (X-shredding) or the disruption X-linked haploinsufficient genes (X-poisoning) can be used to bias the sex ratio of progenies towards males thereby reducing the number of malaria-transmitting females. My PhD work focuses on the use of CRISPR-Cas9 tools for the functional validation of X-linked genes with putative role in male gametogenesis, hybrid male sterility or female survival that can be targeted to develop novel genetic control tools. Alongside the characterization of candidate genes my work allowed to describe mechanisms of formation and inheritance of DNA mutations derived from CRISPR nuclease expression in the germline providing new knowledge and tools to develop new technologies to suppress malaria mosquito populations and transferrable to other major vector-borne diseases.

Keywords: CRISPR cas9, gene, b2 tubulin, deletion, and sterility

14 Progress in *Anopheles stephensi* gene drives and modeling

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Gene drive alleles bias inheritance in their favor, allowing them to quickly spread throughout a population after a small release of transgenic individuals. They could combat vector-borne diseases such as malaria and dengue from mosquitoes by rapidly spreading a cargo gene that blocks pathogen transmission or by directly suppressing vector populations. However, CRISPR gene drives often generate resistance alleles when DNA cleavage is repaired by end-joining instead of homology-directed repair, which impedes the spread of the drive. To overcome resistance allele formation, we generated a multiple-gRNA drive in the invasive urban malaria mosquito *Anopheles stephensi*. It successfully eliminated cage populations of mosquitoes. We've also constructed another drive using a new "toxin-antidote" mechanism that allows confined population modification. These experiments are supported by our computational modeling, which can predict the outcome of gene drive strategies on small and large scales.

Keywords: gene drive, homing suppression drive, *Anopheles stephens*i, resistance, computational modeling

15 Harnessing a naturally occurring mosquito symbiont to block malaria transmission

Authors: Thomas Onchuru, Cassandra Purity Ronnie and Jeremy Herren

Malaria remains one of the world's most persistent infectious diseases, and new approaches are urgently needed to complement existing control strategies. One promising strategy is to harness naturally occurring microorganisms that can alter the ability of mosquitoes to transmit malaria parasites. Microsporidia MB is a naturally occurring microorganism found in Anopheles arabiensis mosquitoes, one of the major malaria mosquito vectors in Africa. When present in mosquitoes, Microsporidia MB reduces their ability to support infection by Plasmodium, the parasite responsible for malaria, making them less capable of transmitting the disease under both laboratory and natural conditions. For a biological control strategy to succeed, a beneficial microorganism must be able to persist and spread within mosquito populations. Our work shows that Microsporidia MB has unique characteristics that support its natural dissemination. The microorganism establishes itself in mosquito reproductive tissues, allowing infected females to pass it to their offspring through eggs. This inheritance is highly efficient and is influenced by the amount of Microsporidia MB carried by the mother, suggesting that stronger infections promote more reliable transmission across generations. In addition, we demonstrate that Microsporidia MB can also spread between mosquitoes through mating, providing a second route for its movement within populations. Together, these findings reveal Microsporidia MB as a naturally occurring mosquito-associated microorganism with both strong malaria blocking activity and the ability to spread through mosquito populations. This work provides important insights into how beneficial microbes can be harnessed as innovative tools for malaria control and supports the development of future strategies that reduce malaria transmission by increasing natural resistance to the parasite within mosquito populations.

16 Lessons for genetic biocontrol from Wolbachia release programs in mosquitoes

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Abstract

The deployment of mosquitoes carrying *Wolbachia* endosymbionts is now one of the most successful approaches to control dengue and other arboviruses spread by mosquitoes. Compared to other genetic approaches targeting mosquitoes, research on *Wolbachia* is relatively mature and several release programs have reached an operational phase across large scales. Consequently, there are important lessons to be learned that are relevant to genetic biocontrol tools like gene drives as they progress from closed laboratory tests to field trials. I will present a broad overview of *Wolbachia* release programs in mosquitoes globally and highlight some of the key successes and challenges with this approach. I will draw on examples from Queensland, Australia, where the very first *Wolbachia* replacement releases occurred over 15 years ago. I will then discuss how our knowledge of *Wolbachia* release programs can be used to inform other similar approaches, including the release of genetically modified mosquitoes to suppress or modify populations.

17 Engineered sex-ratio distorters for mosquito control

Author: Philippos Papathanos

Engineered sex-ratio distorters are promising new tools for mosquito population control. They bias offspring sex ratios towards males, reducing female numbers over successive generations. Here we will describe progress towards the development of complementary CRISPR-based strategies for inducing prezygotic and postzygotic sex-ratio distortion in mosquitoes. We will also cover our work on overcoming transgene expression problems from the male-specific Y chromosome, where silencing during spermatogenesis has been a long-standing barrier. Together, these advances provide a versatile platform for engineering next-generation male-linked genetic control systems.

18 A sex-specifically spliced intron confers male-biased expression on a bisexually expressed transgene in *Anopheles gambiae*

Author: Ebrima SM Kolley

Homing Endonuclease Gene Drives (HEGs) are among the most promising genetic control strategies for *Anopheles gambiae* (*An. gambiae*) population suppression. The doublesex (dsx) homing gene drive has been the most effective mainly due to its location at an ultraconserved functionally constrained intron-exon boundary, resulting in homozygous intersex females. However, the rarity of such conserved female-specific targets and the emergence of resistance alleles due to sequence polymorphisms limit the broader applicability and flexibility of current HEG designs. To address these challenges, we are developing an intronic HEG strategy that leverages sex-specific alternative splicing to convert bisexual traits into female-specific traits. This expands the suitability of HEG targets to the most conserved regions of the *Anopheles gambiae* genome. As a proof-of-concept, we leveraged the sex-specifically spliced intron of 007 to convert a bisexually expressed fluorescent marker to a male-specifically expressed phenotype while hosting an X-shredder sgRNA. To do this, the coding sequence of the DsRed2 marker was interrupted by the intron, resulting in correct splicing of the intron in males and its retention in females. 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 β2-Cas9 with transheterozygous males generating 96% male offspring when crossed to wild-type females. This sex-specific expression and transgene hosting capacity demonstrates the feasibility of using the 007 sex-specifically spliced intron to develop novel HEGs. To transfer this to native genes, an analysis of ultraconserved 20bp Cas9 target sites in the genome identified 3 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. These targets offer expanded opportunities to develop gene drives with greater flexibility and reduced risk of resistance. 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 could be applied to a wide range of applications, for example, *Anopheles gambiae* population suppression or modification gene drives.

19 Establishment of Sex-Linked Transgenic Lines In *Anopheles Funestus*

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Background: Advanced genetic technologies for malaria vector control have been developed in *Anopheles gambiae*, but their application to *Anopheles funestus* remains limited by inefficient genetic transformation tools. Establishing transgenic docking lines is an important step toward enabling genetic technologies in this malaria vector. Sex-linked docking lines are particularly valuable for studying sex-chromosome biology, developing genetic sexing approaches, and supporting future sex-specific strategies.

Methods: PiggyBac-mediated germline transformation was used to generate An. funestus carrying a 3xP3-EYFP fluorescent marker and attP docking sites. Embryos were co-injected with donor construct and either a heat-shock promoter-driven (hsp) or germline-specific vasa-driven piggyBac transposase helper. G_1 progeny were screened for fluorescence, and transgenic lines were established and characterized. Inheritance analysis and inverse PCR followed by sequencing were used to identify sex-linked insertions.

Results: Both transposase systems supported germline transformation and generated transgenic founders. The vasa-

driven system produced a higher estimated germline transformation rate than the hsp-driven system (7.5% vs. 4.7%). Multiple stable transgenic lines were recovered, with variation in fluorescence intensity consistent with positional effects of genomic integration. Importantly, we identified an X-linked transgenic line based on its sex-specific inheritance pattern, and sequencing confirmed integration on the X chromosome.

Conclusion: We established a piggyBac-based transformation platform in *An. funestus* and recovered a stable X-linked transgenic docking line. This provides an important foundational genetic resource for *An. funestus,* with potential applications in studying sex-chromosome biology, developing genetic sexing approaches, and supporting future sex-specific genetic technologies for malaria vector control.

Keywords: *Anopheles funestus*, Germline transformation, piggyBac transposon, Transgenesis, Vector control.

20 Spermatogenic context controls outcomes of engineered sex distortion in malaria mosquitoes

Author: Lee Lamdan

Sex ratio distorters (SRDs) are a promising genetic strategy for controlling insect pest populations by biasing offspring toward males, thereby suppressing or eliminating target populations. In species with heteromorphic sex chromosomes, where males transmit the X chromosome to daughters, SRDs can induce pre-zygotic male bias by overrepresenting Y-bearing sperm or post-zygotic male bias (X-poisoning) by reducing the fitness of daughters inheriting a mutated X-linked gene. Here, we utilized a CRISPR-Cas9 bipartite system to target X-chromosome-linked genes in Anopheles gambiae at distinct spermatogenesis stages, leveraging independent Cas9 and gRNA lines for flexible evaluation of multiple combinations without generating extensive transgenic lines. Trans-heterozygous males (F1) from crosses between homozygous Cas9 and gRNA lines were mated with wild-type females, and the development and sex ratios of their offspring (F2) were assessed. Our results demonstrate that spatial-temporal modulation of Cas9 expression significantly influences SRD outcomes. Targeting X-linked ribosomal genes with the beta2-tubulin promoter during meiosis yielded a strong pre-zygotic male bias. Conversely, using the zpg promoter for early germline Cas9 expression produced varied phenotypes depending on the target gene, including reduced fitness in F1 trans-heterozygotes, with some failing to pupate or emerge as adults, and others exhibiting sterility. We further targeted wupA, an X-linked troponin muscle gene recently identified as haplo-insufficient in Drosophila melanogaster. When driven by the beta2-tubulin promoter, wupA targeting resulted in robust pre-zygotic male bias. However, zpg-driven Cas9 expression led to X-poisoning, with most female offspring failing to reach pupation or, if emerging, unable to fly. These findings provide the first evidence of an X-poisoning system in *Anopheles gambiae* and underscore the critical role of precise Cas9 expression timing in developing effective SRDs for malaria vector control.

21 Quality Assurance Mechanisms for the assessment of the production of Modified Mosquito Products – a pilot by the World Health Organization prequalification unit

Authors: FOSTER[1], Geraldine Marie, TAPHOUSE[1], Maggie, PEREZ NUENO[1], Violeta Isabel, SCHULER[1], Dominic Joseph.

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Significant advancements are underway in the field of mosquito modifications that aim to prevent or interrupt the transmission of vector borne diseases. Given the variety of potential modifications, and the possible spectrum of modified mosquito products (MMP), Member States of the World Health Organization (WHO) may seek guidance from WHO about such products prior to full WHO recommendations becoming available. As such, WHO should consider a regulatory approach to assess the quality and capability for performance of MMPs that is not reliant on epidemiological data.

The WHO Quality Assurance Mechanism for Modified Mosquito Production (QAM) is a proposed regulatory mechanism designed to address the growing needs for quality assessments and manufacturing site audits of MMPs which may be intended for use in public health programmes to reduce transmission of vector borne diseases. Currently under pilot by the Special Prequalification Programme for Vector Control Products at WHO, the purpose of the QAM is to establish an independent assessment by WHO of MMPs and their manufacturing facilities to support Member States and other UN bodies.

Expressions of Interest for participation in the QAM pilot will be open for 12 months. Descriptions of dossier format(s), data requirements and applicable technical considerations are available to all participating manufacturers. These are supported by 15 implementation guidance documents which provide considerations for how applicants may wish to generate the required supporting data.

The proposed outputs from the QAM, once launched as an official programme, are a certification of the declared

manufacturing site, supported by a quality assessment of the product and inspection reports. These outputs will declare that the MMP manufacturing site has demonstrated the ability to consistently produce the described product in accordance with the declared quality standards.

Keywords: Regulation, Modified Mosquito Product, WHO, Quality Assurance

22 Risk Assessment of the Release of Genetically Modified Male-Biased Mosquitoes (Ac(PMB)1) in a Village in Western Burkina Faso

Author: Massouroudini Akoudjin

Sub-Saharan Africa accounts for nearly 90% of global malaria-related deaths. Current control methods (insecticide-treated nets, insecticides, and antimalarial treatments), while contributing to a reduction in disease incidence, remain insufficient to eradicate malaria from the African continent. Genetic control based on genetically modified mosquitoes constitutes a promising alternative for achieving this objective. It is within this framework that genetic control strategies employing genetically modified mosquitoes are currently being developed. Accordingly, male-biased mosquitoes of the Ac(PMB)1 strain were evaluated for a controlled release in a village in western Burkina Faso. The assessment was conducted in accordance with regulatory frameworks (international and national) and comprised four steps: (i) identification of risk hypotheses, (ii) estimation of the probability of risk occurrence, (iii) estimation of the severity of potential adverse effects, and (iv) estimation of the overall risk level, incorporating uncertainties and risk management measures. The potential adverse effects considered were (i) human and animal health and (ii) the environment. With regard to human health, toxicity/allergenicity, disease, and injury/illness were analyzed as potentially adverse effects. For the environment, the following elements were analyzed as potentially adverse effects: toxicity to non-target organisms, loss of biodiversity, increased adverse effects of pathogens/pests, emergence of new pests, disruption of biotic communities, and degradation of the abiotic environment. Each hypothesis was analyzed by means of a causal pathway (a sequence of events, each assigned a likelihood rating: P = probable, IP = improbable, HP/HIP = highly improbable), leading to an estimated risk substantiated by scientific evidence, the characteristics of the receiving site, and the planned activities. A total of 19 risk hypotheses were identified, divided into two categories. For human and animal health, the hypotheses can be summarized as follows: (i) facilitation of the transmission of malaria or other diseases via transgenic proteins, and (ii) toxicity and allergenicity of proteins (eGFP, DsRed, I-PpoI) to humans and animals. For the environment, the hypotheses concerned toxicity to predators, proliferation of transgenic females, instability/persistence/invasiveness of the transgene, increased resistance to insecticides, transfer of the sex-distortion gene to other species (related or unrelated), horizontal gene transfer (eukaryotic and prokaryotic), transfer of transgenes to Plasmodium, the emergence of new pests, cross-border dispersal, and impacts on wetland management. Of the 19 hypotheses, 6 underwent detailed analysis and were all classified as posing negligible risk. The overall risk associated with the controlled release of Ac(PMB)1 was estimated to be negligible for both human/animal health and environmental safety, in light of prior assessments (confined trials) and the present analysis. This conclusion provides the basis for decision-making regarding the controlled release and recapture of male-biased mosquitoes, aimed at collecting the biological and ecological data required for a future release of gene-drive mosquitoes.

Keywords: Genetically modified mosquitoes, Risk assessment, Malaria control, Gene drive, Male-biased

23 Myths, misperceptions, risk perceptions versus scientific risk assessment in decision-making for genetics-based vector control in Africa

Moussa Savadogor.

Decisions to advance innovative, genetics-based vector control strategies in Africa, particularly those involving gene drive technologies for malaria control, are to be made in a complex environment where myths, misperceptions, and culturally rooted risk perceptions often diverge from formal scientific risk assessment. Scientific evaluations rely on internationally standardized principles and methodologies, measurable probabilities, ecological impact analysis, and objective biosafety criteria; however, in parts of the continent, public and stakeholder interpretations of risk are shaped by misperceptions, mistrust, overly precautionary considerations regarding ecological and social disruption, broader geopolitical apprehensions surrounding externally driven technologies, and, in some cases, conspiracy theories. To some extent, these perceptions overshadow the potential disease-control benefits of innovative vector control tools. Drawing on examples, this presentation examines how these divergences can challenge regulatory deliberations, weaken the legitimacy of established processes, undermine the effectiveness of community engagement, and, in some cases, contribute to policy reversals. It also highlights uncertainty around decision-making authority and governance communication, emphasizing the need to closely monitor who holds final decision power and to promote a collegial decision-making structure.

24 Strengthening end-to-end genome editing capacity for genetic biocontrol in Africa

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Background: Genetic biocontrol technologies hold significant promise for addressing vector-borne diseases in Africa. Their responsible development and eventual deployment depend not only on the technologies themselves. It also requires a critical mass of African scientists able to design, execute and evaluate the underlying genome editing work, and to navigate the associated biosafety and regulatory requirements. Building this local capacity remains a major bottleneck. Beginning in 2017 through TReND in Africa, and subsequently through Gene4All, we have developed a hands-on model to strengthen genetic biocontrol capacity across the continent.

Methods: We implement a partnership-based approach combining intensive hands-on genome editing training with online modules, Train-the-Trainers activities, open educational resources and international networking. Training spans the full experimental pipeline relevant to genetic biocontrol, from basic molecular biology and CRISPR-based genome editing to microinjection, insectary practice, biosafety and regulatory literacy, delivered in collaboration with African institutions.

Results: Since 2017, activities have reached more than 200 scientists across seven African countries and over ten institutions, through on-site workshops and online activities. Training has strengthened practical skills directly relevant to gene drive and vector-control research, and regional expertise has begun to consolidate at partner institutions. Early evidence of knowledge multiplication is emerging, with former trainees beginning to establish their own training activities. The network has also contributed to the broader field through African-led collaborative outputs. This includes a co-authored article in Nature Biotechnology, bringing together experts from twelve African and European countries, and engagement with policymakers via a policy brief presented to the Pan-African Parliament.

Conclusions: As genetic biocontrol advances towards field trials, continued investment in local scientific, biosafety and regulatory expertise will remain essential for African researchers and institutions to take a leading role in these technologies. Through hands-on, partnership-based training, we will continue to contribute to this shared effort and to a growing, connected community of expertise across the continent and beyond.

25 AI and the Future of Science Communication Is artificial intelligence transforming science communication or disrupting it?

Milliam Murigi

A few years ago, explaining a complex scientific study meant hours of reading journal papers, interviews with experts and careful translation into everyday language.

But today, that process is changing. With artificial intelligence, a complex scientific paper can be summarised in seconds.

A data set that once required specialist analysis can now be interpreted almost instantly. A draft article can be generated before a journalist even finishes reading the abstract.

This raises a critical question for all of us working in communication, science, and media: is artificial intelligence transforming science communication, or is it disrupting it?

The honest answer is it is doing both at the same time. On one hand, AI is clearly transforming science communication in powerful ways. It is making science faster because what used to take hours of reading can now be condensed into summaries that help communicators quickly grasp the core ideas of a study as well as more accessible since complex terminology can be translated into simpler language.

There is also the power of scale since AI helps organise and interpret massive data in ways that were not previously possible, enabling stronger storytelling grounded in data.

AI is also disrupting science communication in ways we cannot ignore. The first and most obvious risk is misinformation. AI can generate content that sounds confident and accurate but may be factually wrong or misleading. In science communication, where precision matters, this is a serious concern.

There is also the danger of oversimplification. In addition, growing reliance on AI-generated explanations may shift the role of expertise, reduce the visibility of scientists and weaken the connection between research institutions and the public. Finally, trust becomes more fragile, as audiences may struggle to distinguish between human reporting, expert analysis, and machine-generated content in an already contested information environment.

So where does this leave us as science communicators? It means we are at a turning point. On one side, AI offers an opportunity to bridge long-standing gaps. On the other side, it risks deepening inequalities. This is why the role of science communicators is not becoming less important it is becoming more important than ever. Science communicators are not being replaced. They are being repositioned. Their role is shifting from being simple translators of science into public language, to becoming guardians of accuracy, context, and trust and AI can assist us, but it cannot replace the responsibility of verification. It can generate content, but it cannot replace judgment.

In this new landscape, the most important skill is not just writing or reporting. It is knowing how to question outputs, how to verify claims, and how to maintain the integrity of scientific storytelling.

So, when we ask whether AI is transforming or disrupting science communication, the most honest answer is that it is doing both. But the direction it takes will depend on us. If used carelessly, it can distort understanding and weaken trust. If used responsibly, it can expand access to knowledge and strengthen public engagement with science.

26 Machine Learning Enabled Detection and Quantification of Psychographic Narratives Associated with GMO Myths

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Public debate on genetically modified organisms (GMOs) is influenced not only by the availability of scientific evidence but also by how competing narratives are constructed, interpreted, and disseminated. This study developed a machine learning enabled framework to detect psychographic narratives associated with GMO myths and quantify the resulting information asymmetry between scientific evidence and public discourse. Data from publicly accessible social media, news platforms, and online forums were collected, cleaned, deduplicated, and analysed using topic modelling, semantic analysis, and sentiment classification. These outputs were combined with audience profiling to characterize differences in values, beliefs, concerns, and perceptions surrounding major GMO themes.

An Information Asymmetry Index (IAI) was developed from three dimensions: alignment between public narratives and scientific evidence, understanding of the evidence, and disparity in its dissemination. The index was scaled from 0 to 100 and applied to generate an Information Asymmetry Map. The analysis produced an overall IAI of 69, indicating a substantial level of information asymmetry. Corporate control recorded the highest score (83), followed by health risk (78), institutional distrust (69), environmental impact (62), and perceived naturalness (55). These results showed that the strongest asymmetries occurred around issues of corporate influence, health risk, and institutional trust, rather than being evenly distributed across GMO discourse. The framework also incorporated a response-ranking component that prioritised communication interventions according to feasibility and potential impact, with expert review retained as a safeguard against inappropriate or manipulative use of psychographic information. The findings demonstrated that information asymmetry could be operationalized as a measurable feature of contested biotechnology communication rather than treated solely as a problem of misinformation or insufficient public knowledge. The approach provided a basis for identifying specific narrative domains requiring evidence-based engagement and for directing communication resources towards areas of greatest asymmetry. Ethical oversight, transparency, and human judgement remained essential to ensure that psychographic analysis supported informed public engagement rather than targeted manipulation.

Keywords*:* genetically modified organisms; GMO myths; psychographic narratives; machine learning; information asymmetry; risk communication; science communication; biotechnology governance.

27 Trust Before Technology: Risk Communication Lessons from Nigeria's Biosafety Experience for Gene Drive Governance

Dr. Gloria Ogbaki

As genetic biocontrol technologies, particularly gene drives, move closer to potential application, public trust in the institutions responsible for their regulation will be as important as technical readiness. In Nigeria, the National Biosafety Management Agency (NBMA) has spent over a decade navigating public engagement on genetically modified crops and biosafety decisions amid historical skepticism, weak scientific literacy infrastructure, and a rapidly evolving misinformation ecosystem. These challenges have been evident in controversies surrounding BT cotton, genetically modified cowpea and

TELA maize approvals, as well as the National Assembly's motion for a moratorium on genetically modified organisms. These experiences offer practical lessons for understanding how regulatory communication shapes public perceptions of emerging technologies and how these lessons may apply to gene drives, which raise distinct concerns because of their self-propagating nature and potential for effects beyond the immediate intervention site.

This paper argues that trust is not a communication output but a precondition for meaningful engagement. Where trust in the regulator is fragile, technical risk-assessment language may fail to resonate, while misinformation can fill perceived information gaps faster than evidence can correct them. Drawing on NBMA's regulatory communication experience, the paper identifies three recurring dynamics: the gap between regulatory transparency and public perceptions of transparency; the influence of community gatekeepers and informal information networks relative to formal information channels; and the speed with which rumours can outpace official communication. It considers the relevance of these dynamics to Nigeria's current position as a country with an established biosafety regulatory framework for gene drives, but no domestic gene drive research or field activity yet underway.

This anticipatory stage presents an opportunity to establish communication and engagement approaches before potential field application. The paper examines three implications for Nigeria and comparable regulatory contexts: the need for engagement to precede rather than follow technical development; the distinct communication demands of a self-propagating technology; and the limitations of applying generic GMO communication approaches to a technology that the public may perceive differently.

The paper concludes by proposing practical principles for regulatory risk communication during the anticipatory governance stage and ahead of potential field application. These principles are intended to support regulators and implementing partners in building trust, transparency and meaningful community engagement around gene drive research and potential deployment in malaria-endemic regions of Africa.

Keywords: risk communication, regulatory trust, biosafety governance, gene drives, anticipatory governance, public engagement, Nigeria

28 From Vector Genomes to Genetic Biocontrol Decisions: Harnessing Artificial Intelligence for Next-Generation Surveillance in Africa

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Background: Vector-borne diseases, particularly malaria, present severe public health challenges in Africa. While engineered genetic biocontrol offers sustainable solutions, safe deployment requires integrated surveillance combining vector genetics, epidemiology and environmental data. Genomic epidemiology and artificial intelligence (AI) can drive predictive surveillance, yet their convergence within African vector control remains insufficiently characterized.

Objective: To evaluate the convergence of vector genomics and AI in African disease surveillance and establish an operational framework for risk-assessed, decision-ready genetic biocontrol.

Methods: Following JBI and PRISMA-ScR guidelines, major databases and preprint servers were searched for African studies (2010–2026) addressing vector genomics, AI/machine learning (ML), geospatial analytics, and digital surveillance. Data were charted on species, genomic approaches, AI methods, coverage, and implementation considerations.

Results: Of 3,842 records identified, 66 studies across 24 African countries met inclusion criteria (predominantly Kenya, Uganda, Burkina Faso and Nigeria). Anopheles species comprised 83.3% (n=55) of targets. Genomic approaches centered on Whole-Genome Sequencing (Illumina/Nanopore; n=38) and targeted amplicon SNP panels (n=21). AI applications included geospatial ML (Random Forest/XGBoost; n=28), computer vision for species identification (CNNs; n=21), and predictive sequence modeling (n=12). Four critical gaps emerged: (1) poor integration between genomic data and real-time AI models (<8% integrated) (2) insufficient baseline target-site genetic variation data (3) severe local bioinformatic compute deficits and (4) an absence of operationalized AI-genomic governance frameworks for gene drive releases.

Conclusion: Integrating genomic epidemiology and AI can establish adaptive, predictive vector surveillance in Africa. The resulting framework prioritizes real-time multi-modal data integration, baseline target-site monitoring, localized compute infrastructure, and regulatory governance for responsible genetic biocontrol implementation.

Keywords: Genetic Biocontrol, Vector Surveillance, Genomic Epidemiology, Artificial Intelligence, Malaria Vectors, PRISMA-ScR

29 Communicating Genetic Biocontrol Technologies in Africa: Building Public Understanding, Trust, and Informed Engagement

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Genetic biocontrol technologies, including gene drive systems and gene editing applications, are emerging as promising tools for addressing vector-borne diseases and other environmental challenges in Africa. However, successful implementation depends not only on scientific progress but also on public understanding, trust, and meaningful stakeholder engagement.

This presentation explores the role of science communication in supporting informed discussions around genetic biocontrol technologies. Drawing on experiences in science communication, stakeholder engagement, and public dialogue, it highlights practical strategies for translating complex scientific concepts into accessible language, addressing misinformation, and fostering constructive engagement with communities, policymakers, and the media.

The presentation argues that communication should be integrated throughout the research-to-implementation pathway rather than treated as a final dissemination step. By promoting transparency, cultural relevance, and two-way dialogue, science communication can strengthen public confidence and support responsible innovation.

As gene editing and genetic biocontrol technologies continue to advance in Africa, investing in communication capacity will be critical to ensuring that decision-making is informed, inclusive, and grounded in evidence.

Keywords: Science Communication, Genetic Biocontrol, Gene Drive, Gene Editing, Public Engagement, Stakeholder Engagement, Africa

30 Prevalence of Microsporidia MB Symbiont and Malaria Transmission Blocker in Sibling Species of *Anopheles gambiae* s.l. in Rwanda

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Background: Malaria remains a major public health challenge in Rwanda despite the progress made in the deployment of core vector control interventions. The increasing insecticide resistance of malaria vectors and their biting and resting behavior changes highlight the need of innovative tools. *Microsporidia MB*, a natural mosquito-associated symbiont, is a promising biological vector control tool due to its blocking effects of *Plasmodium* parasite in *Anopheles* mosquitoes.

Aim: To investigate the prevalence of *Microsporidia MB* among malaria vector populations in Rwanda.

Methods: *Anopheles* mosquitoes were collected using human landing catching (HLC) in 11 sites across five provinces of Rwanda. The *Plasmodium* sporozoites were tested using ELISA and *Microsporidia MB by PCR*.

Results: Out of 188 *Anopheles gambiae* s.l. tested, 93.8% and 6.2% were respectively *Anopheles arabiensis* and *Anopheles gambiae* s.s. species. In general, 16 specimens of *An. gambiae* s.l. were found positive to *Microsporidia MB*, representing an overall prevalence of 8.5% with a higher prevalence (9.8%, n=153) in *An. arabiensis* compared to (2.9%, n=35) in *An. gambiae* s.s.. *Microsporida MB* was detected in 6 sites out of the 11 surveyed sites, representing all the provinces. In total, five *An. gambiae* s.l. were tested positive to *Plasmodium* infection with a sporozoite infection rate (SIR) of 2.7%. All 16 MB-positive mosquitoes were negative for *Plasmodium* infection while the 172 MB-negative *An. gambiae* s.l, had a *Plasmodium* prevalence of 2.9%.

Conclusion: The *Microsporidia MB* was for the first time detected in *Anopheles* populations in Rwanda with a high prevalence in *An. arabiensis*, with countrywide occurrence. Further longitudinal studies are needed on large samples to assess its prevalence and effects on malaria transmission blocking under laboratory, controlled and field conditions. By targeting vector competence, *Microsporidia MB* could complement integrated vector management and contribute to sustainable malaria control in Rwanda and the Region.

Keywords: Microsporidia MB; Anopheles; malaria; biological control; *Plasmodium*.

31 Environmental Monitoring of Genetic Control in the African Region: the example of *Aedes albopictus* in Reunion Island

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Aedes mosquitoes are the vectors of arboviruses of utmost importance for public health. The situation is particularly problematic in Reunion Island, which is strongly affected by dengue and chikungunya epidemics, with *Aedes albopictus* as a major vector. Innovative control tools are needed. The boosted sterile insect technique (SIT) is a method in which irradiated sterile males also transmit a biocide to wild females, the pyriproxyfen. A strong environmental monitoring is thus needed, even if the transport of biocide is targeted to the larval habitats and the doses very low.

We thus used the PRONTI approach recently proposed to monitor gene drive against Anopheles gambiae to select the best ecological indicators for our programme. We then combined three monitoring methods:

- population dynamics of sentinel beehives using the COLEVAL method and dosage of the pyriproxyfen residuals in honey, wax, bees and pollen;
- biodiversity and density of non-target species (larvae) in sentinel larval sites and dosage of the pyriproxyfen in water;
- biodiversity and density of non-target species (adults) in BG sentinel traps (by-catch) used to monitor the efficacy of the programme.

In addition to a reference morphological identification of non-target species, we constituted a barcoding library of morphotypes and tested metabarcoding and eDNA to assess biodiversity indices using several primers, from general to more specific to Diptera.

Overall, we did not observe any long-term accumulation of pyriproxyfen in the environment nor any impact on the population dynamics of bees and biodiversity of non-target species whatever the method considered. Metabarcoding and eDNA proved very informative and complementary to the reference method, offering new perspectives to improve the cost-efficiency of environmental monitoring of genetic control of mosquitoes in Africa. However, the constitution of a morphotype and barcoding library represents a challenging yet necessary step to use these methods.

Keywords: Vector control, dengue, chikungunya, ecological indicators, barcoding, metabarcoding, eDNA

32 Strengthening Biorisk Management for Emerging Genetic Biocontrol Technologies: Lessons from a High-Containment Laboratory Assessment in Ghana

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Background: New and emerging genetic technologies offer significant potential for addressing public health challenges in diagnosis and treatment, pathogen surveillance, agricultural improvement and research. Their responsible development and application, however, require robust biosafety, biosecurity, risk assessment, ethical and institutional governance frameworks. For institutions in Africa, establishing and strengthening these systems is particularly important as laboratory capacity for handling high-risk agents continue to develop.

Methods/Approach: This report presents lessons learnt from the strengthening and assessment of biorisk management practices at the Noguchi Memorial Institute for Medical Research (NMIMR), Ghana. Two complementary assessments were considered: an Africa Centres for Disease Control and Prevention (Africa CDC) assessment of the Institute's high-containment laboratory using the Regulatory and Certification Framework for Institutions Handling High Risk Pathogens,

conducted in March 2025, and an institutional assessment of biorisk practices across all nine research Departments in the institute. The assessments examined areas including containment, management and operational practices, risk assessment, safe practices, access control, waste management, and emergency preparedness.

Results: The high-containment facility had a total score of 138/160 (86%), placing it within the four-star

(85–94%) category of the Africa CDC certification framework. Management and operational practices demonstrated particularly strong performance, scoring 68/70 (97.1%), while containment design and construction scored 60/75 (80%) and maintenance, commissioning and certification scored 10/15 (66.7%). Opportunities for improvement included documentation of risk assessments, validation and monitoring of decontamination systems, autoclave validation, and the maintenance of occupational health records.

The institutional biorisk practices assessment demonstrated 86.25% overall conformity. Administrative Controls recorded the highest conformity (96.4%), followed by Risk Assessment (93.39%), while Emergency Preparedness recorded the lowest (78.78%). There were significant variations across Departments further underscoring the importance of continuous, Department-specific performance monitoring and evaluation.

Conclusion: The combined findings demonstrate how structured regulatory assessment, high-containment certification, institutional biorisk assessment, and continuous improvement can strengthen the systems required for responsible management of the risks posed by emerging genetic technologies. Although these assessments were not designed specifically for genetic biocontrol technologies, the lessons are transferable to emerging biological technologies that require careful consideration of biosafety, biosecurity, risk assessment, workforce competency, and institutional governance. Strengthening these foundational capabilities in African research institutions would contribute to the safe and responsible advancement of emerging genetic biocontrol technologies.

Keywords: High-Containment management, Biorisk management, Laboratory certification

33 A Risk-Pathway Framework for Biosafety Preparedness for Gene-Drive Mosquito Technologies in Namibia

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Background: Gene-drive mosquito technologies are emerging as promising complementary tools for malaria vector control in Africa. In contrast to conventional genetically modified crops, genetically modified mosquitoes require unique biosafety considerations due to their mobility, mating behavior, inheritance patterns, population-level persistence, and geographic dispersal. For self-propagating gene-drive systems, spreading an engineered trait is often an intended outcome. Consequently, risk assessment must distinguish between biological spread and adverse effects and establish scientifically plausible pathways linking the introduced genetic modification to defined protection goals and adverse endpoints.

Objective: This study introduces a risk-pathway framework designed to enhance Namibia's biosafety preparedness for prospective research involving genetically modified and gene-drive mosquitoes. The framework emphasizes problem formulation, contained research, receiving-environment characterization, regulatory readiness, and transboundary considerations.

Approach: The framework utilizes a case-by-case pathway-to-harm methodology, structured as follows: genetic construct, expressed phenotype, mosquito movement, mating, biased inheritance, population-level spread and persistence, ecological or vector-competence change, and ultimately, human-health or environmental endpoints. It differentiates between population-suppression and population-modification strategies, as these approaches vary in intended outcomes, persistence profiles, exposure pathways, and appropriate comparators. Key evidence domains include molecular characterization, inheritance and genetic stability, vector competence, mosquito fitness and mating behavior, dispersal, population genetics, ecological interactions, and receiving-environment characteristics. The framework follows a tiered development pathway, beginning with institutional and regulatory preparedness, advancing through contained laboratory or insectary studies, and progressing to more representative containment studies before considering environmental release.

Biosafety and governance considerations: The framework prioritizes uncertainty characterization, proportionate risk management, stakeholder engagement, and potential transboundary movement. For mobile genetically modified organisms, the relevant receiving environment may extend beyond the immediate experimental site and potentially cross national borders. Therefore, regional information exchange and engagement with neighboring jurisdictions are essential for responsible assessment. Gene flow, dispersal, and geographic spread are considered exposure processes rather than adverse effects; regulatory significance is established when a credible pathway links such exposure to a defined adverse endpoint.

Conclusion: Proactive development of biosafety capacity would enable Namibia to evaluate emerging genetic biocontrol technologies through evidence-based, proportionate, and case-specific approaches. Enhancing expertise in molecular

biotechnology, contained mosquito research, risk assessment, receiving-environment characterization, and stakeholder engagement would support responsible national and regional participation in future malaria vector control innovation.

Keywords: gene drive; genetically modified mosquitoes; malaria; genetic biocontrol; biosafety; risk assessment; population suppression; population modification; transboundary movement; Namibia

34 Exploring the Mosquito Microbiome for Biological Control: Putative Endosymbionts of *Anopheles gambiae* and *Anopheles arabiensis* in Uganda

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Background: The mosquito microbiome can influence mosquito biology, immunity, and interactions with malaria parasites. Several mosquito-associated bacteria have been investigated for their potential in biological control, but information on microbiome-associated bacteria of malaria vectors in Uganda remains limited. We explored bacterial communities associated with *Anopheles gambiae* and *Anopheles arabiensis* to identify putative endosymbionts of potential interest for future vector-control research.

Methods: A total of 416 adult mosquitoes were collected from four Ugandan sites—Bundibugyo, Entebbe, Kayunga, and Moroto. Of these, 295 *Anopheles* mosquitoes, comprising 216 *An. gambiae* and 79 *An. arabiensis*, were included. Mosquitoes were pooled by species and site, generating eight pooled samples. Bacterial communities were characterized using 16S rRNA gene amplicon sequencing, with ASVs inferred using DADA2 in QIIME 2. Alpha- and beta-diversity analyses and Bray–Curtis-based community comparisons were performed.

Results: Bacterial communities comprised a diverse assemblage of taxa, with Proteobacteria, Firmicutes, Actinobacteria, and Bacteroidetes among the dominant phyla. Several bacterial genera of interest to mosquito biology and biological-control research were detected, including *Asaia*, *Wolbachia*, *Serratia*, *Elizabethkingia*, *Enterobacter*, and *Pseudomonas*. Exploratory beta-diversity analysis indicated differences in bacterial community composition between pooled *An. gambiae* and *An. arabiensis* samples (Bray–Curtis PERMANOVA, $R^2 = 0.331$, $p = 0.024$). Multivariate dispersion did not differ significantly between species groups (PERMDISP, $F = 0.034$, $p = 0.719$). Alpha-diversity measures showed variation among pooled samples, but the limited replication did not support robust statistical inference regarding site-level differences.

Conclusion: This study provides an exploratory baseline characterization of bacterial communities associated with *An. gambiae* and *An. arabiensis* across four Ugandan ecological settings and identifies several putative endosymbionts of potential interest for biological-control research. The detection of taxa such as *Asaia*, *Wolbachia*, *Serratia*, and *Enterobacter* provides a basis for subsequent investigations of their persistence, host association, interactions with *Plasmodium*, and potential for paratransgenesis or other microbiome-based vector-control strategies.

35 Exploring Microsporidia for Mosquito Biological Control: 18S rRNA-Based Detection in *Anopheles gambiae* and *Anopheles arabiensis* in Uganda

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Background: Microsporidia are intracellular microorganisms associated with mosquitoes and are increasingly being investigated for their potential role in mosquito and malaria biological control. Understanding their occurrence in malaria vectors is an important first step toward identifying naturally occurring microsporidian lineages with potential biological-control relevance. This study investigated the occurrence of microsporidia in Anopheles gambiae and Anopheles arabiensis from selected sites in Uganda using molecular detection of the microsporidian 18S rRNA gene.

Methods: Mosquitoes were collected from Bundimasooli, Entebbe, Mpulya and Lusenke between August and October 2020. DNA was extracted from 24 pooled samples containing 5–11 mosquitoes per pool. Samples were screened using the Microsporidia MB primer under optimized PCR conditions targeting the 18S rRNA gene. PCR products were separated by agarose gel electrophoresis and visualized alongside a 100-bp DNA ladder, with positive and negative controls included. PCR positivity was summarized as proportions with 95% confidence intervals. Fisher's exact tests were used to explore differences in detection between mosquito species and sampling sites.

Results: Microsporidia 18S rRNA amplification was detected in 19 of 24 pooled samples (79.2%; 95% CI: 57.8–92.9%).

Positive pools occurred in both *An. gambiae* (14/18; 77.8%) and An. arabiensis (5/6; 83.3%). Site-level detection was 100% at Bundimasooli (6/6), 50% at Entebbe (4/8), 100% at Mpulya (5/5), and 80% at Lusenke (4/5). Fisher's exact testing showed no evidence of a difference in PCR positivity between *An. gambiae* and *An. arabiensis* (p=1.00). Differences among sampling sites were also not statistically significant at the 5% level (p≈0.079). The relatively small and unevenly distributed sample numbers limit the statistical power of these comparisons.

Conclusion: The detection of microsporidian 18S rRNA in a high proportion of mosquito pools from multiple Ugandan sites demonstrates the occurrence of microsporidia-associated DNA in Anopheles malaria vectors. Although species- and site-level differences were not statistically significant, the observed distribution provides a basis for further investigation of these microorganisms as potential biological-control agents. Sequencing of positive 18S rRNA amplicons will enable identification and phylogenetic characterization of the detected microsporidia. Subsequent studies involving individually tested mosquitoes, larger sample sizes, and assessment of mosquito fitness and pathogen-transmission traits will be important for determining their biological-control potential.

36 From readiness to scale: defining pathways for Wolbachia-based dengue control in Africa

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Dengue is expanding across sub-Saharan Africa, with reported cases rising ninefold across 18 African Union Member States between 2019 and 2023.[1] Yet no African country has deployed Wolbachia or established a national Aedes-specific control program. Trial evidence from Asia and Latin America demonstrates substantial reductions in symptomatic dengue[2,3] but pathways to authorize, finance, and operationalize Wolbachia in Africa remain undefined.

CHAI is conducting multi-country scoping in Senegal, Côte d'Ivoire, Ethiopia, Nigeria, and Burkina Faso to assess implementation, regulatory, evidence, and scale-up considerations through document review, key-informant interviews, and engagement with ministries, regulators, and developers.

Initial findings indicate that regulatory classification remains unresolved across all five countries. The appropriate regulatory jurisdiction, including the respective roles of biosafety and medicines authorities, is unclear, and no African authority has yet reviewed a Wolbachia release. With relevant WHO guidance and prequalification pathways still under development,[4] early decisions may need to precede global normative guidance. Burkina Faso's 2025 experience with a genetically modified mosquito release further demonstrates that regulatory authorization alone does not ensure sustained implementation.[5] Across the five countries, dengue vector-control ownership and dedicated financing remain limited, while existing systems are largely Anopheles-oriented. Regulatory readiness also varies substantially across settings, with the greatest gaps emerging in some of the highest-burden countries. Senegal presents the most advanced emerging pathway, providing an opportunity to examine the requirements for moving from trial preparation towards deployment.

The scoping suggests that the near-term constraint is therefore pathway definition, not efficacy evidence. A sequenced framework spanning regulation, program readiness, financing, and deployment could help governments assess readiness, clarify requirements for regulators, funders, and developers, and identify opportunities for regulatory harmonization and reliance.

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37 CRISPR-Cas9 based gene drive targeting the blood metabolism gene HPPD in the malaria mosquito *Anopheles funestus*

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Vector control remains the cornerstone of malaria prevention, yet increasing insecticide resistance threatens the efficacy of current interventions. Innovative control strategies, including genetic-based approaches, are being developed to enhance and complement existing vector control efforts. However, *Anopheles funestus* remains understudied, with relatively few validated genetic targets. Identifying and evaluating novel genetic targets in this major malaria vector is therefore an important step toward developing alternative control strategies. The gene encoding 4-hydroxyphenylpyruvate dioxygenase (HPPD) constitutes a key enzyme in the tyrosine degradation pathway. Here, we generated and characterised a CRISPR-Cas9-mediated gene drive line targeting the HPPD gene in *Anopheles funestus*. A genetically knockout GFP-marked line was generated by targeting the exon 2 of HPPD gene. Phenotypic, developmental, and reproductive parameters were evaluated to assess the fitness cost associated with the gene knockout in heterozygous and homozygous transgenic individuals. Subsequently, a CRISPR-Cas9-based gene drive cassette targeting the same locus was generated. Our results showed that homozygous HPPD knockout females exhibited complete mortality within 24 hours following a blood meal. There was no statistic difference in heterozygous individuals' life parameters compared to wild-type control, suggesting that *HPPD* is an haplosufficient gene. The gene drive line exhibited high transmission rate (>95%) with undetectable fitness cost on female heterozygote in both maternal and paternal lines. This study provides the first successful demonstration of a CRISPR-based gene-drive system in *Anopheles funestus* mosquito and, establishes HPPD as a strong candidate for suppression-based genetic control strategies.

Keywords: *Anopheles funestus*, genetic control, gene knockout, HPPD, CRISPR-Cas9-based gene drive

38 Awareness and perceptions of concerns on genetically modified mosquitoes in malaria control in Mali: The need for socially and culturally legitimate governance

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Background: Africa carries the highest global malaria burden, with over 90% of cases and deaths. The disease is primarily driven by the deadly Plasmodium falciparum parasite and transmitted by the highly efficient Anopheles gambiae mosquito. Sustained investment and innovation remain crucial to reducing malaria's impact on the continent. New ways of combating malaria include genetically modified mosquitoes (GMMs). However, like genetically modified organisms in general, GMMs raise concerns and governance questions that need to be addressed.

Methods: A qualitative study consisting of six focus group discussions (FGDs) was conducted in Koulikoro (rural) and Bamako (urban) in Mali. FGDs were conducted in the local language of Bamanankan, recorded, and transcribed for collaborative analysis. Data were coded manually, with themes and sub-themes extracted to address the study objectives.

Results: GMMs are increasingly promoted as an innovative tool for vector control, yet public interpretations of this technology remain unevenly understood. Deep-rooted concerns about GMMs in different demographic and behavioral groups are revealed, such as anticipated effectiveness, risk profiles, institutional trust, perceived cost, and perceived fairness. This study highlights both convergences and divergences in the governance of GMMs in community perspectives on the introduction of GMMs across gender, geographic, and experiential lines. Interpretations of GMMs vary by gender, geography, and experience, yet communities share a common set of priorities.

Conclusion: It is not enough for GMMs to be scientifically effective for them to be accepted and used by beneficiary

communities. They must also be socially and culturally legitimate and guided by governance that addresses both rational and emotional concerns. An information, education, and communication plan on GMMs needs to be developed with potentially beneficiary communities, without excluding any socio-professional strata.

Keywords: Malaria, Governance, Concerns, Genetically Modified Mosquito.

39 Deploying Sterile Insect Technologies for Precision Crop Protection

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Agragene is advancing next generation crop protection with its technology, Precision-Guided Sterile Insect Technique (pgSIT). The pgSIT technology builds on the proven traditional Sterile Insect Technique (SIT) which relies on the use of radiation to sterilize insects. pgSIT is CRISPR-based and enables for the simultaneous sexing and sterilization of the pest insect prior to releases. Agragene has advanced the development of pgSIT in the Spotted Wing Drosophila (SWD), a major small fruit pest. A series of open and enclosed field trials within the U.S. were approved and conducted with the pgSIT sterile SWD males (KNOCKOUT SWD) to demonstrate its effectiveness at controlling SWD populations in a field setting. Agragene seeks to obtain EPA product registration of the KNOCKOUT SWD sterile insects for use in the U.S. in 2027. pgSIT on new agricultural insect pest targets are currently under development at Agragene.

Keywords: Precision-guided Sterile Insect Technique (pgSIT), CRISPR gene editing, Drosophila suzukii, Insect Control Genetic insect control

40 Cyberbiosecurity Readiness in Biomedical Research Centers in Mali: A Cross-Sectional Study from Point G (2025)

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Background: Cyberbiosecurity, the integration of biosecurity and cybersecurity, aims to protect sensitive biological data. Given its growing global importance and the limited number of studies conducted in Mali, we sought to assess the current state of cyberbiosecurity at biomedical research centers in Point G.

Methods: We conducted a cross-sectional study in September and December 2025 at six biomedical research centers in Point G, Bamako, Mali. Two aspects were examined: (i) database infrastructure; and (ii) the knowledge and practices of researchers, laboratory technicians, and trainees. We obtained informed consent from each participant before including them in the study. The confidentiality and anonymity of the participants were respected. Data was collected using KoboToolbox and analyzed with Python 3.14.

Results: The study covered seven databases and 99 participants. All databases were in a secure environment, but one lacked two-factor authentication. Of the 99 participants, 14.1% had heard of cyberbiosecurity, and 1% had trained in cyberbiosecurity. Among the participants, 42.4% reused the same password, and 13.1% never locked their computers. Furthermore, locking the computer when not in use was correlated with knowledge of best practices ($p = 0.014$) and gender ($p = 0.003$).

Conclusion: Despite a secure infrastructure, the human factor remains the primary vulnerability. It is essential to implement cyberbiosecurity training programs.

Keywords: Cyberbiosecurity; Biosecurity; Biosafety; Biomedical databases; Research; Human behavior.

41 Using gene drive mosquitoes to eliminate malaria in the western equatorial coast of Central Africa

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The University of California malaria initiative (UCMI) is a not-for-profit research collaborative whose objective is to contribute to malaria elimination using a genetically modified *Anopheles* mosquito with gene drive, modifying mosquito populations so that they are incapable of transmitting the malaria parasite to humans. UCMI works with local partners to support governments' malaria elimination efforts in the western equatorial coast of Central Africa.

UCMI began working in the Gulf of Guinea, first beginning in 2019, partnering with the Island nation of São Tomé and Principe (STP), and more recently establishing a partnership with the Republic of Equatorial Guinea. Thus, the oceanic island sites were chosen based on stringent selection criteria that guarantee safe and responsible testing of gene drive mosquitoes (the presence of *Anopheles* vectors of malaria, geographic and environmental features that limit mosquito dispersal, and restricted migration between target and non-target mosquito populations). UCMI aims to deliver this technology in a responsible, sustainable and scalable fashion, in alignment with national strategies, and rooted in transparency, ethical rigor, and local ownership. The UCMI strategy is to eliminate malaria, not mosquitoes.

My presentation will focus on providing an overview of the UCMI program and the important work that has been done with local partners in preparation for conducting the first field trial with this technology.

42 Building Unified Biosafety and Biosecurity Governance for Advanced Vector Engineering in Africa: A Regulator Perspective

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Advanced vector modification strategies-such as clustered regularly interspaced short palindromic repeats (CRISPR)-based gene drives, paratransgenesis, and self-limiting genetic constructs-offer unprecedented possibilities for eliminating persistent vector-borne diseases such as malaria across Africa. However, the self propagating, highly mobile nature of these biological interventions creates complex challenges that exceed the capacity of traditional risk management systems. Addressing transboundary movement, ecological disruptions, long-term population dynamics, and dual-use biosecurity risks requires adaptive regulatory and governance structures. Assessing current governance environments across malaria-endemic African states reveals a highly fragmented regulatory landscape. Operational friction and regulatory ambiguity frequently stem from overlapping mandates among public health authorities, environmental protection agencies, and agricultural bodies. Concurrently, essential biosecurity safeguards-such as standardized facility containment, institutional biosecurity protocols, and dual-use research of concern (DURC) and ethical oversight-remain unevenly integrated into existing national biosafety laws. To address these systemic challenges, this paper introduces a tailored, harmonized governance model designed for the African context. The framework rests on four (4) core pillars: dynamic transboundary risk assessment, standardized laboratory containment and dual-use research protocols, regional policy harmonization, and structured public engagement. Ultimately, building robust, comprehensive biosafety and biosecurity ecosystem is essential to accelerating the safe deployment of life-saving vector control technologies and reducing the scourge of malaria across Africa.

Keywords: Gene drives, Biosafety governance, Biosecurity harmonization, Vector control, Transboundary risk management

43 Governance Structures for One Health Initiatives in Africa: A Comparative Analysis

Misheck Mulumba, Agnes Asagbra and Royden

Background: The success of One Health initiatives in Africa is contingent on an appropriate governance structure, yet no consensus model exists.

Methods: This paper analyses existing One Health governance models across African countries, including Ministry of Health-centric, Veterinary Services-centric, and high-level executive-anchored models (Prime Minister's / Vice President's Office). The attempt by the African One Health Network (AfOHNet) to propose a generic continental framework is also reviewed, with attention to the inclusion of environmental health stakeholders.

Results: Ministry of Health-centric structures benefit from established funding flows but risk marginalizing other sectors. Veterinary-centric models leverage animal health expertise but face similar sectoral dominance challenges. Governance anchored at the Prime Minister's/Vice President's Office promotes equity among ministries, enabling balanced convening power and resource allocation. Across all models, inadequate integration of environmental sector colleagues remains a critical gap. AfOHNet's generic model proved untenable, demonstrating that no one-size-fits-all solution exists.

Conclusion: One Health governance must be context-specific, tailored to each country's institutional systems, political economy, and inter-ministerial dynamics. The analysis provides guidance on advantages and challenges of each model to inform country-specific selection.

44 PGRRI's Farmer and Community Engagement Model: A Communication Blueprint for Emerging Agricultural Technologies.

Ama Kudom-Agyemang

Effective communication and community engagement are central to the responsible introduction of emerging agricultural technologies, especially in contexts where farmers and rural communities are key stakeholders. This presentation examines the engagement model of the CSIR - Plant Genetic Resources Research Institute (PGRRI), Ghana, highlighting how its long-standing practices in farmer outreach, participatory knowledge exchange, and community trust-building offer valuable lessons for scientists, researchers, and communicators working in emerging technology spaces. Drawing on the CSIR-PGRRI's experience in plant genetic resources conservation, seed systems, agroecology, and farmer-led innovation, the presentation distills practical strategies that have enabled the Institute to maintain credibility, strengthen relationships, and foster informed participation among diverse community groups. Through this case study, participants will gain insights into replicable communication approaches such as: culturally grounded messaging, gender-responsive engagement, transparent dialogue, and the integration of indigenous knowledge that can support responsible research and innovation. While the CSIR-PGRRI's mandate is not primarily genetic biocontrol, its engagement philosophy provides a robust blueprint for institutions navigating public perceptions of new technologies. The session ultimately demonstrates how community-centered communication models can enhance trust, reduce misinformation, and create enabling environments for science-driven solutions in agriculture and environmental management.

45 Advancing Next-Generation Precision Technologies for Invasive Insect Control

Marc Schetelig
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For decades, genetic sexing strains (GSS) have been among the most powerful enabling technologies of the Sterile Insect Technique (SIT), allowing efficient male-only releases that improve operational efficiency and reduce production costs. Their development, however, has traditionally relied on rare spontaneous mutations, extensive classical breeding and species-specific genetic architectures. The globally deployed Mediterranean fruit fly GSS illustrates both the remarkable success and the limitations of this approach: they transformed operational SIT programmes worldwide, yet the molecular basis of their key traits remained unresolved for decades. We present the scientific journey from deciphering these classical strains to rebuilding genetic sexing as a modular, transferable engineering platform. Identification of the molecular basis of the temperature-sensitive lethal (tsl) phenotype, together with molecular characterization and genomic rescue of the white pupae (wp) marker, transformed historically selected mutations into defined genetic components. These discoveries enabled the development of neoclassical Mediterranean fruit fly strains in which selectable markers, conditional lethality, chromosomal linkage and genetic rescue can be rationally designed and optimized. This transition from phenotype-driven selection to molecular engineering fundamentally changes genetic sexing strain development. Instead of relying on chance mutations, strain architectures can now be built around conserved genetic targets, engineered rescue elements and species-specific sex-determination pathways. The Medfly, therefore, serves not only as one of the most successful SIT target species but also as a blueprint for developing next-generation GSS for other economically important pests and disease vectors. We are now translating this framework to species like Drosophila suzukii and Aedes species by combining conserved LysRS-based temperature sensitivity with visible markers and sex-specific rescue strategies. Together, these advances establish a scalable platform that links fundamental discoveries in insect genetics with practical technologies for sustainable pest and vector management, accelerating the development of robust genetic sexing strains for future agriculture, public health and global biosecurity.

Keywords: Genetic Biocontrol, Genome Engineering, SIT, genetic sexing strains

46 Genome Editing of Egg Allergens: Development of Hypoallergenic Layer Chickens via Platinum TALEN technology

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Egg allergy is among the most common food allergies affecting infants and children worldwide, driven primarily by a small number of dominant egg-white allergen proteins such as ovomucoid with heat tolerance. This presentation describes a project applying targeted genome editing to reduce or eliminate expression of allergen genes in layer chickens, retain normal nutritional and functional properties while substantially lowering their allergenic potential.

We discuss the strategy for selecting and validating target genes based on their relative contribution to clinical allergenicity, the editing approach and delivery method used in primordial germ cells or embryos, and preliminary results on allergen protein reduction. We also touch on the regulatory pathway relevant to eventual commercialization, noting that Japan's notification-based framework for genome-edited food and food additives — under which products without residual foreign DNA can proceed via simple notification rather than full safety review — offers one comparatively efficient route to market, alongside the different regulatory requirements in other target jurisdictions.

This work illustrates how precision genome editing can directly address a persistent public health and food-safety challenge, and highlights the cross-border technical and regulatory coordination required to bring such hypoallergenic animal products from laboratory validation to commercial availability.

47 Assessment of Male Mating Competitiveness of Genetically Modified MMCP *Anopheles gambiae* against Wild-type Males under Laboratory Conditions

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

48 From laboratory capacity to environmental readiness: building African systems for innovative mosquito control technologies in Burkina Faso

Hamidou Maiga, Inoussa Toe, Mahamadi Kientega, Nouhoun Traore, Jeremy Bouyer Alessandra Lanfrancotti, Tony Nolan, Abdoulaye Diabate

Vector control has contributed substantially to reductions in malaria transmission in sub-Saharan Africa. However, widespread insecticide resistance, changing epidemiological patterns, and rapid environmental change increasingly threaten the effectiveness and sustainability of existing interventions. Innovative approaches, including gene drive-based genetic technologies, therefore need to be accompanied by strengthened local scientific capacity and robust entomological and environmental surveillance systems.

Future evaluation and deployment of these technologies will require baseline data to characterise vector populations, their habitats, and associated biological communities, alongside monitoring systems capable of detecting and interpreting potential changes following an intervention.

In Burkina Faso, capacity-building and environmental monitoring activities have been progressively established to support readiness for the potential future evaluation of gene drive mosquitoes. Investments have strengthened laboratory and

insectary infrastructure, as well as molecular, genetic, and entomological expertise. Students and researchers from Burkina Faso have received specialised training at the Liverpool School of Tropical Medicine and the University of Cambridge in mosquito genome editing and generating transgenic mosquito lines, contributing to the development of national expertise in genetic vector control technologies. In parallel, field studies are establishing ecological baselines through longitudinal monitoring of mosquito populations, characterising larval habitats, and assessing associated aquatic communities, including non-target organisms.

These activities demonstrate the feasibility of implementing integrated entomological and environmental monitoring in operational field conditions and provide insights into the spatial and temporal variability of mosquito populations and their associated biological communities. Such baseline data are essential for distinguishing natural ecological variability from potential changes following future interventions.

This platform also offers opportunities to integrate complementary approaches, such as environmental DNA (eDNA) and genomic surveillance, to enhance the sensitivity and robustness of monitoring. Together, strengthened local capacity and comprehensive baseline surveillance provide a foundation for evidence generation, environmental risk assessment, and the responsible evaluation of gene drive and other innovative mosquito control technologies in Africa.

49 From Capacity Building to African-Led Innovation: ACEME Establishes Genetic Engineering Capability for Malaria Vector Research in Mali.

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Background: Genetic responsible development requires strong African scientific capacity, appropriate infrastructure, and the ability to generate and evaluate locally relevant evidence. ACEME (African Center for Excellence in Molecular Engineering), established at the University of Sciences, Techniques and Technologies of Bamako (USTTB), was created to place African scientists at the centre of this emerging field.

Progress and Results: Through sustained investment in human capacity, laboratory infrastructure, regulatory readiness, and international and South-South collaboration, ACEME has progressed from capacity building to the independent implementation of advanced genetic engineering work in Mali. A major milestone was achieved with the successful development, under contained laboratory conditions, of a transgenic Anopheles mosquito strain carrying a fluorescent marker. ACEME reports this achievement as a first in Mali and the wider West African region.

This milestone demonstrates that advanced mosquito genetic engineering workflows, including construct preparation, embryo microinjection, screening, and subsequent maintenance and characterization, can be established and implemented by an African research team within an appropriately equipped and regulated institution. The achievement builds on a longer-term capacity-strengthening pathway involving training, mentorship, infrastructure development, and collaboration with international and African partners.

Leadership and Significance: Beyond the generation of a transgenic mosquito strain, the ACEME experience demonstrates a broader model for African scientific leadership in emerging genetic biocontrol technologies: building expertise locally, retaining technical knowledge within African institutions, strengthening regulatory and biosafety capacity, and creating platforms through which these competencies can be shared regionally. ACEME is now positioned to further develop its research and training portfolio and to contribute to a growing African ecosystem capable of evaluating genetic vector-control approaches responsibly.

Conclusion: The ACEME experience illustrates how sustained capacity building can translate into tangible scientific capability and African-led innovation. The next step is to consolidate this platform, expand regional training and collaboration, and strengthen the evidence and institutional capacity needed to support informed and responsible decision-making on emerging genetic vector-control technologies.

50 Generation and characterisation of genetically modified *Anopheles funestus* mosquitoes expressing antimicrobial peptides

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Malaria is a life-threatening disease transmitted to humans through the bites of infected female *Anopheles* mosquitoes and remains a major cause of mortality, particularly in Africa. Current prevention strategies rely largely on mosquito control, primarily through insecticide-based interventions. However, the rapid emergence of insecticide resistance in mosquito populations highlights the urgent need for alternative approaches. One promising strategy involves genetically modified mosquitoes that are refractory to malaria parasites, enabling population modification through the spread of anti-parasitic transgenes. This study aimed to generate, for the first time, genetically modified *Anopheles funestus* mosquitoes using the PiggyBac transposon system, which allows semi-random insertions and therefore robust effector function regardless of genomic insertion site. In parallel, we evaluated the ability of a putative carboxypeptidase A1 promoter to drive midgut-specific expression of two antimicrobial peptides, Magainin and Melittin, to ensure maximum efficacy against midgut stages of parasite development. To reach this objective, we first identified putative carboxypeptidase A1 promoter and terminator sequences in *An. funestus* using an in silico approach based on available genomic data. We then constructed a piggyBac donor plasmid containing the two antimicrobial peptide genes under the control of the selected promoter. We successfully generated several transgenic mosquito lines, demonstrating that piggyBac can mediate germline transformation in this species, with an overall transformation efficiency of approximately 7.8%. Molecular characterization confirmed that insertions occurred at canonical TTAA sites, consistent with piggyBac-mediated transposition. We also showed that the *An. funestus* carboxypeptidase A1 promoter can drive midgut-specific expression of a fluorescent marker following a blood meal. In conclusion, these findings provide an important foundation for future genetic and vector biology research, particularly for developing population replacement strategies using gene drive technologies in this major malaria vector.

Keywords: *Anopheles funestus*; genetic modification; antimicrobial peptides; Magainin-2; Melittin; malaria-refractory mosquitoes.

51 Development of transgenic cytoplasmic incompatibility based on wAnD *cif* genes in *Anopheles gambiae* G3

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Background: *Wolbachia,* invade its host through cytoplasmic incompatibility (CI), a conditional sterility resulted in crosses between infected males and uninfected females. Two genes, *cifA* and *cifB* are responsible for the cytoplasmic incompatibility phenotype. CI is a very promising alternative method in dengue control. However, *Wolbachia* strain which induces cytoplasmic incompatibility is not known to infect Anopheles natural population.

Objective: Here, we aimed to develop transgenic cytoplasmic incompatibility in *Anopheles gambiae G3* based on *w*AnD (*Wolbachia anopheles demeilloni*) *cif* genes, *Wolbachia* strain which naturally infect *anopheles demeilloni*.

Method: To achieve these objectives, we designed *silico* 04 different donor constructs based on piggyBac system with *cif* genes. The *cifA* was under *vasa* and *cifB* under *ß2 tubulin* and 2 muted version of *ß2 tubulin* promoter at -271 and -244 referred to the start codon. RFP and YFP markers were respectively used for *cifA* and for *cifB* constructs. Each donor construct and a helper plasmid with the transposase gene controlled by *vasa* were co-injected in *Anopheles gambiae G3* freshly laid embryos. We performed inverse PCR followed by sanger sequencing and qPCR to characterize cif lines and quantify cif expression level. In addition, fertility assays were performed to analyse the ability of *w*AnD *cif* expression to recapitulate transgenic CI.

Results: *w*AnD *cif* transgenic lines with different integration sites were successfully generated. It seems that *w*AnD *cif* genes expression recapitulates transgenic CI in *Anopheles gambiae* G3.

Conclusion: Our work will report for the first time that the transgenic expression of *cif* genes from *Wolbachia* strain *(w*AnD) which naturally infect Anopheles recapitulates transgenic CI in *Anopheles gambiae G3*. These will pave the way for the development of new approaches for malaria vector control based *Wolbachia cif* genes such as the transgenic incompatibility technique and cif-gene drive combined with anti-plasmodium peptides.

Keywords: *Anopheles gambiae*, *cif*, *Wolbachia*, malaria, vector control.

52 Readiness for Emerging Genetic Biocontrol Technologies: An Institutional Readiness Profile for KEMRI

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Genetic biocontrol technologies are advancing rapidly and offer new opportunities for vector control and public health. As these technologies move from laboratory research towards contained studies and field evaluation, research institutions need to be prepared not only scientifically, but also in the people, infrastructure, governance and biorisk management systems required to support their safe and responsible development.

This presentation examines the readiness of the Kenya Medical Research Institute (KEMRI) to support research and capacity development in emerging genetic biocontrol technologies. The readiness profile considers key institutional domains including scientific and technical expertise, workforce capacity, laboratory and containment infrastructure, biosafety and biosecurity systems, institutional oversight, training capacity, regulatory interfaces and national and international partnerships.

KEMRI has an established platform in biomedical and vector research upon which capacity for emerging genetic biocontrol technologies can be strengthened. The readiness assessment considers how these existing capabilities can be leveraged, while identifying areas requiring further development, particularly specialized competencies, appropriate containment infrastructure, institutional biorisk management systems and sustained training and partnerships.

The KEMRI experience provides a practical case for considering what institutional readiness for genetic biocontrol should entail in Africa. Rather than waiting until technologies are ready for advanced testing, scientific capacity, workforce development, governance and biorisk management should be strengthened alongside the research. An institutional readiness approach can help identify existing strengths, define gaps and guide targeted investments needed to enable African institutions to participate safely and meaningfully in the development and evaluation of emerging genetic biocontrol technologies.

Keywords: *Genetic biocontrol; institutional readiness; capacity building; biorisk management; biosafety; biosecurity; vector control; Africa*

53 Burkina Faso National IVM platform: What's the future following the premature termination of Target Malaria project?

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A multisectoral and multi-level approach that addresses health, environmental and social factors influencing vector-borne diseases is important for effective management. Burkina Faso is a key country in the genetic based vector control (GBVC) space, as the country has established since 2018 a national multisectoral Integrated Vector Management (IVM) platform consisting of various stakeholders including governmental and non-state actors engaged in policy formulation, research and development, regulatory functions, communications, and community governance to ensure evidence-based decisions are made on GBVC technologies.

Following the premature termination of the Target Malaria project in August 2025, the National IVM platform continues to implement activities in the country related to innovative technologies against vector born disease. Activities including stakeholders' meetings, reference documents development, targeted communication with the several radio shows covering malaria, dengue and innovative technologies, training on risk assessment and biosafety oversight, … have been conducted during this sensitive period to increase population awareness, share scientific information and evidence and reinforce local capacity for regulators. Adaptative management, protection of stakeholder relationships, restoration of technical dialogue and maintenance of national capacity have been the key words for the IVM platform during this sensitive period.

The Burkina Faso IVM Platform is positioned as a national risk-governance and coordination mechanism, not merely as an activity-delivery structure. In the present national context, its strategic value lies in maintaining a neutral, science-

based space for dialogue among health, biosafety, environment, research, ethics, communication and community actors; preserving institutional memory following the disruption of the Target Malaria project; and supporting evidence-informed decision preparedness for genetic based vector control tools and other emerging biotechnology applications.

54 Building African Capacity for Mosquito Control and Elimination Through PAMCA Networks: Integrating Conventional Approaches and Emerging Technologies

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Pan-African Mosquito Control Association -Kenya Chapter

Introduction: Africa continues to bear a disproportionate burden of mosquito-borne diseases, particularly malaria, as the epidemiology and ecology of mosquito vectors are rapidly changing. Sustaining progress toward malaria control and elimination and addressing other mosquito-borne diseases require strong African capacity to generate evidence, adapt technologies, implement interventions, and guide policy. Capacity building is therefore central to sustainable, locally led mosquito control across the continent.

The Pan-African Mosquito Control Association (PAMCA) provides a continental platform for strengthening this capacity through its network of African scientists, public health practitioners, national programs, academic and research institutions, policymakers, and partners. PAMCA's networks can develop the next generation of African vector-control leaders through training, mentorship, professional exchange, collaborative research, institutional strengthening, and the sharing of knowledge and best practices across countries and regions.

Methods: Capacity building must encompass both conventional mosquito-control approaches, including entomological surveillance, insecticide-treated nets, indoor residual spraying, larval source management, environmental management, insecticide-resistance monitoring, and integrated vector management, and emerging technologies, including genetically modified mosquitoes, gene-drive approaches, Wolbachia and other endosymbiont-based strategies, classical biological control, novel genetic and molecular tools, digital surveillance systems, and artificial intelligence. Importantly, emerging technologies should complement, not replace, effective conventional interventions, and their adoption must be supported by appropriate biosafety, regulatory, ethical, community-engagement, and risk-assessment capacity.

Results: PAMCA can serve as a continental capacity-building and innovation network, linking centers of excellence and emerging institutions across Africa and creating pathways for African scientists to develop expertise in molecular biology, genetics, genomics, bioinformatics, vector ecology, modeling, technology assessment, regulatory science, community engagement, and implementation research. Such networks can reduce reliance on external expertise, promote South–South collaboration, and ensure that technologies developed in Africa are evaluated and adapted to African ecological, epidemiological, regulatory, and social contexts.

Conclusion: Build a strong, connected, Africa-led PAMCA network to provide the human and institutional foundation needed to accelerate mosquito control and elimination, responsibly harness emerging technologies, and translate scientific innovation into sustainable public health impact across the continent.

55 CRISPR/Cas Mediated Genome Editing, A Novel Tool in the Areawide Insect Pest Management: Potentials and Prospects from India Perspective

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It is the continuous human endeavor to looking for newer, safer avenues to mitigate the pestilence inflicting serious concerns for the wellbeing and economic returns. This unsatiated inquiry has witnessed several new approaches being tested, validated and put to final use. In this regard, insects as pest of crops, vectors of crop and human & animal pathogens pose a great challenge in their containment. In this regard, synthetic chemicals have long been the main stay in their management albeit their negative impact on the environment. This requires identification, development and deployment of new and novel genetic biocontrol tools such as CRISPR/Cas mediated genome editing for its application in agricultural, public health, medical research. In this regard the advent CRISPR/Cas has revolutionized the way we are enabled to make locus/loci specific, random mutations, generally aimed at loss-of-function of the target gene. These CRISPR/Cas mediated mutations are regulated at three levels such as SDN1, SDN2 and SDN3 and the first two levels of genome editing have been recognized as safe for environmental release in many countries as the frequency and nature of mutations are considered to be equivalent to the mutations caused in nature. In our lab we have carried out loss-of-function of several key genes in the insect development, coloration, sex ratio, male sterility etc in various species of insect pests mainly through the embryonic delivery of ribonucleoprotein of the target genes. The study species include fall armyworm, *Spodoptera*

frugiperda; diamondback moth, *Plutella xylostella*; egg plant shoot and fruit borer, *Leucinodes orbonalis*; Oriental fruit fly, *Bactrocera dorsalis*; melon fly, *Zeugodacus cucurbitae*; sweet potato whitefly, *Bemisia tabaci*; pod borer, *Maruca vitrata* etc. We have also demonstrated for the first time the use of ribonucleoprotein mediated precision editing using prime editor 3b in editing the eye color gene of *S. frugiperda* and the non-embryonic editing in *B. tabaci*. With reference to the Indian context, biosafety guidelines are already made available for transgenic insects for research purpose. With reference to insect genome editing, standard operating procedures are being formulated for further consultation and operationalization and cross learning. In this regard, CRISPR/Cas mediated genome editing will definitely lead to successful development of suitable gene drive methods such as homing gene drive, split homing gene drive; Cas12a based reversable, containable gene drive, all that follow the non-mendelian way of inheritance. The recent emphasis given for genetic biocontrol of mosquitoes, spotted wing Drosophila in the USA will propel a new wave of interest in application of this technology in the areawide management of agricultural pests such as fruit flies, red palm weevil, pink boll worm etc. India being a biodiversity hot spot, CRISPR/Cas mediated genome editing offers a safe and effective way of insect pest management without interfering environment and biosafety.

56 **Genome-Editing Technologies for Productive, Healthy and Climate-Resilient Tropical Livestock**

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Tropical livestock, particularly buffalo, is vital for food security, rural livelihoods and sustainable animal production worldwide. However, conventional genetic improvement is relatively slow and may not adequately address emerging challenges related to productivity, animal health and climate change. We integrates advanced animal cloning and CRISPR-mediated genome editing to develop precision approaches for genetic improvement and conservation of tropical livestock. Our studies established and applied somatic cell nuclear transfer (SCNT) for multiplication of elite buffalo germplasm and conservation of valuable genetic resources. Building on this foundation, we have integrated genome editing with SCNT to introduce targeted traits of economic, nutritional and health significance. A major focus has been myostatin (MSTN) gene editing to enhance muscle growth and production efficiency. We established a CRISPR–SCNT pipeline for generating MSTN-edited buffalo embryos and successfully produced an MSTN-knockout buffalo, demonstrating the potential of precision editing for improving meat-production traits. In parallel, we developed targeted editing of β-lactoglobulin (BLG) to modify milk protein composition. The next phase focuses on multiplex genome editing and combining production, health and adaptation traits within genetically valuable indigenous livestock. Particular emphasis will be placed on heat tolerance, disease resilience, feed efficiency, metabolic fitness and adaptation to tropical climatic stressors. Thus, our research is progressing from "cloning the best" to "precision editing of the best." The integration of cloning and CRISPR genome editing offers a powerful platform for developing productive, healthy, climate-resilient and genetically sustainable tropical livestock production.

Keywords: Genome-editing, Muscle growth, β-lactoglobulin (BLG)-free milk, and multiplex genome editing

57 **Natural dynamics of *Serratia marcescens* and *Enterobacter cloacae* in the *Anopheles gambiae* midgut: implications for paratransgenic malaria control**

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Blood feeding alters the mosquito gut microbiota and influences vector competence. Members of *Enterobacteriaceae* residing in the mosquito midgut show proliferation 24 hours post blood meal. However, studies that have demonstrated this have often relied on antibiotic-treated mosquitoes and have re-introduced high bacterial loads to assess their anti-plasmodial potential. This design limits the observation of inter-bacterial dynamics and may lead to over-representation of microbial effect, presenting a critical knowledge gap for microbial-based vector control strategies. In this study, we employed a time-course experiment to investigate the natural dynamics of *Serratia marcescens* and *Enterobacter cloacae*, two members of *Enterobacteriaceae* with anti-plasmodial properties, in the midgut of wild *Anopheles gambiae* mosquitoes following a blood meal, and after introduction of bacterial cells into the mosquito midgut through a sugar-meal. Absolute quantitation of bacteria was achieved with standard curves and qPCR. We show that *S. marcescens* abundance in the mosquito midgut peaks at approximately 12 hours post blood meal, increasing by ~87-fold from 1.5 × 104 to 1.3 × 106 CFU/

mL (p = 0.022). A generalized additive mixed model (GAMM), which accounts for temporal smoothing, predicted a slightly later peak at approximately 19 hours post blood meal whilst *E. cloacae* showed no significant increase. After introducing 1000X the load earlier observed, the concentration of S. marcescens at 12hrs post-blood meal was maintained at 1.01 ×106 CFU/mL. These findings suggest that, prior to traversal of the midgut wall by *Plasmodium* ookinetes, *Serratia*, but not *Enterobacter*, proliferates naturally following blood feeding, and that bacterial load is tightly controlled by the mosquito midgut physiological factors. Understanding the molecular and transcriptomic basis of this regulation is key to developing stable, ecologically relevant bacteria-driven paratransgenic strategies for malaria control. Accordingly, omics approaches will be used to analyse *Anopheles gambiae* mosquitoes responses following supplementation with these symbionts.

Keywords: *Anopheles gambiae*, mosquito midgut, *Serratia marcescens*, *Enterobacter cloacae*, paratransgenic, malaria control, transcriptomics.

58 Potential of VectorGrid-Africa mosquito observatories as a platform for monitoring genetically modified mosquitoes and their environmental effects

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Background: Responsible evaluation of genetically modified mosquitoes, including those carrying gene drives, requires evidence on local vector populations and ecological conditions before and after any authorised release. Fragmented, short-term surveillance limits the baselines needed to interpret changes in mosquito populations, disease transmission and the wider environment.

Methods: VectorGrid-Africa is establishing a locally owned network of permanent mosquito observatories across Kenya, Madagascar, Mozambique, South Africa and Tanzania. Standardised monthly sampling and seasonal surveys will integrate mosquito abundance, species composition, host feeding, pathogen detection and genetic variation with climate, land use and vector-control data. Planned genomic analyses will characterise population structure and gene flow, supported by in-country analytical capacity and specimen archives. Non-mosquito bycatch will be preserved for future studies of arthropod diversity.

Implementation and relevance: Early implementation has focused on observatory design, standardised protocols, site selection and data governance. Adaptable molecular workflows could incorporate validated assays for specific genetic constructs, supporting monitoring of their occurrence and spread following authorised releases. Repeated sampling could document changes in target and other mosquito species. With suitable comparison sites, longitudinal data could help distinguish intervention-associated changes from seasonal variation and concurrent environmental or vector-control changes. Broader environmental assessment would require targeted ecological studies alongside routine surveillance. Monitoring priorities and reporting responsibilities should be agreed with regulators, developers and affected communities, with local data stewardship and access for independent scrutiny.

Conclusion: VectorGrid-Africa could provide shared infrastructure for baseline characterisation and long-term monitoring of genetic mosquito control. Early collaboration can help define detection requirements and ecological indicators so that surveillance generates evidence relevant to environmental risk assessment and decisions about future use.

Keywords: VectorGrid-Africa; gene drive; genetically modified mosquitoes; environmental monitoring; genomic surveillance; governance

59 Prospects and limitations of *Anopheles gambiae*-based gene drives for malaria control in Eastern and Southern Africa

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Background: Gene drives targeting *Anopheles gambiae* sensu stricto could contribute to malaria control in Eastern and Southern Africa, where transmission involves several vector species. Their potential public-health value depends on the target species' contribution to transmission, local ecological conditions and the effectiveness of other interventions.

Approach: We conducted a narrative synthesis of entomological and population-genomic evidence to examine the opportunities and limitations of *An. gambiae*-targeted population suppression and modification. We considered species-specific infectious biting, changing vector composition, population connectivity, target-site variation and gene flow among sibling species.

Findings: The reviewed evidence indicates substantial spatial and temporal variation in the contributions of *An. gambiae*, *An. arabiensis* and *An. funestus* to transmission. Documented declines in *An. gambiae* coexist with local persistence and resurgence, supporting evaluation where it remains important or could regain importance as control conditions change. Continued transmission by other vectors may constrain overall benefits. Population connectivity and seasonality can influence drive spread and persistence, while target-site suitability requires separate genetic assessment. Evidence of gene flow among sibling species warrants assessment of both efficacy and biosafety; it does not establish reliable extension of control to *An. arabiensis*. *An. funestus* lies outside the *An. gambiae* complex and requires separate control approaches. Possible ecological compensation following suppression remains uncertain and should be investigated through longitudinal surveillance.

Conclusion: *An. gambiae*-targeted gene drives merit evaluation within locally appropriate malaria-control programmes. Site selection should consider contemporary species-specific transmission, plausible future changes and the distinct implications of suppression and modification. Entomological and genomic surveillance, sustained community engagement and transparent communication of expected benefits and uncertainties are needed to support ethical evaluation. Additional approaches targeting *An. funestus* and *An. arabiensis* remain important research priorities.

Keywords: Gene drive; *Anopheles gambiae*; malaria; vector ecology; population genomics; Eastern and Southern Africa

60 Evaluation and regulation of *Aedes aegypti* mosquitoes infected with the Wolbachia bacterium: Anvisa's (Brazil) experience and learned lessons

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Background: The introduction of Aedes aegypti mosquitoes inoculated with the Wolbachia bacterium is an effective method for controlling arboviral diseases, significantly reducing case incidence and hospitalizations. This experience report describes how the National Health Surveillance Agency (Anvisa) structured and conducted the evaluation and regulation of the Wolbachia method as a complementary strategy for controlling arboviruses in the country.

Methods: The work carried out by Anvisa required a multidisciplinary team and the temporary classification of the product - first as a pesticide and subsequently as a sanitizing product - in order to guide the initial safety and efficacy requirements. Temporary and exceptional mechanisms were used to authorize the use of the method in Brazil.

Experience Report and results: Anvisa's initial action took place in 2014, involving the granting of a Special Temporary Registration for the product on an experimental basis and for limited use. In 2022, exceptional authorization was granted for the implementation of the method, utilizing domestic production. Approval was contingent upon the submission of epidemiological data. Since then, the use of the method has expanded, with two biofactories established in the country. Key challenges included difficulties regarding the regulatory framework; the need for agile mechanisms to respond to disruptive technologies; the monitoring of national and international experiences to inform decision-making; and the definition of roles and collaborative engagement between the Agency and the Ministry of Health, which coordinates the national strategy for arbovirus control and epidemiological surveillance activities in the country. Concurrently, Anvisa is conducting a Regulatory Impact Analysis to support future regulations on the subject

Conclusions: Dynamic and adaptive regulatory processes and shared responsibility among various national institutions were necessary to ensure the method was implemented gradually and safely, subject to continuous evaluation. The conclusion of the Regulatory Impact Analysis will be another important step that will guide future regulatory actions.

61 More than a decade of feasibility research on the Sterile Insect Technique for *Anopheles arabiensis* in South Africa: progress, challenges, and future directions

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Residual malaria transmission remains a major challenge to malaria elimination in South Africa, partly because *Anopheles arabiensis*, an important malaria vector, exhibits substantial outdoor biting and is less effectively targeted by conventional indoor-focused vector control interventions. The Sterile Insect Technique (SIT) is being investigated as a complementary strategy for targeting outdoor-biting populations. This talk will review over a decade (2010–2026) of research undertaken to assess the feasibility of implementing SIT against *An. arabiensis* under South African settings. The programme followed a phased approach, progressing from assessments of national technical capacity and pre-feasibility studies to a small-scale open-field trial. Key achievements include the establishment of local mosquito colonies; generation of entomological baseline data, including mark–release–recapture estimates of mosquito population size; development of irradiation protocols; construction and operationalisation of Africa's first mosquito mass-rearing facility; and implementation of a knowledge, attitudes, and practices survey that informed community engagement strategies. The presentation will also focus on a sustained small-scale field trial in Mamfene, KwaZulu-Natal, that demonstrated the operational feasibility of sterile-male releases and provided preliminary evidence of entomological effects. Discussions on the progress has been in mass-rearing, irradiation, handling, transportation, field release and community engagement. Lastly the operational, regulatory, and social experience gained will be presented and how this will provide a foundation for evaluating SIT as a potential addition to existing malaria elimination efforts in South Africa and other low-transmission settings, including how this may inform future development of other genetic-based vector control technologies.

62 From genetic sexing to field release: An integrated, quality-assured production and deployment platform for *Anopheles arabiensis* within the South African sterile insect technique (SIT) programme

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Translating genetic biocontrol technologies from laboratory development to field implementation requires integration of biological, production and logistical processes that maintain product quality throughout the deployment pathway. We describe the development and operationalisation of an integrated production-to-release platform for *Anopheles arabiensis* within the South African sterile insect technique (SIT) programme. The platform integrates genetic sex separation, mass

rearing, X-ray sterilisation, fluorescent marking, quality assurance and quality control (QA/QC), packaging, long-distance transport and field release.

Stage-specific QA/QC criteria were established to monitor colony performance, development, adult quality, sex separation, irradiation and delivery. Production targets incorporated anticipated losses across processing stages and were scaled to support field releases maintaining an approximate 10:1 sterile-male-to-wild-male ratio across the 48-ha release area. A target of ⩾98% male purity was applied before irradiation, while ⩾85% pupation and ⩾90% adult flight ability were used as key production-quality benchmarks. X-ray irradiation was standardised around a 100–120 Gy target, supported by Gafchromic® film dosimetry. A custom 3D-printed irradiation system achieved a dose-uniformity ratio of 1.06 and enabled processing of approximately 180,000 adults per batch; 259,948 males were subsequently sterilised to support the release programme. Following marking and recovery, sterile males were transported approximately 500 km by road under monitored environmental conditions to field release sites in KwaZulu-Natal.

This experience demonstrates that the principal challenge in *Anopheles* SIT is not optimisation of individual technologies alone, but their reliable integration into a quality-assured production and deployment system. The South African programme provides practical lessons for scaling genetic control of malaria vectors from laboratory and semi-field development towards sustained field implementation in Africa.

Keywords: Malaria vector control; residual transmission; sterile male release; mass rearing; genetic control

63 Assessment of Containment Effectiveness and Dissemination Risk of Genetically Modified Mosquitoes in a Containment Facility in Mali

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Mosquitoes are the deadliest animals in the world because of their role in transmitting diseases such as malaria, which remains a major public health challenge in Mali and across sub-Saharan Africa. Despite significant advances in vector control, the limitations of existing strategies highlight the need for innovative approaches, including the use of genetically modified mosquitoes (GMMs). While promising, throughout their development, these technologies require rigorous biosafety and biosecurity measures to minimize the risk of accidental release into the environment.

This study aimed to assess the effectiveness of the containment system of the transgenic laboratory at the Infectious Diseases and Medical Entomology Research and Training Center (IDMERTC), an Arthropod Containment Level 2 (ACL-2) facility. Weekly entomological surveillance was conducted both inside and outside the containment facility over a seven-year period to evaluate the potential risk of mosquito escape and environmental dissemination.

The results revealed a high predominance of *Anopheles gambiae* s.l. within the containment facility, confirming the successful maintenance and control of experimental mosquito colonies. In contrast, mosquito collections outside the facility were largely dominated by *Culex* spp., reflecting the natural composition of local mosquito populations. No evidence of significant dissemination of laboratory-reared mosquitoes into the surrounding environment was detected during the study period.

Overall, these findings demonstrate the effectiveness of the containment system and indicate an extremely low risk of environmental release. The study highlights the importance of continuous entomological surveillance as a key component of biosafety and biosecurity programs. Furthermore, it provides support for the safe development and application of innovative biotechnologies based on genetically modified mosquitoes as part of integrated malaria control strategies.

Keywords: Genetically Modified Mosquitoes, Biosafety, Containment, Entomological Surveillance, *Anopheles gambiae*.

64 Challenges of Acceptance of Biotechnology and Emerging Biotechnology in Africa and Solutions

Rufus Ebegba

The acceptance of biotechnology and emerging biotechnology remains low in Africa despite its potential to address food insecurity, health challenges, and environmental degradation. This paper examines the challenges hindering the low acceptance of biotechnology and emerging biotechnology in Africa and proposes sustainable solutions. The paper is motivated by the slow adoption of innovations such as genetically modified crops, gene editing, synthetic biology, and bio-manufacturing, even as African countries face poor economy, poor agricultural practice, climate change and population pressure.

The paper adopts qualitative desktop research relying on information from reports journals, and policy documents. Findings reveal that the major challenges include poor public awareness, inadequate political will from governments, misconceptions, weak regulatory frameworks and enforcement, inadequate scientific infrastructure and funding, cultural and ethical resistance, distrust of foreign multinational companies, and limited capacity of public administrators to coordinate stakeholders.

Safe and transparent deployment of biotechnology are critical to sustainable food security and wealth creation in Africa. Strengthening biosafety regulatory institutions, investing in human capital and public enlightenment, promoting participatory policy formulation involving farmers, traditional leaders and religious institutions, encouraging indigenous biotechnology research, and developing clear benefit-sharing models for smallholder farmers and SMEs are critical to acceptance of biotechnology and emerging biotechnology.

65 Advances in the development of a Microsporidia MB endosymbiont-based Plasmodium transmission-blocking strategy

Jeremy Herren

We have established the SYMBIOVECTOR project to investigate the prospect of deploying a recently discovered Anopheles symbiont, Microsporidia MB, as a Plasmodium transmission blocking tool. The ability of Microsporidia MB to block Plasmodium transmission together with vertical transmission and avirulence makes it an excellent candidate for symbiont-based transmission blocking. We show that a vertically transmitted microsporidian symbiont (Microsporidia MB) in the *An. gambiae* complex can impair Plasmodium transmission in the laboratory and field. Microsporidia MB is present at moderate prevalence in geographically dispersed populations of An. arabiensis in Kenya, localized to the mosquito midgut and ovaries, and is not associated with significant reductions in adult host fecundity or survival. We investigated the mechanistic basis and efficiencies of Microsporidia MB transmission between *Anopheles arabiensis* mosquitoes. We show that Microsporidia can be transmitted both vertically (mother to offspring) and sexually between adult mosquitoes. The dynamics of spread and optimal dissemination strategies have been investigated under semi-field conditions and used to determine the likely outcomes of releasing Microsporidia MB in the field.

66 Optimizing the flight propensity as an easy quality control test for mass-reared tsetse fly *Glossina brevipalpis*

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[*]Correspondence: D.T.Barro@iaea.org>Assessing the quality of mass-reared insects prior to their release in area-wide integrated pest management programmes that incorporate the Sterile Insect Technique, is essential for the success of these interventions. Male insects intended for release must undergo regular quality control assessments both in the rearing facilities and in the field. Therefore, simple, reliable and easy-to-perform quality control tests are highly desirable. In this study, flight cylinders of different dimensions were used to evaluate the flight ability of irradiated (120Gy) and non-irradiated (0Gy) of *Glossina brevipalpis* males by measuring their escape rate. Three experiments were conducted to assess five flight tube heights 10, 15, 20, 25, 30 cm and three diameters 5, 7.3, 9 cm. The flight propensity of the irradiated males was successfully differentiated from that of the non-irradiated males using a flight tube hight of 25 cm and a diameter of 5 cm. Survival under stress conditions further confirmed the flight test results, demonstrating that radiation at 120 Gy negatively affected the quality of *G. brevipalpis* males. Based on these findings, a flight tube height of 25 cm and a diameter of 5 cm are recommended as the optimal parameters for a laboratory quality control flight test for *Glossina brevipalpis*.

Keywords: Sterile insect technique, Tsetse, Quality control (QC), Flight propensity, Mass-rearing.

67 Preparing Annobón Island for population modification: household mapping, vector characterization and a baseline malaria indicator survey, Equatorial Guinea

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Background. Annobón is a 17 km^2 island province of Equatorial Guinea, 350 km offshore, whose isolation from other vector populations makes it a candidate site for a first release of *Anopheles coluzzii* carrying a gene drive that blocks *Plasmodium* transmission. The National Malaria Control Program, MCD Global Health and the University of California Malaria Initiative have generated baseline data on the local vector population as well as the human population and its prevalence of malaria so that the effect of the release can be measured.

Methods. Three activities ran between November 2025 and May 2026. Teams visited every building on the island and gave each structure and household a unique identifier, effectively conducting a human census. Larval sites were identified and immature anopheline mosquitoes collected. Adult mosquitos were collected with human landing catches in all four localities and used to characterize the local vector population. The first malaria indicator survey (MIS) conducted on Annobón sampled all houses in San Antonio de Palé, the only permanently inhabited settlement on the island. All data were collected within a spatial decision support system (SDSS).

Results. Mapping of all buildings identified 928 occupied households for a total population of 2,912 inhabitants. The larval source scouting mapped 81 aquatic habitats of which 13.6% were found positive for anopheline immature stages. Adult mosquito collections detected *Anopheles coluzzii* and no other *Anopheles* species. During the MIS, 805 households were visited, 2,531 residents were registered and 1,877 were tested for malaria with a rapid diagnostic test upon consent. Parasite rate was 10.7% in the general population and 5.1% in children under five (n=253). Bed net ownership and use were high (89.3% and 70.7%, respectively).

Conclusion. The surveys described mark the first baselines for malaria epidemiological and entomological surveillance on the island of Annobón. These are critical for the activities that lead to a first in kind genetically modified mosquito release for malaria control at scale.

SCIENCE COMMUNICATION MEDIA AWARD FOR TRANSFORMATIONAL SCIENCE STORIES ON GENETIC BIOCONTROL TECHNOLOGIES

Award competition initiated by the African Genetic Biocontrol Consortium, supported by the Science Communication Forum (SCICOM)

Introduction

The Science Communication Media Awards is an award aimed at recognizing and encouraging excellence, accuracy, factual and innovative science stories and publications across the media fraternity in raising awareness science matters with a focus on genetic biocontrol technologies (which include gene drive/editing or synthetic biology). The overall purpose of the award is to promote coverage of information on genetic biocontrol technologies in the local, national and international media and to have a positive influence on policymakers, the private sector, the civil society as well as individuals. The Awards will also build and maintain strong relations between scientists and communicators' in order to improve dissemination of scientific findings in a simplified manner thus bridging the gap between science and society. A key expected outcome of the award is a increased media engagement and coverage of science-based stories. The awards seek to inspire media stakeholders to go beyond and produce stories and publications of highest standard that communicates and breaks down the science to make it consumable to the public.

Objectives

- To promote professionalism in media engagement of scientists and build capacity in documentation of stories technologies on genetic biocontrol technologies in Africa. To reward and encourage excellence, innovation and originality in science reporting, implementation that bridge the gap between scientists, science communicators and journalists while at the same time bring together science and society. on genetic biocontrol technologies.
- To provide visibility for science journalism and strengthen the Science Communication Forum (SCICOM) a multi-disciplinary network for professionals who include scientists, researchers, journalists, communicators, policy makers and regulators from industry, government, academic institutions, and the private sector and non- state actors in Africa.

Nomination, Eligibility and Judging

The competition is open to all practicing journalists in the mainstream media. Focus will be on journalists who write or report science stories on genetically modified organisms (GMOs) and biotechnology related subjects. The Science Communication Media Awards intend to provide recognition to those journalists who deliberately and consistently make public awareness of science matters. Stories on genetic biocontrol biotechnologies will be an added bonus and their related development issues a priority. The Media Awards will target science communicators from research, universities and related institutions, scientists, mainstream media with specific focus on TV, Print, Online, and Radio.

Only a single article or documentary is eligible. Series will not be accepted for review; however, a single article from a series may be submitted for judging as standalone work.

A committee consisting of two scientists, two editors and two professional science journalists and/or communications experts will determine the winners.

MAIN CATEGORY **Create a google form with choices to assist in selection of the categories**	**SUB-CATEGORY**	**KEY PARAMAETERS**
Print/ Newspaper/ Magazines	1. *News Stories: features* 2. *Photos* 3. *Graphics*: Illustrations /Cartoons/animations Also create choices for this	Does it address key issues in science Longevity in news Angle Quote sources Style Analysis Quality of investigative journalism demonstrated

Television	1.News Stories: features/ documentaries	Does it address key issues in science Longevity in news Angle Quote sources Style Analysis Quality of investigative journalism demonstrated
Radio	Radio Programme: radio shows/features/dramas (authentic and non-sponsored programs	Issues covered Quote sources Style Analysis Angle
	Radio News: features	
Online (Has to be exclusively an online story/article) story not drawn from TV or radio related news	*Online Stories:* features/ photo stories/ new stories/ blogs	Issues covered Quote sources Style Analysis Angle Perspective / what is the picture? Message Picture quality2 Interactivity – between author / reader

Guidelines for Application

The individual should be a practicing Journalist / attached to media house.

- Entry must be on science related issues with a bias on emerging biotechnologies
- Individual entries are limited to only two categories per entrant
- Must present original works of the author with publication date.
- Timeline – within the period June 1, 2026 and January 28, 2027.
- Submissions should not have been previously submitted for similar awards and won.



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