

Opening Ceremony

Monday, Oct. 27, 2025



o Anthems

o Introduction of special Guest

PRO

o Welcome Address HRH-CERID

Prof. Olusola Ojurongbe

o Welcome address, Provost
CHS

Prof. A. Olugbenga-Bello

o Traditional Performance

o Goodwill Messages

- DAAD
- Humboldt Ambassador
Nigeria
- Bayer Foundation
- Alexander von Humboldt
Foundation
- National Biotechnology
Research and Development
Agency (NBRDA)

Prof. Adesola Ajayi, VC TECH-U

Prof. Oluwatoyin Odeku

Dr. Tatjana Gust

Dr. Charlotte Baeuml

**Prof. Mustapha Abdullah,
DG, NBRDA**

o Speech: Consul General,
German Embassy, Lagos,
Nigeria

Ambassador Daniel Krull

o Vice Chancellor's Address

Prof. Rasaq O. Rom Kalilu



Royal Father
of the day:

His Imperial Majesty, **Oba Ghandi Afolabi Olaoye
(Orumogege III), The Sun of Ogbomoso Land**

Program of Events

Date	Time	Schedule	Speaker	Facillitators
Monday, Oct. 27, 2025	8:00–11:00	Registration of participants	-	-
	11:00 – 12:00		Opening ceremonies	
	12:00–12:45	Keynote Address: Battling Infectious Diseases in Southeast Asia and sub-Saharan Africa: Insights into Host-Pathogen genetics	Prof. T.P. Velavan	Chairman: Prof. Ademowo
	12:45–13:45	Panel Discussion 1: Navigating Change: Building Resilient Nigerian Scientists through Institution Leadership	Prof. C. Adebooye, Prof. J. Babalola, Prof. T. C. Babalola, Prof. T. Adejumo, Prof. A. Ajayi, Prof. A. Mustapha	Moderator: Prof. A. Akinyele
	13:45 – 14:30		Networking Lunch	
	14:30–15:00	Plenary 1: H5N1 and One Health-adaptive evolution from birds to cattle to humans	Prof. B. Thomas	Chairman: Prof. S. Omilabu
	15:00–15:30	Plenary 2: Long lasting epigenetic effects of climate change - lessons from the past	Prof. A. Boldt	Chairman: Prof. M. Osman
	15:30–16:30	Parallel Session 1: Five Selected Abstracts	-	Chairman: Prof B. Iwalokun
	15:30–16:30	Parallel Session 2: Five Selected Abstracts	-	Chairman: Prof. A. Lateef
	16:30 – 17:00		Tea Break	
	17:00–18:00	Parallel Session 3: Five Selected Abstracts	-	Chairman: Prof. B. Thomas
	17:00–18:00	Parallel Session 4: Five Selected Abstracts	-	Chairman: Prof. A. Boldt
	18:00 – 20:00		Welcoming Reception at Ragaray	

Program of Events

Date	Time	Schedule	Speaker	Facillitators
Tuesday, Oct. 28, 2025	09:00–09:30	Plenary 3: Does Schistosomiasis affect malaria in co-endemic areas? Echos from Lambarene in Gabon	Prof. Akeem Adegnika	Chairman: Prof O. Walker
	09:30–10:00	Plenary 4: Leveraging Wavelet Analysis to Enhance Lassa Fever Control in Nigeria Amidst Changing Climate	Prof. Emmanuel Bakare	Co-Chairman: Prof. Simeon Kouam
	10:00–11:00	Panel Discussion 2: Beyond Borders: Collaborative Research on Emerging Diseases in a Climate-Changing Planet	Prof. T. Velavan, Prof. T. Odeku, Prof. M. Groschup, Prof. E. Bakare, Prof. S. Omilabu	Moderator: Dr. A. Olalekan
	11:00 – 11:30		Tea Break	
	11:30–12:00	Plenary 5: Orthonairovirus Infections in Sub-Saharan Africa	Prof. M. Groschup	Chairman: Prof. J. Olopade
	12:00–13:00	Parallel Sessions 5: Five Selected Abstracts	–	Chairman: Prof. Ade-omowaye
	12:00–13:00	Parallel Sessions 6: Five Selected Abstracts	–	Chairman: Prof. A. Akintunde
	13:00 – 14:00		Networking Lunch	
	14:00–14:30	Plenary 6: Next-Generation Vaccines for Zoonotic Disease Control: An African-Led Future.	Prof. Osman Mohammed	Chairman: Prof O.A Olowe
	14:30–15:00	Plenary 7: Vaccines in the Climate Crisis: The Role of Genomic Intelligence in Outbreak Prediction and Preparedness	Prof. Bamidele Iwalokun	Chairman: Prof. O. Opaleye
	15:00–16:00	Panel Discussion 3: From Local Labs to Global Impact: Pathways for Early-Career Scientists	Prof. A. Adegnika, Dr. C. Onwuamah, Ms A. Olorunfemi, Prof. J. Olopade, Dr. M. Ikegbunam	Chairman: Prof. O. S. Bello
	16:00 – 16:30		Tea Break	
	16:30–17:30	Poster Session	–	–

Program of Events

Date	Time	Schedule	Speaker	Facillitators
Wednesday, Oct. 29, 2025	9:00–9:30	Plenary 8: Zoonotic Transmission of Hepatitis E Virus: A Shift in the Paradigm	Dr. Dominik Hans	Chairman: Dr. Tatjana Gust
	9:30–10:00	Plenary 9: Implementing genomic surveillance of Plasmodium falciparum malaria across sub-Saharan Africa with rapid nanopore sequencing	Dr. Jason Hendry	Chairman: Dr. C. Onwuamah
	10:00–11:00	Parallel Sessions 7: Five Selected Abstracts	-	Chairman: Dr. O. Ayelaagbe
	10:00–11:00	Parallel Sessions 8: Five Selected Abstracts	-	Chairman: Prof. B. Iwalokun
	11:00 – 11:30		Tea Break	
	11:30–12:00	Scholarship opportunities: Alexander von Humboldt Foundation, Bayer Foundation and DAAD presentations	Prof. O. Odeku, Prof. A. Ajayi, Dr. T. Gust	Moderator: Prof. S. Oyedeji
	12:00–12:30	Plenary 10: Bioactive secondary metabolites from fungi with special emphasis on anti-infectives	Prof. Marck Stadler	Chairman: Prof. Akinwande
	12:30–13:00	Commercial Talk	Inqaba Biotechnology	Moderator: Dr. R. Funwei
	13:00 – 14:00		Networking Lunch	
	14:00–14:30	Commercial Talk	AGBL	Moderator: Dr. M. Ikegbunam
	14:30–15:30	Parallel Sessions 9: Five Selected Abstracts	-	Chairman: Prof. O.T Adedosu
	14:30 – 15:30	Parallel Sessions 10: Five Selected Abstracts	-	Chairman: Prof. B. Egbewale
	15:30–16:30	Prize, Awards / Closing Ceremony	-	Moderator: Prof. T. Ojulongbe
18.00 – 20:00		Closing Dinner		

Program of Events

Thursday, Oct. 30, 2025

Departure

Departure

Keynote & Plenary Speakers



Prof. Dr. _____
Thirumalaisamy P. Velavan

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Battling Infectious Diseases in Southeast Asia and sub-Saharan Africa: Integrating Pathogen and Host Genetics for Global Health Preparedness

Infectious diseases continue to pose a major challenge to global health security, disproportionately affecting populations in Southeast Asia and sub-Saharan Africa. Our research focuses on the interplay between pathogen genetics, host susceptibility, immune responses, and environmental drivers that shape disease outcomes. Through collaborative platforms in Vietnam, Indonesia, Nigeria, Congo, Gabon, and Cameroon, we apply molecular epidemiology to monitor transmission dynamics, emerging drug resistance, and viral genotype shifts. Complementary host-pathogen interaction and immunogenetic studies reveal cytokine dysregulation patterns that serve as biomarkers of disease severity. Beyond classical approaches, we integrate advanced technologies: nanopore sequencing for rapid meningitis diagnosis, machine learning for mosquito vector classification, and low-cost drones with multispectral imagery to map arboviral habitats. These tools bridge molecular research with public health applications, strengthening surveillance and outbreak preparedness.

Our findings highlight the urgent need for sustained cross-continental networks to embed diagnostics, genomic surveillance, and capacity building into national health systems. By combining pathogen genomics, host genetics, and innovative digital tools, we aim to inform clinical management, therapeutic strategies, and policy interventions that address both current and emerging infectious disease threats.

Keynote & Plenary Speakers



Prof. _____
Bolaji Thomas

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H5N1 and One Health-adaptive evolution from birds to cattle to humans

The escalating spread of the H5N1 avian influenza virus, which has recently jumped to new mammalian hosts, including dairy cattle in the United States, underscores a critical and evolving pandemic threat. With over 70 human cases and the first U.S. death reported in 2024 and early 2025, this outbreak now represents a public health crisis, demanding a radical shift to One Health paradigm.

The situation in Nigeria is no wise less concerning. While existing surveillance has charted the molecular evolution of H5N1 clades from 2006 to 2021, these bioinformatic studies are hampered by a critical lack of primary, on-the-ground data. We can no longer afford to view this as a purely avian disease; its relentless adaptive evolution at the human-animal interface, driven by Nigeria's unique social and economic dynamics, threatens to destabilize global health security.

Our recent evolutionary study on the gene encoding one of highly pathogenic H5N1's surface proteins indicated that it is evolving more in humans than in five other hosts (cattle, swan, chicken, turkey, and goose). This finding challenges the passive surveillance model, and as a result, we propose an active, multi-host investigation into the H5N1 viral ecology in Nigeria. This talk will focus on computational deconstruction of recent H5N1 data from GISAID, with specific focus on the neuraminidase gene, & recommend new approaches.



Prof. _____
Angelica Boldt

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Long-lasting epigenetic effects due to climate change: lessons from the past

Climate change affects gene expression through different epigenetic mechanisms with inter- and transgenerational effects. Despite their evolutionary adaptive value, they appear maladaptive in a rapidly changing environment. Drought and famine cause epigenetic alterations driven by mediators as noncoding RNAs. Produced in the oocyte and introduced in sperm cells through epididymosomes, ncRNAs translate parental metabolic status into specific chromatin regulation programs focused on survival, albeit at the cost of higher risk for cardiovascular diseases and metabolic syndrome in adults.

As an adverse childhood event, nutritional deprivation at the first trimester of pregnancy bears the utmost severe consequences. Apart from being a classical cause for human migrations, climate change also drives humans into armed conflicts and overcrowded provisory shelters, where traumatic experiences are responsible for over activating the hypothalamic-pituitary-adrenal axis, predisposing the immune response to a persistent proinflammatory state. Similar epigenetic mechanisms are elicited by floods, storms, and hurricanes, which generate posttraumatic stress and other mental health disorders. Animals submitted to repetitive stressful events and hunger do also show long-lasting epigenetic transgenerational effects in their behavior and metabolism. Thus, epigenetic alterations revealed by genetic-epidemiological projects may be accounted for as reversible biomarkers in future public health strategies designed for climate emergencies.



Prof. _____
Ayola Akim Adegnika

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Does Schistosomiasis affect malaria in co-endemic areas? Echoes from Lambaréné in Gabon

Malaria and schistosomiasis are co-endemic in many parts of sub-Saharan Africa, yet their interactions in humans remain incompletely defined. Lambaréné, Gabon, provides a unique research setting with high transmission of *Plasmodium falciparum* and *Schistosoma haematobium*, where several cohort studies have examined their interplay. Work from the Centre de Recherches Médicales de Lambaréné (CERMEL) has shown that helminth infections modulate host immune responses to malaria. For example, *S. haematobium* co-infection in Gabonese schoolchildren has been associated with altered cytokine production, including higher IL-10 and reduced TNF- α , which correlate with lower malaria parasite densities and fewer febrile episodes (Adegnika et al., 2011). Further studies indicated that chronic schistosomiasis can impair vaccine-induced and naturally acquired malaria immunity, with evidence of reduced immunogenicity to malaria vaccine candidates in co-infected children (Adegnika & Kremsner, 2012). Longitudinal data from Lambaréné also suggest that helminth infections can modify responses to antimalarial treatment and potentially influence susceptibility to reinfection (Adegnika et al., 2014).

Taken together, findings from the Lambaréné cohorts highlight the role of schistosomiasis in shaping malaria epidemiology, immune regulation, and intervention outcomes in co-endemic areas. These insights have critical implications for malaria vaccine trial design, integrated control strategies, and a better understanding of host-parasite interactions in natural settings.

Keynote & Plenary Speakers



Prof. _____
Emmanuel Bakare

**International Centre for
Applied Mathematical
Modelling & Data Analytics,
Department of
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Leveraging Wavelet Analysis to enhance Lassa fever control in Nigeria amidst a changing climate

Lassa fever is an acute viral illness caused by the Lassa fever virus, transmitted to humans through contact with food or household items contaminated with rodent urine or faeces. It is a significant public health concern in Nigeria, particularly in Edo and Ondo States. Studies have shown gaps in climate change impact, altering the dynamics of Lassa fever transmission, making it essential to develop innovative control strategies. This study aims to identify seasonal patterns and relatively define climate variability (temperature and rainfall) and Lassa fever incidence in Edo and Ondo states, as well as explore the potential of forecasting to inform Lassa fever control measures.

Our study provided insight into the complex relationships between temperature and rainfall and Lassa fever incidence. An annual phase angle of 2.5 radians suggests that the peak (or a characteristic point, depending on how the phase was defined in the analysis) of Lassa fever cases in Ondo State typically occurs around late May or early June each year which indicates a clear seasonal pattern for Lassa fever in Ondo State, with its highest incidence generally observed towards the end of the dry season and the beginning of the rainy season, a period often associated with increased rodent activity and human-rodent contact. Results showed that the peak of Lassa fever cases in Edo State is around late December or the very beginning of January each year. This indicates a clear seasonal pattern, with the highest incidence occurring at the very end or start of the calendar year. The wavelet-based forecasting models developed in this study informed Lassa fever control measures, enabling public health officials to respond more effectively to outbreaks.



Prof. _____
Martin Groschup

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Orthonairovirus Infections in Sub-Saharan Africa

The diagnosis of orthonairoviruses continues to pose a considerable challenge. These viruses include various, sometimes highly pathogenic species such as Crimean-Congo haemorrhagic fever virus (CCHFV), whose detection is complicated by pronounced genetic intraspecies diversity and by an increasing number of other orthonairovirus species. The presentation will discuss the key factors contributing to the complexity of diagnosis, based on own studies. In addition, serological methods will be discussed with regard to cross-reactions with those related viruses. There are also logistical hurdles, such as the need for high-security laboratories and the limited availability of standardized reference materials.

In addition, studies on the geographical and ecological distribution of orthonairoviruses will be presented. Field studies show that vector and reservoir dynamics have a decisive influence on the epidemiological situation and significantly determine the interpretation of diagnostic results. The combination of molecular, serological, and sequencing-based approaches not only enables improved case identifications, but also provide a more accurate picture of regional virus circulation. The presentation illustrates how the integration of diagnostics and epidemiological surveillance contributes to the early detection of risks and, at the same time, places new demands on standardization, validation, and international comparability.



Prof. _____
Mohamed Osman

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From Leishmania Trials to circRNA Vaccines: A Practical Strategy for Building African Vaccine R&D and Manufacturing

Africa faces recurrent outbreaks of emerging and re-emerging infectious diseases, yet the continent imports more than 99% of its vaccines. This dependency delays access during pandemics and compromises health security. Drawing on my leadership of first-in-human clinical trials of a Leishmania vaccine (ChAd63-KH) and current research on circular RNA (circRNA) vaccine delivery for Rift Valley Fever virus and coronaviruses, I propose a practical strategy for Africa to establish its own vaccine innovation and manufacturing capacity.

The talk highlights lessons from Leishmania trials—rigorous immune monitoring, regulatory navigation, and community engagement—that are directly transferable to African vaccine programs. I then outline the advantages of circRNA technology, including enhanced stability, sustained antigen expression, and potential for reduced cold chain requirements. These features make circRNA particularly well-suited for African contexts where infrastructure challenges are significant.

I present a roadmap for regional hubs, beginning with quality control (QC), formulation, and stability testing, and progressing to GMP production and clinical trial readiness within 24 months. This phased approach builds credibility with regulators and funders while training a skilled workforce. Priority diseases for West Africa—Lassa fever, RVF, cholera, and coronaviruses—are identified as early candidates for platform deployment.

By investing in modular facilities, regulatory alignment, and workforce development, Africa can achieve vaccine sovereignty. Next-generation platforms such as circRNA provide a transformative opportunity to strengthen outbreak preparedness and ensure equitable access for future health emergencies.

Keynote & Plenary Speakers



Prof. _____
Bamidele Iwalokun

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Nigerian Institute of Medical
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NIMR, Lagos

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Vaccines in the Climate Crisis: The Role of Genomic Intelligence in Outbreak Prediction and Preparedness

Across the globe with the inclusion of countries such as Nigeria that contribute less to global warming, climate crisis continues to serve as a multiplier of infectious disease outbreaks, fatalities and economic hardship. The aim of this presentation is to describe how pathogen genomics with artificial intelligence as tool for an early warning system towards an effective climate crisis management and vaccine innovations.

Here, in Nigeria's perspectives, two major categories of infectious diseases as health emergencies related to global warming, climate change and extreme weather events (Climate crisis) will be presented and discussed. They are water borne diseases (with special emphasis on cholera) and vector-borne diseases (malaria, Lassa fever and Dengue). Presentation will include the outbreak trends of these health emergencies, associated fatalities and inducing climate change in the past decades. COVID-19 pandemic predictive weakness unveiling and genomic data gap (due to low sequencing capacity and Bioinformatics capacity) associated with these health emergencies before and now will also be presented.

Using a one health approach, the inherent solutions entailed in the use of pathogen sequencing, artificial intelligence and machine learning (Genomic Intelligence) coupled with integration with ecology, epidemiology and climate change data will be presented and discussed. This holistic approach enables early pathogen detection before they cause outbreak, identifies epidemic pathogens in real-time for outbreak prediction and provides opportunities for monitoring vaccine variant coverage, and developing new generation vaccines in the 21st century.

Although climate change intensifies infectious disease risk, genomic intelligence offers powerful tools for early detection and vaccine innovation. By embracing one health, investing in technology and fostering trust, we can predict outbreak and prepare vaccines faster than ever. The future of outbreak preparedness depends on our ability to integrate science, policy and public engagement-the time to act is now.



Dr. _____
Dominik Harms

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Zoonotic Transmission of Hepatitis E Virus: A Shift in the Paradigm

Hepatitis E virus (HEV) is a major cause of acute viral hepatitis worldwide, with an estimated 20 million infections annually. Genotypes 1 and 2 are classically linked to large waterborne outbreaks in endemic regions, whereas zoonotic genotypes 3 and 4 are transmitted in industrialized countries through swine and other animal reservoirs, primarily via direct contact or consumption of undercooked meat. Beyond these established pathways, novel zoonotic transmission routes are increasingly recognized.

Rabbit-associated HEV (HEV-3ra) has been detected in humans, and rat-derived rocahepevirus has been confirmed as a cause of human infection as well, expanding the known host range of HEV and underscoring its cross-species adaptability. Recent reports of HEV-4 in domestic pigs in several African countries further challenge the long-standing assumption that HEV transmission in these regions is exclusively waterborne.

Together, these findings suggest a paradigm shift in the global epidemiology of HEV, with broader implications for viral surveillance, public and one health approaches.



Dr. _____
Jason Hendry

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Implementing genomic surveillance of *Plasmodium falciparum* malaria across sub-Saharan Africa with rapid nanopore sequencing

In sub-Saharan Africa, continental-scale genomic surveillance of *Plasmodium falciparum* malaria is needed to track the spread of antimalarial drug resistance and diagnostic test evasion, as well as to monitor parasite evolutionary responses to vaccine rollout. Yet implementation of malaria genomic surveillance at a continental-scale is hindered by resource constraints, the vastness of the continent, and the lack of sequencing protocols suitable for most local laboratories. In this talk, I discuss the development and deployment of a decentralised approach for *P. falciparum* genomic surveillance that uses nanopore sequencing.

The protocol we developed is rapid (~5 hours), cost-efficient (<\$25 USD/sample), and targets key genes of public health relevance. In addition, a bioinformatics dashboard that runs in real-time on a laptop enables rapid in-country analysis. Working closely with local partners, we have been able to successfully establish malaria genomic surveillance in over six African countries — including at HRH-CERID in Nigeria — and locally sequenced and analysed more than 1,065 *P. falciparum* samples. I conclude by discussing future challenges and opportunities surrounding the continued growth of nanopore sequencing for *P. falciparum* surveillance in sub-Saharan Africa.



Prof. _____
Marck Stadler

**Professor and Head,
Department Microbial
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[http://www.helmholtz-hzi.de/en/
research/research_topics/
antiinfectives/microbial_drugs](http://www.helmholtz-hzi.de/en/research/research_topics/antiinfectives/microbial_drugs)

Bioactive secondary metabolites from fungi with special emphasis on anti-infectives

Currently, there is an innovation gap regarding the discovery of new therapeutic anti-infective agents, while the number of resistant pathogens has substantially increased at the same time. Particularly challenging is the fact that multi-resistant fungal pathogens are now invading temperate climates from the tropics. Since fungal natural products have historically constituted the most innovative sources for antibiotics, we started a large screening program to evaluate them by analytical chemistry methods, paired with bioinformatics, molecular biology, and modern know-how of biotechnological process development.

We are studying hitherto unexplored fungi from tropical areas and even ecologically specialized European species that have never been cultured and studied for secondary metabolite production. The pre-selection of strains for evaluation is based on modern taxonomy. For the isolation of strains, special techniques are being employed. Young scientists worldwide, including many Africans are working together in this interdisciplinary scenario. My talk will focus on the following highlights:

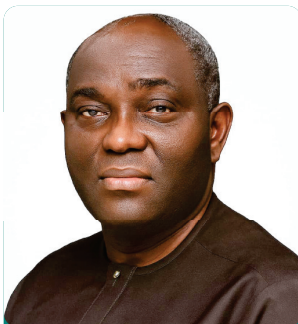
1. the evaluation of the Hypoxylaceae in terms of polythetic taxonomy, phylogenomics and producers of interesting molecules
2. the discovery of novel terpenoid scaffolds from cultures of African Basidiomycota
3. the secondary metabolism of invertebrate-associated (e.g. nematode antagonists, "Zombie Ant fungi") and coprophilous ascomycetes

Meet The LOC



Prof. _____
Oluyinka Opaleye

Chairman, Organising Committee
HRH-CERID, LAUTECH



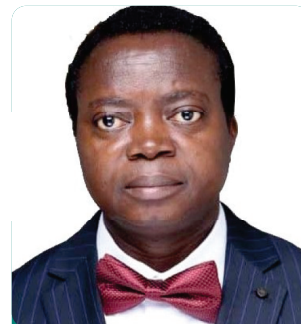
Prof. _____
Olugbenga Olowe

Member
HRH-CERID, LAUTECH



Prof. _____
Segun Oyedeji

Member
FUOYE



Prof. _____
Bolaji Egbewale

Member
HRH-CERID, LAUTECH



Prof. _____
Taiwo Ojurongbe

Member
UNIOSUN



Dr. _____
Adesola Olalekan

Member
UNILAG



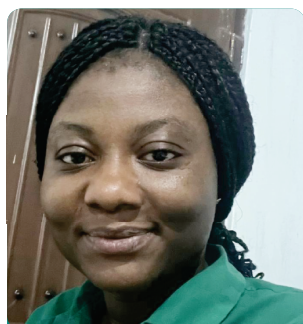
Dr. _____
Moses Ikegbunam

Member
UNIZIK



Dr. _____
Roland Funwei

Member
BABCOCK



Ms. _____
Adedolapo Olorunfemi

Member
HRH-CERID, LAUTECH



We're The

**Local
Organising
Committee**

Oral Presentation Sessions



Monday, Oct. 27, 2025

Parallel Session 1: Time: 15:30 – 16:30

1. **Elizabeth Akande:** Genomic Surveillance of Extended Spectrum Beta-lactamase-producing *Escherichia coli* from Humans and their Environment.
2. **Joseph Tchamgoue:** Fungi-Derived Natural Products in the Fight Against Emerging Diseases.
3. **Dorcas Aboderin:** Molecular Surveillance of Astrovirus In Environmental Water Samples in Lagos State, Nigeria.
4. **Toluwanimi Akinleye:** Genomic Diversity of Human Cosavirus in Nigerian Children with Non-Polio Acute Flaccid Paralysis: Metagenomic Identification of Ten Novel Genotypes.
5. **Samuel Akuma:** Enzymes as Biomarkers for Environmental Surveillance in a Warming World: A Genomic and One Health Approach.

Parallel Session 2: Time: 15:30 – 16:30

1. **Mercy Tebamifor:** Molecular Surveillance of Multi-Resistance in *Anopheles gambiae* in Ota, Ogun State, Nigeria.
2. **Tolulope Oladipo:** Assessment of the Effects of Helminths on the Burden Of Antimicrobial Resistance Among Children In Ibadan Southwestern Nigeria.
3. **Catherine O. Esuola:** Genome Mining for Microbial N-Hydroxylating Monooxygenases (NMOs) Relevance for Siderophore Biosynthesis in Nutrient Depleted Agricultural Soils & ID: 1754008570.
4. **Samuel Ayanwale:** Climate Change and the Emergence of Infectious and Zoonotic Diseases in West and Central Africa.
5. **Ebenezer Ogundana:** Molecular Surveillance of West Nile, Akabane, Wesselsbron, And Middelburg Viruses In Peri-Urban Wildlife Southern Nigeria.

Parallel Session 3: Time: 17:00 – 18:00

1. **Adekemi Adepeju:** Genomic Surveillance of a Typhoid Fever Outbreak in Ibadan, South-Western Nigeria.
2. **Opemiyi Ajuwon:** Genomic profiling of ESBL-producing *Escherichia coli* from food animals in Ibadan, Nigeria.
3. **Jesutofunmi Odeyemi:** Genomic Surveillance uncovers Household Water as a Reservoir for *Salmonella enterica* in Ibadan.
4. **Yahaya Usman:** Genetic characterization and mechanisms of antimicrobial resistance in clinical *Pseudomonas aeruginosa* strains from Northern-western Nigeria.
5. **Seun Okunade:** Drought, Disease, and DNA: Historical Lessons from Livestock Health Crises and the Emergence of Genomic Solutions.

Parallel Session 4: Time: 17:00 – 18:00

1. **Husna Farouq Ibrahim:** Trends in the prevalence of ESBL-producing *E. coli* over the previous decade in Northern Nigeria.
2. **Chidimma Azike:** Metagenomic Characterization of Microbial Communities and their Health Implications in Coastal Waters of Rivers State, Nigeria.
3. **Emmanuel Okechukwu:** Strengthening Genomic and Climate-Sensitive Surveillance through Faith-Based and National Health System Integration: A Multisectoral Model for Epidemic Resilience.
4. **Joyce Mbugua:** Climate Change and Gender: Assessing women's vulnerabilities to climate change and their resilience strategies in Kibwezi, Kenya.
5. **Taiwo Adekunle:** Development of Geo-Computational Based Model for Lassa Fever Outbreak Prediction.

Oral Presentation Sessions



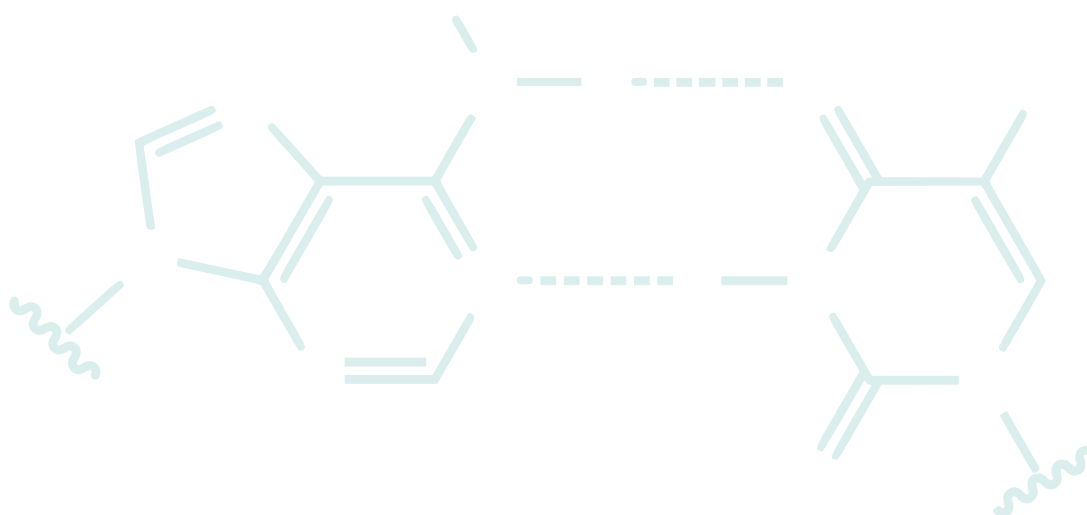
Tuesday, Oct. 28, 2025

Parallel Session 5: Time: 12:00 – 13:00

1. **Foluso Agulanna:** Climate Change and Its Impact on The Health and Livelihoods Of Cocoa Farmers In Nigeria.
2. **Glorious Olajire:** The Social Perspective of Youths' Sustainable Behaviours and Health Motivation In Ibadan North Local Government, Oyo State, Nigeria.
3. **Euslar Onu:** Prevalence of Herpes Simplex Virus Type-2 Infection and factors Affecting its transmission among Youths attending the Sexually Transmitted Infection Clinic of Alex Ekwueme Federal University Teaching Hospital Abakaliki.
4. **Blessing Babalola:** Beyond Crude Antigens: Dot Blot Assay Using Eluted Schistosoma Proteins for Potential Field Diagnosis.
5. **Naomi Ajonloju:** Evaluation of *Plasmodium falciparum* Histidine Rich Protein (Pfhrp2/3) Gene Deletions in Parasite Isolates and Implications for Malaria Control.

Parallel Session 6: Time: 12:00 – 13:00

1. **David Nwachukwu:** Sero-epidemiological Evidence of Zika Virus Exposure and Possible Reinfection Among Pregnant Women in Rivers State, Nigeria.
2. **Celestina Olafusi:** Evaluation of Central Repeats and Haplotype on *Plasmodium falciparum* Circumsporozoite Gene in Isolates Obtained from Ore, Osun State, Nigeria.
3. **Olufunke Oyinloye:** Cross-Species Infection Models Using One Health Data: Predicting the Next Pandemic.
4. **Emmanuel Ikusika:** Co-infection of Extended Spectrum Beta-Lactamase and Carbapenemase Bacteria with Helminths in Ibadan, Nigeria.
5. **Esther Ola:** Molecular Characterization of Zoonotic Helminths in Wild Rodents from Nigeria: Implications for Human Health.



Oral Presentation Sessions



Wednesday, Oct. 29, 2025

Parallel Session 7: Time: 10:00 – 11:00

1. **Alimat Olamide Usamat:** Concurrent Antibiotic Resistance and Virulence Traits in Extremely Drug-Resistant *Burkholderia pseudomallei* from Infected Bovine Milk Samples: Potential for Zoonotic Transmission.
2. **Abiola Ogunleke:** Epidemiology and Burden of Two Human Schistosome Species among School-Aged Children in Osun State, Nigeria.
3. **Saheed Adebisi:** AI-Powered Climate Policy Tools: Data-Driven Insights and Scientifically-Grounded Solutions.
4. **Tawakalt Ayoola:** Mathematical Modelling of COVID-19 under Imperfect Vaccination.
5. **Tasneem Osman:** Interspecific Interactions in Disease Ecology: The Role of Invasive Alien Plants in Modulating Mosquito Vector Performance and Pathogen Dissemination.

Parallel Session 8: Time: 10:00 – 11:00

1. **Olyvia Fadeyi:** Genomic Revolution and Epidemic Control: Advancing a Global Predictive Health Approach.
2. **Bukola Atobatele:** Diversity and Danger: Insights from Antibiotic-Resistant Bacteria in Abattoir Microbiomes in Two Local Governments in Osun State.
3. **Selorme Adukpo:** Bacterial Isolates from Frozen Chicken Are Resistant to Multiple Antibiotics
4. **Motunrayo Ogunyale:** Immunomodulatory Effects of *Bacillus Calmette-Guérin* (BCG) on *Trypanosoma evansi* Rat Model.
5. **Modupe Oluwabiye:** Repositioning Academic Libraries for Research Collaboration and Emerging Disease Response in Nigeria: A Mixed-Methods Study.

Parallel Session 9: Time: 14:00–14:30

1. **Akanbi Gladys:** Influence of Ginger, Garlic and Cayenne Pepper on The Production and Properties of African Yam Bean Snacks.
2. **Oluwafunmilayo Amoran:** Genome Stability of Optimized Micropropagated *Telfairia occidentalis* (Fluted Pumpkin) Seeds.
3. **Salma Suliman:** Comprehensive Genomic Surveillance of *Plasmodium falciparum* in Nigeria and Sudan using Rapid Oxford Nanopore Sequencing.
4. **Felix Agomma:** Environmental Dissemination of Carbapenem-producing Enterobacteriaceae: Lessons from Hospital Effluents in Lagos.
5. **Blessing Shaibu:** Stem-Based Quantification of Ethno-Medicinal Utilization of Woody Plant Species on the Campus of University of Ilorin, Ilorin, Nigeria.

Parallel Session 10: Time: 14:00–14:30

1. **Iheanyi Peter-Ajuzie:** Sero-molecular Detection, Sequence Analysis and Neuro-immunolocalization of West Nile Virus in Nigerian Wildlife.
2. **Alfred Onefeli:** Molecular Characterisation of *Ricinodendron heudelotii* in Nigeria; Genomic Insights for Ethnomedicine, One Health, and Climate-Resilient Disease Management.
3. **Abisola Banji:** Biological and molecular characterization of virus causing mosaic in celosia Argentea in Ibadan.
4. **Mistura Adeleke:** Study of Genetic Diversity of Silver Catfish (*Chrysichthys nigrodigitatus*) in Iwopin Lagoon, Ogun State using ISSR Markers.
5. **Samuel Olawumi:** Biogenic Silver Nanoparticles from Ginger Rhizome Alkaloids as Dual-Action Agents for Diabetic Wound Management and Eco-compatible One-Health Applications.

Scholarship Recipients



Full Scholarship

1. **Joyce Mbugua** — Kenya Institute of Primate Research
2. **Mercy Tebamifor** — Covenant Applied Informatics & Communication Africa Centre of Excellence
3. **Bukola Atobatele** — Bowen University, Nigeria
4. **Tasneem Osman** — University of Bonn, Germany
5. **Praise Adewumi** — Bowen University, Nigeria
6. **David Nwachukwu** — University of Port Harcourt, Nigeria
7. **Joyce Oluokun** — Redeemer's University, Nigeria
8. **Catherine Oluwakemi** — National Horticultural Research Institute, Nigeria
9. **Samuel Ayanwale** — Damien Foundation Centre for Genomics and Global Health, Nigeria
10. **Adekemi Adepeju** — University of Ibadan, Nigeria
11. **Elizabeth Akande** — University of Ibadan, Nigeria
12. **Dorcas Aboderin** — Centre for Human & Zoonotic Virology, Nigeria
13. **Opeyemi Ajuwon** — University of Ibadan, Nigeria
14. **Jesutofunmi Odeyemi** — University of Ibadan, Nigeria
15. **Toluwanimi Akinleye** — University of Ibadan, Nigeria
16. **Naomi Ajoniloju** — University of Ibadan, Nigeria
17. **Olufunke Anuoluwapo** — University of Ilesha, Nigeria
18. **Esther Ola** — Adekunle Ajasin University, Nigeria
19. **Alimat Olamide Usamat** — Osun State University, Nigeria
20. **Blessing Babalola** — University of Medical Sciences, Ondo, Nigeria
21. **Felix Agomma** — University of Lagos, Nigeria
22. **Chidimma Azike** — Rivers State University, Nigeria
23. **Samuel Akuma** — University of Nottingham Malaysia
24. **Selorme Adukpo** — University of Ghana, Legon, Accra, Ghana
25. **Joseph Tchamgoue** — University of Yaounde, Cameroon
26. **Tolulope Oladipo** — University of Ibadan, Nigeria
27. **Emmanuel Olugbenga Ikusika** — University of Ibadan, Ibadan, Nigeria
28. **Yahaya Usman** — Ahmadu Bello University, Zaria, Nigeria
29. **Iheanyi Kেমdirim Peter-Ajuzie** — University of Nigeria
30. **Seun Okunade** — Olabisi Onabanjo University, Nigeria
31. **Abisola Banji** — University of Ibadan, Nigeria
32. **Husna Farouq Ibrahim** — Kano Independent Research Centre Trust, Nigeria

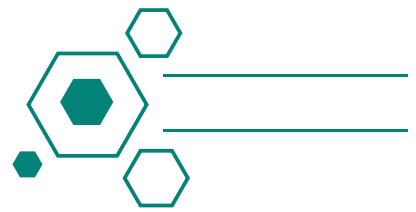
33. **Abidemi Oyalade** — Osun State University
34. **Habeeb Afolabi** — Osun State University
35. **Modupe Oluwabiye** — University of Ibadan
36. **Samuel Olawumi** — Osun State University
37. **Foluso Agunlana** — Cocoa Research Institute of Nigeria

Partial Scholarship

1. **Celestina Olafusi** — Covenant University, Nigeria
2. **Toyosi Igejongbo** — Federal University of Technology, Akure, Nigeria
3. **Saheed Adebisi** — Global Scholars and Leaders Support Network, Nigeria
4. **Tawakalt Ayoola** — Osun State University, Osogbo, Nigeria
5. **Olyvia Gwladys Fadeyi** — University of Parakou (Benin), Nigeria
6. **Oluwafunmilayo Amoran** — National Horticultural Research Institute, Jericho, Ibadan
7. **Emmanuel Okechukwu** — Dept. of Community Medicine & Primary Health Care, Veritas
8. **Fayoke Abe** — University of KwaZulu-Natal, Durban, South Africa
9. **Abiola Ogunleke** — Ladoke Akintola University of Technology
10. **Glorious Olajire** — University of Ibadan
11. **Motunrayo Ogunyale** — Ladoke Akintola University of Technology, Nigeria
12. **Akanbi Gladys** — Ladoke Akintola University of Technology, Nigeria
13. **Blessing Shaibu** — University of Ibadan, Nigeria
14. **Alfred Onefeli** — University of Ibadan, Nigeria
15. **Wasiu Salami** — Lagos State University, Ojo, Nigeria
16. **Abdullah Akinade** — Ladoke Akintola University of Technology, Nigeria
17. **Mistura Adeleke** — Olabisi Onabanjo University, Nigeria
18. **Euslar Onu** — Alex-Ekwueme Federal University, Nigeria
19. **Taiwo Adekunle** — Osun State University, Nigeria
20. **Ebenezer Ogundana** — Institute of Genomics and Global Health

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LAUTECH, Ogbomoso, Oyo State, Nigeria

📅 October 26 – 30, 2025

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Decoding Pathogens, Defending Health