

14th GABRIEL Network International Meeting

June 3–5, 2026

Radisson Blu Hotel, Antananarivo, Madagascar

Organized by: The Mérieux Foundation & Charles Mérieux Center of Infectious disease Madagascar

With the support of: BioMérieux, and the Fondation Pierre Fabre



Special Report

From 3 to 5 June 2026, more than 100 scientists, physicians, academics, and public health professionals from 22 countries gathered at the Radisson Blu Hotel in Antananarivo, Madagascar, for the 14th GABRIEL network international meeting.

The opening ceremony brought together representatives of the Charles Mérieux Center for Infectiology, the Mérieux Foundation, the University of Antananarivo, the Ministries of Health and Higher Education and Research, and the French ambassador to Madagascar. Their remarks reflected a shared commitment to advancing research, diagnostic innovation, and quality patient care in support of the fight against neglected tropical diseases, the focus of the symposium's first day.

For nearly two decades, the GABRIEL network has fostered a trusted and dynamic scientific community. In an increasingly fragmented world, the network plays a vital role in sustaining long-term international scientific partnerships, promoting both south-south and north-south collaborations, strengthening local capacities, and supporting country-led responses to infectious disease challenges. Through initiatives such as the GABRIEL Young Scientist Awards, the network also invests in the next generation of researchers, helping talented

young scientists from low- and lower-middle-income countries advance their careers and contribute to global health.

The annual GABRIEL network meeting provides a unique platform for exchanging knowledge, sharing experiences, and exploring new collaborative opportunities. This year's program focused on antimicrobial resistance, tuberculosis, and acute respiratory infections. The discussions highlighted diagnostic gaps, surveillance needs, and innovative approaches to improving public health and patient outcomes.

This report summarizes the key messages and scientific advances that emerged during the symposium, reaffirming the Mérieux Foundation's long-term commitment to strengthening health systems and improving global health through locally driven solutions.

SYMPOSIUM DAY

June 3, 2026

Innovations in the fight against tropical neglected diseases: from diagnosis to patient care

SESSION I: DIAGNOSTIC INNOVATIONS

Early diagnosis of leprosy: screening strategies, laboratory innovations, role of frontline caregivers



Dr. Tahinamandranto Rasamoelina, from the Centre d'Infectiologie Charles Mérieux, University of Antananarivo, Madagascar

His presentation focused on the challenges and opportunities related to the early diagnosis of leprosy, a neglected tropical disease that continues to affect more than 120 countries and causes significant disability if not detected early. Early detection remains difficult due to the long incubation period, non-specific early symptoms, and limited sensitivity of conventional diagnostic tools, especially in paucibacillary cases. Clinical recognition

therefore remains central, with frontline healthcare workers playing a critical role in identifying suspicious lesions, assessing nerve involvement, and referring patients promptly. The presentation highlighted the importance of targeted screening strategies, including contact tracing and active case finding in endemic areas. Evidence from Madagascar and the Comoros demonstrated that household contacts and nearby neighbors are at significantly higher risk, underlining the value of localized screening approaches.

Recent laboratory innovations were also discussed. Molecular methods such as qPCR improve diagnostic sensitivity, while simpler techniques like LAMP offer promising alternatives for low-resource settings. In parallel, several biomarkers (molecular, serological, immunological, and transcriptomic) are under investigation, although none are currently sufficient on its own for early diagnosis. Operational research showed that combining active case finding with serological tools (e.g., anti-PGL-I rapid tests) and post-

exposure prophylaxis can significantly reduce transmission. These tools also help identify high-risk individuals and monitor intervention impact.

Overall, the presentation emphasized that effective early diagnosis requires an integrated approach combining clinical expertise, targeted screening, and appropriate use of laboratory innovations. Strengthening the role of frontline caregivers and prioritizing high-risk populations are essential to improving detection and reducing transmission.

Latency dynamics: post-exposure and prophylactic intervention strategies



Dr. Lovasoa Mbolamanana Joseph Andrianiriana, from the National Leprosy Control Program at the Ministry of Public Health of Madagascar, highlighted the importance of latency in leprosy transmission and the role of post-exposure prophylaxis in disease control. Latency represents a critical phase during which infected individuals remain asymptomatic, contributing to hidden transmission and delayed diagnosis.

Leprosy is mainly transmitted through prolonged close contact, with household members, neighbors, and social contacts being at highest risk. WHO-recommended strategies include contact tracing and targeted prophylaxis to interrupt transmission early.

The use of single-dose rifampicin PEP (SDR-PEP) was presented as an effective, low-cost, and widely accepted intervention that reduces progression from infection to disease and protects high-risk contacts. Evidence from international programs shows a significant reduction in incidence.

Results from the PEOPLE trial in Madagascar and the Comoros demonstrated that combining door-to-door screening with expanded prophylactic coverage provides the greatest impact. Transmission was shown to be highly localized, often within a 75-meter radius of index cases.

Despite promising results, challenges remain, including long incubation periods, stigma, logistical constraints, and the need for stronger surveillance systems. Overall, integrated strategies combining screening and prophylaxis are essential to reduce transmission and advance leprosy control.

Overall, the presentation underscored that proactive screening combined with targeted post-exposure prophylaxis is critical to reducing transmission and accelerating progress toward leprosy control.

Implantation mycoses: advances in diagnostic tools



Dr. Cécile Garnaud from the Grenoble Alpes University Hospital, France, addressed implantation mycoses, a group of neglected tropical diseases caused by environmental fungi introduced through skin trauma. These infections, including chromoblastomycosis and sporotrichosis, mainly affect low-income populations in tropical and subtropical regions and are associated with chronic disease, significant morbidity, and difficult, prolonged treatment.

She highlighted the diagnostic challenges linked to these diseases, which often require a combination of clinical suspicion and laboratory confirmation. Conventional diagnostic methods include direct microscopy, histopathology, and culture, which remain essential but have limitations such as long turnaround times, variable sensitivity, and the need for specialized expertise. Recent advances in diagnostic tools were presented, including MALDI-TOF mass spectrometry for species-level identification and molecular techniques such as PCR and sequencing, which improve sensitivity and accuracy. However, these tools are not yet widely available in routine settings. Biomarkers and antifungal susceptibility testing are also under development but lack standardization. Despite progress, major gaps remain in access to reliable, affordable diagnostics. Strengthening laboratory capacity, developing simple and accessible assays, and improving training are essential to enhance diagnosis, surveillance, and patient management for these neglected diseases.

Challenges in differential diagnosis: identifying Dengue and other arboviruses among similar febrile diseases



Dr. Felipe Gomes Naveca from the Oswaldo Cruz Foundation (Fiocruz), Brazil, focused on the complexity of diagnosing dengue and other arboviral infections in regions where multiple viruses co-circulate. Arboviruses such as dengue, Oropouche, and Mayaro often present with similar non-specific febrile symptoms, making clinical differentiation challenging and leading to frequent misdiagnosis. Dr. Felipe Gomes Naveca emphasized that overlapping clinical presentations, combined with limited laboratory confirmation capacity, can result in inaccurate epidemiological

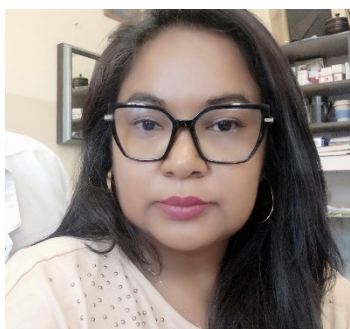
interpretations. An example from Brazil illustrated this issue, where a large proportion of suspected dengue cases were later identified as Oropouche virus infections, highlighting the risk of underestimating emerging pathogens.

A key point was the importance of selecting appropriate diagnostic tools based on the timing of infection. Different methods, including molecular assays and serological tests, have specific diagnostic windows, and failure to consider these can lead to false-negative results. Molecular techniques, particularly PCR-based assays, were highlighted as the most reliable tools for early detection. The presentation also underscored the role of genomic surveillance in improving pathogen identification and tracking outbreaks. Integrating molecular diagnostics with surveillance systems can strengthen outbreak detection and

response. In summary, the need for integrated diagnostic approaches and improved laboratory capacity was identified as essential to enhance accuracy and support effective public health interventions.

SESSION II: THERAPEUTIC INNOVATIONS

Leprosy care: innovations in treatment and prevention



Prof. Lala Soavina Ramarozatovo from University of Antananarivo, Faculty of Medicine, Madagascar reviewed recent advances in the treatment and prevention of leprosy, a neglected tropical disease that continues to cause significant morbidity, with around 200,000 new cases reported annually worldwide.

The WHO-recommended multidrug therapy (MDT) remains the standard of care, but it presents several limitations, including long treatment duration, toxicity, and challenges with patient adherence. Emerging therapeutic innovations include new drug candidates such as Bedaquiline and Telacebec, as well as alternative regimens like Rimoxclamin, which show promising bactericidal activity and potential improvements in neurological outcomes. However, current evidence suggests that these approaches do not yet demonstrate clear superiority over MDT and should be used cautiously.

Prof. Lala Soavina Ramarozatovo also addressed the management of leprosy reactions, highlighting the limitations of corticosteroids and the potential role of steroid-sparing agents such as methotrexate and other immunomodulatory treatments.

In terms of prevention, post-exposure prophylaxis with rifampicin and enhanced regimens combining rifampicin with bedaquiline were discussed. Active case detection and targeted screening strategies were identified as key to reducing transmission.

In conclusion, while promising innovations are emerging, strengthening health systems and ensuring effective implementation remain essential for achieving long-term impact in leprosy control.

Improving therapeutic and diagnostic management of Schistosomiasis in mothers and young children



Prof. Raphael Rakotozandrindrainy from University of Antananarivo, presented the freeBILY study, a major clinical research initiative aimed at improving the diagnosis and treatment of schistosomiasis in pregnant women and young children in Madagascar, one of the countries most heavily affected by this neglected tropical disease. Schistosomiasis remains a significant public health challenge in sub-Saharan Africa, where access to safe water and sanitation is limited. Despite WHO elimination goals, pregnant women and preschool-aged children have historically been overlooked in

control programs.

The freeBILY project, funded by EDCTP and sponsored by the Bernhard Nocht Institute for Tropical Medicine, evaluates the feasibility, effectiveness and safety of a test-based schistosomiasis treatment strategy using rapid POC-CCA (Point of Care – Circulating cathodic antigen) urine testing and praziquantel therapy. Conducted across 42 study sites in Madagascar, the cluster-randomized trial enrolled more than 5,100 pregnant women and followed both mothers and their children over a two-year period.

Results demonstrated a very high baseline prevalence of schistosomiasis, with 88.8% of women testing positive at enrolment. Positivity rates decreased during follow-up after treatment, while praziquantel showed a favorable safety profile, with only mild or moderate adverse events reported. The study highlights the practicality of integrating test-based diagnosis and treatment into primary healthcare services and supports the inclusion of pregnant women and young children in national schistosomiasis control programs.

Female Genital Schistosomiasis and treatment challenges



Dr. Myriam Lassmann from the Bernhard Nocht Institute for Tropical Medicine, Germany, presented an overview of the challenges associated with Female Genital Schistosomiasis (FGS), a neglected manifestation of chronic *Schistosoma haematobium* infection affecting an estimated 56 million women and girls worldwide, predominantly in sub-Saharan Africa. Despite its major health impact, FGS remains underdiagnosed, frequently misidentified as a sexually transmitted infection, and is rarely integrated into routine reproductive health services.

The presentation highlighted the clinical consequences of FGS, including chronic genital symptoms, infertility, ectopic pregnancy, increased susceptibility to HIV infection, and a possible association with HPV infection and cervical cancer. While praziquantel remains the cornerstone of schistosomiasis treatment, its effectiveness against the inflammatory and chronic lesions characteristic of FGS is limited, underscoring the need for improved therapeutic approaches.

Several innovative initiatives underway in Madagascar were presented, including the FIRM-UP project, which integrates colposcopy-based screening and follow-up care into primary healthcare services, and the WINGS4FGS/CARE-M program, which will evaluate combination therapies aimed at improving treatment outcomes. The role of artificial intelligence in supporting colposcopic diagnosis was also discussed as a promising tool to increase diagnostic capacity in resource-limited settings.

The presentation concluded that controlling FGS requires a comprehensive strategy combining earlier diagnosis, innovative treatments, integrated reproductive healthcare services, prevention, community awareness, and strengthened public health program.

Improving access to diagnosis through teledermatology



Pr. Ousmane Faye, from Bamako Dermatology Hospital, Mali, presented the experience of the Mali Teledermatology Project, highlighting how digital health solutions can improve access to dermatological diagnosis and care in resource-limited settings. Skin diseases represent a major public health burden worldwide and are a leading cause of non-fatal disability, yet access to dermatologists remains extremely limited across many West African countries. In addition, a large proportion of patients with skin conditions are initially managed by frontline healthcare workers with limited dermatology training, resulting in frequent misdiagnosis, inappropriate treatments, and increased healthcare costs.

Building on the success of the “Bamako Project,” which improved healthcare workers’ diagnostic skills and prescribing practices through training and access to essential dermatological medicines, a teledermatology initiative was launched in Mali in 2015. Using a store-and-forward model, healthcare workers in primary health centres submit clinical information and photographs to dermatology specialists who provide expert advice remotely.

Over the past decade, the program has expanded considerably, involving 284 healthcare workers, 112 health centers, and national coverage across all regions of Mali. More than 10,000 patients have benefited from specialist support, with an average response time of approximately 24 hours. The project has demonstrated improvements in diagnostic accuracy, healthcare worker knowledge, and patient outcomes.

The presentation concluded that teledermatology is a scalable and sustainable strategy for strengthening dermatological care in underserved areas, while future developments may include artificial intelligence, tele-expertise, and integration into routine health systems.

SESSION III: Public health strategies

Integrating neglected disease programs



Dr. Alphonse José Nely representing the Neglected Tropical Diseases (NTD) Control Program of the Ministry of Public Health of Madagascar, presented the national strategy for integrating NTD control programs to improve efficiency, coverage, and sustainability. Madagascar continues to face a high burden of NTDs, including lymphatic filariasis, leprosy, schistosomiasis, soil-transmitted helminthiases, and cysticercosis, all of which remain endemic in large parts of the country.

The presentation highlighted the limitations of traditional vertical disease programs. While such approaches provide specialized expertise and dedicated funding, they often lead to duplication of activities, fragmentation of health services, inefficient use of resources, and excessive demands on community health

workers. These challenges can weaken health system performance and reduce the sustainability of disease-control gains.

To address these issues, Madagascar has adopted an integrated approach at strategic, operational, and community levels. Key interventions include integrated mass drug administration campaigns combined with other public health activities, joint training and supervision of community distributors, harmonized reporting systems, and the involvement of polyvalent community health agents in disease screening and pharmacovigilance. Integrated campaigns have reportedly achieved substantial cost reductions while improving geographical and therapeutic coverage.

The presentation concluded that program integration is essential for resource-limited settings. Continued success will depend on strong political commitment, improved data harmonization, inter-program collaboration, and sustainable financing aligned with the WHO NTD Roadmap 2021–2030 and Sustainable Development Goal 3.3.

Global web-based surveillance at WHO for data collection, analysis and dissemination on leishmaniasis and skin NTDs

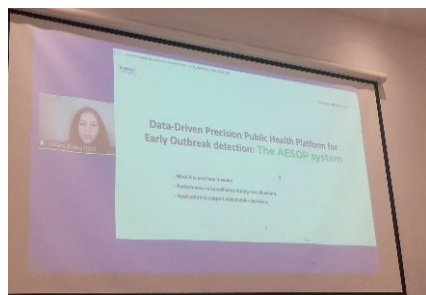


Dr. Carme Carrion Ribas from the University of Girona, Spain, presented recent advances in the development and validation of the WHO SkinNTDs application, a digital decision-support tool designed to strengthen the detection, diagnosis, surveillance, and management of skin-related neglected tropical diseases (NTDs). Developed in line with the WHO NTD Roadmap 2021–2030, the application has evolved from an initial version focused exclusively on skin NTDs to a more comprehensive platform that now includes algorithms covering 12 skin NTDs and 24 common dermatological conditions.

The presentation reviewed the progressive development of the application, including the integration of artificial intelligence (AI) to support frontline healthcare workers in settings where access to dermatological expertise is limited. Internal, external, and field-based validation studies were conducted in several countries, including Kenya, Côte d'Ivoire, Madagascar, Malawi, Guinea, Brazil, and Cameroon. Preliminary results demonstrated encouraging levels of diagnostic performance, particularly for common skin diseases and selected NTDs such as cutaneous leishmaniasis and scabies. Usability assessments also showed high levels of user satisfaction among healthcare professionals.

Pilot implementation studies highlighted the potential of the application to improve diagnostic accuracy, support capacity building, and strengthen integrated skin health services at primary healthcare level. The presentation emphasized the importance of rigorous real-world validation, user training, implementation research, and patient engagement to ensure the safe and effective deployment of AI-powered diagnostic tools in endemic settings.

Data-driven precision public health platform for early outbreak detection: The AESOP system



Dr. Viviane Boaventura from Fiocruz, Brazil, presented AESOP, an innovative surveillance platform developed in Brazil to support the early detection and monitoring of outbreaks with epidemic or pandemic potential. The platform integrates multiple data sources, including primary health care consultations, over-the-counter drug sales, and digital information such as social media signals and rumors. By combining artificial intelligence and

machine learning approaches with epidemiological, environmental, socioeconomic, mobility, and genomic data, AESOP enables the rapid identification of unusual health events, investigation of their potential causes, and monitoring of their spread.

The presentation highlighted how AESOP leverages large-scale routine datasets and applies data quality assessment and anomaly detection algorithms to generate real-time alerts. Results from pilot implementations demonstrated the system's ability to detect increases in respiratory illnesses several weeks before traditional surveillance systems. In the Amazonas region, for example, AESOP identified a surge in respiratory cases 3 to 4 weeks ahead of conventional surveillance during the Parintins Festival.

Dr. Boaventura also described the expansion of the platform to arboviral and diarrheal diseases and its implementation across several Brazilian states. AESOP was presented as a valuable tool to support public health decision-making, optimize sentinel surveillance networks, and strengthen preparedness for emerging infectious disease threats.

SESSION IV: CLIMATE CHANGE AND NEGLECTED TROPICAL DISEASES

Arbovirus dissemination and climate changes in global diseases impact and control



Dr. Felipe Gomes Naveca from the Oswaldo Cruz Foundation (Fiocruz), Brazil, presented an overview of the growing impact of climate change on the emergence, dissemination, and control of arboviral diseases. The presentation emphasized that arbovirus transmission is driven by a complex interaction of environmental, ecological, and societal factors, including land-use changes, urbanization, increasing human mobility, and climate variability. These factors contribute to the expansion of mosquito vectors and increase opportunities

for pathogen transmission.

Drawing on recent evidence from Brazil and other regions of the Americas, Dr. Naveca demonstrated how rising temperatures and persistent climate anomalies have facilitated the geographical expansion of dengue, including into previously protected high-altitude

areas. Temperature was shown to be a major determinant of *Aedes aegypti* vector competence, with optimal dengue transmission occurring around 29°C. Extreme weather events, floods, droughts, and El Niño-related climatic disturbances further influence vector distribution and disease dynamics.

The presentation also reviewed the changing epidemiology of other arboviruses, including chikungunya, yellow fever, Zika virus, and Oropouche virus (OROV). Recent outbreaks of OROV in the Amazon region were associated with extreme climatic conditions, while environmental changes and agricultural expansion may contribute to its spread. Predictive modelling and machine-learning approaches were highlighted as valuable tools for identifying emerging risk areas.

The presentation concluded that climate change is becoming a major driver of arboviral emergence and geographic expansion, requiring strengthened surveillance, predictive modelling, and integrated public health responses to anticipate and mitigate future outbreaks.

Climate change and plague dynamics in Madagascar: a deep learning approach for early risk prediction



Dr. Parfait Rakotonindrainy from University of Antananarivo, Madagascar, presented a study exploring the relationship between climate change and plague dynamics in Madagascar, with a particular focus on the use of deep learning approaches for early risk prediction. Madagascar remains one of the countries most affected by plague worldwide, and its high vulnerability to climate change raises important questions about the influence of environmental factors on disease transmission.

The study adopted a One Health approach, integrating epidemiological, climatic, and environmental datasets collected over several decades. Data included plague surveillance records, temperature and rainfall measurements, and environmental indicators such as altitude, land cover, and deforestation. The objective was to determine how climate anomalies affect plague transmission and whether artificial intelligence could improve the identification of high-risk situations.

Analysis revealed significant climatic trends in endemic regions, including increasing temperature anomalies and decreasing rainfall. The highest incidence of plague was observed during periods characterized by positive thermal anomalies and low precipitation levels. Statistical analysis demonstrated a significant association between climate anomalies and plague occurrence, supporting the hypothesis that environmental changes influence disease resurgence.

Building on these findings, the study developed a deep-learning framework to predict plague risk and improve early warning capabilities. The presentation highlighted the potential of combining climate information, environmental monitoring, and artificial intelligence to strengthen plague surveillance, guide public health interventions, and enhance preparedness in the context of ongoing climate change.

5-MINUTE ORAL POSTER PRESENTATIONS

Strengthening infection control through air sampling: insights from Brazilian hospitals and autopsy facilities



Dr. Layla Honorato from the Institute of Tropical Medicine of the University of São Paulo, Brazil, presented a pilot study on the use of active air sampling for respiratory pathogen surveillance in Brazilian healthcare settings. The project explores how air surveillance can complement traditional infection control and public health monitoring by providing a non-invasive approach to detecting airborne pathogens.

The study is being conducted in four contrasting healthcare environments across Brazil: an emergency observation unit and an autopsy facility in São Paulo, a municipal emergency room in Jataí (Goiás State), and a remote emergency room in Atalaia do Norte (Amazonas State). These sites were selected to represent diverse patient populations, infrastructure levels, and transmission-risk profiles.

Using Apollo™ Ambient Air Samplers, air samples are collected twice weekly over a six-month period. Molecular analyses include qPCR screening for major respiratory viruses (including influenza, SARS-CoV-2, RSV, adenovirus, and rhinovirus/enterovirus), detection of *Mycobacterium tuberculosis* complex, and metagenomic sequencing of selected samples.

Preliminary results from São Paulo demonstrated the feasibility of the approach. During an influenza outbreak in the emergency department, Influenza A was successfully detected in air filters, while all analyzed samples met quality control criteria. These early findings suggest that active air sampling is a simple, safe, and effective tool for monitoring respiratory pathogens and may strengthen infection prevention, outbreak detection, and epidemic preparedness across a variety of healthcare settings.

Evidence of non-tuberculous mycobacteria among tuberculosis presumptive cases in Cameroon



Dr. Valerie Flore Donkeng-Donfack, from Centre Pasteur du Cameroun, presented a study investigating the presence of non-tuberculous mycobacteria (NTM) among patients suspected of having tuberculosis (TB) in Cameroon. The study was motivated by the observation that many presumptive TB cases present symptoms that overlap with other respiratory diseases, including infections caused by NTM, leading to potential misdiagnosis and inappropriate management. Using a combination of microscopy, culture, and molecular identification techniques, the research aimed to characterize NTM species circulating among TB

presumptive cases and evaluate their contribution to the burden of respiratory disease in the country.

The findings revealed that 4.5% of the 5,267 patients investigated were infected with NTM, corresponding to 236 confirmed cases. Importantly, more than half of these NTM infections

(52.1%) were smear-negative and therefore would likely have been missed through routine TB screening procedures. The most frequently identified species were *Mycobacterium fortuitum* (32.4%) and *Mycobacterium intracellulare* (19.4%), both commonly associated with environmental reservoirs such as water and soil.

The study highlights a significant diagnostic gap in TB-endemic settings and suggests that a proportion of individuals classified as TB-negative may actually suffer from NTM disease. It also emphasized the need to strengthen NTM surveillance, expand species-level diagnostic capacity, and use whole-genome sequencing to better understand NTM epidemiology, transmission dynamics, and clinical relevance in Africa.

Socio-behavioral drivers of mpox risk in the Republic of Congo: a cross-sectional analysis of knowledge, attitudes, and practices



Dr. Claujeans Chastel Mfoutou Mapanguy from Fondation Congolaise pour la Recherche Médicale, Republic of Congo, presented the results of a cross-sectional study investigating the socio-behavioral drivers of mpox risk in the Republic of Congo. Conducted in response to the growing mpox burden and the limited availability of local data to guide risk communication strategies, the study aimed to assess knowledge, perceptions, and practices related to mpox among populations living in endemic and neighboring areas. The analysis was based on the socio-

ecological systems framework and covered districts in Likouala, Cuvette, Plateaux, and Brazzaville. A structured questionnaire was administered to adult participants to collect information on socio-demographic characteristics, knowledge of mpox, risk perception, and preventive and healthcare-seeking behaviors.

The results revealed substantial knowledge gaps within the surveyed population. Only 5% of participants demonstrated good knowledge of mpox, while more than half had never been exposed to mpox-related information. Although 45% expressed concern about the disease, misconceptions remained common: 29% believed mpox was not real and 34% approved discrimination against infected individuals. Nevertheless, willingness to adopt preventive measures was encouraging, with 56.3% reporting acceptance of mpox vaccination. Trusted sources of information included radio, television, and healthcare workers.

The study concluded that mpox prevention in the Republic of Congo is hindered more by knowledge gaps and structural barriers than by resistance to public health measures. Strengthening community engagement, improving access to reliable information, and implementing integrated socio-ecological interventions were identified as key priorities for enhancing mpox preparedness and response.

Prospective pediatric CAP cohort integrating serial biomarker measurements, pathogen detection, and a longitudinal biobank to investigate disease severity and recovery



Pr. Graciela Russomando from National University of Asunción, Paraguay, presented a prospective pediatric cohort study conducted in Paraguay to improve the understanding of community-acquired pneumonia in hospitalized children. The project combines serial biomarker measurements, pathogen detection, clinical follow-up, and the establishment of a longitudinal biobank to investigate disease severity, treatment response, and recovery processes. The study follows patients at three key time points: hospital admission, 48 hours after treatment initiation, and discharge, allowing researchers to characterize changes in host inflammatory responses throughout the course of illness.

The main objectives are to describe the inflammatory profile of children with CAP, identify biomarkers associated with disease severity and progression, evaluate predictors of favorable treatment response, and develop prognostic models integrating clinical and biological data. Particular attention is given to pathways involved in innate immunity, tissue injury, immune regulation, and vascular activation.

Microbiological analyses revealed a substantial burden of respiratory pathogens and co-infections. Among 103 nasopharyngeal swabs, 26 *Streptococcus pneumoniae* isolates were recovered, of which 20 showed resistance to at least one antibiotic and 6 were multidrug-resistant to more than five antibiotics. Viral and bacterial co-infections were also frequently detected using multiplex diagnostic technologies.

The study demonstrated that serial monitoring of biomarkers such as high-sensitivity C-reactive protein, procalcitonin, and leukocyte counts provides more informative insights than single measurements at admission. The resulting cohort and biobank represent a valuable platform for future biomarker discovery and for advancing personalized approaches to pediatric pneumonia management.



Dr. Rayane Rafei, from the Lebanese University, Lebanon, presented a multicenter cross-sectional study investigating the prevalence, virulence factors, and antimicrobial susceptibility of *Clostridium perfringens* in North Lebanon using a One Health approach. The study addressed an important knowledge gap regarding the circulation of this foodborne pathogen across human, animal, and food sources in the Middle East and North

Africa region. *C. perfringens* is a spore-forming anaerobic bacterium capable of causing foodborne illness, gas gangrene, and enteric diseases in both humans and livestock.

A total of 490 samples were collected, including 167 human diarrheal stool samples, 300 raw meat samples, and 23 cattle stool samples from hospitals, butcher shops, and farms in North Lebanon. Isolates were cultured under anaerobic conditions, identified by MALDI-TOF, characterized for neuraminidase genes, tested for antimicrobial susceptibility according to EUCAST guidelines, and analyzed using IR-Biotyper strain typing.

The highest prevalence of *C. perfringens* was observed in cattle stool samples (50%), followed by acute diarrhea cases (23.7%), hospital-acquired diarrhea cases (15.7%), and raw meat samples (5.7%). Neuraminidase genes were highly prevalent, with all raw meat isolates carrying *nanI*, *nanH*, and *nanJ*. Most isolates remained susceptible to commonly used antibiotics, although resistance to clindamycin, moxifloxacin, and tigecycline were detected in some strains. IR-Biotyper analysis revealed both genetic diversity and clustering among isolates, suggesting multiple circulating strain profiles.

The study highlights the value of a One Health framework for understanding transmission pathways of *C. perfringens* and supports future investigations using whole-genome sequencing, toxinotyping, and environmental sampling to strengthen surveillance and prevention strategies

GABRIEL NETWORK INTERNATIONAL MEETING

June 4–5, 2026

The GABRIEL network: main achievements



Dr. Florence Komurian-Pradel, from the Mérieux Foundation presented an overview of the GABRIEL network, an international scientific consortium coordinated by the Mérieux Foundation that brings together 22 research institutions, universities, hospitals, and NGOs across Africa, Asia, and South America. The network aims to strengthen local research and surveillance capacities in low- and middle-income countries through collaborative projects, capacity building, and South–South partnerships focused on infectious diseases of major public health importance.

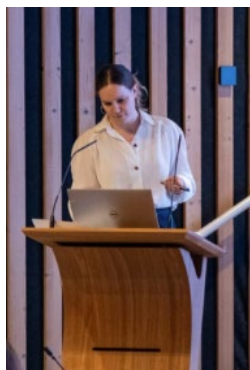
The GABRIEL network's activities are centered on key thematic areas, including tuberculosis, antimicrobial resistance (AMR), acute respiratory infections, and emerging pathogens. Current multicountry projects address innovative tuberculosis diagnostics, AMR surveillance in humans and animals, climate change impacts on antimicrobial resistance, and respiratory pathogen epidemiology and biomarker discovery. The network supports these efforts through seed funding, external partnerships, scientific meetings, webinars, and specialized working groups.

A major component of the network is capacity strengthening. The GABRIEL network promotes laboratory quality improvement, training workshops, e-learning activities, doctoral fellowships, and the Young Scientist Award program. Since 2019, thirteen doctoral scholarships have been awarded, while fourteen young researchers have received scientific awards recognizing outstanding contributions. The network has also produced nearly one hundred collaborative scientific publications since 2012.

The presentation also highlighted strategic partnerships, including collaboration with Fiocruz, which aims to strengthen research on arboviruses and wastewater-based epidemiology. Finally, participants were introduced to three One Health working groups focused on tuberculosis transmission, antimicrobial resistance in poultry production

systems, and multidrug-resistant bacteria at the patient–healthcare worker–hospital interface, laying the groundwork for future collaborative projects and funding opportunities.

Applying biostatistics to support the GABRIEL network



Emilie Westeel from the Mérieux Foundation, presented an overview of the bioinformatics, biostatistics, and training activities implemented within the GABRIEL network to support partner laboratories in the analysis and interpretation of increasingly complex research datasets. As sequencing technologies become more accessible, many laboratories are now able to generate large volumes of genomic and epidemiological data. However, transforming this data into meaningful, reproducible, and actionable public health information remains a significant challenge.

The presentation highlighted three complementary areas of support: bioinformatics, biostatistics, and capacity strengthening. Activities in bioinformatics include pathogen characterization, antimicrobial resistance analysis, phylogenetic investigations, and the development of reproducible analysis pipelines using Illumina and Nanopore sequencing data. Biostatistical support encompasses data management, visualization, statistical modelling, diagnostic test evaluation, sample size calculation, and assistance with scientific publications and reporting. Capacity-building activities focus on strengthening analytical autonomy through training in R, statistics, command-line tools, workflow reproducibility, and next-generation sequencing data analysis.

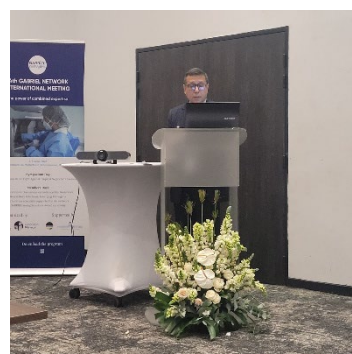
Between 2025 and 2026, support was provided to teams in eight countries through five training sessions and five research projects, reaching 26 trainees in addition to more than 145 enrollments in the INSEQBIN online bioinformatics course. Practical examples included training on reproducible whole-genome sequencing workflows in Burundi and statistical evaluation of mpox diagnostic assays in the Democratic Republic of Congo.

The presentation emphasized that generating data alone is no longer sufficient. Sustainable impact requires strong analytical capacities, reproducible methodologies, and long-term collaborations that enable laboratories to independently analyze and interpret their own data.

SESSION I: ANTIMICROBIAL RESISTANCE

AMR surveillance with One Health Approach: AMR surveillance in human households and pets: what role do they play in transmission routes?

Study in Bangladesh



Dr. Rofiqur Rahman from the Institute for Developing Science and Health Initiative, Bangladesh, presented a One Health study investigating the potential transmission of antimicrobial-resistant (AMR) bacteria between pregnant women and their companion animals. The research focused on carriage of extended-spectrum β -lactamase (ESBL)-producing *Escherichia coli* during the sixth and ninth months of pregnancy.

Whole-genome sequencing of 95 isolates was used to characterize antimicrobial resistance genes, virulence factors, plasmids, serotypes, and sequence types. The analysis revealed a high prevalence of resistance determinants, particularly *bla*CTX-M-15, *bla*TEM-1B, *bla*DHA-1, and the quinolone resistance gene *qnrS1*, together with several virulence genes and multidrug resistance-associated plasmids. Considerable genetic diversity was observed among the isolates. However, despite the widespread presence of AMR genes in both human and animal samples, genomic analysis found no significant overlap between mother-animal pairs and no evidence of direct transmission. The study highlighted the circulation of important AMR determinants in households and demonstrated the value of a One Health approach for AMR surveillance

Study in Brazil



Dr. Nazareno Scaccia from the University of São Paulo, Brazil,

presented the Brazilian arm of the project, conducted in São Paulo. The study assessed the prevalence and genetic characteristics of ESBL-producing *E. coli* in pregnant women and companion animals. Among 180 women sampled at six months of pregnancy, 8.3% carried ESBL-producing *E. coli*, while prevalence decreased to 2.5% among 122 women sampled at nine months. ESBL-producing isolates were also detected in pets, although at lower frequencies.

Whole-genome sequencing of 23 isolates identified several clinically relevant *bla*CTX-M variants and revealed substantial genomic diversity, including sequence types such as ST131 and ST744 in both humans and animals. No identical ESBL-producing strains were detected in the same host over time, and genomic comparisons provided no evidence of direct pet-to-human transmission. The findings nevertheless confirmed the circulation of important resistance determinants in both populations and highlighted the need for further investigation of household transmission dynamics.

Study in Paraguay

Dr. Graciela Russomando, on behalf of Dr. Rosa Guillen from the Instituto de Investigaciones en Ciencias de la Salud in Paraguay, presented the Paraguayan component of the study. Conducted in the Central Department of Paraguay, the cohort included 59 pregnant women and 31 companion animals at six months of pregnancy, with follow-up of 38 women and 18 pets at nine months. The prevalence of ESBL-producing *E. coli* was higher than that observed in Brazil, reaching 15.3% and 18.4% among women at six and nine months, respectively, while prevalence among pets increased from 16.1% to 33.3%. Longitudinal analyses revealed dynamic patterns of acquisition and clearance of ESBL colonization in both women and animals. Whole-genome sequencing of 22 isolates showed high genetic variability, with *bla*CTX-M-15 and *bla*CTX-M-55 as the predominant ESBL genes. Most isolates were multidrug resistant, and all carried the *mdf(A)* efflux pump gene associated with resistance to multiple antimicrobial classes. Genomic comparisons did not support direct transmission between women and their pets, emphasizing the complexity of AMR circulation in community settings and the importance of integrated One Health surveillance.

Genome-based insights into extended spectrum β -lactamase and carbapenemase-producing *Escherichia coli* involved in urinary tract infections (UTIs) in Yaoundé, Cameroon

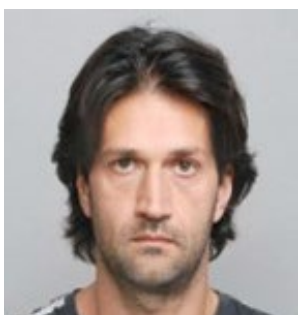


Dr. Pierrette Simo from the Centre Pasteur du Cameroun, presented the results of a genomic study on ESBL- and carbapenemase-producing *Escherichia coli* associated with urinary tract infections (UTIs) in Yaoundé, Cameroon. She first highlighted the growing global burden of UTIs and the increasing challenge posed by antimicrobial resistance, particularly in Cameroon, where genomic data on uropathogenic *E. coli* remain scarce. The study was conducted between September 2024 and March 2025 through a collaboration between the Centre Pasteur du Cameroun and four referral hospitals in Yaoundé. Among 121 multidrug-resistant *E. coli* isolates collected from both hospital and community settings, whole-genome sequencing was performed on a subset of 63 ESBL-producing strains. The findings revealed extensive resistance to multiple antibiotic classes and a predominance of the ESBL gene *bla*CTX-M-15. Carbapenemase genes, including *bla*NDM-1, *bla*NDM-5 and *bla*OXA-181, were also detected in both sectors.

Genomic characterization identified several high-risk and emerging clones, notably ST131, ST410, ST156, ST73 and ST1193, as well as a predominance of strains belonging to the virulent B2 phylogroup. Phylogenetic analyses demonstrated strong genetic similarities between hospital and community isolates, suggesting possible circulation of resistant strains between the two settings.

Dr. Pierrette Simo concluded that the spread of hypervirulent and multidrug-resistant *E. coli* strains underscores the urgent need for genomic surveillance, early detection of antimicrobial resistance, and strengthened prevention and control strategies to mitigate the impact of antimicrobial resistance in Cameroon.

Evaluation of a rapid diagnostic test for detecting antibiotic resistance in bacteria responsible for community-acquired urinary tract infections in Madagascar



Dr. Milen Milenkovic from the Mérieux Foundation, presented the ESBL-UTI project, a prospective study conducted in primary healthcare facilities in Antananarivo, Madagascar, addressing the growing challenge of extended-spectrum beta-lactamase (ESBL)-producing *Escherichia coli* in urinary tract infections (UTIs). The high prevalence of community-acquired ESBL-producing strains in Madagascar reduces the effectiveness of commonly prescribed third-generation cephalosporins and contributes to inappropriate antibiotic use.

The study aims to evaluate the clinical utility of the NG-Test® CTX-M MULTI, a rapid point-of-care test that detects CTX-M-type ESBLs directly from urine samples. Approximately 900 patients presenting with UTI symptoms will be enrolled to assess ESBL prevalence, describe

antibiotic prescribing practices, and determine the diagnostic performance of the test compared with standard culture-based methods.

In parallel, bacterial isolates will undergo phenotypic and genomic characterization to identify antimicrobial resistance mechanisms and examine potential links with strains circulating in the community, building on data generated through the WHO Tricycle surveillance initiative.

The project is expected to generate important evidence on the feasibility and impact of implementing rapid antimicrobial resistance diagnostics in routine care in low-resource settings. By supporting more appropriate antibiotic prescribing, it has the potential to strengthen antimicrobial stewardship and improve patient outcomes.

SESSION II: RESPIRATORY INFECTION

Epidemiological insights and respiratory microbiome diversity in upper acute respiratory tract infections: assessing risks in the aftermath of the COVID-19 pandemic



Dr. Rofiqur Rahman from the Institute for Developing Science and Health Initiatives in Bangladesh, presented a study exploring the epidemiology of acute upper respiratory tract infections (URTIs) and respiratory microbiome diversity in Bangladesh in the post-COVID-19 era. The presentation emphasized the substantial global burden of acute respiratory infections and the complex interactions between host, pathogen, and environmental factors that influence disease transmission and severity. Particular attention was given to the context of Bangladesh, where high population density, air

pollution, widespread malnutrition, passive smoking, and the use of biomass fuels may contribute to an increased burden of respiratory disease.

The study was designed as a 24-month prospective case-control investigation aimed at assessing respiratory microbiome diversity and its association with URTI severity. The objectives include comparing microbial profiles between symptomatic cases and healthy controls, identifying microbiota patterns linked to disease severity, and characterizing pathogens, antimicrobial resistance genes, virulence factors, and emerging variants through shotgun metagenomic sequencing. Clinical and laboratory work is being conducted at ideSHi in Bangladesh, with metagenomic analyses performed in collaboration with CML in China.

He reported that recruitment and sample collection had been completed, including 300 cases and 150 controls. Primary PCR screening of the first samples detected viral pathogens more frequently than bacterial pathogens, with Influenza A showing similar detection rates in symptomatic and control groups, while RSV and bacterial pathogens were detected at low frequencies.

This project is expected to address important post-pandemic knowledge gaps by characterizing microbiome changes, pathogen diversity, and antimicrobial resistance

patterns in Bangladesh. The integration of microbiomes and clinical data may contribute to a better understanding of respiratory disease severity and support the development of more targeted prevention and treatment strategies.

Host biomarkers for RSV severity and diagnosis



Dr. Marilda Siquiera from Fiocruz, Brazil, presented a collaborative project aimed at identifying and evaluating human biomarkers associated with the clinical severity of respiratory syncytial virus (RSV) infection in Brazil. She first highlighted the epidemiological importance of RSV and its seasonal circulation across different Brazilian regions, emphasizing the burden of severe acute respiratory infections caused by the virus.

The project, developed in collaboration with the Christophe Mérieux Laboratory in China, seeks to establish a structured RSV biorepository containing respiratory and serum samples stratified according to disease severity. Its main objectives are to identify biomarkers associated with RSV diagnosis and severity, quantify selected molecular targets including osteopontin, p53 and CXCL4, characterize inflammatory cytokine profiles, and evaluate associations with viral load, RSV subgroups, and clinical outcomes.

The study will enroll participants of all age groups and classify them into RSV-negative controls, RSV-positive mild cases, and RSV-positive severe cases. Comprehensive demographic, clinical, and virological data will be collected, including hospitalization status, intensive care admission, respiratory support requirements, clinical outcomes, and RSV subtype. Biomarker analyses will be performed using ELISA, RT-qPCR, and viral genomic investigations, supported by multivariate statistical approaches.

She reported that the project relies on an expanding network of national collaborators, including several hospitals and research institutions across Brazil. Expected outcomes include the validation of biomarkers for RSV diagnosis and severity, the creation of a database to support future research, integration into international collaborative studies, publication in peer-reviewed journals, and presentation of findings at scientific conferences. She also noted current limitations, including restricted availability of serum samples and ongoing ethical approval processes for new study sites.



Dr. Lili Ren from Christophe Mérieux Laboratory, National Institute of Pathogen Biology, China addressed the pathogenesis of respiratory syncytial virus (RSV) infection and the identification of biomarkers associated with severe disease. RSV is a major cause of respiratory tract infections in children and older adults and represents an important global public health burden. Building on previous work describing the epidemiological patterns of RSV in China, including the alternating circulation of RSV-A and RSV-B, she emphasized the need to better understand the mechanisms underlying

severe RSV infection.

To better understand the mechanisms driving severe RSV infection, she presented two complementary research strategies combining functional genomics and single-cell multi-omics approaches. Genome-wide screening identified platelet factor 4 (PF4/CXCL4) as a host factor with strong antiviral activity against RSV. PF4 levels were found to be higher in RSV-infected patients, particularly in severe cases, and PF4 was identified as a candidate biomarker for disease severity. Experimental data also showed that preventive PF4 treatment reduced viral loads and inflammation.

Using optimized single-cell RNA sequencing, an atlas of more than 330,000 cells was generated from airway and peripheral blood samples. The analyses revealed that immune characteristics in the airway differed markedly from those observed in peripheral blood. Significant differences between mild and severe cases were observed in airway immune cell populations, while peripheral blood showed limited changes. Specific macrophage subsets were associated with disease severity.

Dr. Lili Ren concluded that these findings provide new insights into RSV pathogenesis from a single-cell perspective and support the identification of PF4 as a promising biomarker of severe RSV infection.

Evaluating innovations for the differential diagnosis of tuberculosis and pneumonia among children in Bangladesh (RISK4KIDS)



Dr. Zakir Hossain from the Bangladesh Institute of Tropical and Infectious Diseases, presented the RISK4KIDS study, which aims to improve the differential diagnosis of tuberculosis (TB) and pneumonia among children in Bangladesh. Childhood TB and pneumonia remain major causes of morbidity and mortality, particularly in low- and middle-income countries, where overlapping clinical symptoms and limitations of current diagnostic methods frequently lead to misdiagnosis, inappropriate treatment, and increased antimicrobial resistance.

The study evaluates two innovative non-sputum-based triage tools: the RISK6 blood transcriptomic signature and digital chest X-ray combined with qXR computer-aided detection. RISK6 is a host RNA-based biomarker measuring six immune-related transcripts, while qXR uses artificial intelligence to support standardized interpretation of chest radiographs. The primary objective is to assess the feasibility, acceptability, and diagnostic accuracy of these tools, individually and in combination, for differentiating TB from pneumonia in children under 10 years of age.

This multicenter study is being conducted at the Bangladesh Institute of Tropical and Infectious Diseases (BITID) and icddr,b, with laboratory analyses performed at the Rodolphe Mérieux Laboratory. Participants undergo clinical assessment, blood testing, microbiological investigations, digital chest X-rays, and RISK6 analysis.

As of May 2026, 121 children had been enrolled at the BITID site, including 83 presumptive pneumonia cases and 38 presumptive TB cases. Five TB cases were confirmed, while all pneumonia cases received treatment and recovered. Technical challenges have delayed qXR and RISK6 analyses, but these issues are being resolved. The study is expected to provide important evidence on the feasibility and diagnostic performance of RISK6 and qXR,

and to determine whether their combined use can improve early and accurate differentiation between TB and pneumonia in children. Such innovations could support better clinical decision-making, reduce inappropriate treatments, and inform future diagnostic strategies in resource-limited settings.

Zoonotic aspects of tuberculosis in the southeast region of Madagascar



Dr. Joëlle Razafimahefa from the Faculty of Medicine of Fianarantsoa, Madagascar, presented a One Health study investigating the zoonotic aspects of tuberculosis (TB) in the Haute Matsiatra region of southeast Madagascar, an area characterized by extensive zebu farming, rich wildlife biodiversity, and a substantial burden of extrapulmonary tuberculosis (EPTB). The study was designed to assess the burden of zoonotic tuberculosis (zTB) and bovine tuberculosis (bTB), identify circulating *Mycobacterium* strains, investigate possible interspecies transmission, and evaluate knowledge and practices among populations at risk.

The project adopted a cross-sectional approach and involved human, animal, and wildlife components. Human patients presenting histopathological lesions compatible with EPTB were recruited through 34 primary healthcare centers and two university hospitals. Parallel investigations were conducted in zebu cattle at the main slaughterhouse of Fianarantsoa, while wildlife surveillance included fecal sampling from lemurs and fossas in protected areas. Samples with suspected TB lesions were analyzed using GeneXpert, culture, and molecular characterization methods.

Preliminary findings showed that 52 of 155 human cases (33.5%) were diagnosed as EPTB, with 28 GeneXpert-positive MTBC cases and a culture confirmation rate of 12.1%. Among 179 examined zebus, 20 cases of bovine TB (11.2%) were identified, including 11 GeneXpert-positive cases and a culture positivity rate of 22.2%. MTBC DNA was also detected in wildlife samples, including lemurs, while ongoing surveys revealed limited awareness of zTB and risky practices among exposed occupational groups, particularly abattoir workers.

The study highlights the potential importance of zoonotic transmission at the human-livestock-wildlife interface and underscores the need for strengthened One Health surveillance, improved awareness, and enhanced collaboration between public health and veterinary sectors. Future genomic analyses are expected to clarify transmission pathways and support evidence-based TB control strategies in Madagascar.

Evaluation of a rapid respiratory test and a rapid salivary test, non-invasive, for the screening and treatment monitoring of tuberculosis in Cameroon and Madagascar (LAM4RO project)



Dr. Valerie Flore Donkeng Donfack, from the Centre Pasteur du Cameroun introduced the LAM4RO project, a multicountry operational research study conducted in Cameroon and Madagascar to evaluate innovative, non-invasive approaches for tuberculosis (TB) diagnosis and treatment monitoring. The project explores the use of lipoarabinomannan (LAM), a *Mycobacterium tuberculosis* antigen detectable in exhaled breath condensate and saliva, as an alternative to sputum-based diagnostics that are often difficult to implement in community settings.

The study includes two cohorts: patients with microbiologically confirmed pulmonary TB followed throughout treatment, and household contacts monitored over 18 months to identify active or subclinical TB. Clinical information and biological samples are collected at scheduled visits and analysed using LAM-based tests. Diagnostic performance is evaluated against national standard-of-care algorithms, with laboratory analyses conducted in a blinded manner.

The project aims to generate evidence on the sensitivity, specificity, operational feasibility, and cost-effectiveness of respiratory and saliva-based LAM testing under real-world conditions. By facilitating early detection, decentralized screening, and treatment monitoring through easy-to-collect samples, LAM4RO has the potential to address important gaps in TB diagnosis and contribute to more effective TB control strategies in high-burden settings.

YOUNG SCIENTIST AWARD SESSION

RISK6 transcriptomic signature predicts progression to active Tuberculosis and improves risk stratification among household contacts in Cameroon and Madagascar



Etienne Yuh Jam from Centre Pasteur du Cameroun, presented research on the use of the RISK6 host blood transcriptomic signature, as a tool to identify household contacts at increased risk of developing active tuberculosis. The work was conducted within a prospective cohort of household contacts in two high-burden African settings and addressed a key challenge in tuberculosis prevention: distinguishing individuals who are merely infected from those who are most likely to progress to disease.

The study compared the performance of RISK6 with conventional tests currently used for tuberculosis infection assessment and examined its added value for risk stratification.

Results highlighted the ability of transcriptomic approaches to capture biological processes associated with disease progression rather than simple evidence of exposure. The findings suggested that RISK6 may provide clinically relevant information for identifying individuals who could benefit most from targeted preventive interventions.

Additional analyses evaluated the combination of RISK6 with existing diagnostic tools and explored its role alongside demographic and clinical factors. The overall results support the use of transcriptomic biomarkers as a promising avenue for precision prevention strategies. The presentation concluded that further validation in larger populations and diverse epidemiological settings is warranted, as well as continued efforts to simplify implementation in resource-limited environments and to assess its operational and economic feasibility for tuberculosis control programs.

Challenges in schistosomiasis diagnostics: comparing UCP-LF CAA and POC-CCA in preschool-aged children in three endemic regions of Madagascar



Matthieu Razafindralav from the Charles Merieux Center of Infectious Disease in Madagascar, presented a study comparing two antigen-based diagnostic tools, the Point-of-Care Circulating Cathodic Antigen (POC-CCA) test and the Up-Converting Phosphor Lateral Flow Circulating Anodic Antigen (UCP-LF CAA) assay, for the detection of schistosomiasis in preschool-aged children living in three endemic regions of Madagascar (Bongolava, Itasy and Amoron'i Mania). Schistosomiasis remains a major public

health challenge in Madagascar, where approximately half of the population requires preventive treatment. Conventional parasitological methods often lack sensitivity for detecting low-intensity infections in young children. The study included 2,008 children aged 6 to 24 months recruited from 42 primary healthcare centers between 2020 and 2021. Urine samples were collected, biobanked and tested using both POC-CCA and UCP-LF CAA assays. The analysis compared prevalence estimates and diagnostic concordance between the two methods. Results showed substantial discrepancies between the tests, particularly for POC-CCA "trace" results, which represented about one-third of positive POC-CCA findings and were often not confirmed by UCP-LF CAA. The presentation highlighted the superior specificity and sensitivity of UCP-LF CAA, especially in preschool children, due to its antigen concentration step and quantitative laboratory-based approach.

The findings support the integration of highly sensitive diagnostics such as UCP-LF CAA into surveillance and elimination programs to improve infection mapping, guide control strategies and contribute to the WHO 2030 schistosomiasis elimination goals.

Antimicrobial resistance in *Mycoplasma genitalium*: clinical outcomes and temporal trends from São Paulo, Brazil



Victor Cabelho Passarelli from the University of São Paulo, Brazil, presented research on antimicrobial resistance in *Mycoplasma genitalium*, an emerging but often overlooked sexually transmitted pathogen. The presentation highlighted growing concerns regarding resistance to commonly used antimicrobial classes and the limited epidemiological and resistance surveillance data available in low- and middle-income settings.

The study assessed clinical samples collected in a specialized HIV/STI outpatient setting in Brazil and investigated resistance-associated mutations linked to key therapeutic options. Clinical information and treatment outcomes were also reviewed to

better understand the relationship between antimicrobial resistance and patient management. The analysis explored temporal trends in resistance patterns and examined differences according to clinical presentation.

The findings underscored the importance of strengthening surveillance of *Mycoplasma genitalium* and antimicrobial resistance, as well as the need to adapt diagnostic and treatment strategies in response to evolving resistance patterns. The presentation emphasized the public health implications of emerging resistance in sexually transmitted infections and the challenges it poses for syndromic management approaches. Future directions include expanding national surveillance initiatives, fostering international collaborations, improving awareness among healthcare professionals and communities, and generating evidence to inform clinical guidelines and antimicrobial stewardship strategies.

Genomic and phylogenetic insights of the 2023–2024 dengue outbreak in Bangladesh



Md Ridwan from the Institute for Developing Science and Health Initiatives, Bangladesh, presented genomic and phylogenetic findings from the 2023–2024 dengue outbreak in Bangladesh, the largest dengue epidemic ever recorded in the country, with more than 321,000 reported cases and 1,705 confirmed deaths in 2023.

The study aimed to characterize the viral strains responsible for the outbreak through whole-genome sequencing, phylogenetic analysis, mutation profiling, and evolutionary investigations. A total of 405 dengue patients were enrolled at Kurmitola General Hospital,

Dhaka, and positive samples underwent RT-qPCR serotyping and Nanopore whole-genome sequencing. Most cases occurred between July and November, with the highest burden observed among young adults aged 20 to 35 years.

Results revealed a major serotype shift, with DENV-2 accounting for 69.6% of infections, replacing the previously dominant DENV-3 lineage. Phylogenetic analyses demonstrated extensive regional connectivity while also showing evidence of sustained local transmission.

Nearly all sequenced viruses belonged to the DENV-2 Cosmopolitan genotype, with near-exclusive dominance of lineage 2II_F.1.1. Evolutionary analyses suggested a recent population bottleneck followed by rapid viral expansion with limited adaptive changes.

The findings highlight the importance of integrating genomic surveillance into public health systems to support outbreak preparedness, monitor viral evolution, assess vaccine effectiveness, and guide targeted dengue control strategies in Bangladesh and the region.

Evaluation of humoral and cellular immune responses to influenza and SARS-CoV-2 vaccines: impact of previous immunity, co-administration and population variables



Artur Capão from Oswaldo Cruz Institute - Fiocruz, Brazil, presented research evaluating humoral and cellular immune responses to influenza and SARS-CoV-2 vaccines, with a particular focus on the impact of prior immunity, viral variants, and vaccine co-administration. The study addressed key challenges related to vaccine effectiveness, immune protection, and vaccination strategies following the COVID-19 pandemic.

The investigation assessed antibody and cellular responses in healthy adults receiving influenza vaccines and different SARS-CoV-2 vaccine regimens. Immune responses were measured using hemagglutination inhibition assays for influenza, spike-specific IgG detection, plaque reduction neutralization tests, and flow cytometry activation-induced marker assays. Responses against multiple SARS-CoV-2 variants, including Alpha, Beta, Gamma, Delta, Omicron, Eta, and Iota, were evaluated.

Results demonstrated significant increases in antibody titres following vaccination. Influenza vaccines provided high seroprotection, although responses against influenza B were lower and antibody levels declined after six months, supporting the need for annual vaccination. For SARS-CoV-2, strong humoral and cellular responses were observed, with higher responses following Pfizer vaccination and among previously infected individuals. Immune responses remained broadly effective against the variants studied and showed no significant long-term decline. Co-administration of influenza and COVID-19 vaccines did not negatively affect immunogenicity.

These findings support the safety and effectiveness of co-administration strategies and highlight the beneficial role of prior immunity in vaccine-induced protection.

SESSION III: EARLY CAREER SCIENTISTS SUPPORTED BY THE GABRIEL NETWORK AND THE MÉRIEUX FOUNDATION

Development and evaluation of diagnostic tools for leprosy and other neglected tropical diseases in Madagascar



Jonah Claude Luca Maharavo from the Charles Merieux Center of Infectious Disease in Madagascar, presented ongoing research on the development and evaluation of innovative diagnostic tools for leprosy and other neglected tropical diseases in Madagascar. The work addresses the continued transmission of leprosy in the country, which reports approximately 1,500 new cases annually and remains off track for elimination. The presentation highlighted three complementary research areas. First, the evaluation of host-derived biomarkers, including protein and transcriptomic signatures, to improve diagnosis and distinguish multibacillary from paucibacillary leprosy, thereby supporting more tailored patient management. Preliminary findings showed differential expressions of biomarkers such as anti-PGL-I IgM, CCL4, CRP, ApoA1, and cytokine markers among leprosy patients compared with healthy controls.

Second, a large serological survey is assessing recent *Mycobacterium leprae* transmission among 2,000 schoolchildren aged 5 to 9 years in urban and rural settings using the new PGL-I QURapid rapid test.

Third, molecular surveillance is being conducted to characterize *M. leprae* genotypes and monitor drug resistance using Deeplex Myc-Lep sequencing. Preliminary results confirmed the predominance of genotype ID in Madagascar and identified only one strain carrying a mutation of uncertain clinical significance.

Overall, the project aims to strengthen leprosy diagnosis, surveillance, transmission monitoring, and resistance detection in Madagascar.

Extended-spectrum beta-lactamase-producing *Escherichia coli* at the human-environment-animal interface: experience in Burkina Faso during the first year of implementation of the Tricycle project



Hervé Kafando from the Laboratory of Emerging and Re-emerging Pathogens, Université Nazi Boni, Burkina Faso, presented the first-year results of the WHO Tricycle Project implementation in Burkina Faso, assessing the prevalence and antimicrobial resistance patterns of extended-spectrum beta-lactamase-producing *Escherichia coli* (ESBL-Ec) across the human, animal, and environmental interface using a One Health approach.

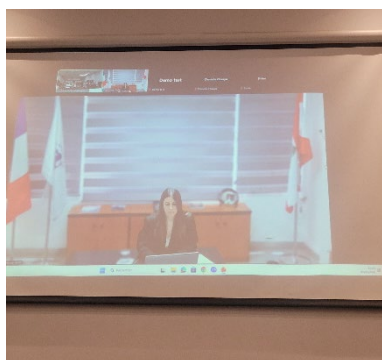
This cross-sectional study was conducted in 2024 in Ouagadougou and Bobo-Dioulasso. Samples included rectal swabs from 465 pregnant women, 3,840 blood cultures, 388 chicken caeca samples, and 49 environmental water samples collected from rivers,

slaughterhouses, and wastewater treatment plants. ESBL-Ec were identified using culture methods, MALDI-TOF identification, and antimicrobial susceptibility testing following EUCAST guidelines.

The results revealed a high prevalence of ESBL-Ec among human carriers (66%) and in environmental waters (77.6%), while prevalence was lower in poultry (29.3%). In bloodstream infections, ESBL-Ec represented approximately 70% of all *E. coli* bacteremia isolates. Wastewater treatment plants reduced bacterial loads by 1.5 to 2 log units but did not eliminate resistant strains. High levels of co-resistance to cotrimoxazole and fluoroquinolones were observed, whereas carbapenems, ceftazidime-avibactam, amikacin, and fosfomycin largely remained effective.

These findings highlight the widespread dissemination of ESBL-Ec in Burkina Faso and underscore the importance of integrated One Health surveillance to guide antimicrobial resistance control strategies

Resistance to new antituberculosis drugs and phylogenetic diversity of the *Mycobacterium tuberculosis* complex: an *in silico* and experimental study conducted in Lebanon.



Marianne Antar from the Rodolphe Mérieux Laboratory in Lebanon, presented an integrated bioinformatic and experimental study investigating the relationship between phylogenetic diversity within the *Mycobacterium tuberculosis* complex (MTBC) and resistance to new and repurposed anti-tuberculosis drugs. The work was conducted in collaboration with the Lebanese National Tuberculosis Reference Laboratory, the National Reference Center for Mycobacteria (CNR-MyRMA) in France, and the IAME Research Unit.

The study focused on genetic determinants of resistance to pretomanid, delamanid, bedaquiline, linezolid, and clofazimine. Using the TB-Annotator platform and a database of approximately 124,000 MTBC genomes, the team performed an *in silico* analysis to identify single nucleotide polymorphisms associated with resistance and assess their distribution across phylogenetic lineages. Particular attention was given to lineage-specific differences, including the reduced susceptibility to pretomanid previously reported in Lineage 1 strains.

Experimental validation was conducted on clinical isolates from Lebanon selected through whole-genome sequencing. A total of 196 high-quality strains were retained for analysis and subjected to minimum inhibitory concentration testing using the EUCAST reference methodology.

The study highlights the importance of integrating phylogenetic information into antimicrobial resistance surveillance and contributes to a better understanding of the mechanisms underlying resistance to novel TB therapies.

Evaluation of innovative approaches to enhance screening of tuberculosis infection and asymptomatic forms of active TB in Cameroon



Erika Londi from the Centre Pasteur du Cameroun presented a research project evaluating innovative non-sputum-based approaches for the early detection of tuberculosis (TB) infection and asymptomatic active TB among household contacts of TB patients in Cameroon and Madagascar. The study addresses a critical diagnostic gap, as a large proportion of TB infections and active TB cases remain asymptomatic and therefore escape conventional screening strategies.

The project investigates two novel diagnostic approaches: detection of lipoarabinomannan in exhaled breath condensate using the LIODETECT® point-of-care assay, and detection of *Mycobacterium tuberculosis* DNA in peripheral blood mononuclear cells using digital PCR. A secondary objective is to characterize TB transmission patterns through next-generation sequencing of clinical isolates.

Preliminary retrospective analyses included household contacts followed for 18 months in the APRECIT cohort. Close contact with the index case was the strongest risk factor for progression to active TB. Traditional infection markers, including tuberculin skin test positivity and quantitative T-SPOT.TB responses, as well as host biomarkers such as BATF2 and a three-gene TB score, were associated with subsequent disease progression. In contrast, blood-based *M. tuberculosis* DNA detection showed limited discriminatory performance when used alone.

The findings support the development of a multi-marker screening strategy combining microbial and host biomarkers to improve early identification of individuals at risk of TB before symptom onset.

Spotlight on Brucella epidemiology in Lebanon: A One Health approach



Fatima Fayad from the Microbiology, Health and Environment Laboratory, Lebanon, presented a One Health research project investigating the epidemiology of brucellosis in Lebanon, where the disease remains endemic with approximately 300 reported cases annually and recurrent outbreaks linked to animal contact and consumption of unpasteurized dairy products.

The project aims to estimate the prevalence of *Brucella* infection in humans, livestock, and dairy products; characterize circulating species, clones, and antimicrobial resistance profiles; identify transmission risk factors; and support integrated control strategies.

The study combines microbiological, serological, molecular, and epidemiological approaches, including strain characterization by MALDI-TOF, PCR, antimicrobial susceptibility testing, and planned whole-genome sequencing.

Preliminary analyses of a strain collection maintained between 2011 and 2025 revealed concerning resistance patterns, with all tested isolates resistant to ciprofloxacin and 85% resistant to trimethoprim-sulfamethoxazole.

The presentation also reported findings from a retrospective clinical study conducted at Nini Hospital in North Lebanon. Among 3,504 individuals tested between 2013 and 2025, 108 confirmed brucellosis cases were included. The study described demographic characteristics, clinical manifestations, complications, diagnostic challenges, and treatment outcomes, including rare cases of neurobrucellosis and *Brucella spondylitis* with epidural abscess.

Overall, the work highlights the need for integrated human-animal-food surveillance to improve understanding of transmission dynamics and strengthen brucellosis control in Lebanon.

The GABRIEL network Young Scientists Award ceremony

The Mérieux Foundation's GABRIEL network Young Scientist Award is a key initiative that supports the next generation of scientists and encourages excellence in research among early-career investigators.

The two award recipients were selected based on the scientific merit, originality, and public health relevance of their research, as well as the clarity and quality of their presentations.

Following a thorough evaluation and careful deliberation, the jury members, Dr. Lili Ren, Dr. Graciela Russomando, Dr. Rayanne Rafei, Pr. Abdoul-Salam Ouedraogo, and Dr. Zakir Hossain, decided to confer the 2026 GABRIEL network Young Scientist Award to:

Mr. Etienne Yuh Jam from Centre Pasteur du Cameroun, for his presentation on "RISK6 transcriptomic signature enhances detection of latent TB and accurately predicts progression to active tuberculosis in a Cameroonian cohort"

Mr. Victor Cabelho Passarelli, from the Institute of Tropical Medicine, Sao Paulo University, Brazil, for his presentation on "Antimicrobial resistance in *Mycoplasma genitalium*: clinical outcomes and temporal trends from São Paulo, Brazil"



Closure of the GABRIEL network international meeting



To close this edition of the GABRIEL network international meeting, **Dr. Robert Seybag**, the vice president of the Mérieux Foundation' expressed his sincere gratitude to all participants for their valuable contributions, commitment, and shared expertise throughout the event.

He emphasized that the Mérieux Foundation remains fully committed to advancing public health and strengthening education and capacity-building programs across all member countries.

Bringing together professionals from around the world, including Bangladesh, Brazil, Burkina Faso, Cambodia, Cameroon, China, the Democratic Republic of the Congo, India, Laos, Lebanon, Madagascar, Mali and the Republic of the Congo, and many others, the GABRIEL network demonstrates the strength of international collaboration. Despite our diverse cultures and contexts, we face many of the same public health challenges. The world is interconnected, and our collective response must be equally united.

He reminded participants that every GABRIEL network member is an ambassador of this unique community, sharing a common vision and a common purpose: improving health for all through cooperation, knowledge sharing, and innovation.

Finally, he reflected on the meaning of the name Gabriel, known as a messenger and an angel in many religions and cultures around the world. In this spirit, he described the GABRIEL network as "the angel of the Mérieux Foundation", carrying its values, its message of solidarity, and its commitment to serving communities worldwide.