Pasteur Network Annual Meeting

2025

October 21-23
Ho Chi Minh City
Vietnam

40 UNDER 40
PNAM 2025

PASTEUR NETWORK

Pasteur Institute in Ho Chi Minh City

Xin chào,

We warmly thank the Pasteur Institute in Ho Chi Minh City for hosting the 2025 Pasteur Network Annual Meeting in this vibrant and dynamic city. As Vietnam's largest metropolis and economic center, Ho Chi Minh City is a fascinating blend of rich history, bustling markets, delicious street food, and modern innovation.

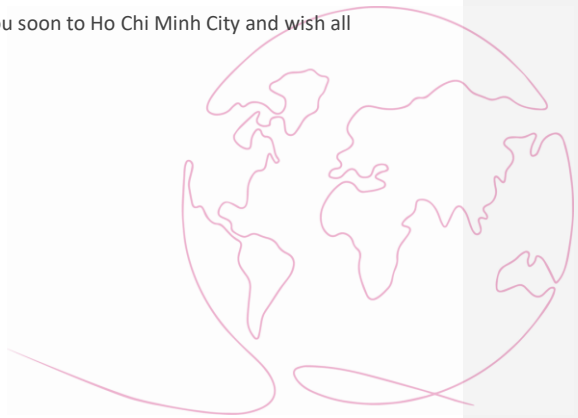
Vietnam itself is a land of stunning natural beauty and deep cultural heritage. It is also home to two other esteemed members of the Pasteur Network: the Pasteur Institute in Nha Trang and in Hanoi, the National Institute of Hygiene and Epidemiology. Together, these institutes play a vital role in advancing scientific research and public health across the region.

For staff of member institutions who are unable to attend in person, we are pleased to offer a virtual link to follow the opening ceremony, on October 21st, 2025. Our goals remain to strengthen the Pasteur Network community through shared research and public health efforts, fostering stronger connections and collaboration among members, and to enhance the Network's international visibility.

On this website, you will find all the essential information to attend the Meeting, including connection links, the program agenda, and updates. We will keep this page regularly updated to ensure you have the latest details.

If you have any questions or need assistance, please don't hesitate to contact our dedicated event organizing team. We look forward to welcoming you soon to Ho Chi Minh City and wish all participants safe travels!

Hẹn gặp lại!



Agenda overview

DAY 1 - Tuesday, October 21st

10:00 Board Meeting ***[Closed Meeting, by invitation only]***

16:00 Registration Opens for All Participants

17:00 Welcome Ceremony & Keynote

Opening remarks

- Madam Lan Hong Dao – *Minister of Health, Vietnam*
- Trung Nguyen – *Director, Institut Pasteur in Ho Chi Minh City*
- Mario Moreira – *President, Pasteur Network*
- Rebecca Grais – *Executive Director, Pasteur Network*
- Yasmine Belkaid – Vice *President, Pasteur Network*

Keynote Speaker

- Shomy Hasan Chowdhury - Award-winning WASH Activist & Co-Founder, Awareness 360

18:45 Cocktail

Agenda overview

DAY 2 - Wednesday, October 22nd

8:00 Welcome & **PNLink**

9:30 Opening remarks - Prof. Huong Lien Thi Nguyen, Deputy Minister of Health, Vietnam

9:40 Talent Award

9:50 **40u40 Plenary Session 1**: Arboviruses: Surveillance, Immunity & Pathogenesis

Moderator: Hichem Ben Hassine - Pasteur Network

- Sebastian Baumgarten - Institut Pasteur, Paris, France
- Idrissa Dieng - Institut Pasteur de Dakar, Senegal
- Enrico Palermo - Institut Pasteur in Italy – Cenci Bolognetti Foundation, Italy
- Hermann Landry Munshili Njifon - Centre Pasteur du Cameroon, Cameroon
- Samar Akbi - Institut Pasteur d'Algérie, Algeria
- Pritesh Lalwani - Fundação Oswaldo Cruz (FIOCRUZ), Brazil

11:00 Coffee Break

11:30 **40u40 Plenary Session 2**: Community Involvement in Research and Surveillance

Moderator: Paula Reges - Pasteur Network

- Wannes Van Hoof - Sciensano, Belgium
- Le Hoang Thieu - Pasteur Institute in Nha Trang, Vietnam
- Grégoire Davigon - Institut Pasteur de Nouvelle Calédonie, New Caledonia

12:15 **Climate & Health Session**

Moderator: Nick Chung - Pasteur Network

- Saren Sovann - Institut Pasteur du Cambodge, Cambodia
- Quang Quan Le - Pasteur Institute in Ho Chi Minh City, Vietnam
- Manilath Nalongsack - Institut Pasteur du Laos, Laos
- Thai Pham - National Institute of Hygiene and Epidemiology (NIHE), Vietnam

13:00 Lunch Period

- Lunch & **PNLink** ***[All Attendees]***
- Regional Working Lunches ***[Closed, by invitation only]***

14:30 **Women in Science**

Moderator: Sophie Diallo - Institut Pasteur de Dakar, Senegal

- Isabella Delgado - Fondation Oswaldo Cruz (Fiocruz), Brazil
- Marième Ndoye - Institut Pasteur de Dakar, Senegal
- Ildikó Csóka - Szeged University, Hungary

15:30 Roundtable: Under 40: "The Early Career Reality Check"

Moderator: Renaud Vatrinet - Pasteur Network

- Le Phan Khoi Nguyen – Pasteur Institute of Ho Chi Minh City, Vietnam
- Cyrine Chenaoui – Institut Pasteur de Tunis, Tunisia
- Gwladys Monamele – Centre Pasteur du Cameroun, Cameroon

16:00 Network & **PNLink** & Coffee Break

17:45 Transfer to PNAM 25 dinner venue ***[Closed, by invitation only]***

23:30 Dinner cruise ends

Agenda overview

DAY 3 - Thursday, October 23rd

8:30 Coffee - **PNLink**

9:30 **40u40 Plenary Session 3**: Respiratory Viruses: Detection, Surveillance & Immunity

Moderator: Yanis M'Zali – Institut Pasteur, Paris, France

- Wuji Zhang - Hong Kong University - Pasteur Research Pole, Hong Kong
- Ali Maleki - Institut Pasteur in Iran, Iran
- Pham Van Khang - National Institute of Hygiene and Epidemiology (NIHE), Vietnam
- Karidja Yakoura - Institut Pasteur de Côte d'Ivoire, Côte d'Ivoire
- Dung Truong Thi Thuy - Pasteur Institute in Ho Chi Minh City, Vietnam

10:20 **40u40 Plenary Session 4**: Enteroviruses & Emerging Viruses

Moderator: Meryem Lemrani - Institut Pasteur du Maroc, Morroco

- Joël Dote - Institut Pasteur de Bangui, Central African Republic
- Anna Dolgova - Saint-Petersburg Pasteur Institute, Russia
- Chittaphone Vanhnollat - Institut Pasteur du Laos, Laos

11:00 Coffee Break

11:30 **Roundtable:** "When I Was in Your Shoes"

Moderator: Rebecca Grais - Pasteur Network

- Samia Menif - Institut Pasteur de Tunis, Tunisia
- Ehsan Mostafavi - Institut Pasteur in Iran, Iran
- Christophe Peyrefitte - Institut Pasteur de la Guyane, French Guyana
- Leo Poon - The University of Hong Kong - Pasteur Research Pole (HKU-PRP), Honk Kong

12:00 Vaccine Manufacturing in the Network

Moderator: Marco Nascimento - Fundação Oswaldo Cruz (FIOCRUZ), Brazil

- Ndeye Mareme Ba - Institut Pasteur de Dakar, Senegal
- Khalid Zemzoumi - Institut Pasteur du Maroc, Morocco
- Safouane Benazzouz - Institut Pasteur d'Algérie, Algeria
- Dionyssios Sgouras - Hellenic Pasteur Institute, Greece

13:00 Lunch & **PNLink**

14:00 **40u40 Plenary Session 5**: Bacteria & Microbiota

Moderator: David Chatenet - INRS - Armand-Frappier Santé Biotechnologie Research Centre, Canada

- Sébastien Bontemps-Gallo - Institut Pasteur de Lille, France
- Antsa Harinavalona Rakotonirina - Institut pasteur de Madagascar, Madagascar
- Isaure Quétel - Institut Pasteur de Guadeloupe, Guadeloupe
- Nikolaos Vakirlis - Hellenic Pasteur Institute, Greece
- Siyeon Yang - Institut Pasteur Korea, Korea
- Iliyan Manoylov - Stephan Angeloff Institute of Microbiology, Bulgaria
- Sokleaph Cheng - Institut Pasteur du Cambodge, Cambodia

15:30 Coffee Break

16:00 **40u40 Plenary Session 6**: Parasites

Moderator: Jose Badano - Institut Pasteur de Montevideo, Uruguay

- Aissata Camara - Institut Pasteur de Guinée, Guinea
- Florencia Díaz Viraqué - Institut Pasteur de Montevideo, Uruguay
- Ryan D. Pardy - INRS, Canada
- Emna Harigua - Institut Pasteur de Tunis, Tunisia
- Imane El Idrissi Saik - Institut Pasteur du Maroc, Morocco
- Celia Florimond - Institut Pasteur de la Guyane, Guyana
- Mamane Salé Noura - CERMES, Niger

17:00 Wrap-Up!

17:45 Transfer to Pasteur Institute of Ho Chi Minh City

18:15 Cocktail and visit of Pasteur Institute HCM - ends 9 pm

Agenda overview

DAY 4 – Friday, October 24th

10:00 General Assembly of the Pasteur Network ***[Closed Meeting, by invitation only]***

In accordance with the Rules and Procedures, each institution's official representative should be accompanied by no more than one additional participant.

10:00 General Assembly Lunch ***[by invitation only]***

Biographies

Opening remarks and Keynote Speaker

Madam Lan Hong Dao

Minister of Health, Vietnam

Madam Lan Hong DAO is the Minister of Health of Vietnam and a member of the 13th Central Committee of the Communist Party of Vietnam. She holds a Master's degree in Economics from the National Economics University and a high-level certificate in political theory. Madam DAO has extensive experience in public administration and political leadership, with nearly three decades of service in the government sector. She began her career at the Ministry of Labour - Invalids and Social Affairs, where she held various senior positions, including Deputy Director-General and Chief of the Ministry's Office. She was then promoted to Deputy Minister of Labour - Invalids and Social Affairs in 2014. In 2018, she was appointed Deputy Secretary of the Bac Ninh Provincial Party Committee and became the province's first female Secretary in 2020.

In October 2022, she was officially appointed Minister of Health. Madam DAO plays a role in leading Vietnam's health sector at the Ministry of Health, particularly in governance, policy-making, and system strengthening. Her leadership continues to shape health administration and intersectoral coordination efforts in Vietnam. She received several awards during her career and has recently been awarded the World No Tobacco Day Award 2025 by WHO for her leadership in efforts to ban electronic cigarettes and heated tobacco products in Vietnam.

Trung Nguyen

Director, Institut Pasteur in Ho Chi Minh City

Associate Professor Trung Vu NGUYEN is the Director of the Pasteur Institute in Ho Chi Minh City, with over two decades of experience in clinical microbiology and infectious disease research. Associate Professor Trung holds a doctoral degree in odontostomatology (1994) and an MSc in microbiology from Hanoi Medical University, a PhD from Karolinska Institute (2005), and completed his post-doc research program in microbiology and molecular biology at Kyoto University (2006). Associate Professor Trung has held prominent academic and leadership roles at Hanoi Medical University, the National Hospital of Tropical Diseases, and the Administration of Science, Technology and Education - the Ministry of Health (Hanoi) at the country level in Vietnam.

His research focuses on antimicrobial resistance, viral and bacterial respiratory infections, vector-borne diseases, and infection control. He led several microbiological research efforts to provide reliable evidence to inform public health responses to outbreaks and emerging infections of H5N1, H1N1pdm, cholera, Streptococcus suis, rickettsial diseases, antimicrobial resistance, and dengue. He is also interested in developing point-of-care diagnostic tests for infectious diseases. A respected scientist and educator, he has made significant contributions to Vietnam's medical education and public health system.

Mario Moreira

President, Pasteur Network

At the Oswaldo Cruz Foundation (Fiocruz) since 1994, Mario Moreira holds a PhD in Public Policy from the Federal University of Paraná, with a doctoral internship at the University of Coimbra, Portugal, and a master's degree in public health from the National School of Public Health Sergio Arouca (Ensp/Fiocruz) and in Technology and Innovation Management from the University of Sussex, UK.

Dr Moreira also holds an MBA in Public Management from the Getúlio Vargas Foundation. In 2017, he became Vice President of Management and Institutional Development at Fiocruz. He was elected President of Fiocruz in March 2023.

Rebecca Grais

Executive Director, Pasteur Network

Rebecca F. Grais is the Executive Director of the Pasteur Network. She previously worked as the Director of Research at Epicentre, an epidemiology and research satellite created by Médecins Sans Frontières, an international medical humanitarian organization. Her primary areas of interest focus on prevention of infectious diseases and emerging infections in low- and middle-income countries. She has particularly focused on population-based studies of the effectiveness of public health interventions and efficacy trials of novel vaccines and therapeutic agents. An additional aspect of her work concerns professional development, mentoring and management training for underrepresented populations in scientific research to advance their individual careers and contribute to adapted healthcare innovations. Dr. Grais holds a doctorate, two masters degrees and a bachelor's degree from Johns Hopkins University She holds a Habilitation à diriger des Recherches from the Faculté de Médecine Paris Saclay (France). She has published over 200 peer-reviewed publications, is a member of diverse scientific, funding and international organization committees and advisory groups with a focus on vaccine development trials, effectiveness and epidemiologic studies among vulnerable populations. She is also a member of the Strategic Advisory Group of Experts at WHO.

Yasmine Belkaid –

Vice President, Pasteur Network

Pr. Yasmine Belkaid is the President of Pasteur Institute (Paris) and the head of the Metaorganism Immunity laboratory at Pasteur Institute. She obtained her Master in Biochemistry at the University of Science and Technology Houari Boumediene in Algiers, Algeria and her PhD from Pasteur Institute in France. Following a postdoctoral fellowship at the National Institute of health (Bethesda) on immune regulation during infection, she started her research program at the Children's Hospital Research Foundation in Cincinnati. In 2005, she joined the National Institute of Allergy and Infectious Diseases (NIAID) where she served as department chair of the Laboratory of Host Immunity and Microbiome, Director of the trans-NIH Center for Human immunology and founder and Director of the NIAID Microbiome program prior to joining Pasteur Institute in 2024.

Her work explores fundamental mechanisms that regulate tissue homeostasis and host immune responses and uncovered key roles for the microbiota and dietary factors in the control of immunity and protection to pathogens. Her work also explores the role of the immune system in organismal remodeling and the impact of infections on maternal child DYAD.

Dr Belkaid is a member of the National Academy of Sciences, the American Academy of Arts and Sciences, the National Academy of Medicine and recipient of numerous awards including the Lurie Prize in Biomedical Sciences, the Emil von Behring Prize, the Sanofi-Institut Pasteur Award, the Robert Koch Award and the AAI Excellence in Mentoring Award.

Shomy Hasan Chowdhury

Award-winning WASH Activist

Shomy Hasan Chowdhury is an award-winning Water, Sanitation and Hygiene (WASH) activist from Bangladesh, and the Co-Founder of the global non-profit Awareness 360, through which she empowers young people across 70+ countries in advancing the UN Global Goals. She is a development professional with over a decade of experience in community development. Her notable recognitions include Forbes 30 Under 30, President's Volunteer Service Award (Gold) by President Barack Obama, Putra Icon Award, and The Diana Legacy Award. She is also the first and only Bangladeshi to sit on the 2021 Diana Legacy Award Judging Panel, a high-level Judge of the UN SDG Action Awards, Global Citizen Advocate, Asia Pacific's first Samsung Global-UNDP Generation17 Leader, McCain Global Leader, Specialist for the CEE program of the US State Department, Global Fellow in Courage by Brown University, Advisor to the Queen Elizabeth Commonwealth Trust, Youth Combating NTDs, Social Enterprise World Forum, and Democracy Moves, and sits in leadership & advisory positions of multiple international organizations. Shomy, an Economics graduate, also holds a Master's in Global Affairs from Tsinghua University in Beijing, China, as a Schwarzman Scholar, one of the most competitive graduate scholarships in the world. In 2018, Shomy was invited to Pakistan as an International Election Observer to observe the Pakistan General Elections, appointed by then Commonwealth Secretary-General Rt Hon Patricia Scotland. Most recently, she has been named a 2025 Young Global Leader by the World Economic Forum.

Shomy, an internationally renowned public speaker, regularly addresses keynotes and has already inspired millions in over 50 countries across 6 continents. She spoke at the Global Citizen Festival in Central Park, New York, addressing a crowd of over 60,000 people. Other remarkable speaking engagements include the likes of the United Nations Headquarters, The White House, Solidays Festival France, Misk Global Forum, Commonwealth Heads of Government Meeting, COP, the Conference of Commonwealth Education Ministers, the Asian Leadership Conference, the Global Baku Forum, and many more. Shomy has been invited to high-level platforms such as the BBC, MSNBC, TEDx, Nasdaq, World Bank, WHO, Forbes, Kensington Palace, Buckingham Palace, Hello!, Humans of Kuala Lumpur, and more.

Prof. Huong Lien Thi Nguyen

Deputy Minister of Health in Vietnam

Assoc. Prof. Huong Lien Thi Nguyen, MD, PhD was appointed Deputy Minister of Health of Vietnam in May 2022. She previously held senior roles at the Ministry of Health, including Director General of the Health Environmental Management Agency (2010–2022), Operational Manager for occupational health and injury (2005–2010), and Health Expert in preventive medicine (1997–2005). She currently serves as a Senior Expert in Preventive Medicine, Health Science Management, and Health Administration.

Dr. Huong holds a Doctor of Medicine from Hanoi Medical University, two Master's degrees in Health Care Administration and Public Health (Nagoya University, Japan; University of London, UK), and a Ph.D. in Social Hygiene and Health from the National Institute of Hygiene and Epidemiology (Vietnam).

With over 26 years of experience, she specializes in preventive medicine, health emergencies, climate and environmental health, and injury prevention. She has authored nearly 200 research papers in leading national and international journals.

40u40 Plenary Session 1: Arboviruses: Surveillance, Immunity & Pathogenesis

Sebastian Baumgarten
Institut Pasteur, Paris, France

I was 100% sure that I would become an ocean explorer and marine biologist pretty much since I went to primary school. This dream was still very much alive when I started studying biology in landlocked southern Germany, so in parallel I trained as a scientific

diver at the German Polar Institute (AWI). The opportunities that came with this training to work as diver on research expeditions in Chilean Patagonia and arctic Svalbard were by far one of my best scientific experiences. Staying true to the marine realm, I joined

the Red Sea Research Center at KAUST in Saudi Arabia for my PhD work, yet I swapped the diving equipment for a computer keyboard and delved into the genomic underlying of corals and their intracellular, symbiotic algae. Being fascinated of how one eukaryotic cell can live and proliferate within another eukaryotic cell is what then ultimately brought me to the malaria parasite.

Plasmodium falciparum evolved seemingly extreme measures in terms of (post-)transcriptional regulation that allows it to efficiently replicate within and transmit between a human host and mosquito vector, making it a unique model to study these processes. The fascination for this parasite keeps growing the more I learn about it, and together with my G5 'Parasite RNA Biology' Team at the Institut Pasteur, we now dive into a new unknown with every day in the lab in the hope that our research on the particular RNA regulatory processes can ultimately benefit those that are affected most by malaria.

Idrissa Dieng

Institut Pasteur de Dakar, Senegal

Dr. Idrissa Dieng is a molecular virologist at the Institut Pasteur de Dakar (IPD), where he conducts research in the Molecular Virology Laboratory under the supervision of Dr. Ndongo Dia. He holds a PhD in Molecular Biology and Virology from Cheikh Anta Diop University in Dakar, preceded by a Master's degree in Genetics and Molecular Biology. His academic journey was driven by a strong interest in infectious diseases, particularly those with epidemic potential in West Africa.

Dr. Dieng has over a decade of experience in the field of viral genomics, diagnostics, and molecular epidemiology. He has authored 36 publications in international peer- reviewed journals. At IPD, he plays a central role in the genomic surveillance of arboviruses, including Dengue, Zika, Chikungunya, and Yellow Fever viruses, using cutting-edge sequencing technologies and bioinformatics tools. His work contributes to early detection, outbreak response, and regional preparedness, aligning closely with the Pasteur Network's strategic axis on "Preparedness and Response to Epidemics." He is actively involved in several national and international collaborations, notably with the Africa CDC, WHO, and the West African Regional Center for Surveillance. Dr. Dieng also contributes to capacity building through the supervision of graduate students and the facilitation of regional training workshops in molecular diagnostics and bioinformatics. Looking ahead, Dr. Dieng aims to expand his research on computational biology, viral evolution and host-pathogen interactions, with a focus on integrating multi-omics approaches to better understand disease emergence and inform public health interventions across the region.

Enrico Palermo

Institut Pasteur in Italy – Cenci Bolognetti Foundation

As an early-career virologist and immunologist, my scientific interest is to investigate the molecular processes underlying type I interferon response to viral infections and the immune evasion strategies adopted by viruses.

I hold an MSc in Medical Biotechnology from Sapienza University of Rome - Policlinico Umberto I Hospital, where I examined the role of residual viremia in people living with HIV during antiretroviral therapy, along with diagnostic activity in viral infectious diseases (HIV, HBV, HDV, Coxsackie Virus).

During my PhD at Institut Pasteur Italy, I developed novel therapeutic approaches to clear latent HIV-1 infection, based on innate immunity stimulation and epigenetic reprogramming.

Currently, my team investigates the mechanisms of immune-escape of SARS-CoV-2 and the effects of cellular metabolism modulation on immune response against Dengue virus infection and in cancers.

Giving the significant contribution of climate change to the spread of infectious diseases into regions that were previously unaffected, a coordinated global response is essential to strengthen pandemic prevention and preparedness. My work aims at determining how cellular metabolism shapes immune response against Dengue virus in order to identify potential biomarkers associated with an increase in viral replication and disease severity.

In my mentorship activity, I am supervising MSc students and co-supervising a PhD candidate from Fiocruz Rondonia (Brazil), in a research project on Alphavirus and Orthobunyavirus in neglected arboviruses.

Looking forward, I aspire to play a leading role in a global, collaborative scientific community committed to addressing future health threats and promoting a diverse, equitable, and inclusive vision of science.

Hermann Landry Munshili Njifon

Centre Pasteur du Cameroon

I hold a Ph.D. in Medical Microbiology (Virology) from the University of Yaoundé I in Cameroon (July 2021) and an International Diploma in One Health (Emerging Infections) from the University of Montpellier in France (2022). My research focuses on zoonotic and emerging infectious diseases, emphasizing surveillance, diagnostics, and public health preparedness. I began my scientific career with an internship at the Centre Pasteur du Cameroun (CPC) in Garoua in 2014 as part of my master's degree program in bacteriology and virology.

Under the mentorship of Prof. Richard Njouom, Head of the Virology Unit, I contributed to influenza surveillance. After graduating, I joined the CPC in Garoua as a project scientist. From 2014 to 2015, I worked on several field-based studies across northern Cameroon, especially those concerning respiratory viruses. In 2016, I began my Ph.D. studies on the genetic characterization of influenza viruses while continuing to contribute to CPC-led surveillance activities. After completing my doctorate, I undertook an NIH-funded postdoctoral fellowship, collaborating with the University of Utah (Prof. Daniel Leung) on the seroepidemiology of cholera, SARS-CoV-2, and arboviruses. Since 2024, I have been a full-time researcher. Currently, I am coordinating the AFRICAM/PREZODE One Health project on arbovirus transmission and contributing to an ERC-funded consortium studying long-term disease dynamics in Africa. My work aligns with the Pasteur Network’s pillars of epidemic preparedness, innovation, and equitable collaboration. I am dedicated to building capacity, promoting gender equity, and mentoring young scientists, positioning CPC Garoua as a regional hub for interdisciplinary research and training.

Samar Akbi
Institut Pasteur d'Algérie, Algeria

I am a Doctor of Pharmacy and Clinical Microbiology Specialist, graduating from the Faculty of Pharmacy of Algiers in December 2024. I completed a four-year residency in Clinical Microbiology at a university hospital in Algiers, where I developed a strong scientific interest in antimicrobial resistance (AMR). During this time, I participated in several leadership programs focused on AMR from a One Health perspective. This experience motivated me to engage actively with various African associations and institutes, where I delivered lectures, organised training sessions and workshops to raise awareness about AMR among young African students from diverse backgrounds. These activities helped shape my leadership, teaching, and scientific communication skills early in my career.

Following my residency, I joined the Virology Department at the Pasteur Institute of Algeria, shifting my focus to vector-borne diseases, particularly West Nile virus (WNV). I was honoured to be selected for the Pasteur Network's Climate and Health

Observatory Accelerator Fellowship, enabling me to integrate climate perspectives into vector-borne disease research. Currently, I am developing a predictive model of WNV circulation in Algeria, utilising climatic and environmental data to enhance the existing national surveillance system. This model aims to improve preparedness by supporting earlier and more targeted preventive interventions. Beyond advancing scientific understanding, this work fosters strong policy engagement through cross-sectoral collaboration on climate and health issues.

Looking ahead, I am committed to sharing the knowledge gained throughout this journey. Leveraging the visibility provided by this fellowship, I aim to raise awareness of climate change's impact on health, strengthen policymaker engagement, and advocate for the integration of climate perspectives across surveillance and public health management of climate-sensitive diseases.

Pritesh Lalwani
Fundação Oswaldo Cruz (FIOCRUZ), Brazil

I trained in biotechnology in India (BSc, 2005), specialized in virology (MSc, 2007), and completed my PhD in Immunology at Charité – Universitätsmedizin Berlin (Dr. rer. nat, 2012). These experiences shaped my focus on viral immunopathogenesis and translational research, which I have since applied to pressing public health challenges in the Amazon.

My research combines field-based surveillance, immunology, and community engagement to study emerging and re-emerging viruses such as Oropouche, Mayaro, hantaviruses, and arboviruses of regional and global concern. I have co-developed diagnostic assays, filed two patents, and published more than 42 peer-reviewed papers. A central theme of my work is applying a One Health perspective to understand how climate change, deforestation, and infrastructure expansion drive zoonotic disease emergence.

This approach directly supports the Pasteur Network's strategic pillars by strengthening epidemic intelligence in climate-sensitive regions, fostering diagnostic innovation, advancing multidisciplinary collaborations, and building equitable partnerships with Indigenous and riverine communities.

Beyond research, I am committed to capacity building and outreach. I mentor MSc, PhD, and postdoctoral researchers, train Indigenous health agents, and developed the course The Art of Reading a Research Paper, which has improved critical analysis and communication skills for students and faculty since 2014. I also contribute to policy, serving on biosafety committees and advising health authorities during the COVID-19 pandemic.

Looking ahead, I aim to consolidate One Health surveillance programs in the Amazon as global exemplars, expand international collaborations, and continue training the next generation of scientists.

Hichem Ben Hassine

Pasteur Network

Hichem Ben Hassine joined the Pasteur Network in April 2024 as Knowledge Sharing platform coordinator. His task is to develop and coordinate a platform who will be open to all the members of the Pasteur Network (PN). The aim of this platform is to facilitate collaboration and communication among the members of the PN and also a tool for sharing knowledge, issues, project ideas, expertise, etc. Hichem is also in charge of the Pasteur Network Monthly Seminars and contribute to several coordination and communication actions within the PN. Before joining the Pasteur Network, he was Head of the Unit "Communication, Science and Society "at the Institut Pasrteur de Tunis for almost 15 years. During this period, he developed and implemented the overall communication and public engagement strategy of the Institut Pasteur de Tunis. Hichem has a background in public and scientific communication and sociology of information/communication.

40u40 Plenary Session 2:
Community Involvement in Research and Surveillance

Wannes Van Hoof
Sciensano, Belgium

Wannes Van Hoof (28/10/1986) studied philosophy and anthropology at KU Leuven. He obtained his PhD in philosophy in 2014 from the Bioethics Institute Ghent titled 'Ethical problems related to cross-border reproductive care'. He worked as a postdoc at Ghent University and Ghent University Hospital on a project about safe and ethical pediatric drug development. He currently works at Sciensano, the Belgian Institute of Public Health. Between 2016-2024 he led a team within the cancer center working on patient/citizen engagement and the ethical aspects of the secondary use of health data, innovative cancer therapies and the implementation of genomic technologies in healthcare. He is currently the head of the Ethical, Legal and Societal Issues (ELSI) unit, focusing on good data governance, AI and cocreation in ELSI. He has given oral presentations at many international conferences (EUPHA, ESPMH, ESHG,...), guest lectured at Ugent, UAntwerpen, VUB and Sciences Po and takes part in many EU research consortia (JANE, JA PREVENTNCD, B1MG, Genome of Europe, TEHDAS, ...).

Le Hoang Thieu

Pasteur Institute in Nha Trang, Vietnam

Dr. Le Hoang Thieu is a medical doctor and public health specialist with a background in preventive medicine and global health. Dr. Thieu obtained Doctor of Preventive Medicine from Hue University of Medicine and Pharmacy in Vietnam and earned a Master of Public Health in Global Control of Infectious Diseases from Yonsei University, South Korea.

Since 2017, Dr. Thieu has been working as an epidemiologist and medical researcher at the Department for Disease Prevention, Pasteur Institute in Nha Trang, focuses on infectious disease surveillance and control, zoonotic disease monitoring, emergency preparedness, and risk communication. And Dr. Thieu has also served as a lecturer and mentor in Vietnam's Field Epidemiology Training Program (FETP) and currently holds the position of Youth Union Secretary at the Institute.

Dr. Thieu's research contributes to several of the Pasteur Network's strategic pillars, particularly in epidemic intelligence, climate-sensitive diseases, and multi-disciplinary collaboration. Dr. Thieu has published extensively on rabies, diphtheria, hepatitis, and vaccine-preventable diseases, and has presented at both national and international scientific forums. The recent projects include evaluating rabies prevention using a One Health approach and assessing immunity gaps to inform vaccination policy.

Looking ahead, Dr. Thieu is dedicated to strengthening global and regional health security through equitable collaboration, capacity-building, and translational research. Dr. Thieu is especially passionate about bridging local expertise with global innovation to improve preparedness and response to emerging health threats.

Grégoire Davigon

Institut Pasteur de Nouvelle Calédonie, New Caledonia

Dr. Grégoire Davignon is a molecular and cellular biologist currently working as a research engineer at the Institut Pasteur of New Caledonia and as an associate researcher at the University of New Caledonia. His research focuses on the environmental adaptation and persistence of Leptospira interrogans, with particular expertise in biofilm formation and gene regulation. He investigates how Leptospira survives in soils, freshwater systems, and within chronic animal carriers—an essential but still poorly understood phase of its epidemiological cycle. His work combines classical microbiology, transcriptomics, and advanced imaging to characterise biofilm development and survival strategies in tropical environments. Notably, he has shown that Leptospira biofilm formation leads to the differential regulation of nearly one-third of the genome, with a strong intracellular stress signature. However, the expression pattern suggests a finely tuned adaptive response that may support its persistence and reactivation following heavy rainfall events. These findings contribute to a deeper understanding of leptospirosis transmission pathways and open avenues for targeted interventions in hyperendemic areas. His research aligns with several strategic axes of the Pasteur Network: epidemic preparedness, research and innovation, and multi-disciplinary collaboration. Dr. Davignon has presented his work at international conferences and contributes to initiatives promoting regional research in the Pacific. He has taught over 180 hours at the undergraduate level and mentors early-career scientists. As a former president of the New Caledonian Doctoral Association, he has actively supported equitable access to science. His vision is to connect fundamental microbial research with public health strategies tailored to vulnerable and climate-affected communities.

Paula Reges

Pasteur Network

Medical Doctor on Infectious Diseases, MSc Clinical Research on Infectious Diseases, working as ID consultant and researcher at Evandro Chagas National Institute of Infectious Diseases (INI/Fiocruz) and Global Health affairs Advisor at Presidency/Oswaldo Cruz Foundation (Fiocruz). Invited researcher of PAHO/WHO Collaborating Center for Global Health and South-South cooperation at Fiocruz Global Health Center (CRIS/Fiocruz).

Climate & Health Session

Saren Sovann

Institut Pasteur du Cambodge, Cambodia

I graduated with a Master of Molecular Biology from Lund University, Sweden and I hold a Bachelor of Bio-Engineering from the Royal University of Phnom Penh, Cambodia. I started working with the Epidemiology and Public Health Unit at the Institut Pasteur du Cambodge in 2019. My work focused on clinical studies of infectious diseases (TB, HIV, and HBV) in Cambodia. Currently, I am working as a Climate and Health Fellow for the Pasteur Network's Climate and Health Observatory Accelerator Project. My research aims to evaluate the knowledge gaps, public perceptions, and practices in response to health implications and infectious diseases burden linked to climate change across Cambodia using One Health approach.

Quang Quan Le

Pasteur Institute in Ho Chi Minh City, Vietnam

Le Quang Quan is a researcher in the Department of Disease Control and Prevention at the Pasteur Institute in Ho Chi Minh city. He holds a Doctor of Preventive Medicine degree and is currently a Fellow in the Climate & Health Observatory Accelerator Program.

His work focuses on disease surveillance, outbreak response, and research on infectious diseases, including vector-borne diseases, hand foot and mouth disease, and vaccine-preventable diseases. His research interests include infectious diseases, climate change, and sustainable prevention strategies.

Thai Pham

National Institute of Hygiene and Epidemiology (NIHE), Vietnam

Manilath Nalongsack

Institut Pasteur du Laos

Manilath Nalongsack is a climate–health researcher with a dual degree in Master of Global Health and Health Leadership and Management in Australia. She previously worked with the World Health Organization in Lao PDR as a Health Information System Support Officer, where he contributed to strengthening national data systems, integrating climate modules into DHIS2, and supporting evidence-based responses to climate-sensitive diseases.

Building on this experience, she is now a Climate & Health Research Fellow at the Institut Pasteur du Laos under the Climate & Health Accelerator Program. In this role, she leads a project on dengue transmission predictive modeling in Central Laos. Her research integrates entomological monitoring, socio-behavioral surveys, and climate data to forecast dengue transmission and develop early warning systems. By linking scientific evidence to policy and engaging with national stakeholders, her work aims to strengthen climate-resilient health systems and inform adaptation strategies in Lao PDR and the wider Southeast Asian region.

Nick Chung

Pasteur Network

I contribute to drive public health collaboration across the Asia-Pacific by fostering partnerships among research institutes, funders, and national and regional health authorities to achieve real-world impact, with a focus on equitable governance and inclusive representation.

Women in Science

Sophie Diallo
Institut Pasteur de Dakar, Senegal

Commenté [SA1]: Bio manquante

Isabella Delgado
Fondation Oswaldo Cruz (Fiocruz), Brazil

Marième Ndoye
Institut Pasteur de Dakar, Senegal

Ildikó Csóka
Szeged University, Hungary

Prof. Ildiko Csoka, is Director – General for Strategy at University of Szeged, Operative Director of Centre of Excellence for Interdisciplinary Research, Development and Innovation and Head of Institute of Pharmaceutical Technology & Regulatory Affairs.

As a leader in both academic and management fields, fulfills a bridge role in the knowledge translation from science into practice; representing researchers' aspects and also understanding the expectations of the society in order to highly meet the needs.

She is a pharmacist by profession with PhD. degree and dr. habil., having MSc. in Health Care Management and holding four specialization post-graduate degree in the fields of Pharmaceutical Technology, Quality Management, Pharmaceutical Care and Pharmacy Administration.

She is the Head of Pharmaceutical Sciences Working Group of the Szeged Regional Committee of the Hungarian Academy of Sciences, Hungarian delegate to the International Pharmaceutical Federation and Scientific Secretary for the Hungarian Chemical Society's Cosmetics and Household-chemicals Divison.

Pro bono acts as the President of the Foundation for the Development of Pharmacy Education at University of Szeged.

Roundtable: Under 40: "The Early Career Reality Check"

Renaud Vatrinet
Pasteur Network

As a member of the Pasteur Network team, Renaud is dedicated to supporting the growth of staff through training and education, while also fostering collaboration, advancing capacity-strengthening initiatives, and helping raise the network's visibility within and beyond.

Renaud is trained in Biology, Epidemiology and Public Health. His experience includes several years of fundamental research in Europe, clinical research in West Africa, and coordination activities across diverse scientific organizations and networks operating globally.

Le Phan Khoi Nguyen
Pasteur Institute of Ho Chi Minh City, Vietnam

Dr. Nguyen Phan Khoi Le is a highly-motivated and well-trained biomedical scientist with international academic and research experience in infectious diseases and preventive medicine through training in the United Kingdom, France, and Germany (PhD fellowship from DAAD).

He is currently working as a core researcher at the Enterovirus Laboratory of Pasteur Institute in Ho Chi Minh City (Vietnam). He plays a critical role in surveillance and research (clinical diagnosis, serotyping and genetic characterization) of enterovirus infections (hand-foot-mouth disease (HFMD), acute flaccid paralysis, aseptic meningitis, acute gastroenteritis) in Southern Vietnam.

Cyrine Chenaoui

Institut Pasteur de Tunis, Tunisia

Cyrine is currently a Fellow in the Climate & Health Observatory Accelerator Program at the Institut Pasteur de Tunis, where she applies complex systems modeling to study the impacts of climate change on vector-borne diseases, with a particular focus on leishmaniasis.

Before moving into decision-support modeling, she built a strong foundation in fisheries management, emphasizing sustainability, ecosystem approaches, and stakeholder engagement to inform evidence-based decisions.

She is also eager to expand her career toward knowledge brokerage and science diplomacy, where she can bridge science, policy, and society to foster more impactful solutions.

Gwladys Monamele

Centre Pasteur du Cameroun

Gwladys is a Climate and Health Fellow at the Centre Pasteur du Cameroun, where she studies how climate variability shapes public-health risks to strengthen preparedness for climate-sensitive diseases.

Trained as a microbiologist, she holds a PhD with a specialization in influenza virology and has contributed to research and surveillance initiatives on respiratory viruses. Alongside her research, she lectures at a Cameroonian university, helping train the next generation of scientists.

40u40 Plenary Session 3: Respiratory Viruses: Detection, Surveillance & Immunity

Yanis M'Zali
Institut Pasteur, Paris, France

Wuji Zhang
HKU - Pasteur Research Pole, Hong Kong

Dr. Wuji Zhang is a Research Assistant Professor at the HKU-Pasteur Research Pole, specializing in adaptive immune responses to respiratory viruses. He completed his PhD and postdoctoral training at the University of Melbourne, Australia, where his groundbreaking research provided world-first evidence that Australian First Nations peoples mount robust immune responses following COVID-19 vaccination. This work, published in Nature Immunology, was featured on the journal cover and highlighted in News & Views and Nature Briefing.

Dr. Zhang's current research focuses on T cell immune responses to circulating and emerging respiratory viruses, including influenza and coronaviruses. He investigates the functionality and cross-reactivity of virus-specific T cells, with a particular emphasis on vulnerable populations, including individuals with chronic comorbidities. By elucidating correlates of broad and robust T cell immunity and exploring the interplay with viral mutations, his research aligns well with the Pasteur Network's strategic pillars of researching high-risk infectious diseases with zoonotic potential, and the R&D of innovative vaccines and therapeutics.

As a highly collaborative researcher, Dr. Zhang has co-authored 12 publications in high-impact journals, including Lancet Infectious Diseases and Immunity. His efforts have earned him 20 academic awards, including the Presidential Research Assistant Professor Scheme (HKU) and the Chinese Government Award for Outstanding Self-financed Students Abroad (China Scholarship Council). Dr. Zhang is actively involved in scientific leadership, organizing scientific events, mentoring undergraduate and high school students, and engaging in public outreach. He is dedicated to advancing research on viruses with pandemic potential and fostering the next generation of researchers.

Ali Maleki
Institut Pasteur in Iran

Dr. Ali Maleki holds a Ph.D. in Medical Virology and is a researcher affiliated with the Pasteur Institute of Iran (PII). His work centers on the molecular epidemiology of respiratory viruses and the development of innovative environmental surveillance tools particularly wastewater-based monitoring of infectious diseases. With over five years of experience, he has led several interdisciplinary projects applying RT-qPCR technology to both clinical and environmental contexts.

Ali is currently focused on designing and validating multiplex RT-qPCR assays for avian influenza virus detection and implementing wastewater surveillance strategies aligned with the Epidemic Intelligence and Preparedness axis of the Pasteur Network. His research bridges laboratory innovation with real-world application, particularly in densely populated settings such as hospitals wastewater systems.

Beyond peer-reviewed publications, he contributes to international collaborations and national programs such as Iran's external quality assessment (EQA) for COVID-19 diagnostics and the respiratory sentinel surveillance project. As a PNAM 2025 candidate, he will present findings from Iran's EQA initiative, highlighting lessons learned during the pandemic and their impact on diagnostic reliability.

Looking ahead, Ali aims to expand his work to focus on the monitoring and detection of emerging and re-emerging respiratory viruses, reinforcing global preparedness through integrated molecular surveillance in public health strategies. He brings a passionate voice to global conversations on infectious disease preparedness.

Pham Van Khang

National Institute of Hygiene and Epidemiology (NIHE), Vietnam

I am a Doctor of Philosophy in Preventive Medicine with over 12 years of experience in disease prevention and expanded immunization. Currently, I am a researcher focusing on infectious disease control and vaccination. In addition to my research, I teach undergraduate and postgraduate courses in preventive medicine and public health at several medical universities.

My current research project is "Assessing the Risk of Measles Outbreaks in Northern Vietnam and Proposing Vaccination Strategies". The project aims to characterize the epidemiology of measles from 2019-2023 and assess the risk of outbreaks in the context of declining vaccination coverage. To achieve this, I conducted an extensive study, collecting and analyzing measles case data in 28 provinces and cities, and applied the World Health Organization (WHO) risk assessment tool to identify high-risk areas. Our results indicate that Ha Noi and Nghe An are at medium risk, while Ha Tinh is the highest risk area. These findings provide a comprehensive picture of the measles epidemiological situation, helping us to make appropriate and effective strategic recommendations, especially in strengthening vaccination coverage and surveillance systems. This work is of great significance in protecting public health and contributing to Vietnam's goal of eliminating measles.

Karidja Yakoura
Institut Pasteur de Côte d'Ivoire

Holder a PhD in microbiology and biotechnology from Nangui Abrogoua University in Côte d'Ivoire, I have built a scientific career focused on microbiology and public health. I completed internships for my Master's and PhD at the Molecular Biology Laboratory, the Environment and Health Department, and the Mycology and Parasitology Department at the Pasteur Institute of Côte d'Ivoire. I have been on the front lines during several epidemics in Côte d'Ivoire, including SARS-CoV-2 and dengue fever. In these projects, I work on aspects related to genomic surveillance, NGS sequencing, and bioinformatics. I am currently a research fellow at the Pasteur Institute of Côte d'Ivoire, where I provide technical supervision of the molecular diagnostic activities of the Respiratory Virus Laboratory. I coordinate technical activities related to the surveillance and investigation of respiratory infections.

My expertise lies in molecular detection of emerging pathogens, RT-PCR diagnostics, genomic sequencing, and data analysis. I actively contribute to several strategic projects, including surveillance of influenza, RSV, SARS-CoV-2, measles, rubella, and genomic sequencing of Mpox, as well as the implementation of innovative approaches such as measles detection in wastewater. This work illustrates my commitment to developing integrated surveillance tools, which are essential for improving early detection and understanding the dynamics of pathogen circulation.

My research is fully aligned with the strategic priorities of the Pasteur Network, particularly epidemic preparedness and response, scientific innovation, and local capacity building. I also participate in national and international collaborations, contributing to scientific data sharing and training and skills transfer activities.

My future prospects are to consolidate integrated genomic surveillance in Côte d'Ivoire and strengthen interdisciplinary approaches in order to anticipate epidemic threats and position Côte d'Ivoire as a key player in the Pasteur Network and the global scientific community.

Dung Truong Thi Thuy

Pasteur Institute in Ho Chi Minh City, Vietnam

Dr. Dung Thi Thuy Truong is a Vietnamese preventive medicine doctor with a strong commitment to immunization and disease prevention. She holds a Doctor of Preventive Medicine from Hue University of Medicine and Pharmacy and a Master of Public Health in Global Health Security from Yonsei University, Korea.

Since 2016, Dr. Dung has worked for the Vaccination Unit within the Pasteur Institute in Ho Chi Minh city, where she supports the sub-national Immunization Program and vaccine-preventable disease surveillance across southern Vietnam - a population-dense region with over 35 million people. Her responsibilities include providing technical guidance, coordinating outbreak responses, training health workers, and strengthening immunization systems. She is also active in education, teaching medical students about vaccine-preventable diseases.

As an early-career researcher, she has published in five international peer-reviewed journals. She has also taken part in several clinical trials, notably contributing to the development of Vietnam's first seasonal influenza vaccine. Her areas of expertise include vaccinology, epidemiology, and strengthening health systems.

In 2023, Dr. Dung was selected to attend the Vaccinology Course at the Institut Pasteur in Paris - an experience that deepened her connection with the Pasteur Network and broadened her global perspective on immunization challenges.

Dr. Dung is passionate about improving vaccine access in underserved communities and developing practical, evidence-based approaches to public health. Her work closely aligns with the Pasteur Network's mission in public health preparedness, training, and research.

She aims to take on a leadership role in public health research and contribute to strengthening collaboration within the Pasteur Network to improve health outcomes across Vietnam.

40u40 Plenary Session 4: Enteroviruses & Emerging Viruses

Meryem Lemrani
Institut Pasteur du Maroc, Morroco

As a Research Director at the Institut Pasteur of Morocco, Meryem Lemrani is dedicated to advancing research on leishmaniasis. She is committed to fostering scientific collaboration, capacity building, and sustainable health initiatives. Her research focuses on the molecular epidemiology of leishmaniasis and the environmental factors influencing its distribution in Morocco; the use of artificial intelligence for rapid Leishmania diagnosis and Biosafety, biosecurity, and biorisk management in research and diagnostic laboratories.

As Principal Investigator and coordinator, Meryem Lemrani has led and contributed to numerous national and international projects resulting in several peer-reviewed publications. Her laboratory is recognized as a national center of excellence, providing molecular and AI-based diagnostic tools for Leishmania detection and genotyping.

Joël Dote

Institut Pasteur de Bangui, Central African Republic

Holder of a Doctorate in Medicine obtained in January 2017 from the University of Bangui and a Master's degree in Applied Biochemistry obtained in 2022 from the University of

Bangui, I am a third-year doctoral student in Virology at the University of Bangui.

Employed as Deputy Scientific Manager of the Enteric Virus and Measles Laboratory at the Institut Pasteur in Bangui since May 2017.

My Laboratory houses three WHO reference laboratories: WHO Regional Reference Laboratory for Poliomyelitis, WHO National Reference Laboratory for Rotavirus, WHO National Reference Laboratory for Measles

I joined CESRI in January 2021 as a Research Assistant. In 2023, I received a Pasteur Network thesis grant worth €75,000, with a thesis project titled Epidemiology and diversity of enteroviruses in the Central African Republic. I also supervised a Master of Science student and a Master of Water Quality student, both of whom are now employed as technicians in the laboratory I co-direct, promoting multidisciplinary knowledge.

I teach modules on virology to second-year medical students, Master of Water Quality students, and molecular biology to the Master of Medical Biology students at the University of Bangui.

My collaborations include IP, Paris, and other institutes of the Pasteur Network, such as Cameroon and Madagascar. I also collaborate with the Luxembourg Institute of Health and CDC, Atlanta.

My future plans involve establishing genomic and metagenomic technics in my lab and basic science research to develop local scientists, cultivating a new scientific community at the pole of excellence.

Anna Dolgova
Saint-Petersburg Pasteur Institute, Russia

I graduated from MSU in 2008, and received my PhD in molecular genetics at the Institute of Gene Biology (2008-2015). Since 2014, I have been working in the Rospotrebnadzor system, first in Moscow, and at the St. Petersburg Pasteur Institute since 2019. I am currently the head of the Laboratory for Molecular Genetics of Pathogens. I supervise various students (undergraduate, master's students, postgraduate theses) and have taught a course on molecular genetics at ITMO University. I participate in the Institute's international activities, coordinating a number of projects with Senegal, Iran and Venezuela.

The projects I coordinate are related to the development of diagnostic approaches and proactive monitoring of high-risk infectious. So far, my team has developed over 30 diagnostic kits (CRISPR/Cas, RPA, DNAzymes, real-time RT-PCR). These serve the needs of the other countries with which we cooperate (under Rospotrebnadzor federal programs in collaboration with the Pasteur Institutes in Dakar and Iran).

In addition to identifying viruses, it is necessary to understand the threat they pose to public health. My current work focuses on predicting the pathogenicity of new, or poorly understood, viruses found through monitoring and characterization (nucleic acid testing, genomic sequencing). One of the methods for assessing the pathogenicity of viruses with a lipid membrane is the pseudotyped viral particle method. It is this approach that I see as one of the most promising and necessary in the modern world for implementation in the epidemiological surveillance system.

Chittaphone Vanhnollat

Institut Pasteur du Laos

Chittaphone holds a medical degree and a PhD in internal medicine. After completing his academic training, he developed a scientific interest in the field of virology, which led to a focus on emerging viral threats with implications for public health and outbreak preparedness.

Since 2022, Chittaphone has been working as a research scientist at the Institut Pasteur du Laos, where he currently leads the Pathogen Discovery group within the Virology laboratory.

His work focuses on managing scientific projects and conducting research to investigate zoonotic viruses with spillover potential. His expertise includes virology, with a particular focus on emerging zoonotic viruses.

Chittaphone's main research project involves active pathogen surveillance in Laos through collaboration with international and local partners, which includes ecological field missions to collect samples from wildlife, such as bats, rodents, and ectoparasites, followed by laboratory testing and high-throughput sequencing to detect and characterize novel/known pathogens.

This work contributes directly to two of the Pasteur Network's strategic pillars: Epidemic Intelligence & Preparedness with a Focus on Climate-Sensitive Diseases and Multi-Disciplinary Knowledge Communities.

Looking ahead, Chittaphone aims to apply the lessons learned to strengthen national research programs and to actively share expertise with local and regional scientists. Future research directions will explore pathogen-host interactions using ecosystem approach, with expanded collaboration among Lao and international researchers.

Roundtable: "When I Was in Your Shoes"

Samia Menif

Institut Pasteur de Tunis, Tunisia

Samia Menif is the General director of the Pasteur Institute of Tunis, she is a Professor of medicine, specializing in hematology biology.

Her medical training was further enriched by an advanced degree in Genetics and Molecular Biology.

Professor Samia Menif directed the hematology laboratory at the Pasteur Institute in Tunis since 2005. Her professional career is marked by her significant contribution to molecular diagnosis of leukemia in Tunisia.

As a member of the Molecular and Cellular Hematology Research Laboratory, Professor Samia Menif brought strategic expertise and enlightened vision to guide research initiatives in the field of leukemia. she was particularly interested in the resistance mechanisms of Chronic Myeloid Leukemia to Tyrosine Kinase Inhibitors (TKI).

She served on the board of the Tunisian Society of Hematology as Treasurer. She was an elected member of the Scientific Council and the Board of Directors of the Pasteur Institute of Tunis.

Her expertise has been widely recognized in the scientific community, and she has been invited to participate in numerous conferences where she presented her diagnostic and research results.

Professor SM has also contributed significantly to the international scientific literature, with several publications in renowned journals,

Ehsan Mostafavi

Institut Pasteur in Iran

Christophe Peyrefitte

Institut Pasteur de la Guyane, French Guyana

Christophe Peyrefitte is the Director of the Institut Pasteur de la Guyane since 2021. A PharmD and PhD in virology, from Université Claude Bernard in Lyon and Université Aix-Marseille. He has built an international career studying arboviruses, hemorrhagic fever viruses, and orthopoxviruses, with experience at institutions including the Institut de Médecine Tropicale du Service de Santé des Armées, the Walter Reed Army Institute of Research, the Fondation Mérieux, and the Institut Pasteur de Dakar, where he served as Scientific Director. He has contributed to national and international reference laboratories, represented France in NATO working groups, and participated in epidemic responses such as Ebola in Guinea and SARSCoV-2 in Senegal. Alongside his research and public health leadership, he has taught virology at Institut Pasteur in Paris for over a decade and more recently at the University of Guyane.

Leo Poon

HKU - Pasteur Research Pole, Honk Kong

He is as a Chair Professor in the School of Public Health, HKU. He is a co-director of HKU-Pasteur Research Pole. Professor Poon is a world-leading virologist and public health scientist. Over the years, he has published about >300 peer-reviewed articles and has been named as a Highly Cited Researcher since 2015. Thus far, his work has been cited over 43 thousand times and he has an H-index of 101. Professor Poon studies emerging viruses for over 25 years. He studies both human and animal influenza and coronaviruses. His work ranges from basic virology to public health virology. Professor Poon serves as an expert for several international organizations. He is an advisor in different task groups for infectious disease control in WHO, FAO and WOAH.

Vaccine Manufacturing in the Network

Marco Nascimento

Fundação Oswaldo Cruz (FIOCRUZ), Brazil

Commenté [SA2]: bio

Ndeye Mareme Ba

Institut Pasteur de Dakar, Senegal

Ndeye Mareme Ba is the Lead of the Cell-Based Vaccine Platform at Institut Pasteur de Dakar. She specializes in upstream vaccine development and technology transfer, leading the design, scale-up, and transfer of cell-based vaccine production processes with contributions to Measles, Rubella, and Marburg vaccine projects. She is also an active researcher and mentor committed to training the next generation.

Khalid Zemzoumi

Institut Pasteur du Maroc, Morocco

Dr. Khalid Zemzoumi is a recognized leader in vaccine, research, development and innovation in North Africa. As coordinator of the Moroccan co-secretariat for the North Africa Regional Capacity & Capability Network (RCCN) at the Institut Pasteur du Maroc, he advances vaccine development, workforce training, and cross-regional collaboration. His expertise spans translational research on respiratory and inflammatory diseases, vaccine development, and biomanufacturing. He has designed and led specialized training programs in vaccine platforms and biomanufacturing, building a skilled workforce aligned with Africa's vaccine self-sufficiency goals. Acknowledged by Africa CDC and other continental bodies, Dr. Zemzoumi is valued for his ability to connect science, training, and partnerships, positioning Morocco as a hub for vaccine R&D and innovation. His leadership combines scientific rigor with a vision for empowering the next generation of biomanufacturing professionals in Africa.

Safouane Benazzouz
Institut Pasteur d'Algérie, Algeria

BENAZZOUZ Mohamed Safouane is an Associate Professor in Pharmacology at the Faculty of Pharmacy of Algiers and is Head of the Therapeutic Serums Production Laboratory at Pasteur Institute of Algeria (PIA). He holds a degree in Pharmacy, a Specialized Medical Studies degree in Pharmacology, and a Doctorate in Medical Sciences from the University of Algiers, as well as a Master's degree in Drug Discovery and Pharmaceutical Management (MSc) from University College London. His career began at the National Laboratory of Control of Pharmaceutical Products, where he worked in regulatory affairs, quality control, and bioequivalence studies, before joining the University of Algiers and the PIA in 2015. Since then, he has been teaching Pharmacology, Clinical Pharmacy and Industrial Pharmacy, and led quality control and production activities for biopharmaceutical products. Appointed Head of the Therapeutic Serums Production Laboratory in 2020, he leads national antivenom production for scorpion and snake envenomation, and conducts applied and translational research on therapeutic serums and vaccines.

He is a member of the Pasteur Network Scientific Working Group on R&D&I on Therapeutics, the Scientific Committee of the Department of Pharmacy at the University of Health Sciences, the Regional Pedagogic Committee of Pharmacology, and a founding member of the Algerian Society for Biological Developments and Pharmaceutical Innovations.

Dionyssios Sgouras

Hellenic Pasteur Institute, Greece

Dr. Dionyssios Sgouras is a Research Director of the Lab. of Medical Microbiology of the Hellenic Pasteur Institute (HPI) and Head of the Vaccine Unit at HPI, following approval by the National Organization for Medicines in Greece. He is a member of the National Committee for Immunization Practices (NCIP) which mandates the annual vaccination program of children and adults in Greece, including vaccination against COVID-19 and an elected member of the Executive Board of the Hellenic Society of Biochemistry & Molecular Biology. Through his post-doctoral studies, he was a U.S. National Institutes of Health-Fogarty International Research Fellow, at the Laboratory of Molecular Oncology at the Frederick Cancer Research and Development Center in Frederick, MD. Research interests focus on bacterial pathogenesis and most specifically, Helicobacter pylori virulence factors and their effect on host intracellular signaling pathways. He runs the Vaccines Unit of HPI, a fill-finish infrastructure, supporting small-scale, productions of sterile parenteral solutions for human and veterinary use, operating under EU-GMP. Dionyssios brings over thirty years' experience in biomedical laboratory research and more than a decade involvement in pharmaceutical regulatory compliance.

40u40 Plenary Session 5: Bacteria & Microbiota

David Chatenet
INRS - Armand-Frappier Santé Biotechnologie Research Centre, Canada

Director of the INRS - Armand-Frappier Santé Biotechnologie Research Centre and full professor at the National Institute for Scientific Research (INRS), Prof. David Chatenet is a recognized expert in medicinal chemistry, pharmacochemistry, and peptide engineering. His work focuses on G protein-coupled receptors (GPCRs), with a particular interest in studying their oligomerization, as well as developing biased ligands and allosteric modulators. His team designs innovative therapeutic agents targeting signaling pathways involved in cardiovascular, inflammatory, and neurodegenerative diseases.

As director of the center, he ensures the scientific and strategic influence of one of Quebec's leading health research hubs, while promoting cross-sector partnerships and the development of cutting-edge technology platforms.

Sébastien Bontemps-Gallo

Institut Pasteur de Lille, France

Dr. Sébastien Bontemps-Gallo is a microbiologist with expertise in bacterial stress adaptation and vector-borne diseases. He earned his Ph.D. in Life and Health Sciences from the University of Lille (France) in 2013. Following a postdoctoral fellowship at the Rocky Mountain Laboratories (NIAID, NIH, USA), he joined the Institut Pasteur de Lille in 2018, where he now holds a permanent CNRS research position. His research explores bacterial pathogenesis—how pathogens colonize hosts, evade host defenses, and cause disease. He uses an integrative approach combining genetics, biochemistry, omics, microscopy, and medical entomology to study in vivo regulatory networks involved in pathogen adaptation. After working on Borrelia burgdorferi, the Lyme disease agent, and its transmission by ticks, he now focuses on Yersinia pestis, the causative agent of plague, and its transmission by fleas. His aim is to identify novel therapeutic targets to fight vector-borne infections. Dr. Bontemps-Gallo is actively involved in science communication, contributing to media platforms such as The Conversation, participating in public engagement events at the Institut Pasteur de Lille, and coordinating the social media presence of his research unit. He also serves as an Academic Editor for PLOS Pathogens and is a member of several national scientific committees. He is currently developing an independent research program supported by early-career funding, with the long-term goal of leading a collaborative, international team within the Pasteur Network.

Antsa Harinavalona Rakotonirina

Institut pasteur de Madagascar, Madagascar

My passion for arthropods and the diseases they transmit began during my studies in Madagascar, where I earned a Bachelor's in Applied Entomology and a Master's in Sciences and Biotechnology.

Internships at the Institut Pasteur de Madagascar (IPM) gave me hands-on experience in mosquito identification, flea population genetics, and strengthened my laboratory skills.

In 2018, I received the Calmette & Yersin doctoral grant from the Pasteur Network to pursue a PhD at the Institut Pasteur de Nouvelle-Calédonie. My research focused on using MALDI-TOF mass spectrometry and AI for arthropod identification and micro-organism detection, contributing to the Network's Research, Development & Innovation pillar and involving regional collaborations across the Pacific and international involving several Instituts Pasteur in the Network.

From 2021 to 2024, I continued this work as a postdoctoral fellow at the Institut Pasteur du Cambodge, where I advanced MALDI-TOF/AI applications and contributed to studies on vector-borne disease risks across ecosystems. This work, aligned with the Epidemic Intelligence & Preparedness pillar, was supported by the French Embassy and NIH.

Since 2024, I have been a researcher at IPM, leading projects on ticks and tick-borne diseases, an emerging public health concern in Madagascar. I collaborate with national, regional, and international partners, while also mentoring students and public health staff and presenting at scientific congresses.

Looking ahead, I aim to deepen my focus on the emergence of tick-borne diseases and vector ecology, in line with the Pasteur Network's mission to promote interdisciplinary research, capacity building, and equitable global collaboration.

Isaure Quétel
Institut Pasteur de Guadeloupe

Isaure Quétel has been working since 2022 as a bioinformatician at the Institut Pasteur de la Guadeloupe, where she specializes in metabarcoding and prokaryotic genome analysis. She is part of the Microbial Ecology team but collaborates closely with other laboratories and research units, including the Vector-Borne Diseases Laboratory and the Amoeba Team, reflecting her strong commitment to interdisciplinary science.

Her research focuses on characterizing microbial communities and understanding host–microbiome–environment interactions through both computational and ecological approaches. She contributes to biodiversity assessments, environmental monitoring, and pathogen surveillance.

In 2023, Isaure Quétel served as the main organizer of JOBIM (Journées Ouvertes en Biologie, Informatique et Mathématiques), a major conference in the French-speaking bioinformatics community. She also gave an oral presentation and was awarded the Best Poster Prize, recognizing the scientific relevance and clarity of her work.

Alongside her research, she is actively engaged in training and mentoring. She has supervised a student intern, teaches at the university level, and contributes to professional training initiatives.

Notably, she co-led a training session in Roscoff, in collaboration with IFREMER and the Roscoff Biological Station, and co-organized a similar course in Guadeloupe, again in partnership with IFREMER.

Isaure Quétel's multidisciplinary expertise, coupled with her dedication to collaboration and knowledge sharing, make her a dynamic figure in the fields of microbial ecology and bioinformatics.

Nikolaos Vakirlis
Hellenic Pasteur Institute, Greece

I am a computational biologist specialized in evolutionary genomics. I have a PhD from Sorbonne University in Paris, France and I have worked as a postdoctoral researcher in Ireland, Germany and Greece. My main focus throughout my career has been to understand how and why novel genes originate during evolution and my research has helped elucidate the mechanism of de novo gene birth. Since October 2024, I have been a G4 group leader at the Hellenic Pasteur Institute, at the head of a multidisciplinary, international team. Our work now focuses on antimicrobial peptides, short proteins used as natural defense against pathogens by all organisms. By detecting them and studying their evolutionary dynamics at the scale of all animals, we aim to ultimately be able to harness them as alternative antibiotics. We also study the origins and evolution of novel 'microproteins' in bacteria to understand how they function in both antibiotic resistance and antimicrobial activity.

Throughout my career I have passionately sought opportunities to serve the scientific community, mentor younger scientists and engage with the general public. I have organized an EMBO Lecture Course (Greece) and co-organized the first-ever scientific meeting on de novo gene birth (US). Through the Hellenic Evolutionary Society I promoted general public activities like annual Darwin Day events and I have participated in events like the Pint of Science festival. As building multi-disciplinary approaches are now indispensable to tackle tough scientific challenges, I am involved in international collaborations across France, the Netherlands, Czech Republic, Switzerland, the US and more.

Siyeon Yang
Institut Pasteur Korea

I majored in veterinary pathology in graduate school, and I participated in research focused on viral vaccine development. Currently, I lead the Animal research and operation lab at the IPK. I am responsible for developing and managing various infectious disease animal models. My primary work has involved in vivo efficacy evaluation of novel tuberculosis(TB) therapeutics, and I am also actively researching standardization strategies for non-tuberculous mycobacteria(NTM) models using different mouse strains.

In response to emerging research needs, I have recently initiated studies on dengue virus and SARS-CoV-2. My long-term goal is to establish advanced animal models that closely mimic human immune responses by utilizing transgenic and humanized mice. These models aim to bridge the gap between basic research and clinical application, supporting more accurate preclinical evaluation of vaccines and therapeutics.

In addition to research, I lectures on preclinical animal studies for drug development and One Health, highlighting the links between humans, animals, and the environment. I am looking for international collaboration on in vivo models for diverse pathogens to support global infectious disease preparedness.

Iliyan Manoylov
Stephan Angeloff Institute of Microbiology, Bulgaria

An immunologist, I graduated from the French Language School in Sofia, then earned my Bachelor's in Molecular Biology and Master's in Cell Biology and Pathology from Sofia University. My Master's thesis on anti-HIV vaccine immune response was completed in Grenoble, France. I later earned my PhD in Immunology from the Stephan Angeloff Institute, focusing on Type 1 Diabetes therapy in mouse models.

With 17 years in Immunology, I'm certified in Flow Cytometry, Animal Experiment Design, Mouse surgery and cryopreservation and Vaccinology. I'm part of the Pasteur SWG R&D&I Vaccines. I've presented at 3 European and 3 International congresses in Immunology and, for the past three years, have organized the Sofia Teen Summer School of Microbiology and Immunology, inspiring future scientists. In 2022, I secured a €100,000 grant for my research on the Zbtb20 gene and its influence on immune responses.

Currently, I'm an assistant professor and lead the institute's animal facility, conducting diverse molecular biology techniques – Flow cytometry, ELISA, PCR etc. and animal surgery. My research focuses on Type 1 Diabetes and immunogenetics, exploring how genes impact immune responses in autoimmune and infectious diseases. I also mentor high school interns, promoting multi-disciplinary knowledge.

As an educator, I'm a teacher in my high school and a visiting scientist at a children's science museum where I engage 16-18 year olds. My collaborations include IP, Paris and HAAN University. My future plans involve establishing an Immunogenetics lab and a new animal facility to develop local scientists, cultivating a vibrant new scientific community.

Sokleaph Cheng

Institut Pasteur du Cambodge, Cambodia

Dr. Sokleaph Cheng, Pharm.D., Ph.D., is a medical biologist with over a decade of experience in medical and research laboratories. She holds a Doctor of Pharmacy degree in Medical Biology from the University of Health Sciences, Cambodia, a Diploma in Specialized Medicine in Medical Biology from Université Paris V – René Descartes, France, and a Ph.D. in Health Biology from Université de Montpellier, France. In 2022, she received the Scientific Prize of the French Embassy in Cambodia for her contributions to infectious disease research.

She is currently Head of the Mycobacteriology Laboratory, Head of the Bacteriology and Antibiotic Resistance Group, and Deputy Head of the Medical Biology Laboratory at Institut Pasteur du Cambodge. Her expertise includes tuberculosis, antimicrobial resistance, diagnostic innovation, surveillance systems, and laboratory quality management in accordance with ISO 15189 standards. She is also a member of the National Technical Working Groups on Antimicrobial Resistance.

Dr. Cheng leads and coordinates several multidisciplinary, international research projects aligned with the Pasteur Network's strategic priorities. Her work focuses on tuberculosis, zoonotic transmission risks, and bacterial pathogens such as Burkholderia and Leptospira. Many projects emphasize capacity building, strengthening surveillance, and developing innovative diagnostic and epidemiological tools to improve public health responses.

In addition to research, Dr. Cheng is engaged in teaching, mentoring early-career scientists, and promoting best laboratory practices through training programs. She actively collaborates at national and international levels to address emerging infectious threats, enhance AMR surveillance, and advance One Health–based public health strategies in Cambodia and beyond.

40u40 Plenary Session 6: Parasites

Jose Badano

Institut Pasteur de Montevideo, Uruguay

Aissata Camara

Institut Pasteur de Guinée, Guinea

I trained as a pharmacist and graduated from the Gamal Abdel Nasser University in Conakry. After completing my studies in Guinea, I continued my training in France, where I obtained a Master 2 in Plant Chemistry at the University of Angers, followed by a PhD in Pharmacology at the University Paul Sabatier in Toulouse.

Before my postgraduate studies, I worked as a research associate at the Centre de Valorisation des Plantes Médicinales de Guinée. I contributed to several projects, resulting in about twenty scientific publications. My work focused on ethnomedical and ethnobotanical surveys, as well as phytochemical, biological, clinical, and ethnotherapeutic studies of local medicinal plants.

Since 2021, I am a postdoctoral researcher at the Pasteur Institute of Guinea in the parasitology unit. I actively contributed to research on African trypanosomiasis. In collaboration with national and international partners, our team developed an ultrasensitive molecular method for detecting trypanosomes. This enabled Guinea to eliminate the HAT, which has been certified by the WHO. As infectious diseases are a priority of the Pasteur Network, I am expanding our research to malaria, still a major public health concern in Guinea. This new project aims to enhance molecular diagnostics using innovative techniques to interrupt transmission and support disease elimination.

At the same time, I am also a research associate at the University of Conakry, in the Department of Health Sciences and Techniques where I teach pharmacology to students in pharmacy, medicine, and ondonto. This dual experience, both academic and professional, has enabled me to develop in-depth expertise in the scientific research and teaching.

Florencia Díaz Viraqué

Institut Pasteur de Montevideo, Uruguay

Florencia Díaz Viraqué holds a Ph.D. in Biological Sciences and is currently a Senior Research Associate at the Institut Pasteur de Montevideo, Uruguay. Her academic and professional background combines strong expertise in molecular biology and genomics, with a particular focus on gene expression regulation and epigenetics in parasitic protozoa— pathogens responsible for major infectious diseases worldwide, for which no vaccines are currently available.

Aligning with the efforts in the innovation in public health of the Pasteur Network, her major research interest is to understand how parasites cause diseases: what are the mechanisms by which they subvert host functions? Her projects have contributed to understanding how the spatial organization of the parasite genome and DNA methylation marks influence gene expression.

In addition to her research, Díaz Viraqué is an active member of the Pasteur Network's International Scientific Working Group on Epidemic Preparedness, where she contributes to integrating molecular biology insights to strengthen the network's collective response to emerging infectious threats.

Looking ahead, her goals include consolidating her research program, expanding international collaborations, and strengthening local scientific capacity through training, mentorship, and public engagement.

Ryan D. Pardy
INRS - Armand-Frappier Santé Biotechnologie Research Centre, Canada

Dr. Ryan Pardy obtained his PhD at McGill University (Montreal, Canada) in 2020 in thelaboratory of Dr. Martin Richer. His doctoral work focused on T cell responses to Zika virus infection and identified how epidemic Zika virus isolates evade host immunity by subverting antigen presentation. Dr. Pardy's postdoctoral research took place in the laboratories of Dr. Chris Hunter and Dr. Boris Striepen at the University of Pennsylvany (Philadelphia, USA), where he studied how intestinal epithelial cells respond to interferon-gamma in the context of infection with the parasite Cryptosporidium. In May 2024 Dr. Pardy joined the faculty at INRS – Centre Armand-Frappier Santé Biotechnologie as an Assistant Professor. The Pardy laboratory studies the role of cytokines called interferons in intestinal immunity, with a particular focus on the Apicomplexan parasite Cryptosporidium parvum. This pathogen exclusively infects intestinal epithelial cells (IEC), which form the barrier between the contents of the intestine and the rest of the body. While it is known that interferons act on IEC to control C. parvum infection, our research focuses on understanding interferon signalling to IEC and how these leads to parasite killing within the cell. C. parvum is a zoonotic pathogen that infects both humans and livestock animals and can be spread through contaminated food and water. Improved understanding of how to prevent or treat this infection is in line with the Pasteur Network's strategic axis "Epidemic Intelligence & Preparedness with a Focus on Climate-Sensitive Diseases".

Emna Harigua

Institut Pasteur de Tunis, Tunisia

Emna Harigua is a Bioinformatician and a Data Scientist, with a multi-disciplinary profile. She holds an engineering degree in Analytical Chemistry and a master degree in Information Processing. She did her PhD in Structural Bioinformatics applied to Drug Discovery, at Institut Pasteur in Paris-France, at Michael Nilges' lab as part of a collaboration with Ikram Guizani's lab at Institut Pasteur de Tunis. She has occupied a postdoctoral position since 2016 at IPT, where she was focusing on developing cutting-edge approaches in Structural Bioinformatics in the field of infectious diseases. Her research evolved to involve Artificial Intelligence (AI) research, starting 2019.

She is currently an assistant professor at IPT. She has built a multi-disciplinary team developing Bioinformatics and AI-based approaches for Biomedical research applications. Dr. Harigua leveraged multiple international grants; the latest is the highly competitive EU-funded ARISE grant from the AAS towards implementing an AI-based platform for Drug discovery, called BIND.

Dr. Harigua is identified as an expert in her field, serving as a reviewer for international funding agencies, and is a member of multiple scientific committees. She is a recipient of various awards and distinctions: The international fellowship of UNESCO-L'OREAL "For Women in Science" 2012, the ASTMH society fellowships (2016, 2020), the Yersin and Calmette fellowships (2011-20212).

She is the founder the startup AI4HD, developing AI-empowered digital tools for diagnosis and e-health purposes in the global south.

Imane El Idrissi Saik
Institut Pasteur du Maroc, Morocco

I hold an Msc in Immunology and I have recently obtained a PhD in Parasitology, Molecular Biology and Immunology. During my PhD conducted between the Molecular and Cellular Pathology Laboratory, Hassan II University of Casablanca and the Laboratory of Leishmaniasis, Institut Pasteur du Maroc, I explored cutaneous leishmaniasis, a climate sensitive neglected tropical disease with a significant public health impact in Morocco. The study approach was multidisciplinary combining epidemiology, molecular biology, immunology, and predictive disease modeling to understand the disease's challenging dynamics.

I have been awarded several competitive grants and fellowships including the EFIS-IL Short Term Fellowship for research at the University of Lausanne, the LABEX-CEMEB grant from the University of Montpellier, and the Infravec2 grant in sandfly rearing and experimental infection. In addition, I conducted research stays at IRD Montpellier through the LeiShield-MATI RISE project.

In 2025, I joined the Climate and Health Observatory Accelerator Project as a fellow, focusing on early warning systems for climate-sensitive neglected diseases. This project directly addresses Pasteur Network pillar Epidemic Intelligence & Preparedness. I collaborate with multidisciplinary teams to link climate data, disease modeling, and public health strategies, aiming to strengthen resilience in vulnerable communities.

On another side note, I serve as a board member for associations working on rural development and women's empowerment in Morocco, and I am committed to mentoring aspiring scientists in interdisciplinary research. My long-term aspiration is to bridge science, policy, and community needs to anticipate and prevent climate-driven health threats, ensuring that research translates into real-world solutions.

Celia Florimond
Institut Pasteur de la Guyane, Guyana

Trained in microbiology, molecular biology and cell biology, I earned my PhD in microbiology from the University of Bordeaux (France) through research characterizing cytoskeletal proteins in Trypanosoma brucei. Over the past 16 years, I have specialized in parasitology, developing expertise across diverse extracellular and intracellular parasite models. During doctoral and postdoctoral studies, I conducted research on cellular biology in Trypanosoma brucei and studied the involvement of oxygen-sensors in Toxoplasma gondii host-pathogen interactions.

Currently, as Research Associate at the National Reference Center for Malaria / WHO Collaborating Center for Antimalarial Drug Resistance Surveillance (Pasteur Institute of French Guiana), I lead critical public health research aiming to optimize malaria treatment strategies through collaborations with local and international partners. This work directly contributes to the Pasteur Network's first strategic pillar as it concurs to strengthen epidemic intelligence and preparedness.

In this context, I conduct fundamental research on the molecular mechanisms of resistance to artemisinin partner drugs in Plasmodium falciparum. Key scientific contributions include:

Demonstration of piperaquine's clinical inadequacy due to emerging resistance (validated by treatment failures in French Guiana, a hotspot for selection of antimalarial drug resistance).

Ongoing assessment of first-line artemether-lumefantrine therapeutic efficacy in the region.

My philosophy centers on continuous skill advancement to develop research project aiming to provide public health solutions with measurable impact. To further solidify my scientific leadership in malaria control, I am preparing my professional qualification to become a medical biologist specialized in malaria.

Mamane Salé Noura

CERMES, Niger

Dr. MAMANE SALE Noura, I'm a medical entomologist and researcher at the Centre de Recherche Médicale et Sanitaire (CERMES) in Niamey, Niger. I hold a PhD in Medical Entomology from Abdou Moumouni University of Niamey, with research focusing on the bioecology, diversity, and insecticide resistance of Anopheles mosquitoes, as well as the influence of environmental factors on their abundance.

My scientific work has been published in several peer-reviewed journals, making a significant contribution to the understanding of malaria vectors in Niger. I have also completed advanced training in molecular biology in Belgium and French Guiana, strengthening my expertise in vector genetics and molecular diagnostics.

In addition to my research activities, I have served as a part-time lecturer for five years at Abdou Moumouni University, where I teach Master's students in Medical Entomology. My dedication to education reflects my commitment to knowledge transfer and the development of future scientists.

Deeply committed to innovation, I'm actively involved in the search for alternative vector control strategies to combat malaria and arboviral diseases-both of which are highly sensitive to climate factors. My work aligns closely with the first and second strategic pillars of the Pasteur Network, focusing on public health and translational research.

Abstracts

40u40 Plenary Session 1: Arboviruses: Surveillance, Immunity & Pathogenesis

Sebastian Baumgarten - Institut Pasteur, Paris, France / ***Environmental Parasitology: Unravelling adaptations to host vector transmission in the human malaria parasite***

Objective:
Infecting and transmitting between diJerent host and vector organisms means a Life of extremes for eukaryotic pathogens. This is particularly true for the most virulent human malaria parasite, Plasmodium falciparum, which develops into specific developmental stages that are highly adapted to each environment it encounters during its life cycle.
Background:
Our research program leverages this life of extremes, aiming to understand the RNA-regulatory mechanisms that allow pathogens to anticipate sudden environmental changes in order to arrest and re-initiate development. Our main research focus is on our discovery of a highly divergent, developmentally controlled ribosome that is only activated once the parasite enters the mosquito. We found that this ribosome is co-expressed in the same cell together with canonical ribosomes, making the parasite a uniquely extreme example of ribosome heterogeneity
Methods:
We now combine functional genomics, next-generation sequencing and advanced imaging and structural biology methods to unravel the composition, structure and function of this new gene regulatory pathway.
Results:
We found that this divergent ribosome features a unique genetic makeup andbiogenesis pathway, folds into a distinct three-dimensional structure and localizes to specific regions in the cell, possibly regulating localized translation during parasite transmission.
Implications:
Since the discovery of the genetic code, the question of whether ribosomes have a regulatory function is protein synthesis has been debated. The advent of new technologies, together with our own methodological advancements and P. falciparum as a model organism, we can now answer one of the longest Standing Questions in Molecular Biology: Do specialized ribosomes exist?
Broader Impact:
Our main goal is to use the malaria parasite as a model to unravel new molecular mechanisms that cannot be studied in standard model systems. In parallel, transmission to the mosquito is also a bottleneck when the parasite is most vulnerable to intervention. Hence, finding new Achilles' heels at this stage will open novel avenues to combat the spread of malaria.

Idrissa Dieng - Institut Pasteur de Dakar, Senegal / ***Genomic Surveillance of Dengue Virus in Senegal (2015–2023): A Tool for Real-Time Epidemic Intelligence and Diagnostic Readiness***

Objective:
To strengthen epidemic intelligence and preparedness in Senegal by establishing a genomic surveillance platform for dengue virus (DENV), enabling real-time monitoring of circulating viral strains and informing diagnostics and control strategies.
Background:
Dengue virus is a major public health concern in West Africa, where under-detection and viral diversity hamper timely response. Despite recurrent outbreaks, data on the genetic makeup of circulating strains has been limited. Understanding the dynamics of DENV evolution and cocirculation is crucial for the development of effective diagnostics, vaccines, and outbreak response strategies.
Methods:
We implemented a nationwide genomic surveillance system from 2015 to 2023, combining next-generation sequencing, real-time molecular diagnostics, and phylogenetic analysis. Clinical samples collected through sentinel surveillance were analyzed to identify DENV serotypes, genetic lineages, and key mutations affecting molecular detection.
Results:
Our work uncovered the co-circulation of three DENV serotypes in Senegal, with dynamic shifts over time. Notably, we identified the re-emergence of a sylvatic DENV strain after over two decades of apparent silence. Real-time monitoring revealed the erosion of diagnostic signature regions used in widely implemented RT-PCR assays, prompting the development and validation of updated molecular tools tailored to local viral diversity.
Implications:
This project directly advances the Pasteur Network's pillars: (1) Epidemic Intelligence & Preparedness: Enables early detection of genetic shifts, including sylvatic spillovers. (2) Research, Development, & Innovation:

Supports the creation of region-adapted diagnostics. (3) Multi-Disciplinary Knowledge Communities: Bridges of genomics, epidemiology, and public health. (4) Good Governance & Equitable Collaboration: Provides a model for sustainable surveillance partnerships in Africa.
Broader Impact:
Our approach enhances regional and global readiness for arboviral outbreaks and offers a scalable model for integrating genomics into routine surveillance, informing evidence-based countermeasures and supporting the One Health agenda

Enrico Palermo - Institut Pasteur in Italy – Cenci Bolognetti Foundation, Italy / ***Metabolic regulation of antiviral innate immunity to Dengue virus infection***
Objective:
This project aims to investigate how the modulation of cellular metabolism affects
the antiviral response to Dengue virus (DENV) infection is important.
Background:
DENV is a mosquito-borne pathogen that annually threatens about half of the world's population with an estimated 100-400 million yearly infections. Oxidative stress has been correlated with inflammation and progression towards the severe forms of disease and the maintenance of redox homeostasis is mediated in part through the global transcriptional regulator Nrf2. The endogenous metabolite itaconate, a by-product of Krebs cycle metabolism,
enables Nrf2 activity linking metabolism to anti-oxidant response.
Methods:
We investigated the effect of the Nrf2 cell-permeable agonist 4-octyl-itaconate (4- OI) on DENV replication in various cell lines and in primary monocyte-derived Dendritic Cells (MoDCs). Along with the evaluation of viral replication and innate immune response to DENV, a RNAseq analysis was performed to identify factors modulated by 4-OI that are involved in the regulation of Dengue infection.
Results:
This work demonstrated that 4-OI increased DENV replication in a Nrf2- independent manner and impaired the activation of type I IFN response. Moreover, the proviral effect relied on the 4-OI – induced metabolic switch from glycolysis to β-oxidation through the activation of the PDK4-CPT1 axis, thus identifying PDK4 as a key metabolic factor involved in modulation of viral replication.
Implications:
Geographic expansion of climate-sensitive diseases claims an urgent coordinated global strategy, sharing local expertise and knowledge to strengthen pandemic preparedness (Pillars 1,3 and 4). Considering the diverse effects of 4-OI, this project provides indications for metabolic-derived compounds Repurposing to generate new broad-spectrum antiviral agents (Pillar 2).
Broader Impact:
By identifying metabolic biomarkers linked to enhanced viral replication, the proposed research seeks to provide critical insights that may inform early prognostic tools and targeted therapeutic interventions. These results have strongrelevance to dengue immunopathogenesis, since disease severity has been directly associated with lipid metabolism disorders and chronic inflammation.

Hermann Landry Munshili Njifon - Centre Pasteur du Cameroon, Cameroon / ***Project Title: Strengthening Arbovirus Surveillance in a Climate-Sensitive Zone: Lessons from Northern Cameroon***
Objective:
To investigate the historical and potential circulation of emerging arboviruses in northern Cameroon. This study will assess past exposure through antibody prevalence and identify, future epidemic risks.
Background:
Arboviruses including orthoflaviviruses and alphaviruses pose an increasing threat to public health in sub-Saharan Africa. The ecological conditions and limited surveillance capacity in northern Cameroon make it a likely hotspot for undetected arbovirus transmission. Understanding past circulation is essential for guiding preparedness efforts
Methods:
We conducted a cross-sectional analysis on 276 human serum samples collected at the Centre Pasteur in Garoua during the SARS-CoV-2 pandemic. We used multiplex immunoassays (Luminex, a technique that enables the simultaneous detection of antibodies against multiple viruses), virus neutralization tests (VNT, which assess functional immunity), and RT-qPCR were used to detect viral RNA, this allowed us to make a comprehensive assessment of past and present infections.
Results:
High IgG seroprevalence was detected for several orthoflaviviruses: DENV-3 (51%), DENV-1 (24%), DENV-2 (18%), DENV-4 (12%), West Nile Virus (34%), USUV (54%), and ZIKV (26%). However, neutralization rates were low, indicating historical rather than recent exposure. Alphavirus results showed 29% seropositivity for CHIKV

and 15% for ONNV. There was significantly higher neutralization for ONNV (72.5%) than for CHIKV (14.5%). No viral RNA was found, ruling out ongoing infection.
Implications:
This project contributes directly to the strategic pillars of the Pasteur Network, particularly Epidemic Intelligence and Preparedness with a Focus on Climate-Sensitive Diseases and Multi-Disciplinary Knowledge Communities. The project reveals historical
transmission patterns and highlights the urgent need for proactive surveillance in climatesensitive regions.
Broader
Impact:
This research combines innovative serological and molecular tools to enhance epidemic risk assessment in neglected areas. The findings will inform future phases focused on genomic surveillance and the environmental drivers of arbovirus emergence. These findings will guide integrated response strategies across Africa

Samar Akbi - Institut Pasteur d'Algérie, Algeria ***/ Spatio-temporal identification of suitable areas for West Nile Virus circulation in Algeria using climatic and environmental data*****.**
Objective:
This study aims to develop a predictive spatio-temporal model to identify potential hotspots for West Nile Virus (WNV) circulation in Algeria. By integrating climatic, environmental, and health data, the model will enhance the national WNV surveillance system to improve outbreak forecasting, guide surveillance efforts, and optimise prevention and response strategies.
Background:
Algeria faces increasing risks of vector-borne diseases driven by climate change. WNV is the second most important vector-borne disease in the country, with significant outbreaks in 2023 (170 cases, 11.2% lethality) and 2024 (239 cases, 19.2% lethality). The recent northward spread of WNV into more densely populated areas heightens the urgency for predictive tools to anticipate and mitigate risks effectively.
Methods:
Key climatic and environmental drivers of WNV circulation were identified through a literature review. Selected factors included land surface temperature, soil moisture, vegetation index, water index, and land cover classification. All laboratory-confirmed human cases from 2023 and 2024 with known location and date of symptoms onset were included. For each case, climatic and environmental conditions were compiled for the six months preceding the infection. Also, veterinary and entomological data, along with human data, were used to define pseudo-negative sites. The predictive model will be trained using data from 2023 to 2024 and validated with 2025 data.
Results:
We expect the model to accurately forecast WNV onset and spatial spread up to two weeks in advance under favourable climatic and environmental conditions.
Implications: This predictive tool will support epidemic intelligence and preparedness by enabling early warning for outbreaks, guiding targeted surveillance, informing prevention measures such as localised vector control initiatives, and facilitating efficient resource allocation for proactive interventions.
Broader Impact:
This project lays the groundwork for integrating climate perspectives into the surveillance and management of climate-sensitive diseases. It will strengthen collaboration between the climate and health sectors and support the inclusion of climatic and environmental factors in early warning systems, contributing to improved public health resilience.

Pritesh Lalwani - Fundação Oswaldo Cruz (FIOCRUZ), Brazil / ***One Health Surveillance along the BR-319 Highway: Emerging Viral and Zoonotic Threats in the Amazon***
Objective:
To understand how the reopening of the BR-319 highway in the Amazon is influencing the spread of viruses and zoonotic diseases, and to develop a One Health approach for early outbreak detection.
Background:
The Amazon is one of the world's most biodiverse regions, but it is undergoing rapid change. The reconstruction of the BR-319 highway, which links Manaus to southern Brazil, is driving migration, deforestation, and new patterns of land use. These changes bring people, domestic animals, and wildlife into closer contact, increasing the risk of diseases that can jump between species and cause epidemics.
Methods:
We carried out field studies in communities along with BR-319. Blood samples from people and domestic animals, as well as insects and small mammals, were tested for evidence of
infection using serological and molecular tools.
Results:
We found strong signs of disease risk along the corridor. Exposure to Oropouche virus (OROV) reached ~80% in people and 70% in domestic animals. Infections were more widespread than routine testing suggests, with at

least four recent infections (IgM-positive) for everyone detected by molecular tests. Other threats were also evident: 29% of people showed signs of past leptospirosis, and 8% had antibodies to orthohantavirus. In domestic animals, 28% showed exposure to leptospirosis. Work is ongoing to analyze the insects and small mammals collected.
Implications:
Our findings demonstrate that rapid environmental changes along BR-319 are creating a hotspot for emerging and re-emerging diseases. Integrated One Health surveillance—linking human, animal, and environmental health—can provide earlier warnings and improve epidemic preparedness in the region.
Broader Impact:
This work offers a scalable model for other tropical regions facing similar pressure. It advances epidemic intelligence, fosters multidisciplinary collaboration, and strengthens global health security, directly contributing to the Pasteur Network's mission of preparedness for climate-sensitive diseases

40u40 Plenary Session 2: Community Involvement in Research and Surveillance

Wannes Van Hoof - Sciensano, Belgium / *Healthy Data – an online citizen consultation about health data reuse*
Objective:
Toruminants,a new ethical and legal framework for the secondary use of health data that allows us to break through the collection and storage of health data in silos, while maintaining citizen trust.
Background:
The European Union launched the joint action Towards the European Health Data Space (TEHDAS). A core objective of TEHDAS Work Package 8 (iCitizen) was to explore citizens' perceptions, expectations, and conditions regarding the secondary use of their health data, aiming to co-design governance models for the future EHDS.
Methods:
A large-scale online consultation was conducted in collaboration with Sciensano (Belgium), NHS Confederation (UK), and Health Data Hub (France). A literature review and 53 stakeholder interviews across pilot countries were conducted to prepare for the consultation. Citizens were engaged via a multilingual digital platform. All 5,932 contributions were analyzed using inductive thematic analysis.
Results:
Several core values emerged: support for public-benefit-driven reuse, strong anonymization, clear and transparent regulatory frameworks (e.g., GDPR alignment), and conditional beneficence rooted in trust and accountability. Citizen values were juxtaposed to expert opinions, stakeholder perspectives, and the legal text behind the EHDS to explore ethical tensions and requirements for trust building.
Implications:
Better secondary use of health data will be a driver for research, development and innovation and support epidemic intelligence and preparedness. This project shows how citizen engagement can contribute to public health governance.
Broader Impact:
Citizens strongly advocate being treated as partners in the EHDS, with transparency, communication, and diverse engagement options essential to building and maintaining trust. A flexible yet robust governance framework is needed—combining consent mechanisms, oversight structures, and feedback channels—to respect citizens' values while enabling societal benefits from data reuse. The findings provide a foundation for policy and governance of recommendations to the European Commission and member states.

Le Hoang Thieu - Pasteur Institute in Nha Trang, Vietnam / ***Rabies Epidemiology and Barriers to Prevention: A One Health Approach in Central Vietnam***
Objective:
To describe the epidemiological characteristics of human rabies deaths and identify barriers to rabies prevention and control in the central region of Vietnam (2016-2021).
Background:
Rabies remains a leading cause of death from infectious diseases in central Vietnam. Despite the availability of effective vaccines, challenges in prevention and control persist, posing a significant threat to public health.
Methods:
A cross-sectional study was conducted involving a retrospective analysis of 49 human rabies death cases reported between 2016 and 2021. In-depth interviews were carried out with 67 stakeholders, including healthcare workers, local authorities, and community members, to explore barriers to rabie prevention and response.
Results:

The rabies mortality rate in the region was 0.41 per 100,000 population, with an average of 7.4 deaths per year. Most deaths occurred among individuals aged 15–59 years (59.2%) and those with farming occupations (49.0%). Alarmingly, 96% of those who died had not received any post-exposure vaccination, and the remaining 4% had incomplete prophylaxis. Key reasons for non-vaccination included fear or unwillingness to be vaccinated (91.8%) and lack of awareness (8.2%). Systemic barriers identified were insufficient specialized human resources, limited stray dog management, and low rates of post-exposure healthcare-seeking behavior.
Implications:
This study directly supports the Epidemic Intelligence & Preparedness pillar through enhanced understanding of high-risk populations and gaps in response. It also contributes to Multi-Disciplinary Knowledge Communities and Good Governance & Equitable Collaboration by promoting cross-sectoral engagement and highlighting the need for coordinated actions.
Broader Impact:
Strengthening the One Health approach—through integrated human-animal surveillance, public education, and sustainable vaccine access—can significantly reduce rabies mortality and enhance epidemic preparedness in Vietnam and other resource-limited settings

Grégoire Davigon - Institut Pasteur de Nouvelle Calédonie, New Caledonia / ***Simulating Climate-Sensitive Leptospira Dynamics Through Transparent Soil Microcosms and Community-Centered Approaches in New Caledonia***
Objective:
This project aims to anticipate the impacts of climate change on environmental persistence and transmission of Leptospira in New Caledonia. It integrates microbial ecology, environmental simulation, and sociocultural perspectives to design more effective and locally adapted public health strategies.
Background:
Leptospirosis is a neglected tropical disease with strong environmental and behavioral determinants, particularly in Oceania. In hyperendemic areas of New Caledonia, Melanesian communities are disproportionately affected. Rainfall events are known to resuspend Leptospira from soil to surface waters, increasing exposure risk. However, the mechanisms governing Leptospira persistence and mobilization in soil remain poorly understood, and prevention campaigns often overlook cultural Perceptions of disease.
Methods:
We will use custom transparent soil microcosms that allow real-time, non-destructive imaging to simulate climate change effects on Leptospira persistence. Three parameters will be evaluated; temperature: microcosms will be incubated at climate scenario-based temperatures (SSP1-1.9 to SSP5-8.5), rainfall: flooding simulations using a pressure-driven microfluidic system will evaluate Leptospira leaching and dispersal and, soil texture: microcosms with engineered soils of varying textural composition will assess effects on Leptospira colonization and transport. Pathogen persistence will be monitored by qPCR, and microbial community changes will be assessed to elucidate climate driven dynamics influencing Leptospira survival. Parallel to this, early discussions with anthropologists and Melanesian community members have revealed distinct representations of disease, prompting us to design culturally tailored awareness campaigns and participatory research workshops.
Results:
Transparent soil models confirm the environmental viability and spatial clustering of Leptospira. In a separate field study, we observed increased concentrations of Leptospira in watershed runoff following heavy rain, supporting the hypothesis of rainfall-driven resuspension. Human component insights suggest that standard public health messages may fail to resonate with local conceptions of health and disease, underscoring the need for adapted communication strategies.
Implications:
This interdisciplinary project contributes to the Pasteur Network pillars:
– Epidemic Preparedness, through environmental modeling under climate scenarios
– Innovation, via biofilm-oriented transparent soil systems
– Equitable Collaboration, through culturally aware public engagement
Broader Impact:
This work will provide tools and frameworks for anticipating leptospirosis outbreaks and building longterm community resilience across climate-vulnerable Pacific regions.

40u40 Plenary Session 3: Respiratory Viruses: Detection, Surveillance & Immunity

Wuji Zhang - Hong Kong University - Pasteur Research Pole, Hong Kong / Determinants of robust immune responses to respiratory virus vaccines in individuals with chronic comorbidities

Objective:
Respiratory tract infections, caused by viruses and other pathogens, remain a major global health burden. High-risk groups with chronic comorbidities are especially vulnerable. This research aims to elucidate factors that influence immune responses to influenza and COVID-19 vaccines in people with chronic health conditions.
Background:
Emerging respiratory viruses pose ongoing threats due to their ability to evade established immune memory. Indigenous populations, such as Australian First Nations peoples, have higher rates of chronic diseases like diabetes and kidney disease, yet were not included in vaccine clinical trials. Understanding immune responses in these populations is critical for effective public health strategies.
Methods:
We assessed immune responses, including neutralizing antibodies, SARS-CoV-2-specific B cells, CD4+ and CD8+ T cells, following mRNA COVID-19 vaccination in Australian First Nations and non-Indigenous (mostly Caucasian) participants. Additionally, we analyzed antibody glycosylation patterns and plasma cytokine levels. Building on these findings, we are recruiting Asian individuals with chronic kidney disease at the HKU-Pasteur Research Pole. We will evaluate their responses to influenza vaccination across disease stages and treatment regimens and explore cross-protection against viral variants.
Results:
First Nations participants mounted robust immune responses to vaccination. However, individuals with chronic comorbidities showed reduced levels of antibodies, B cells, and T follicular helper cells targeting SARS-CoV-2. These alterations were linked to abnormal antibody glycosylation and elevated plasma interleukin-18, suggesting an inflammatory environment. The findings highlight that comorbidities and inflammation drive immune perturbations.
Implications:
This research aligns with the Pasteur Network's strategic pillars by enhancing epidemic preparedness for high-risk zoonotic diseases and informing the development of innovative vaccines.
Broader Impact:
Our research provides actionable insights to optimize vaccine strategies and clinical care for vulnerable populations. These findings may also inform public health policies and clinical guidelines for kidney diseases and other chronic diseases, contributing to global health equity.

Ali Maleki - Institut Pasteur in Iran, Iran / *Strengthening Diagnostic Reliability in Epidemics: Insights from Iran's COVID-19 External Quality Assessment Program*

Objective:
This project aims to evaluate and enhance diagnostic accuracy and laboratory performance through the implementation of a national External Quality Assessment Program (EQAP) during the COVID-19 pandemic in Iran.
Background:
Accurate and timely diagnosis is critical during infectious disease outbreaks. EQAPs serve as a cornerstone of laboratory quality assurance by enabling performance benchmarking and reducing diagnostic variability across institutions. During the COVID-19 crisis, Iran's National Reference Laboratory at the Pasteur Institute of Iran led a structured EQAP to ensure consistent and trustworthy molecular testing nationwide.
Methods:
Participating laboratories were assessed using blinded sample panels, scoring criteria based on cycle threshold (Ct) deviations, and evaluation of interpretive accuracy of RT-qPCR results. The program incorporated sample design with internal controls, standardization of reporting, and training feedback loops to address identified deficiencies.
Results:
The EQAP revealed significant variability in Ct values and interpretative accuracy among labs. Key findings included frequent analytical-phase errors related to reagents and assay execution. Performance improved over successive rounds, demonstrating the EQAP's effectiveness in Fostering diagnostic precision and preparedness during crisis conditions.
Implications:
This work supports the Pasteur Network's pillars of Epidemic Intelligence & Preparedness and Good Governance & Equitable Collaboration by enabling national harmonization of testing, empowering laboratories to respond to emerging pathogens, and establishing a reproducible model for other LMICs.

Broader Impact:
The EQAP framework enhances national surveillance, public health confidence, and outbreak containment capabilities. As climate-sensitive and respiratory diseases grow in frequency, Reproducible quality systems like this will be vital for equitable global health responses.

Pham Van Khang - National Institute of Hygiene and Epidemiology (NIHE), Vietnam/ E*pidemiology of Measles in the Northern Region from 2019 to 2023 and Risk Assessment for 2024*
Objective:
The study aimed to describe the epidemiological characteristics of measles in 28 provinces in northern Vietnam from 2019 to 2023 and assess the potential risk of a measles outbreak in 2024.
Background:
Measles, an acute infectious disease, has increased globally partly due to disruptions in vaccination during the COVID-19 pandemic. In Vietnam, the coverage of the first dose of measles vaccine (MCV1) decreased from 96.7% in 2021 to 88.5% in 2023, much lower than the herd immunity threshold of 95%. This situation has created many susceptible people and increased the risk of an outbreak.
Methods:
The study used case series and cross-sectional methods. 1,157 measles cases were collected from 28 provinces in the North during 2019-2023. The Ministry of Health survey forms and the WHO Measles Risk Assessment Tool were used, which includes four components: community immunity, the effectiveness of the Expanded Programme on Immunisation (EPI), the quality of surveillance and other risk factors.
Results:
A measles outbreak was recorded in 2019, accounting for 949 of the 1,157 cases. Children under 5 years of age accounted for 61.3% of all cases, with 79.7% of them having unclear or unvaccinated vaccination histories. The rate of missed vaccination between DPT1 and MCV1 exceeded 10% in some provinces. The measles risk for 2024 shows Ha Noi and Nghe An are at medium risk, while Ha Tinh is high-risk.
Implications:
Contribute to the Pasteur Network by providing evidence for vaccination strategies and enhanced surveillance.
Broader Impact: These recommendations can be applied to strengthen disease prevention systems and prevent future outbreaks

Karidja Yakoura - Institut Pasteur de Côte d'Ivoire, Côte d'Ivoire / *Integrated Epidemiological and Genomic Surveillance of Respiratory Viruses in Côte d'Ivoire (2022–2025)*
Objective:
To assess the circulation and genomic diversity of respiratory viruses in Côte d'Ivoire through integrated epidemiological and molecular surveillance, with the aim of strengthening early detection and epidemic preparedness.
Background:
Acute respiratory infections remain a major public health concern in sub-Saharan Africa, particularly among children and vulnerable populations. Despite existing vaccination programs and surveillance networks, the dynamics of co-circulating viruses such as influenza, SARS-CoV-2 and respiratory syncytial virus (RSV) are not fully characterized. Integrating genomics into surveillance systems is essential to anticipate epidemic threats and inform public Health interventions.
Methods:
Between 2022 and 2025, a total of 16,161 nasopharyngeal samples were collected from sentinel sites in the influenza surveillance network in Côte d'Ivoire. The following points of the national influenza surveillance protocol, objectives, case definition, and notification form were revised to incorporate the specificities related to RSV and SARS-CoV-2 surveillance.
Respiratory viruses were detected by RT-PCR and characterized by next-generation sequencing using Nanopore technology. Epidemiological data were combined with genomic analyses to Describe seasonal trends and the circulation of viral lineages.
Results:
The results revealed the sustained co-circulation of several respiratory viruses (Influenza, SARS-CoV-2, RSV, Parainfluenza, Seasonal Coronavirus, Rhinovirus) with seasonal peaks influenced by local climatic conditions. Distinct strains of influenza and SARS-CoV-2 were identified, reflecting both repeated introductions and local transmission. Genomic analysis enabled the detection of key mutations associated with viral adaptation and the close monitoring Of variants of concern in SARS-CoV-2 positive cases.
Implications:
This work contributes to the Pasteur Network's strategic pillars by enhancing epidemic intelligence and preparedness, fostering scientific innovation, and strengthening multidisciplinary collaborations at both national and regional levels.
Broader Impact: The integrated approach strengthens national capacity for epidemic

preparedness and response to respiratory viruses, while providing a model for capacity building and genomic-informed surveillance across African countries

Dung Truong Thi Thuy - Pasteur Institute in Ho Chi Minh City, Vietnam / *Real-time Epidemiological Analysis for Measles Outbreak Control in Southern Vietnam, 2024–2025*

Background:
In many low- and middle-income countries, measles outbreaks are hard to contain without rapid access to reliable data. This study describes how near real-time review of case reports and laboratory findings helped shape outbreak response during the 2024–2025 epidemic in Southern Vietnam.
Methods:
We examined suspected measles cases with symptom onset from January 1, 2024, to June 30, 2025, across 20 southern provinces (population over 35 million). Case data from the national surveillance system, combined with laboratory results, were compiled weekly to follow patterns over time, by location, and across age groups. These summaries were discussed with national and provincial teams to adjust vaccination and testing activities in line with changing outbreak trends and the supply of vaccines and diagnostic kits.
Results:
During the study period, 73,502 cases were recorded, including 22 deaths. Case counts rose sharply in August 2024, peaked in December (15,269 cases), and began falling from February 2025. Weekly positivity rates climbed from 10–20% early in the outbreak to 95% at the peak, then dropped to 60–70% after targeted measures. Hospital infection control was reinforced, with vaccination history checks and on-site immunization. Vaccination campaigns focused on high-transmission areas and vulnerable groups. An early "dose 0" for infants six months, earlier than the national nine-month schedule, was introduced. Three rounds of outbreak response vaccination between mid-2024 and mid-2025 delivered over one million doses.
Conclusion:
Regular analysis of routine surveillance data supported timely, practical changes to vaccination and testing, contributing to outbreak containment.
Implications:
This approach reflects the Epidemic Intelligence & Preparedness pillar through adaptive surveillance and targeted interventions and advances Good Governance & Equitable Collaboration through coordinated collaboration between clinical, laboratory, epidemiological, and immunization sectors.
Broader Impact:
The model offers a framework for integrating surveillance and vaccination to manage large outbreaks within the limited-resource settings and the Pasteur Network.

40u40 Plenary Session 4: Enteroviruses & Emerging Viruses

Joël Dote - Institut Pasteur de Bangui, Central African Republic / *Characterization of enteroviruses circulating among farm animals and children in Central African Republic*

Background:
Enteroviruses (EVs) belong to the Picornaviridae family. Besides enterovirus (EV) species that mainly infect humans (EV-A, B, C and D), there are species circulating in other mammals: EV-Es, EV-Fs and EV-Gs infect livestock animals, such as swine, goats, sheep, cattle and lamas. Although the number of known specimens of EVs that infect livestock has increased during the last decade because of the introduction of next generation sequencing techniques, these viruses remain under sampled, particularly in Africa were only a few EV-Es, EV-Fs and EV-Gs have been reported. Therefore, EVs can cross the species barrier between primates and pigs, in both directions.
Objective:
Our objectives were to characterize the EV circulating in farm animals and determine whether there are zoonotic exchanges of EV in the Central African Republic. Methods: we screened by molecular biology 192 stools of animals under 12 months (pigs, small ruminants, and cattle) belonging to family farms located in or near Bangui. To assess whether EV exchanges exist between these animals and humans, we also Screened 195 stools of children who lived in contact with farm animals, as well as control stools of 358 children with no contact with farm animals. EVs were typed based on them capsid sequences.
Results:
We detected EV in 20.5% of animal stool pools, 42.9% of contact children and20,6% of children control stool pools. In children, EV belonging to species A, B, and C were detected without a difference between contacts and controls. EV-C are predominant (> 60%), with a majority of EV-C99 and CVA13. No animal EV was found in the children. In animals, 21 EV were identified, belonging to different types of EV-G. No EV-E or EV-F was observed in this study. Five human EV (CVB3, CVA17, CVA24 and PV-1 of vaccine origin) were detected in pigs.
Implications:

The worldwide circulation of EV-Gs is likely due the massive international trade of live animals. Besides, two human EV-Cs (coxsackievirus A17 and coxsackievirus were detected in pigs, suggesting that these viruses could cross the species barrier. Our work provides original data on the epidemiology and ecology of EVs circulating among herd animals in Africa.
Broader Impact:
Transmission of enteroviruses from animals to humans remains rare, but interspecies transmission of human EVs to animals is possible. It is therefore necessary to search for cellular receptors for these enteroviruses in humans and farm animals and to study the determinants of interspecies transmission of EVs in order to prevent the emergence of new viral types that may result from them

Anna Dolgova - Saint-Petersburg Pasteur Institute, Russia / ***Pseudotyped viral particles as a tool for studying tissue tropism of newly discovered viruses***
The rapid development of NGS technologies has led to their wide application in various fields of biology and medicine. For example, studies of the metaviromes of different animals (reservoirs of both known and potential human pathogens) have become the main source of information on new viruses. This has led to a revolution in our understanding of their diversity. Unfortunately, most newly discovered viruses are not studied by classical virological methods. This is associated with the laboriousness of isolation and cultivation work, as well as the need for required biosafety levels.
In this regard, it is impossible to assess the significance of such findings in terms of their possible pathogenicity for humans. Bioinformatic methods can be used to model virus-receptor interactions; however, this is not enough to solve the existing problem. A powerful tool for studying the pathogenicity of lipid enveloped viruses is the pseudotyped viral particle technique.
An example of the successful application of this is the study of the tropism of the new β-coronavirus MOW-BatCoV/15-22. Its genome was sequenced from P. nathusii fecal samples collected in the Moscow region. Phylogenetic analysis has established that the closest related virus is MERS-CoV, and the S protein is closest to coronaviruses detected in hedgehogs. Molecular docking methods showed a high probability of S protein binding to the DPP4 receptors of M. brandtii and E. europaeus, with a lower (but still significant) binding probability to human DPP4. However, interaction studies of MOW-BatCoV/15-22 S protein pseudotyped particles with H1299 cell lines overexpressing human DPP4 and ACE2 showed a high binding affinity for the ACE2 receptor, but not DPP4. This was later confirmed by other studies. This is one example of how modern synthetic biology methods can answer epidemiological questions and contribute to epidemiological intelligence as a scientific interdisciplinary approach.
Chittaphone Vanhnollat - Institut Pasteur du Laos, Laos / ***Uncovering Zoonotic Viruses at the Human-Wildlife Interface***
Objective:
This study aims to investigate zoonotic viruses with spillover potential, to gain a deeper understanding of viral infections in host reservoirs and ultimately unravel some of the mechanisms behind zoonotic spillover.
Background:
Southeast Asia, and particularly the Lao People's Democratic Republic, is recognized as a hotspot for emerging infectious diseases. Timely identification of novel viruses is critical to mitigating the risk of outbreaks, epidemics, or pandemics. However, the country's current surveillance systems remain limited in scope and capacity. Strengthening these systems Through targeted research, it is essential for both national and global health security.
Methods:
To address this gap, field sampling was conducted at selected sites across Laos, focusing on wildlife known to serve as viral reservoirs, including bats, rodents, and their ectoparasites. Collected samples underwent laboratory testing using polymerase chain reaction (PCR) and next-generation sequencing (NGS). Subsequent bioinformatics analyses were applied to detect and characterize viral genomes.
Results:
Preliminary results revealed the presence of viruses in several families, including Coronaviridae, Hantaviridae, Paramyxoviridae, and Flaviviridae. Of particular note, bat-borne hantaviruses were reported for the first time in Laos, expanding the known geographic distribution of hantaviruses in Southeast Asia. While these initial discoveries are important, many of the viruses detected require further genomic and epidemiological investigation to fully assess their public health relevance.
Implications:
This work directly supports two of the Pasteur Network’s strategic pillars. First, it advances Epidemic Intelligence & Preparedness with a Focus on Climate-Sensitive Diseases by establishing a surveillance pipeline for the early detection of emerging pathogens. Second, it contributes to Multi-Disciplinary Knowledge Communities by promoting local and international collaborations.
Broader Impact:

Beyond immediate findings, this project has strengthened local capacity in both field and laboratory-based viral surveillance. It provides a foundation for future research on unknown and poorly characterized viruses and supports public health preparedness by generating data on potential pathogens of concern

40u40 Plenary Session 5: Bacteria & Microbiota

Sébastien Bontemps-Gallo - Institut Pasteur de Lille, France / *Survive to Transmit: How Yersinia pestis Prepares Inside Fleas for Plague Spread*

Objective:
This study aims to understand how Yersinia pestis adapts to the dynamic and hostile environment of the flea gut to colonize the vector and ensure transmission to mammalian hosts.
Background:
Yersinia pestis, the causative agent of plague, remains endemic in certain regions due to a stable transmission cycle between rodents and their fleas. Fleas act not only as vectors but also, as reservoirs that, under certain conditions, can trigger enzootic cycles and epizootic peaks, increasing human exposure. Successful colonization and transmission require the bacterium to adapt to the harsh physiology of the flea gut, an environment that remains poorly characterized.
Methods
We combined in vivo infection models, molecular biology, omics analyses, biochemical assays, microscopy, and medical entomology to dissect Y. pestis adaptation to its vector.
Results:
After characterizing the flea gut environment with unprecedented temporal resolution, we identified novel molecular mechanisms that allow Y. pestis to resist stress, and thrive, as well as those enabling transmissible infections. This work refines our understanding of how a bacterial pathogen achieves vector-mediated transmission, using the Y. pestis-flea Interaction as a powerful model for studying vector-borne diseases.
Implications:
This research contributes to the Pasteur Network's Research, Development & Innovation pillar by identifying potential targets for strategies to block plague transmission, an urgent need given the absence of a vaccine and the emergence of multidrug-resistant strains. It also includes a drug discovery focus, with candidate molecules currently under evaluation for eIicacy.
Broader Impact:
Beyond plague, these findings may support eIorts to fight multidrug-resistant Enterobacteriaceae, extending the relevance of this work from vector-borne infections to the broader field of antimicrobial resistance

Antsa Harinavalona Rakotonirina - Institut pasteur de Madagascar, Madagascar / *Molecular Detection of Tick-Borne Pathogens in Ticks Infesting Domestic Animals in Madagascar: Implications for Public Health*

Tick-borne diseases (TBDs) pose a significant threat to both veterinary and human health worldwide. In Madagascar, these diseases remain largely neglected despite serological evidence suggesting the circulation of pathogens such as Coxiella burnetii (Q fever), Anaplasma spp., and the Crimean-Congo hemorrhagic fever virus (CCHFV) in both animal and human populations. Therefore, strengthening vector surveillance in the country is crucial to understand transmission risks, improve early detection and prevention strategies, and implement effective public health interventions to mitigate zoonotic threats. Our project aimed to improve understanding of the occurrence and diversity of TBDs in Madagascar, with the goal of supporting the long-term protection of animal and human population. Ticks were collected in two pilot regions, Ifanadiana and Morondava, from various hosts including livestock (zebu, goats) and dogs. Morphological identification determined species, sex, and developmental stage. DNA was extracted, and pathogen screening was performed using high-throughput real-time quantitative PCR (qPCR) via Fluidigm microfluidic technology. A total of 4,576 ticks were collected during the sampling. The majority belonged to Amblyomma variegatum (52.34%; n = 2,395) and Rhipicephalus microplus (47.33%; n = 2,166), both of which primarily parasitized ruminants. Pathogen detection revealed multiple parasitic genera (Babesia spp., Hepatozoon spp., Theileria spp.) and bacterial genera (Anaplasma spp., Borrelia spp., Coxiella spp., Ehrlichia spp., Rickettsia spp.), including human pathogens such as Coxiella burnetii, Rickettsia africae and R. conorii, the latter reported here for the first time in
Madagascar. The presence of these pathogens in ticks from domestic and companion animals highlights the potential risk of zoonotic transmission to Humans. This research provides among the first essential baseline data on tick species and associated pathogens in Madagascar. Aligned with the Pasteur Network's pillar on Epidemic Intelligence & Preparedness, it strengthens zoonotic disease surveillance, supports early detection efforts, and informs public health strategies within a One Health framework

Isaure Quétel - Institut Pasteur de Guadeloupe, Guadeloupe / *Impact of Habitat Disturbance on Small Mammal Microbiota and Zoonotic Risk in a Tropical Island Ecosystem*

Objective:
This study focuses on small mammals and aims to (1) analyze gut microbiome composition, and (2) assess the impact of anthropogenic pressure on the fecal microbiome and pathogens carriage in rats.
Background:

Zoonotic disease emergence has surged over the past 40 years, closely linked to anthropogenic environmental change. Habitat disturbance affects wildlife microbiota and may favor generalist species that serve as reservoirs for pathogens. Guadeloupe, with high biodiversity and ecological vulnerability, offers a relevant model. Its rodent community—mainly Rattus rattus, Rattus norvegicus and Mus musculus—includes known vectors of Leptospira and Angiostrongylus.
Methods:
Ninety-six rats were trapped at 36 sites. Fecal samples were collected and DNA extracted. 16S and 18S rRNA regions were amplified and sequenced by the Biomics platform (Institut Pasteur, Paris). Bioinformatic analyses were made.
Results:
Microbiome analyses of rat feces across Guadeloupe's biotopes revealed that both bacterial and eukaryotic communistes vary significantly with habitat and human disturbance. The microbiomes of rats caught in mangroves showed distinct profiles and lower diversity than those in dryland or swamp forests. Pathogenic bacteria carried by rat microbiomes differed notably between those living in dryland and swamp forests, while certain plant and parasite taxa were biotope-specific. Degradation influenced diversity patterns, especially for eukaryotes. Co-occurrence analyses revealed associations between key pathogens, suggesting that environmental change shapes microbial ecosystems with possible zoonotic consequences.
Implications:
Understanding these microbial and ecological dynamics could offer new insights into the mechanisms underlying the emergence of zoonotic diseases in island environments. Thus, our research aligns with the first strategic pillar of the Pasteur Network. Broader Impact: This research highlights how habitat disturbance influences the microbiota of zoonotic reservoirs. It may improve understanding of pathogen transmission dynamics in insular ecosystems and informs preventive strategies at the interface of environment and public health.

Nikolaos Vakirlis - Hellenic Pasteur Institute, Greece / ***Molecular mechanisms of innovation: de novo gene birth and antimicrobial peptides***

How new genes and protein functions evolve is a fundamental biological question. For a long time, we thought new genes resulted exclusively through tinkering of pre-existing ones. However, we now know that entirely novel genes can also evolve from previously non-coding genomic sequences, a process called de novo gene birth. We know relatively little about how this process unfolds, yet understanding it is important for more than evolutionary reasons: as a key to map the functional potential and therefore better annotate genomes, in its relation to the origin of small proteins in human pathogens, even as a process that could inspire new protein design ideas. My group develops and applies innovative bioinformatics approaches to investigate de novo gene birth in diverse organisms. I will present new and recently published work ranging from the origin of unique microproteins encoded in the human genome, to how simple intergenic repeats in the yeast genome evolved de novo into transmembrane proteins, to our analysis of the massive numbers of "orphan" sequences within human gut microbial pangenomes. Understanding the processes of molecular innovation is also critical in the case of antimicrobial peptides (AMPs), short proteins which are used by all organisms in defense against pathogens, and which have significant potential for use as alternative antibiotic drugs. To optimally harness AMPs for therapeutic purposes it is crucial to investigate the evolutionary forces that have shaped their natural diversity, yet little is known about how novel AMPs originate and diversify. I will present our ongoing project in which we are computationally mining novel AMPs across thousands of animal genomes, experimentally validating and analyzing them using machine learning, comparative genomics and computational molecular biology techniques. In doing so, we aim to understand how AMP inn

Siyeon Yang - Institut Pasteur Korea, Korea / ***Infectious disease animal models mimicking human immune responses for bridging preclinical and clinical research***

Non-tuberculous mycobacteria (NTM) respiratory and skin infections pose significant challenges to human health, necessitating the development of animal models that closely mimic human infection states for translational research. In this study, we establish and characterize mouse infection models that replicate human NTM respiratory and cutaneous infections, providing valuable platforms for understanding disease pathogenesis and evaluating therapeutic interventions.
Among mycobacterial diseases, tuberculosis (TB) remains a global health burden, particularly in its chronic infection form. To better emulate human TB pathophysiology, we have developed a humanized mouse model in which Mycobacterium tuberculosis (Mtb) is introduced into immunodeficient mice reconstituted with human immune cells. This approach allows for more accurate representation of the human immune response to Mtb infection, surpassing limitations of conventional mouse models.
To deepen understanding of TB lung pathology, we applied spatial transcriptomics to analyze distinct lung regions infected humanized mice, focusing on granulomatous lesions compared to adjacent normal tissue. This spatially resolved analysis enabled identification of differentially expressed genes and proteins associated with

granuloma formation and immune regulation. Leveraging these findings, we aim to generate transgenic (TG) mice engineered to overexpress key human genes implicated in TB immune responses. The ultimate goal is to establish mouse infection models that closely replicate the human immune system's dynamics during mycobacterial infections. Such models will enhance the translational value of preclinical studies, facilitating the development of novel therapeutics and vaccines with improved efficacy. Through iterative refinement combining spatial multi-omics and genetic engineering, our approach promises to bridge the gap between experimental animal models and human disease, contributing to more predictive and clinically relevant infectious disease research.

Iliyan Manoylov - Stephan Angeloff Institute of Microbiology, Bulgaria / ***Zbtb20 - a transcription factor important for almost everything***

Objective:
The study aims to determine the effect of the Zbtb20 TF on the function of the immune system.
Background:
Zbtb20 is vital for individual development, impacting organ formation, circadian rhythms, and liver regeneration. Its, dysregulation is linked to the development of carcinomas and lymphomas. Studies also indicate its role in lymphocyte development and its ability to modulate the proliferation of cancerous immune cells. Despite these insights, the full scope of Zbtb20's influence on the immune system remains to be understood.
Methods:
The study uses PCR to check the zygosity of the mice. We analyse BM and spleen cells using flow cytometry for phenotyping, CFSE and apoptosis assays, and perform ELISA on serum samples to measure antibody levels.
Results:
Heterozygous mice exhibit alterations in BM populations, with a surprising increase in HSCs, but a reduction in B-1 cells, suggesting an impact on innate immunity. These changes extend to the spleen, showing more B cells and fewer T cells, particularly helper T cells, potentially weakening adaptive immune responses. While conventional B cell development is augmented in the BM and spleen of heterozygous animals, circulating natural IgM antibodies are elevated despite lower B-1 cells.
Implications:
The Zbtb20 mice were provided by neurobiologists from the Max Planck Institute for Biophysical Chemistry, Goettingen Germany. We perform a cross-disciplinary study, that involves Neurobiology, Genetics, and Immunology. Young scientists are recruited during the course of the experiments. By governing the project, leadership and coordination experience are being acquired, and collaborations are being made.
Broader Impact:
With plans of developing models of autoimmune and infectious diseases in animals, much is to be discovered about the effect of the Zbtb20 TF in cancer research and vaccine response. Data from human patients with different immunological conditions will be gathered to check the transcription activity of Zbtb20 and to link it with the malignancy

Sokleaph Cheng - Institut Pasteur du Cambodge, Cambodia / ***CIRCUS: Circulation of multi-drug resistant Enterobacteriaceae (MDR-E) in humans, animals and the environment in Takeo Province, Cambodia***

Objective: The CircUs project in Cambodia investigates the circulation of multidrug-resistant Enterobacteriaceae (MDR-E) and their mobile genetic elements across humans, animals, and the environment in Takeo province.
Background: The World Health Organization identifies controlling Extended Spectrum Beta- Lactamase Enterobacteriaceae (ESBL-E) and Carbapenemase-Producing Enterobacteriaceae (CPE) as a global priority. These MDR-E and their mobile genetic elements carrying these resistances are found in humans, in animals and in the environment and are spreading worldwide. However, knowledge on the extent of resistance in these three compartments remains poorly characterized in low- and middle-income areas, where surveillance is limited.
Methods: The study is a multicentre and multidisciplinary, organized into three work packages (WP): WP1 - Hospital-based surveillance, WP2 – Detection of MDR-E in patient households and surrounding environments, and WP3 - Whole genome sequencing (WGS) of bacterial isolates from all sources.
Results: WP1 enrolled 64 patients (70.3% female), with 55.6% of females and 65.2% of males carrying MDR-E. A total of 73 isolates were collected, predominantly E. coli (75.3%; 61.8% MDR) and K. pneumoniae (17.8%; 53.8% MDR). WP2 collected 406 samples from 36
households: 19.2% from humans, 30% environmental, 22.2% food, and 18.8% animal samples. Over 80% were MDR-E positive, E. coli, K. pneumoniae, or Enterobacter cloacae complex. Selected isolates are scheduled for WGS at Institut Pasteur, Paris, in late 2025. This data will provide a better understanding of antibiotic resistance circulation within a One Health framework by identifying key resistance hotspots and transmission pathways.
Implications: The CIRCUS project supports all four Pasteur Network strategic pillars by enhancing epidemic intelligence and preparedness through One Health surveillance of multidrug-resistant Enterobacteriaceae, driving innovation with whole genome sequencing, and fostering cross-member collaboration. The project also

fosters multidisciplinary knowledge communities by building local scientific capacity and promoting inclusive collaboration between Cambodian and international researchers. Finally, CircUs exemplifies good governance and equity by empowering Cambodian leadership.
Broader Impact: The project will generate extensive data for integrative thematic and transdisciplinary analyses, aiding the development of targeted strategies to combat antimicrobial resistance effectively on a large scale

40u40 Plenary Session 6: Parasites

Aissata Camara - Institut Pasteur de Guinée, Guinea / *SHERLOCK4AAT, a new molecular method for highly sensitive and specific detection of Animal African Trypanosomes*

Objective:
Strengthen epidemiological surveillance of animal trypanosomiases through the development and application of an ultrasensitive molecular diagnostic tool for detecting African trypanosomes in animal reservoirs.
Background:
African trypanosomes are vector-borne parasites that infect both humans and a wide range of domestic animals across sub-Saharan Africa. In livestock, trypanosomiasis (nagana) causes over 3 million cattle deaths annually, threatening 50 million animals in 37 countries. These losses hinder agricultural productivity and socio-economic development. Better detection tools are needed to identify low-density and mixed infections in animal reservoirs.
Methods:
SHERLOCK (Specific High Sensitivity Enzymatic Reporter UnLOCKing) is a CRISPRbased RNA detection platform that uses isothermal amplification followed by Cas13 mediated detection. The method was adapted and validated in the lab to target the main African animal trypanosome species. Field samples from sheep, goats, pigs, and dogs were collected in Guinea, Cameroon, and Côte d'Ivoire to test the tool under real conditions.
Results :
SHERLOCK enables sensitive detection of trypanosomes, even at very low parasite densities and in co-infections. Two species were detected: T. congolense and T.b. gambiense, with T. congolense being most prevalent in Guinea and Côte d'Ivoire. Among Trypanozoonpositive pigs, 16% (Guinea) and 51% (Côte d'Ivoire) were also infected with T. congolense. No T. vivax, T. simiae, T. theileri, or T. suis were detected.
Implications :
This project aligns with two strategic pillars of the Pasteur Network : Global Health, by addressing a neglected tropical disease within a One Health framework, and Innovation, by applying advanced molecular diagnostics in resource-limited settings. SHERLOCK improves the detection of animal reservoirs, supporting more effective surveillance and control strategies.
Broader Impact :
This approach enhances our capacity to identify parasite reservoirs, guide interventions, and strengthen regional efforts toward sustainable elimination of Trypanosomiases

Florencia Díaz Viraqué - Institut Pasteur de Montevideo, Uruguay / *From Chromatin to Infection: Epigenetic Regulation in a Neglected Human Parasite*

Chagas disease is a major neglected tropical disease caused by Trypanosoma cruzi, distributed worldwide, affecting 7 million people and causing 10,000 deaths annually. With no effective treatment or vaccine, it remains a leading cause of disability and premature death in the Americas. Despite the importance in terms of human health, little is known about its biology compared to other parasites causative of diseases. Understanding how the pathogen T. cruzi regulates the infection is still a primary goal in parasitology and a critical point in the pursue for novel therapeutic venues.
The mechanisms described that regulate T. cruzi gene expression are insufficient to explain the critical regulatory changes necessary for pathogenicity, and it has been widely accepted that the control is post-transcriptional. However, based on increasing evidence, our central hypothesis establishes the spatial organization of the genome as a relevant modulator of gene transcription and pathogenesis. We showed that the genome is organized into chromatin domains and compartments affecting genome expression. Our findings support a model where epigenetics centrally regulate gene expression and provide significant new insights into the molecular mechanisms underlying parasite infection. We demonstrated that its genome organization differs from that of humans; therefore, understanding these mechanisms and uncovering vulnerabilities may aid in vaccine development.
Through integrative approaches, we generate insights that may lay the groundwork for new therapeutic strategies against Chagas disease—a neglected, climate-sensitive illness. Besides, my work is focused on a growing field that holds broad relevance and could benefit diverse research projects in resolving long-standing biological questions.

The project fosters Multi-Disciplinary Knowledge Communities in computational biology and parasitology, and promotes Equitable Collaboration through partnerships within the Pasteur Network, including an ACIP-funded collaboration I coordinate with Fiocruz and Institut Pasteur Paris.

Ryan D. Pardy – INRS-Armand Frappier, Canada / *Investigating the dynamics of interferon signalling in the small intestine using Cryptosporidium infection*

Cryptosporidium spp. are intracellular parasites that exclusively infect intestinal epithelial cells (IEC) and are a leading cause of severe diarrheal disease in children and immunocompromised patients. It has long been appreciated that interferon-γ (IFN-γ) is crucial for parasite control, but how IEC respond to and regulate IFN-γ signalling remains unclear. Thus, our objective is to understand the gene programs IFN-γ activates in IEC to attack Cryptosporidium and how IEC balance dual roles in host immunity and barrier maintenance.

To address this objective, we will identify infected and IFN-responsive cells using fluorescent parasites and mice with a fluorescent reporter for IFN signalling,respectively, in combination with flow cytometry, fluorescence microscopy, and single-cell RNA sequencing. In addition, we will use intestinal organoids grown as air-liquid interface monolayers, an in vitro system that provides a highly controlled environment that closely resembles in vivo IEC biology. Our single-cell RNA sequencing data demonstrate robust upregulation of IFN γstimulated genes in IEC during Cryptosporidium infection, particularly in pathways related to intracellular control of infections and antigen processing and presentation. Subsequent studies have shown that IFN-γ has a delayed impact on Cryptosporidium burden, which is due to low basal STAT1 expression in IEC. Importantly, air-liquid interface organoid studies confirmed the requirement for prolonged pre-exposure to IFNγ for parasite control. This work contributes to the pillar of "Epidemic Intelligence & Preparedness with a Focus on Climate-Sensitive Diseases" by providing new insights into immune control of a zoonotic and waterborne pathogen. More broadly, understanding how IFN-γ promotes host immunity in IEC and how these cells respond to IFNs will be relevant to other enteric infections, especially those that lack small animal models. These studies could lead to novel therapeutic strategies to treat Cryptosporidium, such as host directed therapies that amplify IFN responsiveness while limiting barrier disruption

Emna Harigua - Institut Pasteur de Tunis, Tunisia / *The BIND project: Bioinformatics and Artificial Intelligence for Infectious Diseases drug discovery research*

Objective:

The BIND project aims to develop an integrated computational platform combining bioinformatics and artificial intelligence (AI) to accelerate the discovery of new drug candidates targeting neglected infectious diseases, specifically Leishmaniasis, Malaria and COVID-19. It seeks to improve the efficiency, cost-effectiveness, and success rate of early-stage drug discovery through AI-enabled in silico pipelines, complemented by experimental validation.

Background:

Drug discovery is traditionally a time-consuming, costly, and high-risk process. These challenges are exacerbated when addressing neglected tropical diseases that disproportionately affect low-resources regions. Advances in bioinformatics, molecular modeling, and machine learning have opened new possibilities to streamline drug discovery. However, the application of these Technologies in the African context remains limited. The BIND project was conceived to fill this gap and empower data-driven biomedical innovation.

Methods:

The BIND team employs an integrated computational-experimental pipeline for drug discovery. Structure-based approaches were used to model interactions between candidate compounds and pathogen proteins, including docking and molecular dynamics simulations. Additionally, ligand-based approaches thatleverage machine learning (ML) and deep learning (DL) models were implemented. The ML and DL models were trained on manually collated and curated datasets to predict therapeutic activity, followed by QSAR optimization. Both approaches of virtual screening enabled rapid identification of promising compounds, which were then validated experimentally through in vitro and in
vivo assays.

Results:

The research outcomes of the BIND project consisted of a series of highly performing ML and DL models pretrained and optimized towards predicting their potential effects against the pathogens of interest. These models, alongside the corresponding training datasets were deployed through CidalsDB, an AI-empowered open platform for Drug Discovery & Design (Harigua-Souiai et al., 2024): https://cidalsdb.streamlit.app/. We further used these models through multiple virtual screenings to predict the anti-Leishmania
activities of FDA approved drugs (Masmoudi et al., under review). This drug repurposing approach delivered 14 active compounds out of 41 tested in vitro (Oualha et al., 2024; Abdelkrim et al., in prep). We are currently focused on 5 anti-Leishmania drug candidates investigated through preclinical studies
(Oualha et al. in prep). Multiple patents filing are under preparation based on these findings.

Implications:

BIND's integrated approach accelerates early-stage drug discovery and reduces dependence on high-cost screening infrastructures. It provides a replicable model for applying AI in biomedical research and supports the discovery of therapies for diseases with limited commercial interest but high Public health burden. Additionally, through the BIND project, we are building capacity building in
Computer-Aided Drug Discovery that also leverages expertise in Bioinformatics, Artificial Intelligence and Quantum computing. Such technologies bring high value to research, development and innovation to
tackle the challenges of biomedical and health research. Specifically, the research outcomes consist in bringing to the market novel drug candidates against infectious diseases of interest to global health (Leishmania, Malaria, etc). We believe strongly in how multi-disciplinary approaches, integrating AI, can revolutionize Drug Discovery. We work on growing our expertise and technologies into a recoverable product.
Broader Impact:
BIND positions Tunisia, and specifically Institut Pasteur de Tunis, as a regional leader in computational drug discovery. The project enhances scientific sovereignty and innovation capacity in Africa, fosters south-south and northsouth collaborations, and contributes open tools and methods to the global research community. Through its embedded training programs, BIND also builds a pipeline of young African scientists equipped to lead future AI-driven biomedical innovations.

Imane El Idrissi Saik - Institut Pasteur du Maroc, Morocco ***/ Promoting Multidisciplinarity in Approaching Cutaneous Leishmaniasis for Enhanced Epidemic Intelligence & Preparedness***
An integrative approach combining eco-epidemiology, predictive modeling, molecular diagnostics, and immunopathology was used to strengthen Morocco's preparedness against cutaneous leishmaniasis, a climate-sensitive neglected tropical disease. This multidisciplinary framework bridges research, surveillance, and public health action to anticipate outbreaks and improve control strategies.
Objectives:
The project aimed to deliver epidemiological, immunological, and molecular biology tools to tackle some of the challenges posed by CL. This comprehensive approach could strengthen disease control strategies, particularly in the Moroccan context.
Background:
CL transmission dynamics in Morocco are being reshaped by climate change, environmental shifts, and Socio-economic vulnerabilities. Traditional surveillance and diagnostics are insufficient to address the
disease's evolving epidemiology, and little is known about the disease physiopathology. A multidisciplinary approach can therefore help improve detection, prediction, and control of the disease.
Methods:
• Eco-epidemiology & modeling: Spatio-temporal mapping, climatic correlation, and machine learning forecasting of disease risk in a hotspot.
• Molecular biology: development of higher sensitivity PCR assays based kinetoplast DNA to improve detection.
• Immunopathology: In vitro characterization of keratinocyte–Leishmania interactions.
Results
• Identified climatic drivers and predicted cases in a hotspot with a machine learning based approach.
• Developed and validated sensitive, specific molecular diagnostic PCR tool.
• Revealed the potential role of keratinocytes in Leishmania tropical pathogenesis.
Implications & Broader Impact:
The work directly supports the Pasteur Network pillar Epidemic Intelligence & Preparedness by Integrating climate-sensitive disease modeling and novel diagnostics into early warning systems. It Advances Research, Development & Innovation, and provides a transferable approach for other climate sensitive vector-borne diseases, strengthening resilience in vulnerable populations. The future
of the fight against cutaneous leishmaniasis and other vector borne diseases relies on collective mobilization and the integration of innovative solutions, both in fundamental and cross-disciplinary research, that must be tailored to the challenges posed by these diseases

Celia Florimond - Institut Pasteur de la Guyane, Guyana ***/ Piperaquine-resistant malaria parasites hinder treatment efficacy in the Guianas***
Objective:
This study aimed to characterize the emergence and public health implications of piperaquine resistance in P. falciparum in the Guianas.
Background:
Plasmodium falciparum (Pf), an apicomplexan parasite responsible for lethal cases of malaria, is treated with artemisinin-based combination therapies such as dihydroartemisinin-piperaquine (DHA-PPQ) per WHO guidelines. However, DHA-PPQ-resistant parasites were reported in Southeast Asia and suspected in South America.

Methods:
A treatment efficacy study was performed on reported cases of Pf-infected patients treated with DHA-PPQ in French Guiana (n=6, 2016-2018). Additionally, isolates collected in French Guiana (1997-2018) were genotyped for Pfcrt (n=845) and Pfpm2/3 copy number (n=230), phenotyped using the in-vitro piperaquine survival assay (n=86) and analyzed through genomic studies (n=50). Additional samples from five Amazonian countries and one outside the region were genotyped (n=1,440).
Results:
In field isolates, 47% (n=40/86) were resistant to PPQ in-vitro (PPQ-R) and associated with genetic modifications in two genes (PfCRTC350R mutation and Pfpm2/3 amplification, p<0.001). Those markers were also associated with DHA-PPQ treatment failures (n=3/6). A high prevalence of PPQ-R markers was observed in Suriname (n=19/35 [83%]) and Guyana (n=579/791 [73%]). The PfCRTC350R mutation emerged before Pfpm2/3 amplification in a temporal sequence different from Southeast Asia, and in the absence of artemisinin partial resistance, suggesting a geographically distinctive epistatic relationship between these genetic markers.
Implications:
These findings support the Pasteur Network's first strategic pillar, as surveillance of genetic markers for antimalarial drug resistance allows tailored healthcare for infected patients depending on the area of infection. In this case, the high prevalence of PPQ-R markers in parasite populations of the Guianas, and the associated risk of therapeutic failures warrant caution regarding DHA-PPQ use in the region.
Broader impact:
Given the public health implication of these results in French Guiana, national authorities updated malaria-treatment policy. This study further highlights the potential differences in genotype to phenotype mapping across genetically distinct parasite populations from different continents

Mamane Salé Noura - CERMES, Niger / *Diversity, ecology, and characterization of insecticide resistance in* ***Anopheles, mosquitoes, vectors of malaria, in Niamey city.***
Methods:d : Malaria remains a major public health challenge in Niger, particularly in the city of Niamey, which alone accounts for over 10% of the national malaria-related mortality. In the absence of a widely available vaccine, vector control remains the most effective prevention strategy. However, its success depends on updated knowledge of local mosquito vectors, including their ecology, behavior, and insecticide resistance status.
Objective: This study aimed to assess the diversity, ecology, and insecticide resistance of Anopheles mosquitoes in six representative sites of Niamey, while identifying environmental factors influencing their abundance.
Methods: Entomological monitoring was conducted throughout 2020, with two collection rounds per season over three seasons. Larval habitats were surveyed, identified, and characterized, while adult mosquitoes were captured using indoor spraying and CDC light traps. WHO-standard insecticide susceptibility tests and molecular analyses (PCR) were used to determine species composition, Plasmodium infectivity, blood meal origin, and presence of kdr and ace-1 mutations.
Results : Results revealed a rich ecological diversity, with six Anopheles species identified. The most abundant were An. gambiae s.l., especially An. coluzzii and An. arabiensis, both found to be anthropophilic and infected with Plasmodium. These species exhibited significant resistance to pyrethroids and DDT, with high frequencies of kdr mutations, while bendiocarb remained effective. Vector abundance was closely linked to environmental and seasonal factors, with higher densities during the rainy season. Factors such as proximity to breeding sites, presence of livestock, poor sanitation, and agricultural practices also influenced mosquito distribution. Additionally, vector dynamics were positively correlated with rainfall, humidity, and dew point.
Implications: The findings provide critical deverythingaria vector surveillance in the Sahelian context, supporting the design of targeted and effective vector control strategies. This work contributes directly to the strategic pillars of the Pasteur Network, particularly in epidemic preparedness, applied research and innovation, and evidence-based public health policy development.