ibeid

Labex ibeid, 15 years of excellence in research

ADAPTING TO CHANGE

EMERGING INFECTIOUS DISEASES IN A SHIFTING CLIMATE

Scientific

Conference

Program Book

2024

www.labexibeid.fr

ASSISTANCE PUBLIQUE HÔPITAUX DE PARIS | Inserm | EnvA École nationale vétérinaire d'Alfort | anses agence nationale de sécurité sanitaire alimentation, environnement, travail | Santé publique France | INSTITUT PASTEUR

WELCOME

It is with great pleasure that we welcome you to Adapting to Change: Emerging Infectious Diseases in a Shifting Climate, a special event that marks the 15th anniversary of Labex IBEID. Over the past decade and a half, this initiative has been at the forefront of groundbreaking research and innovation to better understand Emerging and Reemerging Infectious Diseases and all the related topics from pathogen diagnosis, host defence mechanisms, and innovative treatments to anticipate and combat efficiently currently and upcoming infectious diseases, and we are thrilled to celebrate this milestone with you.

This congress is not only a platform for sharing cutting-edge knowledge but also a celebration of the collective achievements that have shaped the Labex IBEID. Your participation highlights your dedication to advancing science and your commitment to pushing the boundaries of what is possible.

Over the next few days, we invite you to engage in the rich program featuring insightful presentations, thought-provoking discussions, and ample opportunities for networking. We hope that the collaborations and ideas that emerge from this gathering will pave the way for the next 15 years of scientific breakthroughs.

Thank you for joining us in this celebration of science from all around the globe. We wish you a productive and inspiring congress!

Warm regards,

Carla Saleh **Philippe Bastin**

Labex IBEID coordinators

ADAPTING TO CHANGE

EMERGING INFECTIOUS DISEASES IN A SHIFTING CLIMATE

THIS CONFERENCE HAS BEEN MADE POSSIBLE
THANKS TO THE GREAT SUPPORT
OF OUR SPONSORS

Table of

Contents

01 About the Labex

02 Scientific Committee

03 Our Keynote & Invited Speakers

04 Guest of honor

05 Program of the Conference

06 Short Talk & Poster Abstracts

07 F.A.Q.

About the Labex IBEID

The Labex IBEID, for Laboratory of Excellence Integrative Biology of Emerging Infectious Diseases (IBEID), is a scientific program coordinated by Carla Saleh and Philippe Bastin at the Institut Pasteur of Paris. This program aims at developing a structure to anticipate and tackle emerging infectious diseases (EID) gathering academic institutions (Institu Pasteur, Inserm and ENVA), clinics (AP-HP) and public health authorities (ANSES and Santé publique France).

History of the Labex

Created by the Professors Pascale Cossart and Philippe Sansonetti in 2011, the Labex IBEID has fostered more than 700 scientists, technicians, and infectious diseases experts since its begininng.
In 2019, Carla Saleh, Philippe Bastin and Marco Vignuzzi took the succession to Pascale Cossart and Philippe Sansonetti to pursue the vision of excellence implemented through the project.
In 2021, Marco Vignuzzi moved his lab to Singapore and the Labex is now coordinated by Carla Saleh and Philippe Bastin.
Constantly challenging themselves about how to embrace the immense diversity of pathogens, mechanisms and environments, the Labex topics have evolved always aiming to create the robust scientific knowledge needed to anticipate the infectious emergencies, and enhance innovative solutions.
Since 2021, we supported six very promising young scientists thanks to our unique Springboard 2 Independance fellowship program (S2I). We are very proud to give them the opportunity to present their latest research work today.

ibeid
integrative biology of emerging infectious diseases

Overview

Since the beginning of the Labex IBEID project, our consortium has published a lot of high impact papers, has trained excellent young scientists including some of them who will present their more recent work), and has developed various ambitious collaborative projects. Here is an overview of the consortium work.

1400+ Publications

700+ Scientists involved

80+ Postdocs & PhD Students

56 Patents

Scientific Committee

This conference has been possible thanks to the work of the whole scientific organizing committee

Philippe Bastin
Institut Pasteur, FR

Nadine Cerf-Bensus-
Institut Imagine, FR

Chetan Chitnis
Institut Pasteur, FR

Anna-Bella Failloux
Institut Pasteur, FR

Mélanie Hamon
Institut Pasteur, FR

Sara Moutailler
ANSES-ENVA, FR

Harold Noel
Santé publique France, FR

Cyril Renassia
Institut Pasteur, FR

Carla Saleh
Institut Pasteur, FR

Etienne Simon-Lorière
Institut Pasteur, FR

Our Keynote Speakers

Sarah Gilbert

University of Oxford

UK

Professor Gilbert joined the Nuffield Department of Medicine at the University of Oxford in 1994 and became a member of the Jenner Institute upon its establishment in 2005. Her primary research focuses on developing viral vectored vaccines that elicit strong protective T and B cell responses. She leads efforts in influenza vaccine development and works on vaccines for various emerging pathogens, including Nipah virus, MERS, and Lassa virus. Additionally, Professor Gilbert plays a key role in rapidly advancing vaccines into GMP manufacturing and conducting first-in-human trials through collaborations with the Clinical Biomanufacturing Facility and the Centre for Clinical Vaccinology and Tropical Medicine at Oxford's Old Road Campus.

As Principal Investigator at the Pandemic Sciences Institute, she also serves as the Oxford Project Leader for the ChAdOx1 nCoV-19 vaccine against SARS-CoV-2, a vaccine that has been administered to over 23,000 participants in clinical trials across the UK, Brazil, and South Africa. Now deployed in more than 180 countries, this vaccine is estimated to have saved over six million lives in the fight against the COVID-19 pandemic.

Adrian Hill

University of Oxford

UK

Professor Hill is Director of the Jenner Institute, where he focuses on designing and developing vaccines for infectious diseases prevalent in developing countries, including HIV/AIDS, malaria, and tuberculosis. He also leads a research group at the Wellcome Trust Centre for Human Genetics, which studies genetic susceptibility to common bacterial diseases. A strong advocate for the potential of molecular medicine, Professor Hill is dedicated to creating new healthcare interventions that can significantly improve the lives of the world's poorest populations, particularly in sub-Saharan Africa.

His vaccine research program has advanced one of the most promising malaria vaccines, which is currently undergoing large-scale trials in infants in sub-Saharan Africa. The R21 malaria vaccine, using a matrix-M adjuvant, has demonstrated high efficacy in clinical trials in the UK and Africa and could become the first widely used vaccine to reduce the burden of malaria in Africa.

In early 2020, the Jenner Institute launched a major initiative to rapidly develop a COVID-19 vaccine, which, in partnership with AstraZeneca, is now being deployed globally.

Professor Hill has published over 600 research papers with 60,000 citations and has co-founded several spin-off companies. He is a Fellow of the UK Academy of Medical Sciences, the Royal College of Physicians, and the Royal Society.

Peter Hotez

Baylor College of Medicine

US

Dr. Peter J. Hotez is Dean of the National School of Tropical Medicine and Professor of Pediatrics and Molecular Virology & Microbiology at Baylor College of Medicine, where he also serves as Co-director of the Texas Children's Center for Vaccine Development (CVD) and holds the Texas Children's Hospital Endowed Chair of Tropical Pediatrics. Additionally, he is a University Professor at Baylor University, Fellow in Disease and Poverty at the James A. Baker III Institute for Public Policy, Senior Fellow at the Scowcroft Institute of International Affairs at Texas A&M University, Faculty Fellow with the Hagler Institute for Advanced Studies at Texas A&M University, and Health Policy Scholar in the Baylor Center for Medical Ethics and Health Policy. Dr. Hotez also holds honorary doctoral degrees from several institutions, including the Elmezzi Graduate School of Molecular Medicine, Roanoke College, the National Autonomous University of Honduras, and the City University of New York Graduate School of Public Health and Health Policy.

Internationally recognized as a physician-scientist specializing in neglected tropical diseases and vaccine development, Dr. Hotez leads a team at the Texas Children's CVD focused on developing new vaccines for diseases such as hookworm infection, schistosomiasis, leishmaniasis, Chagas disease, and SARS/MERS/SARS-2 coronaviruses. His work is dedicated to ensuring global and U.S. access to these critical vaccines.

Manu Prakash

Stanford University

US

Dr. Manu Prakash is an Associate Professor of Bioengineering at Stanford University, where he employs interdisciplinary approaches combining theory and experiments to explore how computation is embodied in biological matter. His research delves into topics such as cognition in single-cell protists, morphological computing in organisms without neurons, and the origins of complex behavior in multicellular systems. The Prakash Lab is particularly focused on developing innovative tools for

studying non-model organisms, with a significant emphasis on marine life. The lab investigates fundamental questions, including how cells sense pressure or gravity.

In addition to research, Manu Prakash and his team are committed to creating and distributing "frugal science" tools to democratize access to science globally. These include widely-used inventions like the Foldscope and Abuzz, which have been instrumental in diagnosing deadly diseases such as malaria. The lab also fosters global citizen science communities to address large-scale environmental challenges, such as mosquito and plankton surveillance, helping map the ocean in the Anthropocene era.

Our Invited Speakers

Rogerio Amino

Labex IBEID, Institut Pasteur
FR

Dr Rogerio Amino is a group leader at Institut Pasteur. He discovered the merosomes as they egress from the liver to begin the blood stage of malaria infections. He is also developing a multi-antigenic PE vaccine.

Alejandro Cabezas-Cruz

Labex IBEID, ANSES-ENVA
FR

Dr. Alejandro Cabezas-Cruz is a group leader at ANSES. His research focuses on understanding the molecular mechanisms underlying tick-host-pathogen interactions and the role of the microbiome in tick-borne diseases. Dr. Cabezas-Cruz is also involved in developing novel strategies for controlling tick-borne infections.

Diarmid Campbell-Lendrum

WHO Headquarters
CH

Dr Diarmid Campbell-Lendrum is the Head of the climate change and health unit at WHO, working on the issue for 20 years, contributing to the first quantitative estimates of global health impacts of climate change.

Tineke Cantaert

Institut Pasteur Cambodia
KH

Tineke Cantaert is head of the Immunology Unit at Institut Pasteur Cambodia. She aims to understand the mechanisms driving protective adaptive immune responses to flavivirus infection, helping to design more effective vaccines.

Simon Cauchemez

Labex IBEID, Institut Pasteur
FR

Prof Simon Cauchemez is Head of Mathematical Modelling of Infectious Diseases Unit at Institut Pasteur. He uses a multidisciplinary approach to study infectious diseases through various perspectives, scales and data streams.

Michael Connor

Labex IBEID, Institut Pasteur
FR

Dr Michael Connor is a scientist at Institut Pasteur. He blends chromatin and cellular infection biology with nasal cell culture and organ-on-chip devices to dissect distinct processes triggered by pathogens vs. commensals.

Monika Gulia-Nuss

University of Nevada
US

Dr. Monika Gulia-Nuss is an associate professor in the Dpt of Biochemistry and Molecular Biology at the Univ of Nevada. She developed the first embryo injection protocol for ticks and used it to create a CRISPR-based KO.

Cassandra Koh

Labex IBEID, Institut Pasteur
FR

Dr Cassandra Koh is a vector biologist and geneticist at Institut Pasteur. She focuses on the mosquito virome, studying the impact of mosquito-specific viruses on the arboviral disease ecology and transmission.

Isabelle Louradour

Labex IBEID, Institut Pasteur
FR

Dr Isabelle Louradour is a scientist at Institut Pasteur. She investigates the complex interactions between Leishmania and sand flies, producing hybrids to decipher the insect parameters contributing to the infection.

Sarah Merkling

Labex IBEID, Institut Pasteur
FR

Dr Sarah Merkling leads the Insect Immunity and Infection group at Institut Pasteur. She focuses on understanding interactions between mosquitoes and the arboviruses they transmit to humans

Jorge Moura de Sousa

Labex IBEID, Institut Pasteur
FR

Dr Jorge Moura de Sousa is a scientist at Institut Pasteur mixing comparative genomics and experimental approaches to decipher the role of bacteriophages and their satellites in the ecology and evolution of bacteria.

Sara Moutailler

Labex IBEID, ANSES-ENVA
FR

Dr Sara Moutailler is Scientific Deputy Director of Animal Health Lab at ANSES. Specialized in Medical Entomology and Virology, she combines RNA seq and microfluidic PCR to develop new epidemiological surveillance tools for vector borne diseases.

Bali Pulendran

Stanford University
US

Dr. Bali Pulendran is Professor of Pathology, Microbiology and Immunology at Stanford University. He has recently begun to apply systems biological approaches to predicting the efficacy of vaccine against infectious diseases.

Benjamin Roche

IRD
FR

Dr Benjamin Roche is Research Director at Institut de la Rercherche pour le Développement and an Associate Professor at UNAM. His research focuses on a cross-disciplinary approach between evolutionary ecology and public health.

Boris Striepen

University of Pennsylvania
US

Dr Boris Striepen is Professor of Pathobiology at University of Pennsylvania. He focuses on Cryptosporidium, a pathogen accounting for 50% of all U.S. waterborne disease outbreaks, for which no effective treatment is available.

Nina Van Sorge

Amsterdam Institute for Infection and Immunity
NL

Dr Nina van Sorge is Professor of Translational Microbiology at Amsterdam Institute for Infection and Immunity. She focuses on the human pathogens of global concern Staphylococcus aureus and Streptococcus A, for which no vaccines are available.

Guest of honor

To celebrate 15 years of excellent research o,n Emerging and Reemerging Infectious Diseases by the Labex IBEID partners, we have the pleasure to welcome:

Pascale Cossart

Institut Pasteur
Founder of the Labex IBEID
FR

Professor Pascale Cossart is a renowned French microbiologist who has made significant contributions to the field of infectious diseases. She is best known for her pioneering work on the bacterial pathogen Listeria monocytogenes, which has provided profound insights into the mechanisms of bacterial infection and host-pathogen interactions.

Cossart earned her PhD in biochemistry and, in 1971, joined the Institut Pasteur in Paris, where she spent much of her illustrious career. Her research has been instrumental in understanding how bacteria invade cells and manipulate host processes, leading to advances in both microbiology and infectious disease treatment. Her work has been recognized with numerous prestigious awards, including election to the French Academy of Sciences and the National Academy of Sciences in the United States.

Beyond her research, Professor Cossart has been a dedicated mentor and leader, influencing the next generation of scientists. Her contributions have had a lasting impact on global public health and the scientific community.

Philippe Sansonetti

Institut Pasteur
Founder of the Labex IBEID
FR

Professor Philippe Sansonetti is a distinguished French microbiologist renowned for his groundbreaking work in the field of infectious diseases. His research has significantly advanced our understanding of bacterial pathogens, particularly Shigella, the causative agent of dysentery.

Sansonetti earned his MD and began his career at the Institut Pasteur in Paris, where he has been a leading figure in microbiology and immunology. His pioneering studies on Shigella have revealed critical insights into how this pathogen invades and causes disease in the human gut, contributing to the development of new therapeutic approaches and vaccines.

Throughout his career, Professor Sansonetti has received numerous accolades, including membership in the French Academy of Sciences and international recognition for his contributions to public health. He has also played a vital role as a mentor, shaping the careers of many young scientists and advancing the field of microbiology.

Professor Sansonetti's work continues to influence both scientific research and public health policies worldwide, cementing his legacy as a leader in infectious disease research.

Yasmine Belkaid

General Director of the Institut Pasteur
FR

Professor Yasmine Belkaid is an immunologist celebrated for her pioneering research on the interactions between the immune system and the microbiota, which has provided essential insights into how beneficial microbes influence immune responses and protect against diseases.

Born in Algeria, Belkaid pursued her PhD in France before conducting postdoctoral research at the Institut Pasteur. She later moved to the United States, where she held prominent positions at the National Institutes of Health (NIH). Her research has significantly advanced the understanding of how the microbiota regulates immunity, particularly in the skin and gut, leading to innovative approaches for treating inflammatory diseases and infections.

In 2023, she returned to the Institut Pasteur as its Director General, where she continues to influence the direction of global biomedical research. Professor Belkaid's contributions have earned her numerous prestigious awards and memberships in esteemed scientific societies, including the National Academy of Sciences. She is also a passionate advocate for diversity in science and a dedicated mentor to the next generation of researchers.

Her groundbreaking work and leadership continue to shape the fields of immunology and microbiology, reinforcing her position as one of the most influential figures in contemporary biomedical science.

Program of the Conference

DAY 1 OCTOBER 16, 2024 2:30 PM - 8:00 PM

OPENING

2:30-2:45	**Welcome Coffee**
2:45-3:00	**Carla Saleh & Philippe Sansonetti** *Opening*
3:00-3:45	**Keynote Lecture - Congress Opening** **Manu Prakash** Stanford University, US *Frugal Science: Democratizing scientific tools in global health, ecological monitoring and science education*

SESSION 1
GLOBAL HEALTH IN A SHIFTING CLIMATE

Auditorium CIS, Institut Pasteur.

Chairs: Arnaud FONTANET, Harold NOEL, Carla SALEH, Philippe SANSONETTI

3:45-4:15	**Diarmid Campbell-Lendrum** WHO Headquarters, CH *Preventing infectious diseases driven by climate change: an imperative for WHO Member States*
4:15-4:45	Coffee Break
4:45-5:15	**Simon Cauchemez** Labex IBEID, Institut Pasteur, FR *Modelling the spread of emerging infectious diseases to support risk assessment and planning*
5:15-5:35	**Sarah Merkling** S2I Fellow Labex IBEID, Institut Pasteur, FR *Cellular and metabolic signatures of natural DENV resistance in Aedes aegypti*
5:35-5:50	**Maphepele Sara Mashilo** University of Venda, ZA *Prevalence and risk factors of Drug-resistant MTB in rural communities of South Africa*
5:50-6:05	**Laura Andrea Barrero Guevara** Max Planck Institute for Infection Biology, DE *How causal inference concepts can guide research into the effects of climate on infectious diseases*
6:05-6:35	**Benjamin Roche** Institut de Recherche pour le Développement, FR *Prevention of emerging zoonoses: what do we know and what can we do?*
6:35-6:45	**Yasmine Belkaid** General Director of the Institut Pasteur
6:45-7:30	Welcome Cocktail

DAY 2 OCTOBER 17, 2024 8:30 AM - 8:00 PM

SESSION 2
INFECTIOUS DISEASES STUDY

Auditorium CIS, Institut Pasteur.

Chairs: Sarah BONNET, Carmen BUCHRIESER, Christophe d'Enfert, Louis LAMBRECHTS, Nicole PAVIO, Félix REY, Etienne SIMON-LORIERE, Gérald SPAETH

8:30-9:00	**Coffee**
9:00-9:45	**Keynote Lecture** **Adrian Hill** University of Oxford, UK *All change for malaria: The role of new vaccines in preventing and eliminating malaria*
9:45-10:15	**Boris Striepen** University of Pennsylvania, US *The biology of the parasite Cryptosporidium*
10:15-10:30	**Hebert Echenique Rivera** Labex IBEID, Institut Pasteur, FR *Dual RNA-Seq of Peyer's Patches infected with Yersinia enterocolitica lineage 4 reveal new mechanisms of bacterial virulence and modulation of host responses*
10:30-11:00	**Coffee Break**
11:00-11:30	**Tineke Cantaert** Institut Pasteur of Cambodia, KH *Human immune response to dengue virus infection*
11:30-11:50	**Cassandra Koh** S2I Fellow Labex IBEID, Institut Pasteur, FR *Exploring mosquito viromes and virus ecologies across continents*
11:50-12:05	**Marwan Sharawy** Labex IBEID, Institut Pasteur, FR *A single-cell perspective on age and sex effects on immune response to viral infection*
12:05-12:20	**Idalba Mildred Serrato Pomar** Institut de Recherche pour le Développement, FR *Multiple flaviviruses secrete a viral non-coding RNA in mosquito salivary vesicles to enhance saliva infectivity by reducing early IFN response*
12:20-12:30	**Group Photography**
12:30-2:30	**Lunch Buffet & Poster Session 1**
2:30-3:00	**Bali Pulendran** Stanford University, US *TBC*
3:00-3:20	**Michael Connor** S2I Fellow Labex IBEID, Institut Pasteur, FR *Not just pathogens at the nasal interface*
3:20-3:35	**Diego Sebastian Ojeda** Fundación Instituto Leloir, AR *RNA Spacer located just downstream of the Stop codon of dengue and other flavivirus genomes is essential for infectivity*
3:35-3:50	**Aristide Mounchili Njifon** Centre Pasteur du Cameroun, CM *Identification of NS5B resistance-associated mutations in hepatitis C virus circulating in treatment naïve Cameroonian patients*
3:50-4:10	**Coffee Break**
4:10-4:40	**Sara Moutailler and Alejandro Cabezas-Cruz** Labex IBEID, ANSES-ENVA, FR *Integrative approaches to managing Tick-borne Diseases: Modeling coinfections and harnessing vector microbiome vaccines*
4:40-5:00	**Isabelle Louradour** S2I Fellow Labex IBEID, Institut Pasteur, FR *Leishmania hybrid production: a key driver of adaptation*
5:00-8:30	**Music, Litebites and Poster Session 2**

DAY 3 OCTOBER 18, 2024 8:30 AM - 5:30 PM

SESSION 3
NEW TOOLS FOR DIAGNOSIS, THERAPY AND VACCINE
Auditorium CIS, Institut Pasteur.

Chairs: Philippe BASTIN, Chetan CHITNIS, Pascale COSSART, Mélanie HAMON, Sara MOUTAILLER, Olivier SCHWARTZ, Michael WHITE

8:30-9:00	**Coffee**
9:00-9:45	**Keynote Lecture** **Sarah Gilbert** University of Oxford, UK *Platform technologies for rapid and cost-effective vaccine production.*
9:45-10:00	**Kévin Jean** CNAM, FR *The role of living in flood-prone regions on hindering early childhood vaccination in Bangladesh*
10:00-10:15	**Gerardo Guillen** Center for Genetic Engineering and Biotechnology, CU *Pandemic preparedness: Targeting the mucosal immune system ith Cuban Abdala and Mambisa vaccines*
10:15-10:45	**Coffee Break**
10:45-11:15	**Monika Gulia-Nuss** University of Nevada, US *Progress towards genetic methods for Ticks and Tick-borne Diseases Management*
11:15-11:35	**Jorge Moura de Sousa** S2I Fellow Labex IBEID, Institut Pasteur, FR *The intricate lives of the microbes*
11:35-11:50	**Johanna Bouckaert** Institute of Tropical Medicine, BE *Next generation Dengue virus serodiagnostics: Peptide-Based approaches over traditional protein dethods*
11:50-12:05	**Elena Pérez Antón** Labex IBEID, Institut Pasteur, FR *Development of a SHERLOCK CRISPR/Cas13 toolbox for eco-epidemiological surveillance of animal African Trypanosomiasis*
12:05-2:30	**Lunch Buffet**
2:30-3:00	**Rogerio Amino** Labex IBEID, Institut Pasteur, FR *Neutralizing mechanisms of antibodies targeting malaria sporozoites*
3:00-3:15	**Shima Hadifar** Institut Pasteur of Iran, IRN *Intralesional cytokines expression and activated JAK-STAT molecules in Leishmania tropica-infected patients*
3:15-3:30	**Francisco José Martinez Blazquez** Institut Pasteur, FR *PvDBPII elicits mutltiple antibody-mediated mechanisms that reduce growth in a Plasmodium vivax challenge trial*
3:30-4:00	**Nina Van Sorge** Amsterdam Institute for Infection and Immunity, NL *The rise and fall of bacterial infections: From epidemiological insights to new interventions*
4:00-4:30	**Coffee Break**

CLOSING

4:30-5:15	**Keynote Lecture - Congress Closing** **Peter Hotez** Baylor College of Medicine, US *Vaccines for our new era of global boiling and rising anti-science*
5:15-5:30	**Philippe Bastin & Pascale Cossart** *Wrap up*

Selected Short Talk & Poster Abstracts

Selected Short Talks

1. How causal inference concepts can guide research into the effects of climate on infectious diseases
   Laura Andrea Barrero Guevara Max Planck Institute for Infection Biology, DE

2. Next Generation Dengue Virus Serodiagnostics: Peptide-Based Approaches Over Traditional Protein Methods Dual RNA-seq of Peyer's Patches
   Johanna Bouckaert Institute of Tropical Medicine, BE

3. Dual RNA-Seq of Peyer's Patches infected with Yersinia enterocolitica lineage 4 reveal new mechanisms of bacterial virulence and modulation of host responses
   Hebert Echenique Rivera Institut Pasteur, FR

4. Pandemic preparedness: Targeting the mucosal immune system with Cuban Abdala and Mambisa vaccines
   Gerardo Guillen Center for Genetic Engineering and Biotechnology, CU

5. Intralesional cytokines expression and activated JAK-STAT molecules in Leishmania tropica-infected patients - Speaker: **Shima Hadifar** Institut Pasteur of Iran, IRN

6. The role of living in flood-prone regions on hindering early childhood vaccination in Bangladesh **Kévin Jean** CNAM, FR

7. PvDBPII elicits multiple antibody-mediated mechanisms that reduce growth in a Plasmodium vivax challenge trial
   Francisco José Martinez Blazquez Institut Pasteur, FR

8. Prevalence and risk factors of Drug-resistant MTB in rural communities of South Africa - **Maphepele Sara Mashilo** University of Venda, ZA

9. Identification of NS5B Resistance-Associated Mutations in Hepatitis C Virus Circulating in Treatment Naïve Cameroonian Patients
   Aristide Mounchili Njifon Centre Pasteur du Cameroun, CM

10. RNA Spacer Located Just Downstream of the Stop Codon of Dengue and other Flavivirus Genomes Is Essential for Infectivity
    Diego Sebastian Ojeda Fundación Instituto Leloir, AR

11. Development of a SHERLOCK CRISPR/Cas13 toolbox for eco-epidemiological surveillance of animal African Trypanosomiasis
    Elena Pérez Antón Institut Pasteur, FR

12. Multiple flaviviruses secrete a viral non-coding RNA in mosquito salivary vesicles to enhance saliva infectivity by reducing early IFN response
    Idalba Mildred Serrato Pomar Institut de Recherche pour le Développement, FR

13. A single-cell perspective on age and sex effects on immune response to viral infection
    Marwan Sharawy Institut Pasteur, FR

Selected Posters

1. Floral biology variations in Olea europaea amidst climate change: Implications for Allergy
   Marcello Albanesi University of Bari, IT

2. Faecal carriage of extended-spectrum beta-lactamase-producing escherichia coli in livestock and abattoir workers from sekondi-takoradi abattoir
   Frederick Obeng Amoah Public Health Reference Laboratory, GH

3. Variation in chromatin accessibility in immune cells: population differences and genetic contributors revealed by single-cell approaches Pandemic preparedness: Targeting the mucosal immune system with Cuban Abdala and Mambisa vaccines
   Yann Aquino Institut Pasteur, FR

4. Antimicrobial susceptibility, ESBL production and virulence of enterobacteria isolated from urinary tract infections in Benin
   Funke Faizatou Assouma University of Abomey Calavi, BJ

5. Targeting the Intra-erythrocytic Life Cycle of the Malaria Parasite to Identify Starting Points for Antimalarial Drug Discovery from Drymaria cordata and Macaranga monandra
   Kamche Aubin Youbi University of Yaounde, CM

6. Effect of shifting temperature on transmission dynamics of cholera: Mathematical modeling
   Nassim Ayad Pasteur Institute Of Algeria, DZ

7. Adapting CRISPR-Cas13 as an antiviral tool in insects
   Eugenia Bardossy Institut Pasteur, FR

8. Gut microbiome metabolites regulate innate immune response in Japanese encephalitis virus infection
   Anirban Basu National Brain CResearch Center, IN

9. Surveillance of Crimea-Congo Haemorrhagic fever virus in Central Sahara, Algeria
   Kamal Eddine Benallal Pasteur Institute of Algeria, DZ

10. Drugs Targeting Human Peroxiredoxin 6 as a Novel Class of Antimalarial Agents
    Nur Elyza Binte Zulkifli Institut Pasteur, FR

11. Microbiological monitoring, new horizons for tick-borne diseases: tick and pathogen presence according to the ecosystem in urban and peri-urban environments in the Ile de France region
    Sarah Bonnet Institut Pasteur, FR

12. Probing the intrinsic heterogeneity of viral infections by single-cell genomic
    Pierre Bost Institut Curie, FR

13. Unraveling depletion mechanism of the virulence gene pla in epidemic strains of Yersinia pestis
    Emelyne Bougit Institut Pasteur, FR

14. Deciphering the interactions between RNA viruses and retrotransposons in Drosophila melanogaster
    Mauro Castelló Sanjuán Institut Pasteur, FR

15. The microbiota of Anopheles and Aedes mosquitoes in French Guiana: Investigating microbial communities and their relationship with environmental factors
    Estelle Chabanol Institut Pasteur de la Guyane, GY

16. A multimodal virus-host interactome pipeline as a tool for viral preparedness
    Caroline Demeret Institut Pasteur, FR

17. Characterization of AHSV antagonists of the IFN-I pathway
    Pascal Dujardin ANSES-INRAE-ENVA, FR

18. Population immunity against mosquito-borne diseases in New Caledonia and Vanuatu, Pacific region
Myrielle Dupont-Rouzeyrol Institut Pasteur de Nouvelle-Calédonie, FR

19. Three-in-one Vaccine: A Single Recombinant Measles Virus Expressing Three Arbovirus Antigens Induces Robust Humoral and Cell-Mediated Immune Responses, Conferring Effective Protection in a Mouse Model
Phanramphoei Frantz Institut Pasteur, FR

20. Emergence of Cladophialophora bantiana infections in France
Dea Garcia Hermoso Institut Pasteur, FR

21. Prevalence of Campylobacter infection and the emergence of multidrug-resistant thermophilic clones and their association with climate change in Tunisia
Manel Gharbi Institut Pasteur de Tunis, TN

22. Regulatory events governing host-C. albicans interaction: potential implications for wound healing Targeting the Intra-erythrocytic Life Cycle of the Malaria Parasite to Identify Starting Points for Antimalarial Drug Discovery from Drymaria cordata and Macaranga monandra
Ankita Ghoshal Indian Institute of Science Banagalore, IN

23. Bacteriome composition modulates viral infections in Drosophila melanogaster Adapting CRISPR-Cas13 as an antiviral tool in insects
Rubén González Institut Pasteur, FR

24. Development of Peptide Inhibitors of Influenza Virus Replication by Directed Evolution Surveillance of Crimea-Congo Haemorrhagic fever virus in Central Sahara, Algeria
Darren Hart CNRS, FR

25. Adapting Internet of Things Devices for enhanced vital signs data collection in Viet Nam: a systematic review Microbiological monitoring, new horizons for tick-borne diseases: tick and pathogen presence according to the ecosystem in urban and peri-urban environments in the Ile de France region
Nguyen Ho Xuan Pasteur Institute of Ho Chi Minh City, VN

26. A Multicenter, Randomized, Double-Blind, Controlled, Phase III Clinical Trial (Immunobridging Study) of INAVAC - Vero Cell Inactivated SARS-CoV-2 Vaccine - in Healthy Population Aged 18 Years and Above in Indonesia - a Preliminary Report
Dominicius Husada Universitas Airlangga, ID

27. RNA Interference: paving the way for a CHIKV vaccine in Aedes mosquitoes Deciphering the interactions between RNA viruses and retrotransposons in Drosophila melanogaster
Edith Janssens Institute of Tropical Medicine, BE

28. Recapitulating memory B cell responses in a Lymphoid Organ-Chip to evaluate mRNA vaccine boosting strategies A multimodal virus-host interactome pipeline as a tool for viral preparedness
Raphaël Jeger-Madiot Institut Pasteur, FR

29. Anticandidal guided isolation and UHPLC-Orbitrap-ESIMS/MS analysis of Monotes kerstingii (Dipterocarpaceae) leaves and roots Population immunity against mosquito-borne diseases in New Caledonia and Vanuatu, Pacific region
Sorelle Kache Fotsing University of Yaounde, CM

30. Chikungunya seroprevalence, force of infection, and prevalence of chronic disability after infection in endemic and epidemic settings: a systematic review, meta-analysis, and modelling study
Hyolim Kang London School of Hygiene and Tropical Medicine, KR

31. Designing and testing a simple diagnostic tool for quickly identifying West Nile virus in clinical settings
Marwa Khedhiri Institut Pasteur of Tunis, TN

32. The profile of viral and bacterial pathogens in ticks collected from migratory and non-migratory birds captured for seasonal ringing
Malgorzata Kryzowska Military Institute of Hygiene and Epidemiology, PL

33. Smallpox-vaccinated individuals preserve long-term immunological memory and mount serological reactivity against selected monkeypox antigens
Malgorzata Kryzowska Military Institute of Hygiene and Epidemiology, PL

34. Antibiotic treatment can excise the ISAba125 transposon associated with blaNDM- sh ble allele from the genome of enteric pathogens through xer/integrase recombination mechanism
Shashi Kumari Translational Health Science and Technology Institute, IN

35. MEDILABSECURE A One Health Network to improve preparedness and response capacities to emerging vector-borne diseases increased by environmental and climate change
Vanessa Lagal Institut Pasteur, FR

36. In-host evolution of Yersinia enterocolitica during a chronic human infection
Pierre Lê-Bury Institut Pasteur, FR

37. Seroprevalence of crimean-congo hemorrhagic fever and associated factors in cattle and animal workers in Cameroon: NIH-ARBOCAM Study
Gisele Liliane Machuetum Centre Pasteur du Cameroun, CM

38. Identification of human and porcine interferon response effectors with antiviral activity against HEV-3 infection
Aïlona Marcadet-Hauss ANSE-INRAE-ENVA, FR

39. Effects of Angiotensin Converting Enzyme (ACE2) polymorphisms in the disease severity during Tuberculosis and Covid-19 coinfection in Cameroon
Kameni Mary Ngongang University of Yaounde, CM

40. malaria and climate change a growing threat to public health in Niger
Djedanem Médard Epicentre, NE

41. Unraveling the bioactive potential of Cameroonian medicinal plants with anti-Shigella and antioxidant activity, UHPLC-LIT-MS/MS fingerprints, prediction of pharmacokinetics, and drug-likeness properties of identified chemicals
Yanick Kevin Université of Yaounde, CM

42. Implementation of host genetic diversity in preclinical models of infectious disease: Collaborative Cross mouse strains mirror the range of human disease severity and identify susceptibility loci
Xavier Montagutelli Institut Pasteur, FR

43. A decade-long retrospective study of hepatitis C virus genetic diversity in Cameroon 2013-2023: Presence of a high proportion of unsubtypable and putative recombinant HCV strains
Aristide Mounchili Njifon Centre Pasteur du Cameroun, CM

44. Influenza A virus infection alters endoplasmic reticulum architecture and phosphoinositide turnover to promote vRNP egress
Jean-Baptiste Brault Institut Pasteur, FR

45. In silico genomic surveillance by CoVerage predicts and characterizes SARS-CoV-2 Variants of Interest
Katrina Norwood Helmholtz Centre for Infection Research, DE

46. Factors associated with mosquito-borne disease protective behaviour: a pre-registered cross-sectional study in metropolitan France
Juan Ocampo Institut Pasteur, FR

47. Climate Change shifting Arboviruses Disease Burden to Overtake Malaria in Public Health?
Jack Ogony Jomo Kenyatta University of Agriculture and Technology, KE

48. Uncovering the hidden toll: exploring 130 years of temperature-related mortality in Madrid
Dariya Ordanovich Spanish National Research Council, ES

49. Long term circulation of SARS-CoV-2 related viruses in bats in Cambodia
Tey Putita Ou Institut Pasteur of Cambodia, KH

50. Mother-to-child transmission of yellow fever virus during breastfeeding
Jeanne Pascard Institut Pasteur, FR

51. Survey of prevalence and seroprevalence of rat hepatitis E virus (Rocahepevirus ratti) in rodent populations in different french cities
Marie Pellerin Anses, FR

52. Uncovering Health Disparities in Southern Vietnam Through Hand, Foot, and Mouth Disease Data Analysis, 2017–2022
Thi Ngoc Uyen Phan Pasteur Institute of Ho Chi Minh City, VN

53. Evolution of SARS-CoV-2 JN.1 lineage: viral fitness and antibody evasion
Delphine Planas Institut Pasteur, FR

54. Untargeted metatranscriptomics of ticks from Ile de France
Matthieu Prot Institut Pasteur, FR

55. Resilience of Community Health Systems Confronting Emerging Zoonoses in Cameroon
Salomon Garaobe RAPAEJ, CM

56. Integrative Structural Biology of human and viral protein "players" in the ADP-ribosylation pathway
Georgios Spyroulias University of Patras, GR

57. Antibiotic resistance genes and virulence markers: next-generation sequencing analysis of pseudomonas aeruginosa isolated from various clinical specimens - a single center experience from india
Tarun Kumar Suvvari Squad Medicine and Research, IN

58. Knowledge and Perception on Climate Change and Vector-Borne Diseases among Indian Doctors - A Pilot Study
Tarun Kumar Suvvari Squad Medicine and Research, IN

59. Non-invasive diagnosis method for cutaneous leishmaniasis
Yasaman Taslimi Institut Pasteur of Iran, IR

60. Deployment of in vitro assays, UHPLC-MS/MS fingerprints, and in silico approach to unveil antimalarial drug candidates with good pharmacokinetics, and drug-likeness profiles from Diospyros gilletii
Mriscal Brice Tchatat Tali University of Yaounde, CM

61. Implication of biochemical markers and ACE2 gene mutation in the disease severity in malaria and covid-19 co-infected patients in Yaoundé, Cameroon
Eric Berenger University of Yaounde, CM

62. Modeling tick infection by Hazara and Dugbe viruses to study the survival and spread of Crimean-Congo hemorrhagic fever virus in the environment
Sarah Thibaudeau ANSES, FR

63. Dissecting the viral genetic determinants of differential mosquito transmissibility and mouse pathogenicity between African and Asian lineages of Zika virus
Shiho torii Institut Pasteur, FR

64. Impact of Lactobacillus rhamnosus and Bifidobacterium longum on Entamoeba histolytica invasive process in the human colon
Thomas Tréport Institut Pasteur, FR

65. Associations between influenza and meteorological parameters in four climatic zones of Cameroon: In the grasslands, equatorial forest, Sahel and the highlands from 2017 to 2022
Desmon Toutou Tsafack Centre Pasteur du Cameroun, CM

66. Comparative Analysis of RLR-specific RNA ligands during influenza virus infection
Deniz Uresin Institut Pasteur, FR

67. Modelling the AIRR response to DENV1: a human challenge study
Thomas-Wolf Verdonckt Institute of Tropical Medicine, BE

68. Antileishmanial potential and in silico prediction of pharmacokinetic properties of some synthetic phenolic compounds
Diana Sandra Wendji Monkam University of Yaounde, CM

Short Talks

01 HOW CAUSAL INFERENCE CONCEPTS CAN GUIDE RESEARCH INTO THE EFFECTS OF CLIMATE ON INFECTIOUS DISEASES

L. Barrero Guevara*1-2, SC. Kramer1, T. Kurth2, M. Domenech De Cellès1
1Infectious Diseases Epidemiology, Max Planck Institute for Infection Biology, Berlin, Germany
2Institute of Public Health, Charité – Universitätsmedizin Berlin, Berlin,Germany

A pressing question resulting from global warming is how infectious diseases will be affected by climate change. Answering this question requires research into the effects of weather on the population dynamics of transmission and infection; elucidating these effects, however, has proven difficult due to the challenges of assessing causality from the predominantly observational data available in epidemiological research. Here, we show how concepts from causal inference—the sub-field of statistics aiming at inferring causality from data—can guide that research. Through a series of case studies, we illustrate how such concepts can help assess study design and strategically choose a study's location, evaluate and reduce the risk of bias, and interpret the multifaceted effects of meteorological variables on transmission. More broadly, we argue that interdisciplinary approaches based on explicit causal frameworks are crucial for reliably estimating the effect of weather and accurately predicting the consequences of climate change.

02 NEXT GENERATION DENGUE VIRUS SERODIAGNOSTICS: PEPTIDE-BASED APPROACHES OVER TRADITIONAL PROTEIN METHODS

J. Bouckaert*1, F. Falconi-Agapito2, M. Talledo2, O. Lagatie3, K. Ariën1
1Virology, Institute of Tropical Medicine Antwerp, Antwerpen, Belgium
2Unidad de Virología, Instituto de Medicina Tropical Alexander von Humboldt, Peru, Peru
3Unit of Global Public Health, Janssen Pharmaceutica N.V. /Johnson & Johnson, Beerse, Belgium

Dengue virus, primarily transmitted by Aedes mosquitoes, is spreading increasingly across tropical and subtropical regions. Urbanization, global travel, and mass events contribute to both climate change and widespread dissemination of this virus, placing half of the world's population at risk of contracting dengue. The World Health Organization reported an alarming rise in dengue cases in 2023, with more than 6.5 million cases and 7300 deaths in over 80 countries, and this trend shows no foreseeable improvements. Most dengue cases are asymptomatic or present with general feverish symptoms indistinguishable from other (arbo)viral infections, making diagnosis based on symptoms unreliable.

Consequently, effective disease control relies on laboratory detection, primarily through serological testing. Traditional first-generation serodiagnostics, which utilize whole viral lysates or recombinant proteins, suffer from cross-reactivity, often due to cocirculating flaviviruses. To overcome this issue, we developed next-generation peptide-based serodiagnostic markers that enhance the resolution of antigen tests by targeting the virus at peptide/epitope level, significantly reducing cross-reactivity.

Here, we describe the implementation of a discovery pipeline for dengue-specific peptide biomarkers through high-throughput proteome-wide screening. Specifically, we screened a peptide library (3AA overlap) consisting of 15-mer peptides spanning the entire proteomes and genomic diversity of dengue, Zika, and yellow fever viruses. This high-density microarray screening involved a panel of serum samples (n = 80), including convalescent cases of dengue, Zika, and yellow fever, as well as flavivirus-negative cases. Based on microarray immunoreactivity profiles, we selected a panel of dengue-specific peptides for further evaluation using multiplex peptide immunoassays against a more extensive serum panel. Finally, selected peptides were adapted to a rapid diagnostic test (RDT) platform suitable for field deployment.

While the pipeline has been established, several challenges persist in developing a peptide-biomarker that meets the WHO TPP accuracy standards. To address these challenges, we are employing random forest models to identify peptide combinations that enhance sensitivity while maintaining high specificity. Additionally, we are mapping the epitopes to ultimately develop multi-epitope peptides suitable for implementation in RDTs for dengue, Zika and yellow fever virus at the point-of-care in low-resource settings, in reference centres, as well as in highresource settings such as travel clinics.

03 DUAL RNA-SEQ OF PEYER'S PATCHES INFECTED WITH YERSINIA ENTEROCOLITICA LINEAGE 4 REVEAL NEW MECHANISMS OF BACTERIAL VIRULENCE AND MODULATION OF HOST RESPONSES

H. Echenique Rivera*1, J. Madej1, P. Goosens1, E. Turc2, M. Monot2, C. Savin1, AS. Le Guern1, J. Pizarro Cerda1
1Yersinia Unit, Institut Pasteur, Paris, France
2Biomics Platform C2RT, Institut Pasteur, Paris, France

Yersinia enterocolitica is a Gram-negative bacterium responsible for enteric yersiniosis, the fourth most reported bacterial food-borne zoonosis in Europe. Y. enterocolitica pathogenesis is characterized by early colonization of the intestinal lumen, followed by entry and replication within Peyer's patches. From here, Y. enterocolitica migrates to mesenteric lymph nodes, causing lymphadenitis. In immunocompromised patients, Y. enterocolitica can reach the lymphatic system and then the bloodstream, causing septicemia. Y. enterocolitica molecular mechanisms of pathogenesis have been mainly studied in lineage 1B, which is a very rare biotype in clinical cases. On the other hand, the most common lineage around the world is currently lineage 4, which has been poorly studied until now and belongs to a different genetic cluster compared to lineage 1B. In this study, we have performed a Dual RNA-seq analysis of the interaction of Y. enterocolitica lineage at the entry site of infection (Peyer's Patches) to dissect the mechanisms of bacterial adaptation to cause infection. We have identified iron related proteins as the main group involved in adaptation as well as transcriptional regulators and proteins of unknown functions that represent candidates for virulence factors. Additionally, we have identified the main host mechanisms trigger in response to Y. enterocolitica . Major up-regulated host pathways during infection include the activation of the IL-17 signaling pathway and TNF signaling pathway as the biological process of inflammatory response and neutrophil chemotaxis; on the other hand, functions related to Retinol metabolism and linoleic acid metabolism represent major down-regulated pathways. This study provides a global picture and better understanding of Y. enterocolitica lineage 4 pathogenesis in vivo and highlight new potential virulence factors as host pathways as potential target for new therapies to inhibit infection.

04 PANDEMIC PREPAREDNESS: TARGETING THE MUCOSAL IMMUNE SYSTEM WITH CUBAN ABDALA AND MAMBISA VACCINES

G. Guillen*1-2, G. Lemus1, D. Palenzuela1, Y. Barrese3, I. Figueroa4, M. Alvarez5, J. Aguiar1, M. Vega1, MG. Guzman5, M. Limonta1, M. Ayala1, E. Pimentel6, E. Martinez7
1Biomedical Research, Center for Genetic Engineering and Biotechnology, Havana, Cuba
2Latin American School of Medicine, Havana, Cuba
3Centro Nacional Coordinador de Ensayos Clínicos, Havana, Cuba
4Hospital Hermanos Ameijeiras, Havana, Cuba
5Intitute for Tropical Medicine “Pedro Kouri”, Havana, Cuba 6Biotechnology and Pharmaceutical Industries Group, BioCubaFarma, Havana, Cuba
7Ministry of Science and Technology (CITMA), Havana, Cuba

With the first case of COVID-19 on March 11, 2019, Cuba initiated an extensive vaccine research program to combat the epidemic. The parenteral vaccine, CIGB-66 (Abdala), obtained Emergency Use Authorization in July 2021 after demonstrating 92.28% efficacy in a phase 3 clinical trial. The mucosal vaccine candidate CIGB-669 (Mambisa) is under the registration process. Both subunit vaccines contain the SARS-CoV-2 receptor-binding domain (RBD) and are manufactured using the yeast Pichia pastoris. Abdala contains 50 ug of RBD, and the mucosal vaccine formulation combines 50µg of RBD with 40 µg of HBcAg, leveraging the immune-enhancing properties of the hepatitis B nucleocapsid antigen (HBcAg). During the phase 2 clinical trial, 1040 convalescent individuals were randomly divided into two arms immunized either with Abdala or Mambisa and stratified based on age in subjects younger and older than 60 years. All participants provided written informed consent. The Mambisa vaccine has been shown to elicit high levels of specific IgA and IgG antibodies. These antibodies in serum and mucosa exhibit inhibitory effects on RBD-ACE2 binding and demonstrate neutralization activity against the D614G and Omicron variants of concern. In an independent proof-of-concept study comparing the nasal vaccine with the systemic vaccine, only the nasal vaccine Mambisa induced mucosal tissue-specific memory cells.

05 INTRALESIONAL CYTOKINES EXPRESSION AND ACTIVATED JAK-STAT MOLECULES IN LEISHMANIA TROPICA-INFECTED PATIENTS

S. Hadifar*1, N. Masoudzadeh1, H. Heydari1, V. Mashayekhi Goyonlo2, M. Kerachian2, M. Daneshpazhooh3, A. Sadeghnia4, N. Tootoonchi4, R. Erfanian Salim5, S. Rafati1, A. M. Harandi6
1Department of Immunotherapy and Leishmania Vaccine Research, Pasteur Institute of Iran, Tehran, Iran
2Cutaneous Leishmaniasis Research Center, Mashhad University of Medical Sciences, Mashhad, Iran
3Autoimmune Bullous Disease Research Center, Tehran University of Medical Sciences, Tehran, Iran
4School of medicine, Razi hospital, Tehran, Iran 5Noor Eye Hospital, Tehran, Iran
6Department of Microbiology and Immunology, University of Gothenburg, Gothenburg, Sweden

Cutaneous leishmaniasis (CL) is a complex skin infection caused by over 20 different Leishmania species that are transmitted through the bite of infected sand flies. The resolution of CL disease is known to be associated with the type of immune response and parasite factors. At the host level, the type of T-helper (Th) response and the corresponding cytokine profile play a critical role in determining the outcome of the disease. The JAK-STAT signaling pathway is a central cascade of signal transduction for the myriad of cytokines in which dysregulation has been implicated in disease progression. However, the involvement of this pathway in human CL has not been explored more and requires further investigation. The present study aimed to explore the differential gene expression of several pro- and anti-inflammatory cytokines and their associated jak-stat genes in the skin biopsy samples collected from CL patients infected
with L. tropica by quantitative Real-Time PCR. Further, we evaluate the expression of five inhibitory immune checkpoint genes as well as nine genes related to transcription factors, extracellular matrix, interferon-inducible GTPases, and epidermal barrier function. Our results revealed the overexpression of both Th1 (ifng, il12 (p35/p40), il23 (p19), and Th2 response (il4, il10) in the lesion of patients infected with L. tropica. Further, we highlighted elevated levels of il35, il21, il27 and il24, which are rather understudied in human CL. Notably, most of the genes involved in the JAK-STAT signaling pathway as well as pdl1, ctl4 and corresponding receptors were upregulated. Our finding showed dysregulation of cytokines and related jakstat genes in the lesion of L. tropica-infected patients. This result highlights the importance of further exploration into the regulatory effect of the cytokines and downstream genes in the pathogenesis of, and immunity to, CL to identify the new potential target for intervention.

06

THE ROLE OF LIVING IN FLOOD-PRONE REGIONS ON HINDERING EARLY CHILDHOOD VACCINATION IN BANGLADESH

E. Schwartz1-2, A. Dimitrova3, F. Rerolle3-4, T. Benmahrnia3, K. Jean*5-1
1Institut Pasteur, Conservatoire National des Arts et Métiers, Unité PACRI, 75015 Paris, France, Institut Pasteur, Paris, France, France
2Laboratoire MESuRS, Le Cnam, Paris, France
3Scripps Institution of Oceanography, University of California, San Diego, San Diego, United States
4Department of Epidemiology and Biostatistics, UC San Fransisco, San Fransisco, United States 5IBENS, ENS-PSL, Paris, France

Introduction: Flooding events, which are strongly linked to climate change and variability, have the potential to disrupt communities and health systems. Vaccination, a highly effective public health intervention, plays a pivotal role in preventing numerous deaths annually, particularly among children. However, the relationship between exposure to floods and early childhood vaccination remains unexplored.

Methods: This study utilizes validated flood exposure data from the Global Flood Database (GFD) and five waves of nationally representative survey data regarding the vaccination history of children <3 years from the Bangladesh Demographic and Health Surveys (DHS) collected between 2004 and 2017. Using the geographical coordinates of each surveyed household grouping and matching it with the spatially resolved GFD data, we determined whether children reside in a flood-prone area. We then used Generalized Estimating Equations, accounting for geographical clustering and including an inverse probability of treatment weighting (IPTW) for covariate balance, to assess the relationship between living in a flood-prone area and incomplete vaccination. Incomplete vaccination was defined as having missed at least one does of the four World Health Organization-recommended childhood vaccines: Tuberculosis (BCG), Diphtheria-Pertussis-Tetanus (DPT), Polio (OPV), and Measles (MCV). The sensitivity of the association measure to various definitions of exposure was explored.

Results: Our sample included 9,688 children, of which 30% lived in flood-prone areas and 86% were fully vaccinated. Our findings indicate that children living in flood-prone areas are 1.22 (CI: 1.06-1.45) times more likely to be incompletely vaccinated. This association remained when examining individual vaccines and doses. We estimate that 6% of the children who were not fully immunized, representing roughly 45,000 children in 2019, were incompletely vaccinated due to residing in a flood-prone area.

Discussion: These findings hold critical implications for disaster management protocols, emphasizing the need to ensure uninterrupted access to routine healthcare services during floods, which are becoming increasingly more common due to climate change. Considering that populations in low- and middle-income countries are disproportionately impacted by extreme climate events such as floods and preventable infectious diseases remain some of the leading causes of child death there, ensuring access to essential vaccines is critical for safeguarding public health.

07

PVDBPII ELICITS MULTIPLE ANTIBODY-MEDIATED MECHANISMS THAT REDUCE GROWTH IN A PLASMODIUM VIVAX CHALLENGE TRIAL

F. Martinez Blazquez*1, M. White2, M. Guillotte-Blisnick1, C. Huon1, A. Boucharlet3, F. Agou3, P. England4, J. Popovici5, M. Hou6-7, S. Silk6-7, J. Barrett6-7, C. Nielsen6-7, J. Reimer8, P. Mukherjee9, V. Chauhan10, A. Minassian6-7, S. Draper6-7, C. Chitnis1
1Unite de Biologie et Vaccins, Institut Pasteur, Paris, France
2Infectious Disease Epidemiology and Analytics G5 Unit, Institut Pasteur, Paris, France
3Chemogenomic and Biological Screening Core Facility, Institut Pasteur, Paris, France
4Molecular Biophysics Facility, Institut Pasteur, Paris, France
5Institut Pasteur, Pnom Penh, Cambodia
6Dept. Biochemistry, University of Oxford, Oxford, United Kingdom
7The Jenner Institute, Oxford, United Kingdom
8Novavax AB, Uppsala, Sweden
9Multi-Vaccines Development Program, ICGEB, New Delhi, India 10ICGEB, New Delhi, India

The receptor-binding domain, region II, of the Plasmodium vivax Duffy binding protein (PvDBPII), which binds the Duffy antigen receptor (DARC) during reticulocyte invasion by P. vivax is a leading blood stage vaccine candidate. Immunization with recombinant PvDBPII (variant SalI) formulated with Matrix-MTM adjuvant (PvDBPII/M-M) in a delayed dosing schedule (0, 1, 14 months) resulted in a 50% lower parasite multiplication rate (PMR) compared to unvaccinated controls following challenge with the heterologous P. vivax blood stage parasites isolate PvW1. Immunization with PvDBPII/M-M in a 0, 1, 2-month schedule did not yield any protection. Similarly, immunization with viral-vectored PvDBPII (VV-PvDBPII) delivered by chimpanzee adenovirus (ChAd63) vector followed by modified vaccinia virus (MVA) vector in a 0, 2-month schedule or in a delayed 0, 17, 19-month schedule did not have any impact on PMR following blood stage P. vivax challenge. Here, we present results of the analysis of the polyfunctional antibody responses in these groups in an effort to identify correlates of immune protection. A classification algorithm identified antibody features that significantly contribute to PMR reduction, which include antibody titre, receptor-binding inhibitory titre, dissociation constant of the PvDBPII-antibody interaction, complement C1q and Fc gamma receptor binding and specific IgG subclasses. These data suggest that multiple immune mechanisms elicited by PvDBPII immunization are likely to be associated with protection. Importantly, all the polyfunctional antibody features that correlated with protection cross-reacted with both PvDBPII SalI and PvW1 variants, suggesting that immunization with PvDBPII should protect against diversPe. vivax isolates. The immune correlates identified here could guide the development of an effective vaccine for P. vivax malaria.

08

PREVALENCE AND RISK FACTORS OF DRUG-RESISTANT MTB IN RURAL COMMUNITIES OF SOUTH AFRICA

M. Mashilo*, J.P. Kabue, N. Potgieter, A.N. Traore
Biochemistry and Microbiology, University of Venda, Thohoyandou, South Africa

Background: Drug-resistant tuberculosis (TB) continues to be a threat to public health and health security, making TB the world's largest cause of death. The study aimed to evaluate drugresistant MTB's prevalence and risk factors in rural South Africa.

Methods: A cross-sectional study was conducted among outpatients in rural communities of the Vhembe district, South Africa. Thirty active TB patients were enrolled for this study in rural communities. Patient data were collected using a structured questionnaire on lifestyle behavior and socioeconomic and environmental characteristics. A total of 60 (30 blood and 30 sputum) specimens were collected. A U-rapid test was used on blood specimens to confirm HIV status. For sputum samples, DNA was extracted using Allplex™ DNA extraction. The DNA extract was subjected to multiplex real-time PCR using the Anyplex MTB/NTM and subsequently to Allplex™ MTB/MDR/ XDRe to detect MTB/NTM (Mycobacterium tuberculosis/nontuberculosis mycobacteria) and MTB/MDR-MTB/XDR-MTB (Mycobacterium tuberculosis/Multidrug-resistant Mycobacterium tuberculosis/ Extensively drug-resistant Mycobacterium tuberculosis) respectively.

Results: Among the 35 participants, 54,3% (19/35) were females. The ages of the participants ranged from 23 to 72 years. The estimated prevalence of drug-resistant MTB was 11% (4/35). Unemployment constituted 65% (23/35) of TB patients in this study. Fifty-one percent (18/35) of the patients tested positive for MTB/HIV co-infections. In addition to MTB/HIV, other co-infections included MTB + NTM (40.0%, 14/35), MDR-MTB + NTM (5,7%, 2/35), and XDR-MTB + NTM (2,9%, 1/35).

Conclusion: The study's findings underscore the urgent need for targeted strategies in addressing drug-resistant TB. The high prevalence of co-infection, particularly NTM/DR-MTB, should be a primary focus in MTB control in the Vhembe district. The significant proportion of unemployment among TB patients and the prolonged healthcare consultation period were identified as key risk factors. Therefore, strategies should prioritize TB co-infection diagnosis/ treatment and address unemployment, as these are crucial areas where interventions can significantly impact the health of the individuals and the overall public health and health security of the region.

Keywords: Drug-resistant Mycobacterium tuberculosis, Drug-resistant tuberculosis, Nontuberculous mycobacteria, Risk factors, Rural communities

09 IDENTIFICATION OF NS5B RESISTANCE-ASSOCIATED MUTATIONS IN HEPATITIS C VIRUS CIRCULATING IN TREATMENT NAÏVE CAMEROONIAN PATIENTS

A. Mounchili Njifon*, A. Modiyinji, R. Njouom
1Virology, Centre Pasteur of Cameroon, Yaounde, Cameroon
2Virology, Centre pasteur du Cameroun, Yaounde, Cameroon
3Virology, Centre Pasteur of Cameroon, Yaounde, Cameroon

Background: NS5B polymerase inhibitors form the basis of current treatment for hepatitis C virus (HCV) infection. Direct-acting antivirals (DAAs) offer high efficacy, low risk and short treatment duration. However, the existence of resistance-associated mutations, notably at the NS5B polymerase level, may attenuate the efficacy of DAAs. The aim of this study was to identify possible natural direct-acting antiviral (DAA) mutations in the HCV NS5B gene linked to DAA resistance in treatment-naive Cameroonian patients with chronic hepatitis C.

Methods: Blood samples and treatment data were collected from 925 HCV-infected patients at the Cameroon Pasteur Center between January 2013 and December 2023; plasma was then isolated and stored at -80°C for molecular analysis. NS5B gene fragments from 925 samples were amplified with specified primers and nucleotide sequences were obtained using the Sanger sequencing system. The drug resistance profile of the NS5B gene was analyzed using Geno2pheno [hcv] 0.92.

Results: A total of 925 HCV isolates from patients were classified into three genotypes, including genotypes 1, 2 and 4. NS5B sequence analysis revealed numerous amino acid mutations. The significant S282T mutation, which induces a high level of resistance to SOF, was detected in one genotype 1 patient, while the NS5B C316N polymorphism, associated with resistance to HCV including SOF, was found in 16 genotype 1 sequences, the mutation associated with ribavirin resistance at positions Q309R was detected in 19 genotype 1 sequences, and the polymerase inhibitor L320F mutation was found in one genotype 4f sequence. The following mutations were found to be linked to DAA resistance: E237G, M289L, A333V, D310N, V321A and V321I were found in our study in different genotypes. In addition, several other mutations were found in different positions of our sequences, such as 241, 300, 310, 316, 329, 330 and 333, whose clinical characteristics have not yet been studied.

Conclusion: Our study showed several different mutations in the NS5B gene in HCV patients who had not previously received DAA therapy. These mutations could increase the risk of therapeutic failure in the future.

Keywords: NS5B, resistance mutations, hepatitis C virus, Cameroon.

10 RNA SPACER LOCATED JUST DOWNSTREAM OF THE STOP CODON OF DENGUE AND OTHER FLAVIVIRUS GENOMES IS ESSENTIAL FOR INFECTIVITY

D. Ojeda*, E. Bardossy, C. Filomatori, L. De Borba, H. Pallares, G. Costa Navarro, M. Gonzalez Lopez Ledesma, S. Oviedo Rouco, A. Gamarnik
Molecular Virology Laboratory, Fundación Instituto Leloir, Buenos Aires, Argentina

The dengue virus genome consists of a single open reading frame flanked by highly structured non-coding 5' and 3' UTRs crucial for viral replication. The 3'UTR contains two Stem Loops (SLI and SLII), two dumbbells (DBI and DBII), and a 3' Terminal Stem Loop. The SL and DB structures halt the activity of the host XRN1 exoribonuclease, leading to the accumulation of subgenomic flavivirus RNAs (sfRNAs) associated with immune evasion and pathogenesis. These structures are referred to as xrRNAs. Just downstream of the translation stop codon, preceding SLI, there is an unstructured sequence named the hypervariable region (HVR), which varies in sequence and length across DENV serotypes and genotypes.

Deleting the HVR in a DENV2 infectious clone abolishes viral infectivity. To understand its role in viral replication, we designed a battery of mutants that gradually reduced its length, modified its sequence, or introduced stable RNA structures at different positions. We found that viral replication requires at least 20 nucleotides between the stop codon and the first xrRNA1; otherwise, the viral RNAs are non-infectious. We hypothesize that the compact xrRNA structure following the stop codon interferes with viral translation termination or alters the proper folding of the viral 3'UTR

To investigate the mechanism of this observation, we performed in vivo viral evolution and searched for revertant viruses after transfection of a mutant with a complete HVR deletion. We repeatedly obtained a pseudo-revertant virus that recovered full replication, carrying a single mutation within the xrRNA1 structure. Analysis of RNA folding revealed that this mutation destabilizes the xrRNA1 structure, likely interfering with its ability to halt the XRN1 activity. To confirm this idea, we examine the revertant virus property to generate sfRNAs in infected cell extracts using Northern Blot analysis. We found that the mutation was sufficient to impair sfRNA1 accumulation in infected cells, resulting in the generation of shorter sfRNA species.

Together, our data confirm that the compact xrRNA1 structure following the stop codon at the viral 3'UTR is responsible of abolishing DENV replication. These findings provide new information about the complex interplay between translation termination, sfRNA formation, and viral RNA folding, which is essential for viral infectivity.

11 DEVELOPMENT OF A SHERLOCK CRISPR/CAS13 TOOLBOX FOR ECO-EPIDEMIOLOGICAL SURVEILLANCE OF ANIMAL AFRICAN TRYPANOSOMIASIS

E. Pérez Antón*1, R. Eloiflin2, A. Dujeancourt-Henry1, A. Camara3, S. Boiro3, JM. Bart2, V. Jamonneau2, S. Thevenon2, D. Camara4, M. Kagbadouno4, M. Camara4, M. N'djetchi5, M. Koffi5, B. Doukouré6, Y. Le Pennec6, B. Rotureau3-7, L. Glover1
1Trypanosome Molecular Biology, Department of Parasites and Insect Vectors, Institut Pasteur, Université Paris Cité, Paris, France
2Institut de Recherche pour le Développement, Unité Mixte de Recherche Institut de Recherche pour le Développement (IRD)-CIRAD, Montpellier, France
3Parasitology Unit, Institut Pasteur of Guinea, Conakry, Guinea
4Ministère de la Santé, Programme National de Luttecontre la Trypanosomiase Humaine Africaine, Conakry, Guinea 5Unité de Formation et de Recherche Environnement, Université Jean Lorougnon Guédé, Laboratoire des Interactions Hôte-Microorganisme-Environnement et Evolution, Daloa, Ivory Coast
6Virology Unit, Institut Pasteur of Guinea, Conakry, Guinea
7Trypanosome Transmission Group, Trypanosome Cell Biology Unit, INSERM U1201 & Department of Parasites and Insect Vectors, Institut Pasteur, Université Paris Sorbonne, Paris, France

New diagnostic tools with highly specific and sensitive detection are needed as we move towards control or elimination of a number of neglected tropical diseases. We have adapted SHERLOCK (Specific High-sensitivity Enzymatic Reporter unLOCKing) for the detection of different species of trypanosomatid parasites, including human and animal African trypanosomiasis (HAT and AAT). SHERLOCK harnesses the specificity and sensitivity of CRISPR-Cas13a to detect specific target RNAs in a sample, allowing for the detection of an active infection. We have now developed an (1) 18S Pan-trypanosomatid SHERLOCK, capable of detecting the presence of any trypanosomatid parasite, (2) 18S PanT-rypanozoon SHERLOCK, (3) and species-specific SHERLOCKs (for the detection oTf:. congolense, T. vivax, T. simiae and T. theileri), which can discriminate between species of the same family with high specificity in a single sample. This methodology allows us to detect the presence of parasites in samples at a concentration of 0.5 - 0.05 parasites/mL. We evaluated two populations of pigs, one from farms in forested Guinea (n= 200) and free-range domestic pigs collected in regions of the Ivory Coast (n= 230). With our toolbox we obtained a high presence of positive samples for our first line SHERLOCK that detects any trypanosomatid parasite, and a subsequent percentage close to 45% of positive samples for the Pan-Trypanozoon SHERLOCK. We detected pigs positive forT . congolense in both foci (approximately 9% and 23% respectively), and at least one other species of trypanosome. Our assays revealed the presence of T. b. gambiense in pigs in both regions, highlighting the risk to the human population living in close proximity to the animals. Our SHERLOCK toolbox can be used to perform a detailed analysis of AAT epidemiology, which will inform on the efforts put in place to control potential animal reservoirs to facilitate control of HAT transmission in the face of the spread of the Tsetse fly vector in response to a changing environment.

12 MULTIPLE FLAVIVIRUSES SECRETE A VIRAL NON-CODING RNA IN MOSQUITO SALIVARY VESICLES TO ENHANCE SALIVA INFECTIVITY BY REDUCING EARLY IFN RESPONSE

I. Serrato Pomar*1-2, J. Zoladek3, Q. Narpon1, F. Rey-Cadilhac1, R. Hamel1, S. Rossi1, O. Medianikov2, D. Missé1, S. Nisole3, J. Pompon1
1MIVEGEC, IRD, Montpellier, France 2CD62, Aix-Marseille université, Marseille, France 3IRIM, CNRS, Univ. Montpellier, Montpellier, France

West Nile (WNV) and Zika (ZIKV) viruses are endemic in tropical and subtropical countries and have recently emerged in temperate regions of Europe and North America. There are no therapeutic and prophylactic options, and vector control strategies have limited efficacy. A better understanding of the initial step of bite-initiated transmission will promote novel interventions. All orthoflaviviruses produce a subgenomic flaviviral RNA (sfRNA) with immune inhibitory properties within mosquitoes. Here, we showed that multiple orthoflaviviruses secrete sfRNA in saliva of multiple mosquito species to enhance transmission by inhibiting innate immunity. First, we detected sfRNA in saliva from Culex quinquefasciatus mosquitoes orally infected with WNV, and from Aedes aegypti mosquitoes infected with ZIKV. We further showed that oral infection is not required for salivary sfRNA secretion. Second, we observed that WNV and ZIKV salivary sfRNA were resistant to RNAse degradation unless treated with a detergent, strongly suggesting that salivary sfRNA is packaged inside a lipidbased vesicle. Third, we infected human cells with saliva containing different sfRNA concentrations and showed that sfRNA increased infection. Reproducing the phenotype by transfecting synthetic sfRNA supported that the phenotype was caused by sfRNA alone. We also showed a similar increase in different transmission-relevant cell types. Fourth, we determine how salivary sfRNA increases infection through multiple approaches. Higher sfRNA saliva reduced early innate immune response, in a RIG-I independent manner. RNAseq analysis revealed the gene regulation associated with sfRNA-mediated increased infection. Finally, we determined the effect of salivary sfRNA on transmission by using a mouse transmission model. Wild-type mice were injected with infectious saliva containing different concentrations of sfRNA and their survival was monitored. Overall, our study discovers a salivary transmission enhancer that is conserved across orthoflaviviruses and determines the mechanism.

13 A SINGLE-CELL PERSPECTIVE ON AGE AND SEX EFFECTS ON IMMUNE RESPONSE TO VIRAL INFECTION

M. Sharawy*1, ZHI. Li1, A. Bisiaux1, JAN. Madacki1, Y. Aquino1, M. Rotival1, E. Patin1, D. Duffy2, L. Quintana-Murci1
1Human evolutionary genetic, Pasteur, Paris, France
2Translational Immunology, pasteur, Paris, France

Human immune variability is driven by genetic and non-genetic factors, including age, sex, smoking habits, and latent viral infections. To untangle these effects on the immune landscape, we collected peripheral blood mononuclear cells (PBMCs) from 415 healthy donors of European ancestry, aged 30 to 80, with a balanced sex ratio in each age group. PBMCs were stimulated for 6 hours with SARS-CoV-2 (Omicron), influenza A virus (IAV; PDM09), or a mock control. Using single-cell RNA sequencing, we identified 40 cell types spanning five major immune lineages. Focusing on cell composition, our analyses revealed sex-specific and environment-dependent effects of age on cellular proportions, such as a women-specific decrease in innate lymphoid cell (ILC) frequency with age and a stronger decline in the mucosal-associated invariant T (MAIT) cell compartment with age in CMV+ individuals.

We next examined how age and sex affect the transcriptional profile of immune cells. We detected 1,664 genes whose expression changes with age (FDR<0.01), with over 75% affecting the CD4 T lineage. Similarly, sex displayed widespread effects on transcriptional variability, with 1,161 genes showing differential expression between sexes in at least one cell type, including 83 located on sex chromosomes. In response to virus stimulation, we identified 443 genes displaying stimulation-specific differential expression. Notably, women showed enrichment for differential expression upon stimulation in inflammatory and type 1 and 2 interferon pathway genes in CD56dim NK cells. By inferring transcription factor activity from gene expression data, we revealed a men-specific decrease in NF-KB and IRF1/3 activity in myeloid cells upon stimulation, likely underlying the observed sex-differences in interferon-stimulated responses to viral infection. We finally investigated age-associated mosaic loss of the Y chromosome (LoY), and found that LoY primarily affects the NK and myeloid lineages, as well as specific cell-types such as regulatory T cells, where ~20% of cells lack a Y chromosome. Interestingly, innate immune cells with LoY showed stronger antiviral responses upon stimulation compared to cells without LoY from the same individuals.

Overall, our work provides insights into how age and sex influence immune response variation and reveals new connections between immune senescence and responses to viral infections.

Posters

01 FLORAL BIOLOGY VARIATIONS IN OLEA EUROPAEA AMIDST CLIMATE CHANGE: IMPLICATIONS FOR ALLERGY

Alessandro Cinquantasei MSc 1,5, Stefano Palazzo Eng1,5, Nada Chaoul MSc, PhD 1,2,5, Francesco Russano3, Maria Pia Rossi MSc4, Lucia Anna Giliberti PhD4 and Marcello Albanesi MD, PhD 1,5,6

Background: Olea europaea, an endemic plant of the Mediterranean basin, exhibits a flowering period from April to June, requiring high temperatures and sensitivity to low humidity, rainfall, and windiness. Allergy to O. europaea affects 13.85% of the Southern Italian population. This study investigates the influence of climate change on O. europaea pollen concentration, morphological and biochemical variations, and clinical symptoms over a 6-year period (2017-2022).

Methods: Pollen concentration in Southern Italy was analyzed alongside weather variables (temperature, precipitation, humidity, and windiness) using existing databases (Arpa Puglia; time and date). Optical and fluorescence microscopy techniques were employed to assess pollen morphology and biochemical characteristics. Additionally, the absolute number of prescriptions for various antihistamine drugs (cetirizine, ebastine, bilastine, desloratadine, rupatadine, levocetirizine, fexofenadine, loratadine) was calculated.

Results: The lowest pollen count occurred in 2018 (91.1 pollen per m3 value/week), while the highest was recorded in 2021 (2545.3 pollen per m3/week). In 2019, the pollen peak was delayed by 2 weeks. Notably, 2018 exhibited more rainy days in May and June and higher humidity percentages (April 73%, May 70%, June 72%). In contrast, 2021 had lower humidity values (April 68%, May 61%, June 59%) and fewer rainy days (1 day in May and none in June). No changes in pollen size were observed, but modifications in O.europaea pollen fuchsin fluorescence were noted in 2018 and 2021. The number of drug prescriptions was highest in 2021.

Conclusions: This study highlights that climate change may impact the flowering period, morphology, and pollen production of O.europaea, influencing patient symptomatology and the need for antihistamine medications.

02

FAECAL CARRIAGE OF EXTENDED-SPECTRUM BETA-LACTAMASE-PRODUCING ESCHERICHIA COLI IN LIVESTOCK AND ABATTOIR WORKERS FROM SEKONDI-TAKORADI ABATTOIR

F. Amoah*1-2, B. Egyir2, A. Labi3
1Bacteriology, Public Health Reference Laboratory, Sekondi-Takoradi, Ghana
2Bacteriology, Noguchi Memorial Institute for Medical Research, Accra, Ghana
3Bacteriology, University of Ghana-Medical Microbiology, Accra, Ghana

Background: Antimicrobial resistance (AMR) is a global health and development issue and contributes to high mortality and morbidity worldwide, especially in low and middle-income countries. Transmission of resistance is driven by several factors including the zoonotic route. Animals are known to be colonized by extended-spectrum beta-lactamase (ESBL) producing bacteria. Studies have shown that there is evidence of potential transmission of these organisms from companion pets to humans.

Aim: This study aims to assess the faecal carriage of ESBL-producing E. Coli (ESBL-EC) and its associated risk factors among livestock and abattoir workers at the Sekondi-Takoradi abattoir.

Method: A comparative cross-sectional study will be conducted from March 2024 to May 2024 at Sekondi-Takoradi. Participants which include 300 abattoir workers would be randomly selected after consenting to the study and 200 livestock would be included in the study. Moreover, a comparator population of 300 non-abattoir workers which includes healthy community residents would be sampled after consenting to the study. Samples would be cultured to isolate ESBL-EC and determine their antimicrobial susceptibility patterns. ESBL- EC would be sequenced to assess the genetic similarities between isolates from livestock, abattoir workers, and non-abattoir workers. The potential risk factors associated with ESBL- EC carriage in abattoir workers would be assessed by bivariate analysis using odds ratios as a measure of association. Risk factors would be included in an unconditional logistic regression model used for multivariate analysis at a 5% significance level.

Expected outcome: Data obtained would help determine the carriage of ESBL-EC in livestock and abattoir workers the genetic similarities of resistant bacteria present and risk factors for ESBL-EC carriage in abattoir workers.

03 VARIATION IN CHROMATIN ACCESSIBILITY IN IMMUNE CELLS: POPULATION DIFFERENCES AND GENETIC CONTRIBUTORS REVEALED BY SINGLE-CELL APPROACHES

Y. Aquino*1, A. Bisiaux1, Z. Li1, M. Hasan2, E. Patin1, L. Quintana-Murci1-3, M. Rotival1
1Human Evolutionary Genetics Unit, Institut Pasteur, Paris, France
2UTechS Single Cell Biomarkers, Institut Pasteur, Paris, France
3Collège de France, Paris, France

Transcriptional responses to infection vary widely across individuals and populations. While growing evidence links immune differences with epigenetic variation, the mechanisms through which chromatin remodeling contributes to transcriptional immune heterogeneity remain elusive. We used single-nuclei assays of transposase-accessible-chromatin sequencing (snATACseq) on peripheral blood mononuclear cells from 160 healthy donors of Central African or West European ancestry to delineate the chromatin accessibility landscape across 21 cell types.
We uncovered 2,197 open chromatin regions (OCRs) displaying differential accessibility (|log2FC| ≥ 0.5, FDR ≤ 0.01) between populations (popDA), with K-light-chain memory B cells being the most differentiated (1,013 popDA OCRs). Around 63% of these popDA OCRs are more accessible in African-ancestry memory B cells and enriched in binding motifs for T-box transcription factors involved in the acquisition of immune memory, like T-bet (TBX21). This suggests a preferential switch of memory B cells to T-bet+ phenotypes in individuals of African ancestry. We next mapped the genetic determinants of chromatin accessibility, and identified 20,174 OCRs associated (FDR < 0.05) with nearby genetic variants (cis-caQTL). Notably, 80% of caQTL were detected in a single immune lineage, highlighting the cell context-dependent nature of the genetic determinants of chromatin accessibility. Focusing on population variation, popDA OCRs were enriched in cis-caQTL in all immune lineages (OR > 3.2p, < 2.2×10-16). However, only around 3% of T-bet motif-harboring OCRs displayed a significant caQTL in B cells, pointing to environmental or trans-genetic effects as sources of the African T-bet+ phenotype. Finally, leveraging scRNA-seq data from the same individuals, mock- or SARS-CoV-2-stimulated, we estimated that only up to 5% of caQTL are also associated with gene expression (eQTLsp, < 10-3), suggesting that caQTL and eQTL mapping targets fundamentally different sets of regulatory variants. In line with these observations, we found that while caQTLs are enriched among variants associated to immune traits genome-wide (OR = 4.07, p < 2.2×10-16), over half of these signals (88/169) were missed by previous eQTL mapping. Overall, our results highlight the relevance of mapping caQTL to delineate a potential missing layer of regulation that could enhance the prediction of complex disease risk from genome-wide associations.

04

ANTIMICROBIAL SUSCEPTIBILITY, ESBL PRODUCTION AND VIRULENCE OF ENTEROBACTERIA ISOLATED FROM URINARY TRACT INFECTIONS IN BENIN

L. Baba-Moussa, H. Sina Orou, F. Assouma*
faculty of science and technology, laboratory of biology and molecular typing in microbiology, University of Abomey Calavi, Seme Podji, Benin

Enterobacteriaceae represent one of the main families of Gram-negative bacilli responsible for serious urinary tract infections (UTI). The aim of the present study was to draw the resistance profile and the virulence capability of Enterobacteriaceae strains isolated in urinary tract infections in Benin. Three hundred and nighty urine samples from hospitalized and non-hospitalized patients were collected and the isolation of the Enterobacteriaceae strains was carried out according to standard microbiology methods. The API 20E gallery was used for biochemical identification. All the isolated strains were subjected to antimicrobial susceptibility testing using the disc diffusion method. Extended-spectrum beta-lactamases (ESBL) production was investigated using the Thomson double halo method and the biofilm production was quantified using the microplates method. Multiplex PCR was used for the detection of urovirulence genes, namely: PapG , IronB , Sfa, iucD , Hly, FocG , Sat, FyuA a n d Cnf using commercially designed primers. More than 26% of our samples were contaminated by Enterobacteriaceae strains at different level. Thus, E. coli (31.06%), Serratia marcescens(11.65%), Klebsiella ornithinolytica (8.73%), Serratia fonticola (7.76%) and Enterobacter cloacae (6.79%) were identified. Among the isolated strains, 40% were biofilm-forming and 5.82% of them were ESBL-producing. Isolates were most resistant to erythromycin, cefixime, ceftriaxone and ampicillin (≥90%), followed by ciprofloxacin, gentamycin, doxycycline, levofloxacin (≥50%) and least resistant to imipenem (27.18 %). Concerning the virulence genes, Sfa was the most detected (28.15%), followed by IronB (22.23%), iucD (21.36%), Cnf (15.53%) PapG (9.71%), FocG (8.74%), Sat (6.79%), FyuA (5.82%) and Hyl (2.91%). These data could help to improve the diagnosis of strains of uro-pathogenic Enterobacteriaceae and to design effective strategies and measures for the prevention and management of serious, recurrent or complicated urinary tract infections in Benin.

Keywords: Urinary tract infections, Enterobacteriaceae, Resistance, Biofilm, ESBL, virulence, Benin.

05 TARGETING THE INTRA-ERYTHROCYTIC LIFE CYCLE OF THE MALARIA PARASITE TO IDENTIFY STARTING POINTS FOR ANTIMALARIAL DRUG DISCOVERY FROM DRYMARIA CORDATA AND MACARANGA MONANDRA

K. Aubin Youbi*1-2, M. Tchatat Tali1-2, H. Souleyman1, S. Wendji Monkam1, D. Woutouoba1, G. Yanou1, P. Tsouh1-2, F. Boyom Fekam1-2
1Biochemistry, AntiMicrobial & Biocontrol Agents Unit, Laboratory for Phytobiochemistry & Medicinal Plants Studies, University of Yaounde 1, Yaoundé, Cameroon
2Malaria Drug Discovery, Advanced Research & Health Innovation Hub, Yaoundé, Cameroon

The outbreak and spread of parasite strains less sensitive to artemisinin derivatives and the failure of treatment with artemisinin-based combination therapies underline the emergency of searching for new drugs against malaria. The intra-erythrocytic life cycle of the parasite is responsible for the clinical manifestations and represents a crucial target for the development of new antimalarial drugs to relieve the symptoms of the disease. Medicinal plants, which have long been used to cure various diseases, were reported to possess a number of antimalarial bioactive secondary metabolites. The general objective of this work was to target the intra-erythrocytic life cycle of the malaria parasite to discover new drugs from Drymaria cordata and Macaranga monandra, two plants traditionally used in Cameroon for the treatment of malaria. Aqueous, methanolic, ethanolic and hydroethanolic extracts of the whole plant of D. cordata and of the bark of M. monandra were tested in vitro against chloroquine-sensitive (Pf3D7) and multi-drug resistant (PfDd2) strains of Plasmodium falciparum using the SYBR Green-I test. Subsequently, the effects of active extracts on erythrocyte membrane integrity and on viability of the Vero cell line were evaluated by the spectrophotometric method based on hemoglobin release and resazurin conversion respectively. The most active and selective extract was selected for fractionation. Inhibition kinetics and action specificity of promising fractions on the intra-erythrocytic development cycle of P. falciparum were studied. Only the ethanolic extract of D. cordata showed good antiplasmodial activity (IC50PfDd2:18.9µg/ml; IC50Pf3D7:24.51µg/ml) while all the extracts of M. monandra showed promising antiplasmodial activities (IC50< 8µg/ml). All active extracts showed no haemolytic or cytotoxic effects. Promising ethyl acetate (IC50PfDd2: 0.60µg/ml, IC50Pf3D7: 3.42µg/ml) and n-butanol (IC50PfDd2: 0.92µg/ml, IC50Pf37D: 2.46µg/ml) fractions from M. monandra bark methanolic extract (IC50PfDd2:2.46µg/ml; IC50Pf3D7:1.02µg/ml) have proved to be fast-acting, inhibiting ring development, inducing selective lysis of parasitized red blood cells harboring trophozoites, and blocking the release of new merozoites. Qualitative analysis of this extract revealed the presence of pharmacologically active phytochemicals such as phenols, flavonoids, tannins, anthraquinones, terpenoides and anthocynins. Further investigation of the ethyl acetate and n-butanol fractions from M. monandra bark methanolic extract could reveal powerful starting points for antimalarial drug discovery.

06

EFFECT OF SHIFTING TEMPERATURE ON TRANSMISSION DYNAMICS OF CHOLERA: MATHEMATICAL MODELING

N. Ayad*1, S. Abrouk2, F. Derrar2-3
1Laboratory of Modeling and Biostatistics, Pasteur Institute of Algeria, Alger, Algeria
2Pasteur Institute of Algeria, Algiers, Algeria
3Medical School, University of Algiers 1, Algiers, Algeria

Cholera remains a significant public health threat, especially in regions with limited access to clean water. Climate change has been described to raise outbreaks of cholera disease and increases public health concerns. In this work, we propose a mathematical model to assess the impact of environmental temperature change on transmission dynamics of Cholera. SIR-BT compartmental deterministic model was considered in this study, where B is the environment Vibrio compartment, and T is the environment temperature which influences some model parameters, namely, transmission rates and Vibrio growth rate. System of differential equations with temperature dependent parameters were used to describe cholera dynamics. R software has been used to carry out numerical solution and numerical simulations related to different temperatures hypothesis. We highlighted three different scenarios related to temperature shifting. Total number of infections and epidemic peak were increasing with the rise in environmental temperature, while time to epidemic peak was decreasing. In a population of 10000 susceptible individuals, shifting temperature from 20°C to 30°C will be increasing the total number of infections by 494, and will be decreasing the time to epidemic peak by 3 days. Shifting temperature from 20°C to 40°C will be increasing the total number of infections by 1062, and will be decreasing the time to epidemic peak by 6 days. The simulated scenarios are very useful for public health to estimate the future trend of cholera incidence, with the aim of adopting protective measures in endemic areas.

07

ADAPTING CRISPR-CAS13 AS AN ANTIVIRAL TOOL IN INSECTS

E. Bardossy*1, C. Picciotto2, F. Schweisguth2, MC. Saleh1
1Virus and RNA interference, Institut Pasteur, Paris, France
2Dynamics of Developmental Decisions in Drosophila Unit, Institut Pasteur, Paris, France

Viruses transmitted by insects pose a significant threat to global health, affecting both human health and agricultural productivity. Insect-borne viruses such as dengue and Zika disproportionately affect impoverished regions, while plant viruses reduce crop yields and exacerbate food insecurity. With no effective vaccines or treatments for many human insect-borne viral diseases and incurable plant viral infections, novel prophylactic measures are urgently needed. The current reliance on pesticides raises environmental and health concerns and requires sustainable alternatives for insect control. Here I will present the development of CRISPR/Cas13 systems as programmable antiviral tool in insects. We useD rosophila melanogaster as a model organism and Drosophila C virus (DCV) and Sindbis virus (SINV) as model viruses. We hypothesize that transgenic expression of virus-specific CRISPR/Cas13 in insects will enhance the antiviral immune response, thereby reducing viral load and transmission. We aim to evaluate the efficacy of CRISPR/Cas13 in Drosophila by (i) assessing its ability to suppress viral replication in Drosophila S2 cells, (ii) developing transgenic fly lines expressing virus-specific CRISPR/Cas13 systems, and (iii) testing the ability of these transgenic flies to inhibit viral replication upon viral challenge. This project leverages the tractability and genetic tools of Drosophila to validate CRISPR/Cas13 as a sustainable, environmentally friendly insect control strategy, potentially transforming our approach to managing insect-borne viral diseases in humans and plants.

08

GUT MICROBIOME METABOLITES REGULATE INNATE IMMUNE RESPONSE IN JAPANESE ENCEPHALITIS VIRUS INFECTION

A. Majumdar1, I. Siva Venkatesh11, V. Swarup2, A. Basu*1
1National Brain Research Center, Gurugram, India 2University of California,
2. Institute for Memory Impairments and Neurological Disorders (MIND),USA, Irvine, Ca, United States

The gut-brain axis plays a pivotal role in the physiological state of an organism. One of the key channels of this axis are gut microbial metabolic derivatives such as short-chain fatty acids (SCFAs). These metabolites are produced by anaerobic fermentation of ingested complex carbohydrates and are regarded to have potent immuno-modulatory role. Japanese encephalitis virus (JEV), a neurotropic flavivirus, is associated with life threatening neuro-inflammation and neurological sequelae in infected hosts. Based on known immunomodulatory functions of SCFAs, we hypothesize that the latter's supplementation have potential in mitigating JEV pathogenesis. An SCFA cocktail containing acetate-butyrate-propionate was intraperitoneally supplemented in a group of JEV infected mice prior to infection. Our study contributes to the increasing evidence supporting SCFAs as an anti-inflammatory and neuro-protective agent, we further expand its scope as a potential supplementary intervention in JEV mediated neuroinflammation. Based on known immunomodulatory functions of SCFAs, we hypothesize that the latter's supplementation have potential in mitigating JEV pathogenesis. An SCFA cocktail containing acetate-butyrate-propionate was intraperitoneally supplemented in a group of JEV infected mice prior to infection. The SCFA+JEV group showed delayed onset,of symptoms and increased survival upon infection as opposed to JEV control group (JEVi)n vivo. Significant downregulation of inflammatory cytokines along with reduced glial activation was observed in SCFA+JEV group SCFAs appear to quench inflammatory markers in JEV infected microglial cells. Our study contributes to the increasing evidence supporting SCFAs as an anti-inflammatory and neuro-protective agent, we further expand its scope as a potential supplementary intervention in JEV mediated neuroinflammation.

09

SURVEILLANCE OF CRIMEA-CONGO HAEMORRHAGIC FEVER VIRUS IN CENTRAL SAHARA, ALGERIA

K. Benallal*1, A. Hachid1, M. Tamani1, FA. Khardine1, NA. Gessoum1, I. Lafri2
1Virology, Arboviruses and emergent viruses Laboratory, Institut Pasteur of Algeria, Algiers, Algeria
2Department of Veterinary, Institut Pasteur of Algeria, Algiers, Algeria

Crimea-Congo haemorrhagic fever virus (CCHFV) belongs to Orthonairovirus genus and is transmitted mainly by ticks ofH yalomma genus. Animal such as sheep and cow are considered as amplifiers of the virus and does not show any symptoms while human is severally affected causing between 5% and 80% of mortality. Several studies were conducted in Algeria tackling the circulation of this virus among camels and sheep and the available results showed that up 70% tested camels of the by serology were positive to this virus. So far in Algeria, the only strain of CCHFV was detected in Hyalomma eagyptum collected on tortus which clustered within the AP2 genotype regarded as non-pathogenic for human. In our study, of 450 ticks collected on camels in the Central Sahara, 259 were tested to CCHFV using two different RT-PCR allowed the detection of the virus in twoH yalomma dromaderii and Hy. imputed. The sequencing of the segment S showed that this strain belongs to the Africa I genotype which is considered pathogenic to human. For our knowledge this is the first detection of pathogenic strain in Algeria and the phylogenetic tree showed that the virus evolves solely suggesting the presence of a probable local cycle of this virus in the Central Sahara that merit to be explored further.

10 DRUGS TARGETING HUMAN PEROXIREDOXIN 6 AS A NOVEL CLASS OF ANTIMALARIAL AGENTS

N. Binte Zulkifli*1-2, C. Chitnis1
1Malaria Parasite Biology & Vaccines Unit, Institut Pasteur, Malaria Parasite Biology & Vaccines Unit, Paris, France
2Université Paris Cité, CNRS UMR 3523, Paris, France

As Plasmodium parasites propagate in RBCs, they import and proteolytically digest host hemoglobin to provide amino acids for growth. Hemoglobin degradation releases free heme, which inflicts oxidative damage on both the parasite and the host. Initial observations show the PLA2 inhibitor, Darapladib, inhibits the development of P. falciparum blood stages from ring to schizont and that it binds to human peroxiredoxin 6 (PRDX6). These findings suggest that P. falciparum uses host PRDX6 for membrane repair following oxidative damage during blood stage growth. Human host PRDX6 makes an attractive novel target for antimalarials as it would have lower chances of developing drug resistance. Even though Darapladib has been shown to inhibit progression of P. falciparum, the IC50 value of Darapladib is too high at 0.56 µM, above the levels of bioavailability in humans. Therefore, there is a need to screen for better inhibitors of PRDX6. We established a drug screening pipeline to select for inhibitors of PRDX6 from compound libraries. We used the thermal profiles of PRDX6 with and without inhibitor Darapladib to optimise a High Throughput Fluorescence Thermal Shift Assay (FTSA) Inhibitor Library Screen for PRDX6. The protocol is sensitive, robust, reproducible and allows for the screening of 320 compounds in one 384- well plate. Out of 24,381 compounds screened thus far, 31 were shown to be reproducible and exhibit ΔTm of at least -1°C. Growth Inhibition Assay was subsequently performed to determine the antimalarial activity in P. falciparum strain 3D7 of the compounds. Thus far, eight out of 21 compounds showed at least 50% inhibition at 10 µM. These compounds were also re-evaluated for binding to the PLA2 site of PRDX6 through gel based-Activity Based Profiling Assay and inhibition of PLA2 activity of PRDX6. Following the hit confirmation assays, we will progress to lead optimization where we will generate analogs of our hits with the target of improving its potency as a PRDX6 inhibitor and the most promising inhibitors will be selected for in vivo studies in humanised mice.

11 MICROBIOLOGICAL MONITORING, NEW HORIZONS FOR TICK-BORNE DISEASES: TICK AND PATHOGEN PRESENCE ACCORDING TO THE ECOSYSTEM IN URBAN AND PERI-URBAN ENVIRONMENTS IN THE ILE DE FRANCE REGION

E. Krupa1, L. Levillayer1, M. Bastien2, O. Telle3, B. Combes2, M. Prot4, E. Simon-Loriere4, A. Raffetin5, R. Paul1, S. Bonnet*1
1Ecology and Emergence of Arthropod-borne Pathogens, Institut Pasteur-INRAE-Université Paris Cité-CNRS UMR 2000, Paris, France
2Entente de Lutte et d'Intervention contre les Zoonoses (ELIZ), Malzéville, France
3UMR 8504 Geographie-cités, CNRS, Aubervilliers, France
4G5 Evolutionary Genomics of RNA Viruses, Institut Pasteur-Université Paris Cité, Paris, France
5Tick-Borne Diseases Reference Center-Paris and Northern Region, General Hospital Lucie et Raymond Aubrac, Villeneuve-Saint-Georges, France

Ticks are strict hematophagous arthropod that can transmit a high diversity of tick-borne pathogens (TBPs) including those responsible of Lyme disease, piroplasmosis or Tick-Borne Encephalitis and Crimea Congo Haemorrhagic fever. Environmental, socio-economical and climate changes impact the geographical distribution of these vectors, contributing to the emergence of associated tick-borne diseases. Additionally, urban greening, by providing suitable environments for ticks and their hosts and promoting outdoor activities, increases the risk of encountering ticks and TBPs. In that context, our aim is to provide evidence-based recommendations and tick risk maps for the general public on the green spaces in and around Paris, France. For that purpose, ticks were collected by flagging in spring and autumn of 2022 and 2023, in 166 sites of significant human attendance in 32 different green areas of Ile de France regions, including urban parks, peri-urban woods, green infrastructures and forest . Following tick identification, tick-borne pathogens were detected by dedicated PCR and Next Generation Sequencing. In total, 3456 ticks were collected, most of them being Ixodes ricinus. Forest but also periurban woods hosted the majority of ticks collected. Urban parks and green infrastructures were not exempt of risk, even if they seemed to be less suitable for the installation of tick populations. Borrelia burgdorferi sl, Anaplasma phagocytophilum. Bartonella spp., Rickettsia spp. and Babesia spp. were detected and prevalence varied according to the collection site. In conclusion, whilst the environment is a key parameter in the distribution of ticks and hence tick bite risk and pathogen transmission, exposure is ultimately crucial. Tick abundances and TBP prevalence rates stratified by type of green space will be mapped across the region and contextualised with respect to human frequentation through social media information to generate a population level estimation of risk. In the end, the results obtained will be superimposed on the participatory science data of tick bite reporting (CITIQUE) and the case data of Lyme diseases of the Centre de Référence des Maladies Vectorisées par les Tiques (CRMVT).

12 PROBING THE INTRINSIC HETEROGENEITY OF VIRAL INFECTIONS BY SINGLE-CELL GENOMIC

P. Bost
Institut Curie, Paris, France

Recent viral pandemics caused by emerging viruses such as HIV, Ebola, and COVID-19 have demonstrated that viruses continue to pose a significant threat. Despite considerable research efforts, our understanding of these viruses remains limited, underscoring the need to elucidate the fundamental processes and phenomena involved in viral infections. For example, viral infection of a homogeneous cell population results in a highly heterogeneous viral particles production across individual cells. The mechanisms and reasons for this heterogeneity are still unclear. Furthermore, it is unknown whether this heterogeneity extends to individual viral gene expression.

While this question was technologically challenging to address for many years, we can now directly profile the viral transcriptome of thousands of individual infected cells using single-cell RNA-sequencing (scRNA-seq). I will begin by introducing the general approach of single-cell metaviromics and how it can be utilized to study acute viral infections such as COVID-19 and how it revealed secondary viral infections by hHMPV and HSV-1, as well as their impact on the immune system. Subsequently, I will demonstrate how multiplexed imaging techniques can complement scRNA-seq in studying viral infections, illustrated by the analysis of Respiratory Syncytial Virus infection kinetics. Finally, I will discuss how a new generation of scRNA-seq protocols is ideally suited for studying viral transcriptomes that cannot be assessed using conventional scRNA-seq protocols, and how these protocols can be applied to study complex viral transcriptomes, such as that of HCoV-229E, a non-pathogenic coronavirus.

In summary, I will detail how single-cell genomics methods are revolutionizing the study of viruses and what can be learned both in terms of fundamental and applied virology.

13 UNRAVELING DEPLETION MECHANISM OF THE VIRULENCE GENE PLA IN EPIDEMIC STRAINS OF YERSINIA PESTIS

E. Bougit*, P. Lê-Bury, O. Dussurget, J. Pizarro-Cerda
Yersinia Research Unit, Pasteur Institute, Paris, France

Yersinia pestis is the bacterium responsible for causing deadly plague, a vector-borne zoonotic disease that led to massive epidemics in human history. It is considered a reemerging disease and remains a global health concern due to recent outbreaks in countries like Madagascar. The highly plastic genome of Y. pestis contains pPCP1, a 9.6 kb-plasmid of importance as it carries the major virulence gene pla. Y. pestis strains bearing a 7.6 kb-pPCP1 plasmid characterized by a 2 kb deletion have been identified at the end of the second plague pandemic. This deleted region, named the pla region, encompasses pla and toxin-antitoxin genes. How this deletion occurred is currently unknown. The aim of our study is to decipher the molecular mechanism driving loss of pla. We have identified xrs1 and xrs2 sequences flanking the pla region of 9.6 kb-pPCP1 that are homologous to specific recombination sites of the Xer recombinase Recombination System. This system contributes to dimer resolution in Escherichia coli. Here, we show that plasmid dimers containing Y. pestis xrs2, but not xrs1, can be resolved into monomers in E. coli or Y. pestis. We also highlight that SNP in xrs2 of the Y. pestis reference strain CO92, leads to defective dimer resolution. Lastly, we demonstrate that Xer system proteins XerC and PepA are crucial for dimer resolution in E. coli, but dispensable in Y. pestis. Our findings reveal a functional Xer site-specific recombination system in Y. pestis whose role in excision of the pla region is currently under investigation.

14 DECIPHERING THE INTERACTIONS BETWEEN RNA VIRUSES AND RETROTRANSPOSONS IN DROSOPHILA MELANOGASTER

M. Castelló Sanjuán*1, S. Leach2, J. Nigg1, M.C. Saleh1
1Université Paris Cité, CNRS UMR3569, Viruses and RNA Interference Unit, Institut Pasteur, Paris, France
2University of Colorado Anschutz Medical Campus, Denver, United States

Arthropods are vectors for viruses causing disease in humans, plants, and animals. During viral infection in many arthropods, RNA genomes of non-retroviral RNA viruses are reverse transcribed into viral DNA (vDNA) by reverse transcriptases (RTs) encoded by endogenous retrotransposons. vDNA enhances the RNA interference-based antiviral response by giving rise to transcripts serving as sources of small interfering RNAs. This process keeps viral titers below a lethal threshold and is required for establishment of persistent viral infections in flies, mosquitoes, ticks, shrimps and moths, among other invertebrates. Therefore, virus-retrotransposon interactions are a critical component of the host response to infection and a greater understanding of these interactions may facilitate new strategies to disrupt virus transmission.

Here, we developed isogenic D. melanogaster stocks harboring persistent infections with four naturally infecting viruses of D. melanogaster to explore the impact of virus-retrotransposon interactions on viral infection cycles and host fitness. We analysed how the maintenance of persistent infections affected the transcriptomic profiles of the fly. In addition, we focused on a positive sense, single stranded RNA virus called Drosophila A virus (DAV) to determine how virus-retrotransposon interactions may influence host physiology during persistent viral infection. We found that vDNA forms of DAV are produced during persistent DAV infection and we measured RT activity throughout development to correlate the appearance of vDNA with RT activity. Our results reveal novel spatiotemporal information regarding the synthesis of vDNA and provide insights to further explore virus-retrotransposon interactions.

15 THE MICROBIOTA OF ANOPHELES AND AEDES MOSQUITOES IN FRENCH GUIANA: INVESTIGATING MICROBIAL COMMUNITIES AND THEIR RELATIONSHIP WITH ENVIRONMENTAL FACTORS

E. Chabanol*1, O. Romoli1, V. Behrends2, Y. Epelboin1, S. Talaga1, K. Heu1, G. Prévot3, M. Gendrin1-4
1Institut Pasteur de la Guyane, Cayenne, France
2University of Roehampton, London, United Kingdom
3Université de Guyane, Cayenne, France 4Institut Pasteur, Paris, France

Mosquitoes host microbial communities that influence various aspects of their life, from development to fecundity and lifespan. Additionally, the microbiota can impact the vectorial competence of mosquitoes for diseases such as malaria or dengue fever. The diverse microbial actors within the intestine can interact with pathogens in different ways, either facilitating or hindering the establishment of pathogens within the mosquito's body. Therefore, understanding the effects of the various microbial communities present in mosquitoes is crucial. While sequencing-based studies have analyzed microbial compositions in mosquitoes, it remains unclear whether variations in the microbiota are random or influenced by bacterial interactions or environmental factors, favoring specific compositions. In our study, we focused on a broad range of Aedes and Anopheles mosquitoes from various locations in French Guiana, sampled across several months and years. Using 16S sequencing and MiSeq technology, we analyzed the bacterial composition of individual mosquito midguts. Our findings revealed a varied microbiota, however predominantly dominated by core bacteria, rather than various typical compositions. Furthermore, we gained insights into the influence of capture location, month, and mosquito species on the microbiota and correlated our results with an analysis of mosquito metabolism from two different study locations. These findings enable the identification of typical and dominant bacteria within the mosquito microbiota, which could serve as targets for future functional studies or be utilized in studies involving manipulation of the mosquito microbiota.

16 A MULTIMODAL VIRUS-HOST INTERACTOME PIPELINE AS A TOOL FOR VIRAL PREPAREDNESS

G. Dugied1, E. Laurent2, M. Attia1, JP. Gimeno2, M. Dos Santos1, S. Volant3, S. Van Der Werf4, A. Komarova1, Y. Sofianatos5, E. Coyaud2, C. Demeret*1
1Virology, Interactomics, RNA and Immunity, Institut Pasteur, Paris, France
2Protéomique Réponse Inflammatoire Spectrométrie de Masse - PRISM, University of Lille, INSERM, Lille, France
3Bioinformatics and Biostatistics Hub, Institut Pasteur, Paris, France
4Virology, Molecular Genetics of RNA Viruses, Institut Pasteur, Paris, France
5Institute for Fundamental Biomedical Research, Vari, Greece

We developed and innovative pipeline which both sketches the relative spatial organization of virus and host proteomes and identifies physical virus/host proteins contacts. Benchmarked with the proteins of SARS-CoV-2, this pipeline started by use of proximity-dependent biotinylation (BioID) to generate individual virus proximal interactomes. From these datasets, a 3D virus/host interaction map was modelled, positioning SARS-CoV-2 and host proteins within the cell volume. This 3D map highlights virus invasion of different cell territories and the coordinated hijacking of cellular machineries. Then, a subset of the viral proximal interactome has been probed for direct contacts with the viral proteins, by a semi-quantitative splitnanoluciferase assay. Such profiling the physical virus/host contacts demonstrated the accuracy of the 3D map spatial positioning and generated a solid framework for the structural modelling of several SARS-CoV-2 complexes. We have thus obtained high-confidence structures of virus/host complexes involving proteins that are essential for infection, representing as many candidate interfaces relevant for structure-driven screening of PPIs-disrupting compounds. The versatility of our pipeline for any emerging human pathogen and its applicability as soon as the genome of an emerging virus is sequenced make it a valuable tool for viral preparedness.

17 CHARACTERIZATION OF AHSV ANTAGONISTS OF THE IFN-I PATHWAY

P. Dujardin*, M. Lemesle, A. Fablet, G. Caignard, D. Vitour
UMR Virologie 1161 Anses-Inrae-EnvA, Maisons-Alfort, France

African horse sickness virus (AHSV), is an arbovirus that infects almost exclusively equids. Described as a hemorrhagic fever, African horse sickness is highly pathogenic in horses, with a case-fatality rate of up to 95%. AHSV belongs to the Orbivirus genus within the Sedoreoviridae family, and comprises 9 distinct serotypes. It is transmitted by hematophagous midges of the Culicoides genus, whose different species cover a large part of the planet. The establishment of the virus in areas not endemic to it, due to the global warming, has begun to alarm animal health authorities in many countries. Apart from the symptomatic effects of the disease, very little is known about the molecular mechanisms governing the infection, and in particular the modulation of the type 1 interferon (IFN-I) response by the virus. This project aims to reveal which AHSV proteins inhibit the IFN-I pathway, and to decipher the molecular level of action of those antagonists. Using reporter gene assays that enable the expression of the Firefly luciferase placed under the control of an IFN-B or ISRE promoter following activation of the IFN-I pathway by various agonists, we screened the entire AHSV ORFeome to discern the proteins that inhibit the activity of the reporter gene. Results show that NS3/A, NS4 and NS5 hamper the induction pathway, with NS4 acting upstream of IRF3 activation. NS4 also blocks the JAK/STAT signaling pathway, which makes it a serious proviral actor during the replication cycle. Further investigations are envisioned to understand the mechanisms of action of those antagonists.

18 POPULATION IMMUNITY AGAINST MOSQUITO-BORNE DISEASES IN NEW CALEDONIA AND VANUATU, PACIFIC REGION

K. Huet1, AF. Griffon1, A. Kalulu2, D. Hoinard3, W. Donald2, E. Bloch4, AC. Gourinat5, P. Guyant6, O. O'connor1, P. Domingue Mena7, C. Inizan1, M. White4, J. Vanhomwegen3, M. Dupont-Rouzeyrol*1
1URE Dengue et Arboviroses, Institut Pasteur de Nouvelle-Calédonie, Noumea, New Caledonia, France
2Ministry of Health, Port Vila, Vanuatu 3CIBU, Institut Pasteur, Paris, France
4Epidémiologie et Analyse des Maladies Infectieuses, Institut Pasteur, Paris, France
5Direction des Affaires Sanitaires et Sociales de la Nouvelle-Calédonie, Noumea, New Caledonia, France
6World Health Organization, Port Vila, Vanuatu 7Agence Sanitaire et Sociale de la Nouvelle-Calédonie, Noumea, New Caledonia, France

Arthropod-borne viruses (arboviruses) are one of the most important categories of emerging pathogen and are of public-health concern in the Pacific region as their occurrence has increased over the last decades probably due to climate change and human mobilities. In order to provide health security with elements to assess the risk of vector-borne diseases in New Caledonia and in Vanuatu, a seroprevalence survey was conducted in 2021-2023.
In New Caledonia, 750 healthy volunteers from 18 to 64 years old were included, and 1122 healthy volunteers from 5 to 80 years old were included for Vanuatu. Serum samples were tested for IgG against a range of arboviruses using the Luminex technology.
In New Caledonia, the results showed a 55% (95% CI 49.8-61%), 1.8% (95% CI 0.81-3.9%) and 11% (95% CI 8-15%) standardized seroprevalence of dengue (DENV), Zika (ZIKV) and Ross River virus (RRV) respectively. People living in the North and Loyalty Islands Province or people belonging to the Oceanian community have been significantly more exposed to DENV and RRV. In Vanuatu, results obtained showed a 51% (95% CI 45-58%), 2.6% (95% CI 1.2-5.4%) and 9.5% (95% CI 7.2-12%) standardized seroprevalence of DENV, ZIKV and RRV respectively. The 6-18 years old have been significantly less exposed to DENV compared to the other age categories. RRV seroprevalence was significantly higher in man, those aged 45-64 years or those living in Shefa and Sanma provinces. Furthermore, in both countries, the seroprevalence is nil for the West Nile virus, Japanese Encephalitis virus, Yellow fever virus, Usutu virus and chikungunya virus (CHIKV).
Apart from DENV, where about half of both populations have antibodies, population immunity is very low or nil for the other arboviruses tested. Interestingly, our results highlight an undetected silent circulation of RRV, which is concordant with the recent studies in Fiji and French Polynesia. Our study confirms that the CHIK outbreak that spread through the region 10 years ago did not affect these two countries. In a context of climate change and rapid spread of infectious diseases, our data suggests a significant risk for the populations if these pathogens were to be (re)introduced.

19 THREE-IN-ONE VACCINE: A SINGLE RECOMBINANT MEASLES VIRUS EXPRESSING THREE ARBOVIRUS ANTIGENS INDUCES ROBUST HUMORAL AND CELLMEDIATED IMMUNE RESPONSES, CONFERRING EFFECTIVE PROTECTION IN A MOUSE MODEL

P. Frantz*1-2, C. Ruffié3, C. Combredet3, V. Najburg1-3, E. Simard1-3, F. Tangy*1-2
1Laboratory Commune Institut Pasteur-Oncovita, Insitut Pasteur, Paris, France
2Oncovita, Paris, France
3Innovation Lab; Vaccines, Institut Pasteur, Paris, France

The measles vaccine (MV) delivery platform has undergone development from preclinical to clinical stages, demonstrating its ability to adapt rapidly and effectively to different pathogens. The live pediatric MV holds extensive history of safety and efficacy, along with its established large-scale manufacturing capacity. To further enhance the capabilities of MV vector, we have engineered an improved MV vector using a bacterial artificial chromosome (BAC) plasmid. With the stability of BAC plasmids, this new MV vector can now accommodate and maintain the expression of more than 7 kb of additional heterologous gene/s within a single rescued recombinant MV. Moreover, the incorporation of additional transcription unit sites enables the insertion of multiple additional genes in tandem into measles sequence. Our proof-of-concept demonstrated the successful construction of a combined MV vector that expresses three protective antigens derived from the Chikungunya virus (CHIKV), West Nile virus (WNV), and Zika virus (ZIKV), simultaneously. Immunization of mice with this replication-competent multivalent vaccine elicited robust immunogenicity to all three viruses, both humoral and cell-mediated immune responses, and conferred effective protection from individual challenges.

20

EMERGENCE OF CLADOPHIALOPHORA BANTIANA INFECTIONS IN FRANCE

O. Lortholary, D. Garcia Hermoso*
Institut Pasteur, Paris, France

Background: To circumvent understanding limitations about Cladophialophora bantiana phaeohyphomycosis, we reappraised the epidemiology, clinical presentation, therapeutic strategy in Metropolitan France and French overseas territories.

Methods: All cases were diagnosed and/or confirmed at the Institut Pasteur (Paris, France) between 2002 and 2022.

Findings: There were 23 patients (median age, 57 years). Until 2021, the annual number of cases evolved between zero and two, with six cases notified in 2022, the warmest year ever recorded in France. Central nervous system (CNS) involvement was observed in 15/23 (65%) patients (including three disseminated cases); skin, soft tissue, and osteo-articular infections in 7/23 (30%) and isolated lung infection in one case. Diabetes was observed in five cases, while any immunodepression factor was observed in fourteen. When considering only patients with CNS involvement, nine-month survival appeared higher in patients who underwent surgery (3/4 (75%) versus 3/11 (27%), p=0.24) and significantly in those treated during at least two weeks with liposomal amphotericin B + posaconazole and flucytosine (7/9 (78%) vs. 1/6 (17%), p=0.04). When focusing on patients with non-CNS involvement, 3/7 underwent major surgery and 6/7 survived. Two patients were treated with excision surgery alone (one with success, the other one was lost to follow up).

Interpretation: This study underscores, that clinical presentations and underlying medical conditions are more diverse than previously described. It also emphasizes the extreme severity of CNS location, with a two-thirds mortality rate. The prognosis improved when surgery was performed and triple antifungal therapy was administered.

21 PREVALENCE OF CAMPYLOBACTER INFECTION AND THE EMERGENCE OF MULTIDRUG-RESISTANT THERMOPHILIC CLONES AND THEIR ASSOCIATION WITH CLIMATE

M. Gharbi*, A. Maaroufi
laboratory of Epidemiology and Veterinary Microbiology, Institut Pasteur de Tunis, Belvedere., Tunisia

Thermotolerant Campylobacter is a major foodborne pathogen worldwide, leading to a significant human health burden. To obtain an overview of the occurrence and characteristics of thermophilic Campylobacters in avian environment Tunisia, we investigated a total of 328 isolates taken from chicken flocks. The spread of Campylobacter infections in relation to climate changes associated with seasonal variations were analyzed. Antimicrobial susceptibility testing was performed on all isolates according to the recommendation of the European Committee on Antimicrobial Susceptibility Testing guidelines. The detection of resistance genes was performed using polymerase chain reaction (PCR). Mutations in GyrA and the occurrence of RECmeABC efflux pump were determined by mismatch amplification mutation assay (MAMA) PCR and PCR, respectively. In addition, eleven isolates were selected to determine their clonal lineage by MLST.

Total prevalence of Campylobacter infection in broiler flocks was in the range of 22.4%, with a predominance of C. jejuni (69%), followed by C. coli (41%). A positive correlation has been observed between the degree of infection and warm climate changes. ($P < 0.001$). Antimicrobial susceptibility testing revealed very high resistance rates detected against macrolide, tetracycline, quinolones, and chloramphenicol, ranging from 88.6% to 100%. Lower resistance prevalence was noticed for B-lactams (47% and 61.4%) and gentamicin (12.9%). 17 R-type patterns were observed, and a common pattern was found in 30.3% of isolates. All isolates were multidrug-resistant. Molecular screening of the AMR gene revealed the predominance of the tet(O) and the cmeB genes (99%) among resistant isolates. The blaOXA-61 gene and the specific mutations in the 23S rRNA were detected in 87% and 73.5% of isolates, respectively. The A2075G and the Thr-86-Ile mutations were detected in 85% and 73.5% of macrolide and quinolone-resistant strains, respectively. The eleven isolates studied by MLST belonged to a new sequence type ST13450.

This study provides updates and new data on the emergence of Campylobacter infection and the emergence of multidrug-resistant thermophilic clones and their association with climate change in Tunisia, highlighting the need for better surveillance and rigorous regulation of antimicrobial use.

22 REGULATORY EVENTS GOVERNING HOST-C. ALBICANS INTERACTION: POTENTIAL IMPLICATIONS FOR WOUND HEALING

A. Ghoshal
Microbiology and Cell Biology, Indian Institute Of Science Bangalore, Bangalore, India

Candida albicans accounts for one of the most prevalent opportunistic communities associated with fungus mediated pathogenicity in immunocompromised individuals. It has been shown in literature that fungal pathogens, in particular C. albicans, are associated with chronic non healing wounds. However, detailed investigations have not been conducted. Wounds that exhibit impaired healing, including acute wounds and chronic wounds, frequently enter a state of pathological inflammation due to a slower, incomplete, or uncoordinated healing process that can result in permanent sepsis. Taking this problem into regard, our work aims to explore regulatory molecular mechanisms that may be primarily governing C. albicans mediated delayed wound repair. We have shown that regulation of genes which are key players in modulating homeostatic wound healing is perturbed both in vitro and in vivo by C. albicans infection. In literature, altered regulation of histone demethylase Kdm6a and a global transcription factor, CREB has been shown to be associated with healing wounds. We have elucidated that downregulation of Kdm6a and elevated expression of p-CREB in macrophages upon C. albicans infection is responsible for the deregulated state of key genes involved in wound healing and inflammation. Further, we have also shown that C. albicans regulates p-CREB by Cannabinoid Receptor 2 mediated signalling. Together, we believe that the pathogenic implications of Kdm6a and CREB in perturbing the regulation of key genes involved in wound healing, makes these factors critical targets for host-directed therapy for C. albicans mediated colonisation of wounds.

23 BACTERIOME COMPOSITION MODULATES VIRAL INFECTIONS IN DROSOPHILA MELANOGASTER

R. González*, J. Nigg, O. Romoli, M. Castelló-Sanjuán, H. Blanc, MC. Saleh
Saleh Lab, Institut Pasteur, Paris, France

The bacteriome (bacterial component of organism-associated microbes) plays a crucial role in shaping host-virus interactions. Despite the bacteriome's significant impact on viral infections, there are wide knowledge gaps regarding how its composition modulates host susceptibility to viruses. Our goal is to address this gap by defining the mechanisms of this modulation. To achieve this, we combined the genetic tractability of the fruit fly Drosophila melanogaster with its well-documented array of naturally associated bacteria and viruses.
Preliminary results have shown that flies colonized with a bacteriome rich in Lactiplantibacillus plantarum exhibited reduced accumulation of Drosophila A virus but showed increased host mortality from this virus. Here I present the individual modulation of viral infection by L. plantarum and Acetobacter pomorum, two bacterial species that dominate the fruit fly bacteriome at distinct temperatures. These findings highlight the complex interactions between the host, virus, and bacteriome, and opens new avenues for mechanistic insights into how the bacteriome influences virus accumulation and virulence.

24 DEVELOPMENT OF PEPTIDE INHIBITORS OF INFLUENZA VIRUS REPLICATION BY DIRECTED EVOLUTION

A. Florez-Prada1, B. Sépari1, C. Sturmach2, C. Bourgneuf2, N. Pautrieux1, P. Mas3, W. Burmeister1, T. Crépin1, R. Lartia1, D. Boturyn4, N. Laroui5, C. Pichon2, C. Isel2, N. Naffakh2, D. Hart*1-3
1IBS UMR5075 (Université Grenoble Alpes, CEA, CNRS), Grenoble, France
2Unité Biologie des ARN et Virus Influenza, Institut Pasteur, CNRS UMR 3569, Université ParisnCité, Paris, France
3ISBG UAR3518 (Univ. Grenoble Alpes, CNRS, CEA, EMBL), Grenoble, France
4DCM, UMR 5250 (Université Grenoble Alpes, CNRS), Grenoble, France
5INSERM UMS 55-ART ARNm (Université d'Orléans), Orleans, France

Influenza virus causes hundreds of thousands of deaths every year and can generate serious pandemics. Its high rate of genetic mutation limits the use of currently available antivirals and creates a demand for new drugs targeting alternative mechanisms. Hence, we are exploring new viral- and host-directed anti-influenza therapeutic strategies that could be active against a wide range of influenza viruses and be less prone to drug resistance.
We present our development of peptide inhibitors that block the assembly of key protein complexes necessary for influenza virus replication. The first complex targeted is the heterotrimeric influenza virus RNA-dependant RNA polymerase (FluPol) that catalyses transcription and replication of the viral genome. We are focusing on a highly conserved protein-protein interface within this complex, namely the PB1-PA interface, for which a natural peptide was previously shown to interfere with assembly. The second complex we are targeting is the host REDSMU1 complex, building on previous work showing that its transient destabilisation inhibits splicing of the NS1 viral mRNA and thus viral replication.
We built structure-guided phage display libraries of >108 random variants of natural interacting peptides and selected for high affinity binders to the partner domain. Multiple hits were characterised using ELISA, NGS and BLI, revealing alternative binding sequences that have never been observed naturally. For both systems, biophysical, X-ray crystallography and cellbased methods reveal how these synthetic peptides function. Chemical optimisation and vectorisation strategies are being explored.

25 ADAPTING INTERNET OF THINGS DEVICES FOR ENHANCED VITAL SIGNS DATA COLLECTION IN VIET NAM: A SYSTEMATIC REVIEW

N. Ho Xuan*, U. Phan Thi Ngoc
Pasteur Institute, Ho chi Minh, Vietnam

Introduction: Surveillance plays an important role in response to global health crises. In the Industry 4.0 era, the Internet of Things (IoT) has revolutionized healthcare, offering enhanced data collection for surveillance efficacy.
Context and Aim: This study aims to identify IoT devices for enhancing vital signs collection in line with the Vietnamese government's drive for digital healthcare.
Method: A semi-systematic review was conducted to explore the advantages and limitations of IoT devices. The study design adhered to the Preferred Reporting Items for Systematic Reviews and Meta-Analysis (PRISMA) 2020 statement and the Critical Appraisal Skills Programme assessment tools. The Case Fatality Rate (CFR) and common signs were analyzed using infectious disease data extracted from the Vietnamese Ministry of Health's annual reports for the years 2017 to 2022.
Findings: Out of 1441 articles, fifteen met the inclusion criteria. Four focused on standalone sensors and the remaining eleven explored embedded sensory devices. These articles underscored the accuracy, non-invasiveness, and real-time data monitoring capabilities of IoT devices. The IoT devices that acquire temperature and respiratory rate were determined for the Vietnamese context.
Innovative contribution: Adapting IoT devices is an optimal solution to improve surveillance and reduce pressure on the Healthcare Workforce. Therefore, resources should be allocated to invest in IoT devices.

26 A MULTICENTER, RANDOMIZED, DOUBLE-BLIND, CONTROLLED, PHASE III CLINICAL TRIAL (IMMUNOBRIDGING STUDY) OF INAVAC - VERO CELL INACTIVATED SARS-COV-2 VACCINE - IN HEALTHY POPULATION AGED 18 YEARS AND ABOVE IN INDONESIA - A PRELIMINARY REPORT

D. Husada*1-2, D. Tinduh1-3, L. Wulandari1-3, G. Soegiarto1-3, D. Puspitasari1-3, L. Kartina1-3, I. Moedjito1-3, F. Munawaroh1-3, A. Aryati1-3, J. Nugraha1-3, BE. Rahman1-4, N. Nasronudin1-4, RD. Puspita5, SG. Jati6, CS. Wahono7-8, FA. Rantam9, NT. Puspaningsih10, CR. Prakoeswa1-2
1Faculty of Medicine Universitas Airlangga, Surabaya, Indonesia
2Dr. Soetomo Hospital, Surabaya, Indonesia
3Dr. Soetomo Hospital, Surabaya, Indonesia
4Internal Medicine, Universitas Airlangga Hospital, Surabaya, Indonesia
5Dr. Soebandi Hospital, Jember, Indonesia
6Lung Hospital, Jember, Indonesia
7Internal Medicine, Faculty of Medicine
Universitas Brawijaya, Malang, Indonesia
8Internal Medicine, Saiful Anwar Hospital, Malang, Indonesia
9Institute of Tropical Diseases, Universitas Airlangga, Surabaya, Indonesia
10Universitas Airlangga, Surabaya, Indonesia

Influenza virus causes hundreds of thousands of deaths every year and can generate serious pandemics. Its high rate of genetic mutation limits the use of currently available antivirals and creates a demand for new drugs targeting alternative mechanisms. Hence, we are exploring new viral- and host-directed anti-influenza therapeutic strategies that could be active against a wide range of influenza viruses and be less prone to drug resistance.
We present our development of peptide inhibitors that block the assembly of key protein complexes necessary for influenza virus replication. The first complex targeted is the heterotrimeric influenza virus RNA-dependant RNA polymerase (FluPol) that catalyses transcription and replication of the viral genome. We are focusing on a highly conserved protein-protein interface within this complex, namely the PB1-PA interface, for which a natural peptide was previously shown to interfere with assembly. The second complex we are targeting is the host REDSMU1 complex, building on previous work showing that its transient destabilisation inhibits splicing of the NS1 viral mRNA and thus viral replication.
We built structure-guided phage display libraries of >108 random variants of natural interacting peptides and selected for high affinity binders to the partner domain. Multiple hits were characterised using ELISA, NGS and BLI, revealing alternative binding sequences that have never been observed naturally. For both systems, biophysical, X-ray crystallography and cellbased methods reveal how these synthetic peptides function. Chemical optimisation and vectorisation strategies are being explored.

27 RNA INTERFERENCE: PAVING THE WAY FOR A CHIKV VACCINE IN AEDES MOSQUITOES

E. Janssens*1, T. Teodoro1, M. Brustolin2, K. Bartholomeeusen1, R. Müller2, K. Ariën1
1Virology unit, Institute Of Tropical Medicine, Antwerp, Belgium
2Entomology Unit, Institute Of Tropical Medicine, Antwerp, Belgium

Chikungunya virus (CHIKV), anA edes mosquito-borne alphavirus, is of public health concern given its global spread observed. Current effective control strategies for CHIKV rely on vector management but fall short in terms of sustainability, specificity, and eco-friendliness. This research explores RNA-interference (RNAi) as a promising approach to target CHIKV in Aedes mosquitoes.

We hypothesized that exogenous delivery of CHIKV-specific dsRNA sequences primes the mosquito's natural antiviral immunity, thereby limiting viral replication upon CHIKV infection. In vitro experiments showed significant reduction of CHIKV replication in U4.4 cells treated with CHIKV-dsRNA, but not in RNAi-defective C6/36 cells or U4.4 cells treated with Dengue virus (DENV)-dsRNA.I n vivo studies delivering naked CHIKV-dsRNA through glucose feeding did not replicate the outcomes observedi n vitro. Chitosan-based nanoparticles (Ch-NPs) are being developed to improve dsRNA stability and cellular delivery to mosquito cells in vivo.

We will present recent findings on the optimization of Ch-NPs and potential for CHIKV replication controli n vivo. Future research will focus on enhancing dsRNA stability and delivery efficiency for practical field application.

28 RECAPITULATING MEMORY B CELL RESPONSES IN A LYMPHOID ORGAN-CHIP TO EVALUATE MRNA VACCINE BOOSTING STRATEGIES

R. Jeger-Madiot*1, D. Planas1, I. Staropoli1, H. Debarnot1, J. Kervevan1, H. Mary2, C. Collina1, B. F. Fonseca1, R. Robinot1, S. Gellenencourt1, O. Schwartz1, L. Ewart3, M. Bscheider4, S. Gobaa2, LA. Chakrabarti1
1Virus and Immunity Unit, Institut Pasteur, Paris, France
2Biomaterials and Microfluidics Core Facility, Institut Pasteur, Paris, France
3Emulate Inc, Boston, United States
4Roche Pharma Research & Early Development, Basel, Switzerland

Purpose: Predicting the immunogenicity of candidate vaccines and biologicals in humans based on animal model data remains a challenge. To address this issue, we developed a lymphoid organ-chip (LO chip) model based on a microfluidic chip seeded with human PBMC at high density within a 3D matrix.
Methods: The lower channel of an S1R chip (Emulate) was seeded with human PBMC at 6x108/mL within a collagen-based extracellular matrix, to mimic the high cellular densities characteristic of lymphoid tissue. The upper chip channel, used as a vascular-like compartment, was continuously perfused with nutrients and antigens for 6 to 14 days.
Results: Perfusion of the SARS-CoV-2 Spike protein mimicked a vaccine boost by inducing a massive amplification of Spike-specific memory B cells, plasmablast differentiation, and Spike-specific antibody secretion. The magnitude of Spike- specific B cell amplification in the LO chip, with a median 32.7x increase at d6, was higher than in 2D and 3D static cultures, highlighting the added value of a dynamically perfused culture. Features typical of lymphoid tissue, including the formation of activated CD4+ T cell/B cell clusters, the induction of ICOS in CD4+ T cells within the clusters, CXCL13 chemokine secretion, and the emigration of matured plasmablasts, were recapitulated in the LO chip. Importantly, meyloid cells were competent at capturing and expressing mRNA vectored by lipid nanoparticles, enabling the assessment of responses to mRNA vaccines perfused in the LO chip. Comparison of responses to Wuhan monovalent and Wuhan/Omicron bivalent mRNA vaccine boosts showed equivalent induction of Omicron neutralizing antibodies, suggestive of immune imprinting, as reported in vivo.
Conclusion: We developed a versatile lymph node-on-chip system suitable for the rapid evaluation of B cell recall responses. The model is responsive to protein and mRNA-encoded antigens, highlighting its potential in the preclinical evaluation of vaccine boosting strategies.

29 ANTICANDIDAL GUIDED ISOLATION AND UHPLC-ORBITRAP-ESIMS/MS ANALYSIS OF MONOTES KERSTINGII (DIPTEROCARPACEAE) LEAVES AND ROOTS

S. Kache Fotsing*1, B. Ngadjui Tchaleu1, B. Ndjakou Lenta2, N. Sewald3, G. Wabo Fotso1
1Department of Organic Chemistry, University of Yaounde 1, Yaoundé, Cameroon
2Department of Chemistry, Higher Teacher Training College, University of Yaoundé 1, Yaoundé, Cameroon
3Department of Organic Chemistry, University of Bielefeld, Bielefeld, Germany

The rise of Candida drug resistance relies on the main challenging treatment, needing the search for alternative options. Medicinal plants can be used as an appropriate approach for such treatment. This study was investigated the anticandidal properties of Monotes kerstingii used to treat skin infections in Cameroonian pharmacopeia. Monotes kerstingii root and leaves extracts were prepared and screened against Candida albicans, Candida glabrata, Candida krusei, Candida parapsilosis, and Candida tropicalis using microdilution method following by liquid-liquid partitioning, purification, and characterization of metabolites. The pure compounds were screened for their anticandidal and cytotoxic properties. The potent and major metabolites were selected for the pharmacomodulations and chemical transformations respectively. The metabolome of M. kerstingii was established using ultra-high-performance liquid chromatography- Orbitrap-ESI-LIT-MS/MS coupled with computational tools. The oral acute toxicity of the potent extract was then assessed using the limit test doses. All the investigated extracts were effective against tested Candida spp. with the MIC ranging from 3.9 to 2000 µg/mL with the hydroethanolic leaf extract being the potent one (MIC of 3.9 µg/mL). The tested extracts were safe on Raw and Vero cell lines. Twenty-eight (28) metabolites were isolated and fully characterized. Among these compounds, the stilbene 1-{2-hydroxy-6-[(1E)-2-(4-hydroxyphenyl) ethenyl]-4-methoxyphenyl}-2-methyl-1-propanone was found to be the most effective against the investigated Candida species, with MICs ranging from 7.81 to 15.62 µg/mL and non-cytotoxic on Vero and Raw cell lines (CC50>100 µg/mL). The pharmacomodulation and chemical transformation led the synthesis of eight new bibenzyl derivatives. The UHPLC-Orbitrap-ESIMS/MS analysis led the annotations of metabolites spanning to stilbenes, stilbene-coumarins, terpenoids, flavonoids, lipid and lipid like, alkaloid, and glycosides in the extracts. The LD50 values of the extracts were up to 2000 mg/kg of body weight, indicating low toxicity. These findings justify the uses of Monotes kerstingii in Far North region and suggest that it can be used as started point for the development of new and safe phytodrug for the suitable management of Candidiasis.

Keywords: Monotes kerstingii, anticandida., metabolomic, stilbene, bibenzyl derivatives

30 CHIKUNGUNYA SEROPREVALENCE, FORCE OF INFECTION, AND PREVALENCE OF CHRONIC DISABILITY AFTER INFECTION IN ENDEMIC AND EPIDEMIC SETTINGS: A SYSTEMATIC REVIEW, META-ANALYSIS, AND MODELLING STUDY

H. Kang*1, M. Auzenbergs1, H. Clapham2, C. Maure3, J. Kim3, H. Salje4, C. Taylor5, A. Lim1, A. Clark1, WJ. Edmunds1, S. Sahastrabuddhe3-6, O. Brady1, K. Abbas1-7
1Epidemiology and Population Health, London School of Hygiene and Tropical Medicine, London, United Kingdom
2National University of Singapore, Singapore, Singapore
3International Vaccine Institute, Seoul, South Korea
4Cambridge University, Cambridge, United Kingdom
5GAVI, Geneva, Switzerland
6Centre International de Recherche en Infectiologie, Université Jean Monnet, Université Claude Bernard Lyon, INSERM, SaintEtienne, France, Lyon, France
7Tropical Medicine and Global Health, Negasaki University, Nagasaki, Japan

Background: Chikungunya is an arboviral disease transmitted by Aedes aegypti and Aedes albopictus mosquitoes with a growing global burden linked to climate change and globalisation. We aimed to estimate chikungunya seroprevalence, force of infection (FOI), and prevalence of related chronic disability and hospital admissions in endemic and epidemic settings.

Methods: In this systematic review, meta-analysis, and modelling study, we searched PubMed, Ovid, and Web of Science for articles published from database inception until Sept 26, 2022, for prospective and retrospective cross sectional studies that addressed serological chikungunya virus infection in any geographical region, age group, and population subgroup and for longitudinal prospective and retrospective cohort studies with data on chronic chikungunya or hospital admissions in people with chikungunya. We did a systematic review of studies on chikungunya seroprevalence and fitted catalytic models to each survey to estimate location-specific force of infection. We performed a meta-analysis to estimate the proportion of symptomatic patients with laboratory-confirmed chikungunya who had chronic chikungunya or were admitted to hospital following infection.

Findings: We identified 60 studies with data on seroprevalence and chronic chikungunya symptoms done across 76 locations in 38 countries, and classified 17 (22%) of 76 locations as endemic settings and 59 (78%) as epidemic settings. The global long-term median annual FOI was 0·007 (95% uncertainty interval [UI] 0·003–0·010) and varied from 0·0001 (0·00004–0·0002) to 0·113 (0·07–0·20). The highest estimated median seroprevalence at age 10 years was in south Asia (8·0% [95% UI 6·5–9·6]), followed by Latin America and the Caribbean (7·8% [4·9–14·6]), whereas median seroprevalence was lowest in the Middle East (1·0% [0·5–1·9]). We estimated that 51% (95% CI 45–58) of people with laboratory-confirmed symptomatic chikungunya had chronic disability after infection and 4% (3–5) were admitted to hospital following infection.

Interpretation: We inferred subnational heterogeneity in long-term average annual FOI and transmission dynamics and identified both endemic and epidemic settings across different countries. Long-term average annual FOI was higher in epidemic settings than endemic settings. However, long-term cumulative incidence of chikungunya can be similar between large outbreaks in epidemic settings with a high FOI and endemic settings with a relatively low FOI.

31 DESIGNING AND TESTING A SIMPLE DIAGNOSTIC TOOL FOR QUICKLY IDENTIFYING WEST NILE VIRUS IN CLINICAL SETTINGS

M. Khedhiri
Clinical Labroratory, Institut Pasteur de Tunis, Tunis, Tunisia

West Nile Virus (WNV) causes a serious public health concern in many countries around the world. Virus detection in pathological samples is a key component of WNV infection diagnostic, classically performed by realtime PCR. In outbreak situation, rapid detection of the virus, in peripheral laboratories or at point of care, is crucial to guide decision makers and for the establishment of adequate action plans to prevent virus dissemination. Here, we evaluate a Loop-mediated isothermal amplification (LAMP) tool for WNV detection. Amplifications were performed comparatively on extracted viral RNA and on crude samples using a classical thermal cycler and a portable device (pebble device). qRT-PCR was used as gold standard and two sets of urine samples (n = 62 and n = 74) were used to evaluate the retained amplification protocols and assess their sensitivity and specificity. RT-LAMP on RNA extracts and crude samples showed a sensitivity of 90% and 87%, respectively. The specificity was 100% for extracts and 97% for crude samples. Using the device, the RT-LAMP on extracted RNA was comparable to the gold standard results (100% sensitivity and specificity) and it was a bit lower on crude samples (65% sensitivity and 94% specificity). These results show that RTLAMP is an efficient technique to detect WNV. RT-LAMP provides a rapid, sensitive, high-throughput and portable tool for accurate WNV detection and has potentials to facilitate diagnostic and surveillance efforts both in the laboratory and in the field, especially in developing countries.

32 THE PROFILE OF VIRAL AND BACTERIAL PATHOGENS IN TICKS COLLECTED FROM MIGRATORY AND NON-MIGRATORY BIRDS CAPTURED FOR SEASONAL RINGING

K. Korzekwa1, P. Gorski2, J. Rapczynski2, K. Bylinska1, P. Baska1, M. Krzyzowska*1
1Military Institute of Hygiene and Epidemiology, Warsaw, Poland
2Warsaw University of Life Sciences, Warsaw, Poland

Background and Aims: In the temperate zone of Europe, pathogens transmitted by hard ticks (Ixodidae) are responsible for the majority of the vector-borne diseases. Migratory birds are long-known carriers of ticks, most importantly Hyalomma species. The aim of this work was to access the profile of the vector-borne viral and bacterial pathogens in ticks collected from migratory and non-migratory birds captured for seasonal ringing.
Methods: Birds mist-netted at the ringing station were examined for the presence of ticks, in May and June 2023/2024. Collected ticks were identified morphologically and genetically (sequencing), and next subjected to RNA and DNA isolation. Presence of Borrelia spp., Anaplasma phagocitophylum, Coxiella burnetii, Rickettsia spp., Tick-borne encephalitis virus (TBEV) and Crimean Congo haemorrhagic fever virus (CCHFV) was examined by qPCR and sequencing.
Results: Approximately 1000 Ticks were collected from migratory (Acrocephalus schoenobaenus, Acrocephalus palustris, Acrocephalus scirpaceus, Erithacus rubecula, Hippolais icterina, Phylloscopus collybita, Phylloscopus trochilus, Sylvia communis, Sylvia atricapilla) and non-migratory (Parus major, Turdus merula, Turdus philomelos) birds during two seasonal ringing at multiply sites. Collected ticks included larvae, nymphs and adults belonging mostly to Ixodes spp., I. ricinus, I. arboricola but we also identified 4 Hyalomma species (H.migrans, H. dromaderi). Ticks from migratory birds were single-positive for Borrelia spp., Erlichia sp., Rickettsia sp. and CCHFV (only Acrocephalus palustris - one case). Nonmigratory birds showed the presence of mulitply ticks multi-positive for several pathogens (Borrelia spp., Erlichia sp., Rickettsia spp., Anaplasma phagocitophylum, Coxiella burnetti, and TBEV).
Conclusions: Our results showed that common non-migratory birds can carry multiply ticks containing at least one bacterial pathogen. Therefore, we postulate that non-migratory birds should also be monitored as the source of vector-borne diseases of viral and bacterial origin. The presence of ticks from the genus Hyalomma idicates the risk of carrying CCHFV into the eastern Europe, if the climate change enables hyalomma species to survive and undergo metamorphosis during one summer season.
This research was funded by the Ministry of Defense project no. 33000228382/DWSZdr/2024/ZAG

33 SMALLPOX-VACCINATED INDIVIDUALS PRESERVE LONG-TERM IMMUNOLOGICAL MEMORY AND MOUNT SEROLOGICAL REACTIVITY AGAINST SELECTED MONKEYPOX ANTIGENS

K. Korzekwa, M. Krzyzowska*
Military Institute of Hygiene and Epidemiology, Warsaw, Poland

Purpose: Following the global eradication of smallpox, monkeypox virus (MPXV) has emerged as the most critical orthopoxvirus (OPXV) for public health. MPXV is endemic in certain parts of Africa, but single cases of MPXV infection are also noticed in Europe. Vaccination against smallpox with vaccinia virus (VACV) has been shown to protect from MPXV infection but it had been stopped in Europe in early 80's. The aim of this work was to access memory to smallpox vaccination and cross-reactivity to monkeypox antigens in population of individuals with known medical history of comorbidities.
Methods: Individuals aged 19-60 with or without smallpox vaccination were bled and the blood was used to isolate serum and PBMCs. Serological status to VACV was checked by seroneutralisation and in-house ELISA. MPXV serological response was measured using single antigens (A29, A35R and H3L) as well as pooled antigen ELISAs. PBMCs were assessed for MPXV and VACV-specific B cells using ELISPOT test, VACV-specific tetramers were used to identify possible T cell memory in circulatory PBMCs.
Results: Individuals vaccinated against smallpox and without selected comorbidities such as diabetes and autoimmunological diseases showed good seroneutralisation activity against VACV (approx. 80% of population over 45 years of age) and positive reaction to A35 antigen of MPXV. Sera from vaccinated and MPXV-positive individuals did not differ in seroneutralisation activity from MPXV-negative vaccinees. Unvaccinated individuals (below 45 years), positive to MPXV antigens, showed mild cross-reactivity in seroneutralisation tests with VACV. Activation of B cells upon contact with VACV antigens, but not with MPXV, was demonstrated for some smallpox-vaccinated individuals.
Conclusion: Smallpox vaccination seems to last with age in individuals without comorbidities and allows to mount serological cross-reactivity against selected MPXV antigens. However, MPXV infection and smallpox vaccination induce shared but different serological reactivity towards poxvirus antigens.
This research was funded by the Ministry of Defense project no. 33000228382/DWSZdr/2024/ZAG

34 ANTIBIOTIC TREATMENT CAN EXCISE THE ISABA125 TRANSPOSON ASSOCIATED WITH BLANDM- SH BLE ALLELE FROM THE GENOME OF ENTERIC PATHOGENS THROUGH XER/INTEGRASE RECOMBINATION MECHANISM

S. Kumari
FGL INDIA, THSTI, Faridabad, India

Background: Transposons drive the emergence of multidrug resistance in diverse bacterial pathogens, yet the mechanisms are poorly characterized. The ISAba125 a non-viral integrase transposon propagates resistance to the antibiotic beta-lactam used for severe drug-resistant infections. A prominent IS30-like ISAba125, which is a major source of transfer of blaNDM sh-ble resistance in clinical Carbapenem-resistant Enterobacteriaceae (CRE) and others. As one of the leading causes of hospital-acquired infections, causes diverse, difficult to treat infections. Transfer of blaNDM sh-ble resistance via ISAba125 has already been observed to various genera. which is concerning as carbapenem is commonly used as a last resort antibiotic in the treatment of drug-resistant infections.

Method:

1. To facilitate the transposon encoded functional studies on the IS30/ISAba125 transposons, a chromosomally intact resident of the Providencia stuartii, along with blaNDM sh-ble resistance genes as a selection marker together with its terminal invert repeats (TIRs) were used to construct a donor vector (pBD60 an integrative vector) to monitor its integration/excision efficiency in the V. cholerae (N16961) and E. coli (ATCC 25922) host genome.
2. Furthermore, the frequency of excisions of blaNDM- sh ble allele from the genome of the bacterial host was determined by giving a sublethal dosage of therapeutically relevant antibiotics.
3. And by using plasmid curing, excision assay, PCR, and antibiotic profiling assay the mobility function of IS30/ ISAba125 element was monitored.

Results:

1. Reporter strains carrying distinct combinations of other transposons along with IS30/ISAba125, demonstrated significantly diverse potential of the host organism to retain the plasmid following plasmid curing.
2. Further, through excision assay it was observed that IS30/ISAba125 linked with blaNDM sh-ble allele can excise from the genome of V. cholerae with the help of an integration module (Terminal invert repeats).
3. To our surprise, the MIC concentration of gentamicin was found to be higher for the single copy of IS30/ISAba125 linked to the blaNDM sh-ble resistance gene than with the two copies of IS30/ISAba125 present along with the resistance gene.

Conclusion: Detection and characterization of functional MGEs, especially in clinical isolates, would increase us understanding of the underlying pathways of transposition and recombination that would further allow us to determine interventional strategies to interrupt this process. It may also lay the foundation for the development of novel antibiotic adjuvants for targeting MGEs that can function as broad-acting resistance breakers.

35 MEDILABSECURE A ONE HEALTH NETWORK TO IMPROVE PREPAREDNESS AND RESPONSE CAPACITIES TO EMERGING VECTOR-BORNE DISEASES INCREASED BY ENVIRONMENTAL AND CLIMATE CHANGE

V. Lagal*1, JC. Manuguerra1, MA. Jiménez2, F. Fournet3, MG. Dente4, P. Calistri5, G. Hendrickx6, M. Seguy1
1Institut Pasteur, France
2CSIC-INIA, Madrid, Spain
3IRD, Montpellier, France
4Istituto Superiore de Sanita, Roma, Italy
5IZS-Teramo, Teramo, Italy
6Avia-GIS, Zoersel, Belgium

The geographical distribution and incidence of vector-borne diseases is increasing favoured by environmental degradations and climate change. The implementation of an integrated surveillance is of paramount importance to efficiently prevent vector-borne diseases. MediLabSecure is a capacity-building project funded by the European Commission that aims at reinforcing a OH network of national reference laboratories and public health institutions to improve preparedness and response capacities to vector-borne diseases, in 22 EU neighbouring countries of the Mediterranean, Balkans, Black Sea and Sahel regions.

The main lines of action are capacity building through training activities and multisectoral networking, both centred on the promotion of the added value of a One Health approach.

The key successes of the project are: i) the setting up of rapid detection capacities in case of emergence/re-emergence and epidemics ii) the strengthening of identification, mapping, and control capacities for vectors of interest. iii) the production of 19 operating procedures and 5 tools for vector identification iv) the formulation of recommendations to improve the integration of data between sectors for risk assessment and in national surveillance plans v) the organization of 5 global and regional meetings to foster regional and multisectoral networking and promote OH added value.

MediLabSecure is now a well-established OH network in the peri Mediterranean region bringing together 111 national reference laboratories and public health institutions from the human and animal health sector; and gathering more than 200 multidisciplinary experts. The main achievement in terms of detection capacities, risk mapping and intersectoral networking is the demonstration of how concrete actions can lead to a successful OH implementation approach. The network is now ready for further development to empower members by promoting incountry initiatives and by supporting the OH advocacy to national stakeholders to leverage the political engagement.

This abstract was produced with the financial support of the EU.

36 IN-HOST EVOLUTION OF YERSINIA ENTEROCOLITICA DURING A CHRONIC HUMAN INFECTION

C. Savin1-2, P. Lê-Bury*1-3, J. Guglielmini4, T. Douché5, R. Buzelé6-7, C. Le Brun6, F. Bastides7, M. François8, B. Birmelé8, L. Guichard1-2, N. Cabanel1-2, L. Dortet3-9, M. Matondo5, O. Dussurget1, E. Carniel1-2, P. Lanotte6-10, J. Pizarro-Cerdá1-2
1Yersinia Research Unit, Institut Pasteur, Université Paris Cité, Paris, France
2Yersinia National Reference Laboratory, Institut Pasteur, Université Paris Cité, Paris, France
3Center for Immunology of Viral, Autoimmune, Hematological and Bacterial Diseases (IMVAHB/IDMIT), Université Paris Saclay, Inserm, CEA, Fontenay-Aux-Roses, France
4CNRS USR 3756, Biostatistics and Bioinformatics Hub, Institut Pasteur, Université Paris Cité, Paris, France
5CNRS UAR2024, Proteomic Platform, Mass Spectrometry for Biology Unit, Institut Pasteur, Université Paris Cité, Paris, France
6Service de Bactériologie-Virologie, CHRU de Tours, Tours, France
7Service de Médecine Interne et des Maladies Infectieuses, CHRU de Tours, Tours, France
8Service d'Hémodialyse, CHRU de Tours, Tours, France
9Centre National de Référence Associé de la Résistance aux Antibiotiques, Le Kremlin-Bicêtre, France
10UMR1282, ISP, INRA, Université de Tours, Tours, France

We characterized four Yersinia enterocolitica clonal isolates from successive bacteremia episodes that evolved within a 75-years-old patient in the span of 14 years. Pan-genome analysis and genome comparison showed that their common evolution was characterized by 41 small insertion/deletion events, loss of three large DNA fragments and mutations in 140 genes. A phylogenetic analysis by maximum likelihood identified two genes presenting a positive selection signal, suggesting that these mutations provided a survival advantage to bacteria during chronic infection. Quinolone resistance in the last two isolates was acquired through a so far undescribed deletion in the gyrA gene. Mass-spectrometry analysis revealed a strong proteome remodeling in the last two isolates which was correlated with a truncation in the stringent response regulator DksA. A reduced carbon, energy and purine metabolism supports their severe growth defects in vitro. 3rd-generation cephalosporin resistance of the last isolate was correlated with a truncation of OmpF, the main porin translocating antibiotics through the outermembrane, as well as an increased production of BlaA and AmpC B-lactamases. This is the first report of genetic and phenotypic changes associated to within-host adaptation of a pathogenic Yersinia species under antibiotic pressure.

37 SEROPREVALENCE OF CRIMEAN-CONGO HEMORRHAGIC FEVER AND ASSOCIATED FACTORS IN CATTLE AND ANIMAL WORKERS IN CAMEROON: NIHARBOCAM STUDY

G. Machuetum*1-2, M. Souleymanou1, J.B. Tchatchueng-Mbougua1, D. Djuicy1, G. Essima1, L. Mounchili1, M. Yonga1, C. Nsangou1, R. Poueme1, B. Kamgang3, A. Alkaissou4, A. Sakuntabhai5, K. Koro2, P.A. Tagnouokam-Ngoupo1, R. Njouom1
1Virology, Centre Pasteur du Cameroun, Yaoundé, Cameroon
2University of Douala, Douala, Cameroon
3Centre for Research in Infectious Diseases, Yaoundé, Cameroon
4Ministry of Livestock, Fisheries and Animal Industries, Yaoundé, Cameroon
5Institut Pasteur Japan, Tokyo, Japan 6Laboratoire National Vétérinaire, Garoua, Cameroon

Background: Crimean-Congo haemorrhagic fever (CCHF) is a severe zoonotic disease transmitted by ticks and endemic in several regions of the world, including Africa. Recently, high seroprevalence has been reported in cattle in Cameroon. Although the observed seroprevalence is high in cattle, little is known about the epidemiological status of animal workers. The aim of this study was to determine seroprevalence of CCHFV and associated factors in cattle and animal workers in two regions of Cameroon.

Methods: Between 2022 and 2023, blood samples were collected from cattle and humans including, breeders, slaughterers, butchers and veterinarians in slaughterhouses, farms and markets in the Centre and North regions of Cameroon. Serum was analyzed using the Enzyme-Linked Immunosorbent Assay (ELISA) technique to the detect anti-CCHFV IgG antibodies. Socio-demographic data and the ELISA results were statistically analyzed using R Software Version 4.1.

Results: Overall seroprevalences were 60.2% (649/1078) and 4.8% (34/706) in cattle and humans respectively. In cattle, seroprevalence was higher in the Centre region (78.8%) than in the North region (48.4%) ($p<0.001$), while no difference was observed in both regions in humans (5.2% vs 4.0 %;) ($p=0.47$). Seroprevalence in the rainy (64.0%) and dry (55.6%) seasons was almost similar ($p=0.005$). No significant difference was observed with gender in both study populations. Multiple regression analysis showed that cattle aged ≥4 years old [ORa = 3.20 (95% CI: 1.77-.5.85)] and collected in the Centre region [ORa = 3.41 (95% CI: 1.23–9.12)] were significantly associated with CCHFV seroprevalence in cattle.

Conclusion: Despite the low seroprevalence observed in animal workers, the results of our study nevertheless confirm the presence of anti-CCHFV IgG antibodies in cattle and animal workers in Cameroon. CCHFV is likely endemic in Cameroon, although no clinical case has been reported.

38 IDENTIFICATION OF HUMAN AND PORCINE INTERFERON RESPONSE EFFECTORS WITH ANTIVIRAL ACTIVITY AGAINST HEV-3 INFECTION

A. Marcadet-Hauss*, S. Gellenoncourt, M. Pellerin, N. Pavio, V. Doceul
INRAE, ENVA, ANSES, UMR Virologie 1161, Maisons-Alfort, France

Hepatitis E virus (HEV) is a major cause of enterically transmitted viral hepatitis worldwide. Four main genotypes circulate in humans (HEV-1 to -4). HEV-3 and -4 are zoonotic, whereas HEV-1 and -2 circulate only in human. Swine are the main reservoir of zoonotic HEV that is transmitted mainly via the foodborne route. In France, zoonotic HEV represents a significant public health and food safety problem. The interferon (IFN) response is the first line of defense against pathogens leading to the expression of many IFN-stimulated genes (ISG) establishing an antiviral state within the cell. The objective of this project is to identify and characterize effectors of the host IFN response that have antiviral activity against HEV. We also aim to determine whether their antiviral properties depend on the species (human and swine) and genotype (HEV-1 and HEV-3) involved. To achieve this goal, we have overexpressed more than 40 ISGs from different species (human and swine) in different human cell lines (HepaRG, A549-D3 and HepG2/C3A) using lentiviral vectors before infecting them with HEV-3. The impact of overexpression of these ISG on HEV-3 infection was determined by measuring the amount of HEV-3 genome copies by RT-qPCR and the transduction efficacy was monitored by flow cytometry through reporter gene expression (RFP). We found that RIG-I and IRF-1 interfere with HEV-3 replication as reported previously in the literature. Other ISG candidates with anti-HEV properties were also identified and are now being further characterized. Overall, this work will highlight how the IFN response might influence inter-species transmission of HEV.

39 EFFECTS OF ANGIOTENSIN CONVERTING ENZYME (ACE2) POLYMORPHISMS IN THE DISEASE SEVERITY DURING TUBERCULOSIS AND COVID-19 COINFECTION IN CAMEROON

N. Masumbe Palmer1, J. Assam Assam2, J. Taya Fokou3, E. Tchoupe Kamoua1, K. Mary Ngongang*2
1Department of biochemistry., Molecular diagnostics research group, University of Yaounde 1, Yaounde, Cameroon
2Microbiology ., Molecular diagnostics research laboratory, University of Yaounde 1, Yaounde, Cameroon
3Faculty of medecine and biomedical science, University of Yaounde 1, Yaounde, Cameroon

Background: Many similarities exist between Covid-19 and Tuberculosis (TB) pathogenesis. There is higher co-expression of angiotensin-converting enzyme 2 (ACE2), the entry receptor for SARS-CoV-2 in the lung of TB-infected. ACE 2 genes mutations could alter disease severity in TB/Covid-19 co-infected patients. The present study sought to identify single nucleotide polymorphisms (SNPs) on ACE2 gene and determine the severity of the disease in TB and covid-19 co-infection.

Methods: Participants above ten years, presenting an acute respiratory illness and at least one sign/symptom of respiratory disease were included in this study. 85 participants were retained as convenient sampling during the Covid-19 pandemic from March 2020 to December 2022. Six (6) most frequent SNPs associated with Covid-19 infection were also identified on ACE 2 gene and using Taqman RT-PCR. Nasopharyngeal swabs, sputum and blood samples were collected from each consenting participant. In order to detect cases of Covid-19, RDT and qualitative real-time PCR was carried out on nasopharyngeal samples. TB was tested on participants' sputum using microscopy and RT-PCR. ACE 2 polymorphisms amongst our study population were detected using TaqMan SNP Genotyping Assay after extraction of human DNA. The polymorphisms observed were either wild, heterozygous or mutant. Disease severity was evaluated by measuring liver (ALT and AST) and kidney (UREA and CREA) biomarker levels. Participants data were collected and entered in redcap. The data collected were analysed using Graphpad Prism version 9 software.

Results: We included 54 (63.5 %) males and 31 (36,5 %) females. The average age of the study population was 40 years. Participants were distributed into four clusters, 25 (29,4 %) Covid-19+, 24 (28 %) Tuberculosis+, 21 (24,7 %) Covid-19/Tuberculosis+ and 25 (29,4 %) Negative controls. A total of 6 different mutations (rs2285666, rs4240157, rs4646140, rs147311723, rs2074192 and rs4646179) were identified for the ACE 2 gene. The frequency of ACE 2 mutations was considerably higher in TB and TB/Covid-19 patients than in the other 2 groups. No mutation was observed in the negative control group. There was significant variation in liver and kidney function biomarkers across the 4 groups.

Conclusion: The above findings revealed that ACE 2 mutations observed in TB/covid-19 co-infection was a result of increase in disease severity. This emphasizes the role of considering TB/Covid-19 co-infection in the diagnostics of severe cases as it may have implications on patient's treatment outcome.

Keywords: Covid-19, Tuberculosis, disease severity, mutations.

40

MALARIA AND CLIMATE CHANGE A GROWING THREAT TO PUBLIC HEALTH IN NIGER

D. Médard*, AZ. Abdoussalam Zakari, ZM. Zaneidou Mamane, AE. Adehossi Eric, RJ. Ronan Jambou
1Université Abdou Mmoumouni, Niamey, Niger (The)
2Epicentre, Niamey, Niger (The)
3Université Nazi Boni, Bobo Dioulasso, Burkina Faso 4CERMES, Niamey, Niger (The)
5Institut Pasteur Paris, Paris, France
6Direction de la Surveillance et de la Riposte aux Epidémies, Niamey, Niger (The)

Niger is an arid country where the seasonal presence of water in the rainy season creates favorable conditions for the reproduction of malaria vectors, arboviruses and tick-borne diseases. Despite its Sahelian setting, the region is one of the top ten countries reporting cases of malaria. Climate change is associated with an increase in global rainfall, but in the form of violent climatic events. As a result, transmission is perpetuated by the persistence of residual pools or irrigated perimeters. From September onwards, Anopheles colonize most of the breeding sites, making Niger a high-risk area for malaria transmission and a new endemic zone.

Methodology: this study analyzes routine malaria retrospective data from the last five years (2017-2021) collected by the Ministry.

Results: The average annual number of malaria cases in Niger is 3,542,166±714,343, with an average of 3,765.6±866.99 deaths per year. The average annual growth rate of cases is 8.49% (Mann-Kendall), associated with an increase of 0.001037 deaths per additional case. Severe malaria in children under the age of 5 accounted for 10.75% of cases, and 11.56% of cases in those aged 5-10, underlining an equal risk for both age groups. This should encourage the extension of malaria protection to the 5-10 age group. Climate change is rapidly altering ecosystems. Malaria now occurs late in the dry season until February-March in Niger, and treatment cycles should be considered during the dry season. Similarly, this strategy should be extended to the northern Saharan zones, which receive less than 300 mm of rainfall a year, for children under five, and also to older children to continue protecting them. These changes in biotopes are also associated with changes in vector species, with the rapid return of Anopheles funestus to the Sahel, but above all with the invasion of West and Central Africa by An stephensis.SMC contributed to a 55% and 73% reduction in uncomplicated malaria, and a 42% to 48% reduction in the incidenc of severe malaria.

Conclusion: Despite the country's desert aspect, vulnerable populations in Niger pay a heavy price for malaria. Climate change favors the regular occurrence of malaria epidemics in this country.

Keywords: Malaria, Niger, climate change, threat

41 UNRAVELING THE BIOACTIVE POTENTIAL OF CAMEROONIAN MEDICINAL PLANTS WITH ANTI-SHIGELLA AND ANTIOXIDANT ACTIVITY, UHPLC-LIT-MS/MS FINGERPRINTS, PREDICTION OF PHARMACOKINETICS, AND DRUG-LIKENESS

Y. Melogmo Dongmo*1, B.M. Tchatat Tali1, D. Dize1, C.D. Jiatsa Mbouna1, S. Kache Fotsing2, K. Lunga Paul1, F. Fekam Boyom1
1Department of Biochemistry, Laboratory for Phytobiochemistry and Medicinal plants studies, University of Yaoundé 1, Yaoundé, Cameroon
2Department of Organic Chemistry, Faculty of Science, University of Yaoundé 1, Yaoundé, Cameroon

Shigella is a significant public health concern, causing 700,000 deaths annually. The rise of multidrug-resistant Shigella makes treatment challenging. To address this, exploring medicinal plants used to treat dysentery, and diarrhea in endemic regions could be appropriate option. This study aims to investigate the anti-Shigella and antioxidant properties of some Cameroonian medicinal plants, emphasizing the pharmacokinetic and drug-likeness properties of the identified chemicals. Plants were selected based on their ethnopharmacological uses and the literature. Crude aqueous, ethanolic, methanolic, and hydroethanolic (30:70, v/v) extracts were prepared and screened for their anti-Shigella activity and cytotoxicity against Vero and Raw cells using microdilution and resazurin-based methods, respectively. The antioxidant activities of potent extracts were evaluated using DPPH, ABTS, NO, and FRAP scavenging assays followed by a killing kinetics study. The chemical profile of potent extracts was performed using the UHPLC-LIT-MS/MS and the pharmacokinetic properties, druglikeness, and likely molecular targets of the chemical scaffolds identified were predicted using SwissADME and SwissTargetPredictor. Thirty-nine plants belonging to 26 plant families were harvested. Of the 228 extracts tested, 18 from 6 plants were active (MICs 250 - 1000 µg/mL) and nontoxic toward Vero and Raw (CC50 129.25 - >1000 µg/mL). Six potent extracts from the two plants exhibited moderate to potent DPPH (SC50 8.870-54.410 µg/mL), ABTS (SC50 12.020- 27.36 µg/mL), and NO (SC50 0.02 - 195.85 µg/mL) scavenging activities. These extracts showed interesting ferric iron-reducing power (1.28 to 12.14 µg equivalent NH2OH/g of extract). The shortest onset of action time (4 and 6 hours) observed following killing kinetics studies was observed. The UHPLC-LIT-MS/MS and some databases NIST 14, HMD, MassBank, SuperNatural 3.0, FooDB, and ChEBI allowed the annotation of 18 and 17 metabolites in P. macrophylla a n d B. ferruginea extracts respectively. Pharmacokinetic prediction showed that compound 6 (4,6a-bis(Hydroxymethyl)-9a-methyl-3-oxo-1a,1b,3,5,6,6a,7a,9a-octahydrobis(oxireno)[2',3':5,6;2",3":9,10]cyclodeca[1,2-b]furan-5-yl methacrylate), compound 8 (Corynoxeine), and compounds 35 (Stachybotrydial acetate) demonstrated acceptable druglike and pharmacokinetic properties and might act through inhibition of kinase, transferase, protease, oxidoreductase, and family AG protein-linked receptors. The findings showed that Cameroonian medicinal plants are suitable reservoirs of anti-Shigella and antioxidant agents with good drug candidate properties.

Keywords: Cameroonian medicinal plants, anti-Shigella, antioxidant, cytotoxicity, pharmacokinetic

42 IMPLEMENTATION OF HOST GENETIC DIVERSITY IN PRECLINICAL MODELS OF INFECTIOUS DISEASE: COLLABORATIVE CROSS MOUSE STRAINS MIRROR THE RANGE OF HUMAN DISEASE SEVERITY AND IDENTIFY SUSCEPTIBILITY LOCI

C. Manet1, M. Bourdon1-2, L. Conquet1, M. Prot3, L. Lambrechts4, E. Simon-Lorière3, J. Jaubert1, X. Montagutelli*1
1Mouse Genetics Laboratory, Institut Pasteur, Université Paris Cité, Paris, France
2Helmholtz Zentrum, München, Germany
3Evolutionary genomics of RNA viruses, Institut Pasteur, Université Paris Cité, Paris, France
4Virus-Insects Interactions Unit, Institut Pasteur, Université Paris Cité, Paris, France

Many diseases caused by infectious agents in humans show variable degree of severity between individuals. This is for example the case for vector-borne diseases such as dengue or Zika for which the majority of infected persons show no or mild symptoms, others a self-resolving flu-like syndrome, while a small fraction develop severe complications which can lead to death. Classical mouse models used for deciphering mechanisms of pathogenicity of viral infections fail to reproduce this range of disease outcomes due to their genetic homogeneity. To overcome this limitation, a collection of mouse inbred strains named the Collaborative Cross (CC) has been developed to incorporate >90% of the genetic variants identified in the mouse species and encompass a genetic diversity similar to that of the human population. When challenged with an infectious agent, CC strains display a broad spectrum of responses, generally ranging from resistance with low pathogen burden, to high susceptibility with clinical signs and mortality. Our laboratory has successfully used CC mice to produce a variety of models for Zika virus and SARS-CoV-2 infections. Preliminary experiments show similar results with tick-borne encephalitis virus. By crossing resistant and susceptible strains, we identifiedI rf3 as an important factor controlling Zika virus replication in vitro as well as other genetic determinants of susceptibility in vivo. The CC is therefore an unmatched resource for modelling inter-human variability of susceptibility to infectious disease and for identifying the underlying host genetic determinants. It also allows testing preventive and therapeutic interventions in genetically diverse backgrounds, thereby improving the predictive translational value of preclinical models.

43 A DECADE-LONG RETROSPECTIVE STUDY OF HEPATITIS C VIRUS GENETIC DIVERSITY IN CAMEROON 2013-2023: PRESENCE OF A HIGH PROPORTION OF UNSUBTYPABLE AND PUTATIVE RECOMBINANT HCV STRAINS

A. Mounchili Njifon*1, A. Modiyinji2, R. Njouom3
1Virology, Centre pasteur du Cameroun, Yaounde, Cameroon
2Virology, Centre Pasteur du Cameroun, Yaounde, Cameroon
3Virology, Centre Pasteur du Cameroun, Yaounde, Cameroon

Aim: While treatment options for HCV have expanded considerably over the past decade thanks to the development of pan-genotypic therapies, genotype testing remains a prerequisite for treatment in sub-Saharan African countries, including Cameroon, where multiple HCV genotypes and subtypes exist. The main objective of the present study was to outline the trend in the distribution of HCV genotypes and subtypes from 2013 to 2023 in the Cameroonian population.

Methods: Viral loads were determined using the Abbott Real Time assay, and genotyping/subtyping was based on nested and semi-nested RT-PCR of the core and NS5B regions, respectively, followed by sequencing and phylogenetic analysis.

Results: A total of 512 patients with NS5B and core sequencing results were included in our study. Genotyping revealed a predominance of both genotype 4 (38.48%) and genotype 1 (37.11%), followed by genotype 2, detected in 22.46% of patients. Interestingly, ten samples (1.95%) had discordant genotypes in both regions, suggesting the presence of putative recombinant forms of HCV. Twelve different subtypes were detected during the study period, with a predominance of subtypes 4f (18.95%) and 1e (16.02%). Furthermore, phylogenetic analyses failed to assign a subtype to a relatively high proportion of sequences (38.67%) for the two genomic regions, and their classification was limited to genotypes. The frequency distribution of HCV genotypes showed no statistical difference according to year or sex.

Conclusion: These results confirm the genetic diversity of HCV in Cameroon. Further studies using new sequencing techniques are needed to better describe the molecular epidemiology of HCV in Cameroon.

Keywords: Cameroon, diversity, hepatitis C virus, genotype.

44 INFLUENZA A VIRUS INFECTION ALTERS ENDOPLASMIC RETICULUM ARCHITECTURE AND PHOSPHOINOSITIDE TURNOVER TO PROMOTE VRNP EGRESS

C. Alemany1, J. Da Graça1, Q. Giai Gianetto2, S. Paisant3, T. Douche2, C. Isel3, C. Delevoye1, L. Danglot4-5, M. Matondo2, E. Morel1, JB. Brault3, N. Naffakh*3
1INSERM U1151, CNRS UMR8253, Institut Necker Enfants Malades, Université Paris Cité, Paris, France
2Mass Spectrometry for Biology Unit, Proteomic Platform, Institut
Pasteur, Université Paris Cité, CNRS UAR 2024, Paris, France
3RNA Biology and Influenza Viruses, Institut Pasteur, Université Paris Cité, CNRS UMR3569, Paris, France
4NeurImag facility, Institute of Psychiatry and Neuroscience of Paris (IPNP), INSERM U1266, Université Paris Cité, Paris, France
5Membrane Traffic in Healthy and Diseased Brain team, Institute of Psychiatry and Neuroscience of Paris (IPNP), INSERM U1266, Université Paris Cité, Paris, France

Influenza A virus (IAV) genomic RNAs, in the form of ribonucleoproteins (vRNPs), are replicated in the nucleus of the infected host cell, exported to the cytoplasm and transported to the plasma membrane (PM) at the sites of virion budding. There is strong evidence that the cellular GTPase RAB11A binds vRNPs and regulates the trafficking of vRNP transport vesicles, but the mechanisms involved remain largely unknown. Using electron microscopy, we showed that IAV infection induces a strong remodeling of the endoplasmic reticulum (ER) and proposed that the remodeled ER serves as a platform for the biogenesis of vRNP transport vesicles. Here, using a combination of confocal and STED microscopy, we confirm that IAV infection strongly alters ER architecture, notably the ER sheet distribution. Importantly, we show that RAB11A depletion leads to the accumulation of vRNPs in the vicinity of remodeled ER membranes, suggesting that RAB11A does not recruit vRNPs to ER membranes but rather drives their subsequent transport towards the PM. To identify host factors involved in this process, we characterized the RAB11A proximity interactome in IAV-infected versus mock-infected cells, using a TurboID-RAB11A fusion protein. Cellular regulators of phosphoinositide homeostasis were significantly enriched at the proximity of RAB11A in infected cells. Notably, the PI3P/PI4P phosphoinositide balance was found to be altered upon IAV-infection, through a pathway that involves the autophagy-related protein ATG16L1. Interestingly, ATG16L1 as well as local spots of PI4P co-distribute with vRNPs on ER membrane subdomains. Depletion of ATG16L1 leads to the accumulation of vRNPs in the cytoplasm of infected cells and to a decreased production of IAV infectious particles. Hence, we propose a working model in which IAV infection reshapes ER membranes where vRNPs associate, whilst PI4P is locally generated and RAB11A is concomitantly recruited. These events lead to the biogenesis of pathological vesicles coated with vRNPs that are transported to the PM.

45 IN SILICO GENOMIC SURVEILLANCE BY COVERAGE PREDICTS AND CHARACTERIZES SARS-COV-2 VARIANTS OF INTEREST

K. Norwood*1-2, Z. Deng1, S. Reimering1, G. Robertson1, M. Foroughmand-Araabi1-2, S. Goliaei1-2, M. Hölzer3, A. Mchardy1-2
1Deutsches Zentrum für Infektionsforschung (DZIF), Braunschweig, Germany
2Helmholtz Centre for Infection Research, Braunschweig, Germany
3Braunschweig Integrated Centre of Systems Biology (BRICS), Technische Universität Braunschweig, Braunschweig, Germany
4Genome Competence Center (MF1), Robert Koch Institute, Berlin, Germany

Over the past four years SARS-CoV-2 has demonstrated a propensity for adaptive evolution, with novel variants of concern (VOCs) emerging, with e.g. improved transmissibility or alterations in antigenicity. This has necessitated the early detection of such variants of interest to ensure the continued efficacy of vaccines and to optimize public health management. To address this, large-scale viral genomic surveillance programs have been initiated worldwide with data being deposited in public repositories in a timely manner. However, technologies for their continuous interpretation are currently lacking. We propose CoVerage, a web-based genomic surveillance platform for SARS-CoV-2 viruses (https://sarscoverage.org/), which offers unique analytic and predictive capabilities for SARS-CoV-2 genomic surveillance, with all results being continuously updated to maximize predictive value. Using the establishment of Omicron and its subsequent sublineages, we demonstrate how CoVerage can facilitate the timely identification and assessment of future SARS-CoV-2 Variants of Concern.

46 FACTORS ASSOCIATED WITH MOSQUITO-BORNE DISEASE PROTECTIVE BEHAVIOUR: A PRE-REGISTERED CROSS-SECTIONAL STUDY IN METROPOLITAN FRANCE

J. Ocampo*1, J. Dussault1, J. Mueller1-2
1Emergent Infectious Disease Unit, Institut Pasteur, Paris, France
2Ecole des hautes études en santé publique (EHESP), Paris, France

Background: Mosquito-borne diseases (MBDs) are increasing and expanding their range throughout metropolitan France. Promoting individual protective behaviour is imperative, but research on its determinants is limited to southern regions. This study aims to quantify the knowledge, attitudes, and practice around MBDs and examine factors influencing protective behaviour in the metropolitan French population.

Methods: 2,087 subjects responded an online questionnaire in November 2023. We fitted two mixed effects models to estimate the frequency and count of protective behaviours across different sociodemographic groups and to identify which factors influence protective behaviour.

Results: Frequency of protective behaviour is significantly associated with perceived MBD threat (B = 0.11; 95% CI: 0.06, 0.15), having financial difficulties (B = 0.23; 95% CI: 0.02, 0.43), and getting bitten by mosquitoes often (B = 3.39; 95% CI: 3.10, 3.69) and sometimes (B = 1.54; 95% CI: 1.31, 1.76) compared to almost never. Count of protective behaviours is associated with getting bitten by mosquitoes often (B = 0.39; 95% CI: 0.30, 0.49) and sometimes (B = 0.14; 95% CI: 0.05, 0.23), perceived MBD threat (B = 0.02; 95% CI: 0.00, 0.03), MBD knowledge (B = 0.06; 95% CI: 0.04, 0.08), and having a chronic disease (B = 0.08; 95% CI: 0.02, 0.14). Models were adjusted for place of residence, education, and age. No associations were found for sex, having experienced an MBD, or confidence in public authorities to manage health crises.

Conclusions: This study provides insights into MBD protective behaviour and its associated factors considering all metropolitan French regions. Our results highlight factors which may inform prevention communication and policies focused on increasing protective behaviour.

47 CLIMATE CHANGE SHIFTING ARBOVIRUSES DISEASE BURDEN TO OVERTAKE MALARIA IN PUBLIC HEALTH?

J. Judith Mangeni1, D. Diana Menya1, G. George Ayodo2, J. Joseph D. Tucker3, S. Simon Karanja4, I. Ivy Akinyi5, B. Ben Oyugi2, A. Arthy Yongo2, J. Ogony*4-2
1Moi University, Kenya, Eldoret, Kenya
2Jaramogi Oginga Odinga University of Science and Technology, Kenya, Kisumu, Kenya
3London School of Hygiene and Tropical Medicine, London, United Kingdom
4Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya
5University of Antwerp, Antwerp, Belgium

Background: Climate change is a global threat to human health and has impacted health systems. Vector-borne diseases are among the greatest causes of human suffering associated with climate variability resulting in vector abundance and competence. According to the World Health Organization, about one-sixth of the diseases and disability suffered globally are linked these diseases, Plasmodium and dengue virus infection in humans are caused by the bites of infected female mosquitoe Anopheles and Aedes aegypti respectively. Both mosquitoes are anthropophilic with different biting patterns.

Methods: A three month,cohort, mixed methods study on sample size of 380 children presenting with febrile illness at levels; 2, 3 and 4 public health facilities in Busia and Kisumu Counties in western Kenya. Children were screened for malaria and dengue virus using rapid diagnostic kits. Questionnaire was administered to the parents/guardians.

Result: Time of mosquito bites is a significant predictor of P. falcipurum and dengue fever infection ($p = 0.003$), experiencing mosquito bites during both day and night is 2.13 times (OR = 2.13, 95% CI: 1.29, 3.54) higher risk of infection compared to those bitten only at night (reference category).

Discussion: Due to the exitance of the vector's preferred environment of warm temperatures and increased precipitation and humidity vectors fecundity for both transmitting Aedes aegypti, and anopheles favored in western region. Aedes aegypti, the principal mosquito vector of dengue fever and urban yellow fever viruses is known to be diurnal and tends to travel short distances to obtain its blood meals, while anopheles sp. are predominantly nocturnal feeders.

Conclusion: An exposure to mosquito bite both day and night due to the diurnal and nocturnal behaviours of these vectors explains the rising burden of both malaria and dengue fever as well as the co-infection burden can lead serious and fatal outcomes if left undiagnosed and without timely treatment. If not control now, the burden of the arbovirus diseases like dengue fever may equalize or overtake the known malaria public health burden in the region. This study confirms that there is a biting competition between the two species of mosquito. There is need to up the control measures.

48 UNCOVERING THE HIDDEN TOLL: EXPLORING 130 YEARS OF TEMPERATURE-RELATED MORTALITY IN MADRID

D. Ordanovich*1, A. Tobías2, D. Ramiro1
1Center for Human and Social Sciences, Spanish National Research Council, Madrid, Spain
2Institute of Environmental Assessment and Water Research, Spanish National Research Council, Barcelona, Spain

The association between ambient temperatures and health outcomes was extensively studied in the past decades, especially in the light of exacerbating climate change. Yet long-term studies focusing on the analysis of the changes of mortality answers to extreme heat are rare, particularly in the Mediterranean region. Minimum Mortality, or so-called Optimum temperatures are increasingly used to assess the levels of adaptation to changing temperatures. The warming of the air temperatures in Spain affected the entire national territory since the turn of the XX century. However, the number of studies exploring the evolution of adaptation to heat and relying on multidecadal time-series data in Spain at any administrative level is very limited. To our knowledge, the present research is the first one to leverage daily mortality and temperature data in the city of Madrid since the end of the XIX century until today.
We examined the patterns of adaptation to extreme and moderate heat and cold in the city of Madrid in the period from 1890 until 2020 using daily data on air temperature received from the meteorological stations and all-cause mortality from yearly books and civil registers. Using a distributed-lag nonlinear modelling framework, we explored the complex temperaturemortality relations and estimated the changes in the adaptation metrics by decade.
We observed a gradual increase in the optimum temperatures over time, along with the overall increment of the air temperatures, especially in the last decades. The flattening of the mortality curves over time suggests an extension of the optimal temperature range. We also saw a general reduction in the heat-attributable mortality fractions, which indicates a progressive adaptation to overall warming of air temperatures and intensification of weather extremes.
On the other hand, the dose-response relationship differed between sex- and age-groups, being the highest for older woman and children in the begging of the study period. We also observed a spatially different response of mortality to intense heat within the city due to different housing environment and development of urban infrastructures in each area of the city.

49 LONG TERM CIRCULATION OF SARS-COV-2 RELATED VIRUSES IN BATS IN CAMBODIA

Tey Putita Ou, Erik A Karlsson, Julia Guillebaud, Deborah Delaune, Matthieu Prot, Vibol Hul, Thavry Hoem, Hélène Guis, Heidi Auerswald, Leakhena Prum, Gavin James Smith, Philippe Dussart, Véronique Chevalier, Julien Cappelle, Veasna Duong, Etienne Simon-Lorière
IPC: PTO, EAK, JG, VH, TH, HA, LP, VD
Virology Unit, Institut Pasteur du Cambodge, Pasteur Network, Phnom Penh, Cambodia
IPM: PD
Institut Pasteur de Madagascar, Pasteur Network, Antananarivo, Madagascar
CIRAD: JC, VC, HG
CIRAD, UMR ASTRE (Animal, Santé, Territoires, Risques, Ecosystèmes), TA A 117/E, Campus International de Baillarguet, 34398 Montpellier CEDEX 5, France
ASTRE, CIRAD, INRA, Université de Montpellier, Montpellier, France
IP-Paris: DD, MP, ESL
Institut Pasteur, Université de Paris, G5 Evolutionary Genomics of RNA Viruses, F-75015, Paris, France
Duke-NUS: GJS
Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore, Singapore

Recent studies have identified the Greater Mekong Subregion as a critical zone for Sarbecoviruses presence in bats, particularly insectivorous horseshoe bats of the Rhinolophus genus. The prevalence, maintenance, and evolution of these viruses within Rhinolophids remain largely unknown due to limited sampling efforts that tend to focus on one-time cross-sectional surveys. With the detection of SARS-CoV-2 related viruses in historical R. shameli samples (from 2010) in Steung Treng, Cambodia, further surveillance efforts are crucial, both to understand the extent of the diversity of coronaviruses in the region, and to facilitate surveillance efforts for pandemic preparedness. Live bats catch and release sampling has been implemented in several sites located in Steung Treng province between 2020 and 2023. Rectal swab specimens from these bats were subjected to real-time RT-qPCR testing for SARS-CoV-2 or other sarbecoviruses. RNA samples from bats that tested positive by RT-qPCR were then sequenced through metagenomic and amplicon sequencing. SARS-CoV-2-related viruses have been identified in various species of Rhinolophus bats, including R. shameli, R. microglobosus, R. acuminatus, R. pusillus and R. malayanus. Based on phylogenetic analysis, these viruses were categorized into three groups: viral group 1 was found in both R. shameli and R. micoglobosus; viral group 2 was present in R. acuminatus and R. pusillus; while viral group 3 was detected in R. malayanus. Group 1 viruses closely resemble to the 2010 virus allowing to study the evolution of this lineage over 13 years; Group 2 constitute a new subclade within sarbecoviruses; and Group 3 represents a sub-lineage of SARS-CoV-2 related viruses that clusters with a virus detected in Thailand. Interestingly, the receptor binding motif on the spike protein of viral group 2 shows high similarity with SARS-CoV-2, with only five amino acids mismatches. We implemented a pseudovirus assay to characterize the capacity of selected spike of viral group1 and 2 to mediate entry into cells expressing human receptor ACE2. Overall, our findings highlight the importance of continued surveillance and research on bat populations to better understand the diversity of coronaviruses and their evolutionary processes, to be better prepared for potential future outbreaks.

50 MOTHER-TO-CHILD TRANSMISSION OF YELLOW FEVER VIRUS DURING BREASTFEEDING

J. Pascard*1, S. Desgraupes2-1, P. Jeannin2-1, A. Gessain2-1, PE. Ceccaldi2-1, A. Vidy-Roche2-1
1Université Paris-Cité, Paris, France
2Unité Epidémiologie et Physiopathologie des Virus Oncogènes, Institut Pasteur, Paris, France

Yellow fever virus (YFV) (Flaviviridae, Orthoflavivirus) can cause an acute hemorrhagic disease in humans and is transmitted by mosquitoes. Despite the existence of an effective vaccine (attenuated strain 17D), it causes at least 30,000 deaths/year worldwide. Several cases of 17D strain transmission to infants through breastfeeding have been reported following nursing mothers' vaccination, with some infants developing neurological symptoms. However, wild-type strains transmission through breastfeeding remains under-documented, although likely since the presence of viral RNA has been detected in breast milk from infected mothers.

With the aim of demonstrating and characterizing YFV transmission through breastfeeding, we studied the different stages of this mode of transmission: viral dissemination to the mammary glands, excretion of infectious virus into breast milk, and oral viral transmission to infant with associated mechanisms.

We have demonstrated that YFV disseminates to the mammary glands of infected A129 mice. Moreover, we were able to demonstrate the susceptibility and permissivity of human mammary cells to YFV infection.

Using A129 mice, we showed that YFV infectious particles are excreted into breast milk, as free virus particles and cell-associated virus.

Finally, the susceptibility of pups to oral infection by YFV has been demonstrated, after intragastric inoculation of the virus. In addition, using an in vitro model of tight human intestinal epithelium (Caco-2 cells cultured on Transwell), we demonstrated that YFV is able to infect and cross the epithelial barrier without altering its permeability.

Altogether, these studies provide fundamental knowledge in the mechanisms of mother-to-child transmission of YFV during breastfeeding.

51 SURVEY OF PREVALENCE AND SEROPREVALENCE OF RAT HEPATITIS E VIRUS (ROCAHEPEVIRUS RATTI) IN RODENT POPULATIONS IN DIFFERENT FRENCH CITIES

M. Pellerin*1, V. Doceul1, V. Sauvage2, S. Gellenoncourt1, A. Marcadet-Hauss1, E. Picard Meyer3, S. Daouda Soro4, V. Lattard4, E. Monchatre-Leroy3, N. Pavio1
1UMR Virologie, Anses-Inrae-Enva, Maisons-Alfort, France
2Unite Environnement et risques infectieux, Institut Pasteur, Paris, France
3Laboratoire de la rage et de la faune sauvage de Nancy, Anses, Malzeville, France
4Rongeurs Sauvages, Risques Sanitaires et Gestion des Populations - UR 1233, VetAgro Sup, Marcy L'etoile, France

The Hepeviridae family, whose prototype virus is hepatitis E virus (HEV), comprises several viral species whose host range are not yet well defined. The emergence of cases of acute or chronic hepatitis in humans following infection with rat hepatitis E virus is a cause for concern, and there is a need to acquire new knowledge of the geographical distribution of rodent HEV viruses.

As part of the Ratvar research project (ANRS MIE Emergen program, project ANRS0163), the consortium captured wild rodentsR (attus norvegicus) in the sewers and parks of several major French cities: Besançon, Lyon, Nancy, Marseille, Bordeaux and Nantes. The captures were carried out during spring 2023, in sewers and around social housing units with high human population densities. Over 300 rat liver samples were analysed. Rats of all ages and genders were present and were divided by weight category (correlation between weight/age).

Liver samples were analysed by real-time RT-qPCR. Matched sera were collected and a test to detect anti-HEV antibodies, suitable for rodents, was used. Characteristics of HEV positive animals are available (age, sex, collection site) and will be the subject of epidemiological analyses.HEV (Rocahepevirus ratti) RNA was detected in rat liver samples from all 6 cities, with HEV-C RNA individual prevalence ranging between 7 and 60%. HEV RNA was detected in all weight categories with apparent gender difference (higher for females). The findings suggest that the prevalence of HEV increases with the growth in weight of the animals, especially after 100g when the rats become mature and go look for food. Sequencing is currently underway to analyse the strain variability/heterogeneity as a function of cities.

With climate change, the greening of cities has benefits for human and environmental health, but it can also have negative effects, such as increasing the environment's carrying capacity to support more abundant rat populations, which can harbor and spread a wide variety of zoonotic pathogens. The high presence of rat HEV in major French cities should encourage research into its zoonotic potential and routes of exposure.

52 UNCOVERING HEALTH DISPARITIES IN SOUTHERN VIETNAM THROUGH HAND, FOOT, AND MOUTH DISEASE DATA ANALYSIS, 2017–2022

T. Phan*, Q. Luong
Department for Disease Control and Prevention, Pasteur Institute in Ho Chi Minh City, Ho chi Minh City, Vietnam

Introduction: Annually, Vietnam reports 90,000 Hand, Foot, and Mouth Disease (HFMD) cases. Two sub-regions of the Southern Region, Southeast and Mekong-Delta, have the highest morbidity, and case-fatality is disproportionally distributed. We investigated health disparities between the sub-regions.
Methods: We described the case distribution and severity, defined as central nervous system involvement, using 6-years of HFMD case data (2017–2022). We linked it to provincial socio-economic indicators of the same period to identify risk factors for severe cases. We conducted multilevel logistic regression analyses with random intercepts for province, random slope for time (pre- vs. post-COVID-19 era), and reported odd ratios (OR) and associated 95% confidence intervals (CI).
Findings: Between 2017–2022, the Southeast reported 247,579 HFMD cases, 1,224 (4.9%) severe cases, and 10 (0.04%) deaths. The Mekong-Delta reported 177,370 cases, 2,008 (11.3%) severe cases, and 21 (0.12%) deaths. Younger age, male sex, and ethnic minorities were significantly associated with severe cases. Higher percentage of population using hygienic water (OR 0.97, 95%CI: 0.96–0.98) was associated with fewer severe cases at provincial level.
Contribution: Addressing HFMD severity requires multifaceted interventions. Further studies are necessary to identify the causes of health disparities among HFMD cases in Vietnam.

Keywords: Health disparity; Hand, foot, and mouth disease; multilevel regression analysis.

53 EVOLUTION OF SARS-COV-2 JN.1 LINEAGE: VIRAL FITNESS AND ANTIBODY EVASION

D. Planas*1, I. Staropoli1, V. Michel2, F. Porrot1, F. Guivel-Benhassine1, E. Yab2, B. Jeyarajah2, Y. Rahou2, C. Planchais2, W.H. Bolland1, M. Prot2, J. Buchrieser1, T. Bruel1, F. Lemoine2, L. Hocqueloux3, T. Prazuck3, H. Mouquet2, E. Simon-Loriere2, M.A. Rameix-Welti2, O. Schwartz1
1Virus and immunity, Institut Pasteur, Paris, France
2Hospices Civils de Lyon, Lyon, France
3Institut Pasteur, Paris, France
4CHR d'Orléans, Orléans, France

The unceasing circulation of SARS-CoV-2 leads to the continuous emergence of novel viral sublineages. We isolate and characterize the recent JN.1-derived strains, which circulate in 2024. Recent JN.1 strains have convergently accumulated mutations on the receptor-binding domain (RBD) of the spike, including R346S/T and F456L/V (referred to as "FLiRT" variants). A newly detected variant, designated KP.3, also carries a Q493E mutation. An additional deletion in position 31 has also been detected in FLiRT- and KP.3-derived strains. As of June 2024, the circulation of these variants is increasing in various countries, including France.

Our aim is to understand the mechanisms underlying the selection of these variants. We perform a side-by-side comparison of their replication in human cell lines and relevant primary nasal epithelial cells (hNECs), their binding to ACE2 and fusogenicity. We examine their sensitivity to monoclonal antibodies (mAbs) and antiviral drugs, as well as to sera from a longitudinal cohort of recipients of various vaccine regimens who experienced breakthrough infections.

We demonstrate that SARS-CoV-2 Omicron variants continuously evolve in the context of the mixed immunity of human populations. The selective advantage of JN.1-derived variants combines convergent increased fitness and replication in respiratory cells, along with resistance to prevalent antibodies.

54 UNTARGETED METATRANSCRIPTOMICS OF TICKS FROM ILE DE FRANCE

Matthieu PROT 1, Artem BAIDALIUK 1,2, Eva KRUPA 3, Laurine LEVILLAYER 3, Matthieu BASTIEN 4, Océane CLAUDE4, Olivier TELLE5, Stéphanie FAVIER4, Benoît COMBES4, Alice RAFFETIN6, Richard PAUL3, Sarah BONNET3, Etienne SIMON-LORIERE1

1Institut Pasteur, Université Paris Cité, Evolutionary Genomics of RNA Viruses, F-75015 Paris, France
2Institut Pasteur, Université Paris Cité, Bioinformatics and Biostatistics Hub, F-75015 Paris, France.
3Institut Pasteur, Université Paris Cité, CNRS UMR 2000, INRAE USC 1510, Ecology and Emergence of Arthropod-borne pathogens unit, F-75015 Paris, France.
4Entente de Lutte et d'Intervention contre les Zoonoses (ELIZ), F-54220 Malzéville, France
5Centre National de la Recherche Scientifique (CNRS), UMR 8504 Géographie-cités, F-93322 Aubervilliers cedex, France
6Department of Infectious Diseases, Tick-Borne Diseases Reference Center-Paris and Northern Region, General Hospital Lucie et Raymond Aubrac, F-94190 Villeneuve-Saint-Georges, France

Ticks are blood-feeding arthropods found throughout Europe, and they play a significant role in the transmission of tick-borne pathogens that affect humans, wildlife, and domestic animals. They can transmit a wide variety of microbes, including bacteria, parasites and viruses. While Lyme disease, Tick-Borne Encephalitis and Crimea Congo Haemorrhagic fever are well known tick-borne pathogens, very little is known about the diversity of viral communities in ticks and zoonotic potential of their constituents.

We developed a metatranscriptomic sequencing protocol allowing us to study RNA viruses present in a wide diversity of sample types originating from different hosts, both vertebrate and invertebrate. One of the key steps that increases the amount of virus data is ribodepletion (i.e., the removal of the most dominant RNA species usually reaching 80% of all data – ribosomal RNA). Our protocol deploys custom designed DNA probes that target rRNA of a given host at the appropriate taxonomic level. We used this sequencing approach for virus detection in ticks collected in the green spaces in and around Paris, France. For this study, we designed ribodepletion probes for different tick species. We showed that <10% of the total read number after sequencing came from rRNA, increasing drastically the number of reads of interest. We sequenced a total of 83 ticks (adults and nymphs, and mostly Ixodes ricinus). We used a standard virus discovery workflow based on de novo assembly and sequence similarity search in the nr-prot NCBI database. Our preliminary analysis, focusing on hits of >70% of amino acid sequence similarity, detected members of Bunyavirales, Nairoviridae, Partitiviridae, Rhabdoviridae, and the Flaviviridae virus families. In conclusion, this study on a relatively small number of samples sheds light on the tick virome diversity and highlight the circulation of potential human-pathogenic RNA viruses in ticks from Ile de France. Further analyses and additional sequencing on this tick cohort is under way.

Keywords: ticks, tick-borne viruses, ribosomal RNA depletion, metatranscriptomics, phylogenetic analysis

55 RESILIENCE OF COMMUNITY HEALTH SYSTEMS CONFRONTING EMERGING ZOONOSES IN CAMEROON

G. Salomon
Cellule de recherche et des statistiques, RAPEAJ -Cameroun, Buea Cameroon, Cameroon

Cameroon, situated in the heart of Central Africa, boasts exceptional biodiversity but faces growing public health challenges, particularly concerning emerging zoonoses. As of 2020, 41 zoonoses were identified in Cameroon according to the National Program for Zoonosis Management. The increasingly frequent interactions between humans, domestic animals, and wildlife, combined with climate change and deforestation, significantly increase the risk of zoonotic disease transmission. In this context, community health systems play a crucial role as the first line of defense against these threats. However, these systems face numerous structural and organizational challenges that limit their capacity for effective response.

Our study aims to examine how to strengthen the resilience of these community health systems in Cameroon in the face of the growing threat of zoonoses, within a context of limited resources and multiple vulnerabilities. To address this complex issue, we adopt a mixed methodological approach. This includes a systematic review of literature on zoonoses in Cameroon and community responses, semi-structured interviews with key actors such as community health workers, veterinarians, and health authorities, as well as focus groups in rural and peri-urban communities.

This communication will be structured around four major axes. We will begin by assessing the current state of community health systems, identifying their strengths and weaknesses, as well as their current capacities in dealing with zoonoses. We will then explore the main challenges these systems face.

We will also examine potential opportunities and innovations to strengthen these systems, such as the adoption of a One Health approach at the community level, the use of mobile technologies for participatory surveillance, and the reinforcement of traditional and cultural knowledge. Finally, we will formulate concrete policy recommendations to improve the resilience of community health systems.

56 INTEGRATIVE STRUCTURAL BIOLOGY OF HUMAN AND VIRAL PROTEIN "PLAYERS" IN THE ADP-RIBOSYLATION PATHWAY

G. Spyroulias
Department of Pharmacy, Lab of Biomolecular NMR, University of Patras, Patras, Greece

Macrodomains (MDs) are a group of structural modules with a unique a/b/a sandwich fold. They are present in all living organisms, viruses included, either alone or in combination with larger proteins. In viruses, MDs are components of big, non-structural proteins. Their functional differences contrast with their architectural similarities, while their capacity to bind ADPribose, indicates their importance in the ADP-ribosylation process. Their biological role, which is connected to their ability to identify ribosylated proteins (due to this property are characterized as "readers") and/or de-ribosylate the substrates (therefore they act as "erasers"), leading to the suppression of PARP-mediated antiviral activity (PARP holds for Poly-ADPribose polymerase, enzymes that produce and attach ADPr on proteins). Due to this property, they are recently recognized as potential therapeutic targets. Because of the tandem MDs incorporated into their sequences, which control macroPARPs' subcellular localization and interactions with other cellular constituents, the terms "macroPARPs" relate to PARP9, PARP14, and PARP15. 1, 2
Our recent results of the comparative study between viral and human macroPARPs MDs, with the aim to elucidate the structure, the dynamic properties, and the biochemical characteristics of several unexplored members, will be presented. Our efforts to unravel subtle differences among the physicochemical determinants that underlie the in-silico screening, NMR-driven approaches, biophysical techniques, and biochemical assays to identify and develop selective binders, spanning a wide range of organic scaffolds, overcoming the sequence similarities among the MD family members, will be discussed, as well. 3,4

Acknowledgements: "INSPIRED" (MIS 5002550), under the Action "Reinforcement of the Research and Innovation Infrastructure", funded by the Operational Programme "Competitiveness, Entrepreneurship and Innovation" (NSRF 2014-2020), and European Union's HE programs (2021-2027), "REMOTE-NMR" (GA 101058595)& "ESPERANCE" ERA Chair (GA 101087215). https://bionmr.upatras.gr/

References

1. Rack JGM, Zorzini V, Zhu Z, Schuller M, Ahel D, Ahel I. Open Biol. 2020, 10:200237. doi: 10.1098/rsob.200237. PMID: 33202171.
2. Rack JG, Perina D, Ahel I. Annu Rev Biochem. 2016, 85:431-54. doi: 10.1146/annurev-biochem-060815-014935. PMID: 26844395.
3. Tsika AC, Gallo A, Fourkiotis NK, et al. J Mol Biol. 2022, 434:167720. doi:10.1016/j.jmb.2022.167720.
4. COV19-NMR Consortium et al. Angewandte Chemie Int Ed Engl 2022, 61, e202205858. https://doi.org/10.1002/anie.202205858.

57 ANTIBIOTIC RESISTANCE GENES AND VIRULENCE MARKERS: NEXT-GENERATION SEQUENCING ANALYSIS OF PSEUDOMONAS AERUGINOSA ISOLATED FROM VARIOUS CLINICAL SPECIMENS - A SINGLE CENTER EXPERIENCE FROM INDIA

V. Kandi1-2, T. Suvvari*2
1Microbiology, Prathima Institute of Medical Sciences (PIMS), Karimnagar, India
2Squad Medicine and Research (SMR), Srikakulam, India

Background: Pseudomonas is a ubiquitous bacterium that resides in the environment. It is a saprophytic bacteria that can be found in hospital environments. However, Pseudomonas aeruginosa (PA) and a few other species have been associated with serious infections in the hospitals known as nosocomial infections or hospital acquired infections or healthcare associated infections. These infections are generally noted among debilitated patients like new-born babies/neonates, intubated patients, critically ill patients, and patients admitted in the intensive care units (ICU), among others. Pseudomonas species (spp.) are also known to contaminate antiseptics, survive in the harshest environments, and acquire multi-drug resistance.

Methods: Out of 386 Pseudomonas aeruginosa isolate samples received, 9 bacterial isolates showing multi-drug resistance were identified and further sent to genomic profiling. Identification of the bacteria and antimicrobial susceptibility testing (AST) of isolates was done and Multi Locus Sequence Typing (MLST), Antimicrobial Resistance (AMR) determinants, virulence factors and plasmid replicon types were identified from their whole genome sequences using ARIBA tool v2.14.4 with BIGSdb-Pasteur MLST database, NCBI AMR acquired gene & PointFinder databases and VFDB.

Results: A total of 9 Pseudomonas aeruginosa bacterial isolates showing multi-drug resistance were identified from skin & soft tissue infections and respiratory tract infections. The mean age was 43.33 years and out of 9 samples, 5 were from males and 4 were from females. Most common resistant genes found in samples were aph(3')-IIb, blaPDC, blaOXA. In phenotype analysis, all samples were sensitive to aminoglycoside while in genotype analysis all samples were resistant to aminoglycoside. exoS, lasI, lasR toxA were the most common virulence genes detected. Major plasmid replicon types detected were aroE, nuoD, trpE.

Conclusion: The results of the current study showed discordance in the phenotypic and genotypic antimicrobial susceptibility profiles. Moreover, all the strains in this study revealed multiple resistance and virulence genes and belonged to different sequence types. Given the emerging antimicrobial resistance among bacteria that result in treatment failures, genomic surveillance of isolates for resistance genes and molecular analysis of strain types and virulence determinants assume increased significance both for clinical and epidemiological purposes.

58 KNOWLEDGE AND PERCEPTION ON CLIMATE CHANGE AND VECTOR-BORNE DISEASES AMONG INDIAN DOCTORS - A PILOT STUDY

V. Kandi1-2, T. Suvvari*2
1Microbiology, Prathima Institute of Medical Sciences (PIMS), Karimnagar, India
2Squad Medicine and Research (SMR), Srikakulam, India

Background: Climate change is a growing concern for public health, potentially increasing the spread of vector-borne diseases (VBDs), mostly commonly includes malaria and dengue. Doctors play a vital role in managing VBDs, and understanding their knowledge and perceptions regarding climate change is crucial for effective public health interventions. This pilot study aimed to assess the feasibility of a larger study examining Indian doctors' knowledge and perception of climate change and VBDs.

Methods: A pilot study was conducted and a convenience sample of 140 Indian physicians from various healthcare settings across different states of India participated. A pre-structured self-administered questionnaire was used to collect data on socio-demographic characteristics, knowledge about climate change and its health impacts, perceptions on climate change health risks, and self-reported practices and behaviors.

Results: The study found that 94% of the physicians were aware of climate change, and 78% believed that it can affect the spread and incidence of vector-borne diseases. While 85% of the physicians considered the health impacts of climate change to be serious, only 48% felt that the Indian healthcare system is prepared to deal with these impacts. Gaps were also identified in the physicians' knowledge of specific vector-borne diseases linked to climate change, with 74% being able to correctly identify the diseases most likely to be impacted. Furthermore, 43% of the physicians reported routinely discussing the health impacts of climate change with their patients.

Conclusions: This pilot study successfully evaluated the feasibility of a larger-scale investigation along with crucial insights into the current state of knowledge, attitudes and practices of Indian physicians regarding the health impacts of climate change. The findings can inform the development of targeted educational interventions and policy measures to enhance climate change preparedness in the healthcare sector. The results also contribute to the limited evidence base on this topic from the Indian context.

59 NON-INVASIVE DIAGNOSIS METHOD FOR CUTANEOUS LEISHMANIASIS

Y. Taslimi*1, S. Habibzadeh1, R. Yousefi1, V. Mashayekhi2, A. Akbarzadeh2, Z. Azarpour2, J. Persson3, S. Gharibzadeh4, A.M. Harandi3-5, A. Mizbani6, S. Rafati1
1Immunotherapy and leishmania vaccine research, Pasteur institute of Iran, Tehran, Iran
2Cutaneous Leishmaniasis Research Center, Mashhad University of Medical Sciences, Mashhad, Iran
3Department of Microbiology and Immunology, Institute of Biomedicine, Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden
4Department of Epidemiology and Biostatistics, Research Centre for Emerging and Reemerging Infectious Diseases, Pasteur Institute of Iran, Tehran, Iran
5Vaccine Evaluation Center, BC Children's Hospital Research Institute, The University of British Columbia, Vancouver, Canada
6ETH Zurich, Zurich, Switzerland 7Immunotherapy and leishmania vaccine research, Pasteur Institute of Iran, Tehran, Iran

Background: Pseudomonas is a ubiquitous bacterium that resides in the environment. It is a saprophytic bacteria that can be found in hospital environments. However, Pseudomonas aeruginosa (PA) and a few other species have been associated with serious infections in the hospitals known as nosocomial infections or hospital acquired infections or healthcare associated infections. These infections are generally noted among debilitated patients like new-born babies/neonates, intubated patients, critically ill patients, and patients admitted in the intensive care units (ICU), among others. Pseudomonas species (spp.) are also known to contaminate antiseptics, survive in the harshest environments, and acquire multi-drug resistance.
Methods: Out of 386 Pseudomonas aeruginosa isolate samples received, 9 bacterial isolates showing multi-drug resistance were identified and further sent to genomic profiling. Identification of the bacteria and antimicrobial susceptibility testing (AST) of isolates was done and Multi Locus Sequence Typing (MLST), Antimicrobial Resistance (AMR) determinants, virulence factors and plasmid replicon types were identified from their whole genome sequences using ARIBA tool v2.14.4 with BIGSdb-Pasteur MLST database, NCBI AMR acquired gene & PointFinder databases and VFDB.
Results: A total of 9 Pseudomonas aeruginosa bacterial isolates showing multi-drug resistance were identified from skin & soft tissue infections and respiratory tract infections. The mean age was 43.33 years and out of 9 samples, 5 were from males and 4 were from females. Most common resistant genes found in samples were aph(3')-IIb, blaPDC, blaOXA. In phenotype analysis, all samples were sensitive to aminoglycoside while in genotype analysis all samples were resistant to aminoglycoside. exoS, lasI, lasR toxA were the most common virulence genes detected. Major plasmid replicon types detected were aroE, nuoD, trpE.
Conclusion: The results of the current study showed discordance in the phenotypic and genotypic antimicrobial susceptibility profiles. Moreover, all the strains in this study revealed multiple resistance and virulence genes and belonged to different sequence types. Given the emerging antimicrobial resistance among bacteria that result in treatment failures, genomic surveillance of isolates for resistance genes and molecular analysis of strain types and virulence determinants assume increased significance both for clinical and epidemiological purposes.

60 DEPLOYMENT OF IN VITRO ASSAYS, UHPLC-MS/MS FINGERPRINTS, AND IN SILICO APPROACH TO UNVEIL ANTIMALARIAL DRUG CANDIDATES WITH GOOD PHARMACOKINETICS, AND DRUG-LIKENESS PROFILES FROM DIOSPYROS GILLETII

M. Tchatat Tali*1-2, K. Aubin Youbi1-2, H. Djigang Nana1, Y. Melogmo Dongmo1, C. Jiatsa Mbouna1, D. Wendji Monkam1, J. Claude Tchouankeu3, F. Fekam Boyom1-2
1Biochemistry., Antimicrobial and Biocontrol Agents Unit, Laboratory for Phytobiochemistry and Medicinal Studies., University of Yaounde I, Yaounde, Cameroon
2Malaria Drug Discovery, Advanced Research and Health Innovation Hub, Yaounde, Cameroon
3Department of Organic Chemistry, Laboratory of Natural Products and Organic Synthesis, University of Yaounde I, Yaounde, Cameroon
4Biochemistry, Antimicrobial and Biocontrol Agents Unit, Laboratory for Phytobiochemistry and Medicinal Plant Study, University of Yaounde I, Yaounde, Cameroon

The necessity for the discovery of novel antimalarial drugs is being driven by the emergence of acquired resistance to artemisinin in Africa. This instigates the need for continuous deployment of a holistic approach to the discovery and development of new antimalarial drugs with improved efficacy and safety profiles. Natural products, particularly those derived from plants, have long been a valuable source of antimalarial agents. However, the development of new antimalarial drugs from natural products is not without challenges. In this context, we deployed in vitro assays, UHPLC-MS/MS fingerprints, and anin -silico approach to unveil novel antimalarial drug candidates with good pharmacokinetics and drug-likeness properties from a plant called Diospyros gilletii. Methanolic, ethanolic, and hydroethanolic extracts from D. gilletii bark were obtained by maceration and screened in vitro against chloroquine-sensitive (Pf3D7) and multidrug-resistant (PfDd2) strains of Plasmodium falciparum using the SYBR Green I-based method. The selectivity of potent extracts was assessed on red blood cells using a hemoglobin-releasing test while the resazurin-based method was used on Vero and Raw cell lines. The chemical profile of the potent extract was established through ultra-high-performance liquid chromatography coupled with tandem mass spectrometry (UHPLC-MS/MS). Thein silico antiplasmodial activity, pharmacokinetics and drug target of the identified chemical were predicted using Artificial Intelligence and Machine Learning (AI/ML)-assisted models from the Ersilia Open-Source. Out of the three (03) extracts screened, hydroethanolic extract exhibited the most potent antiplasmodium activity (IC50PfDd2: 7.70 µg/ml; IC50Pf3D7: 7.64 µg/ml) and acceptable selectivity profile against erythrocyte and normal cells (IS>3). The UHPLC-MS/MS-based metabolomics analysis allowed the putative annotation of seventeen (17) metabolites from the hydroethanolic extract ofD . gilletii belonging to a range of chemical families, with a notable majority (47%) being classified as flavonoids. The in silico prediction of antiplasmadium activity unveiled two (2) compounds, Santin (Prediction Score: 0.99 and 0.84) and 3-(benzo[d][1,3] dioxol-5-yl)-7-isopropoxy-2-methyl-6-propyl-4H-chromen-4-one (Prediction Score: 0.65 and 0.70) as the most potent candidate against asexual and gametocytes stages of P. falciparum with acceptable pharmacokinetic and drug-likeness profile targeting mainly kinases. The two unveiled antimalarial drug lead might serve as a starting point for drug development aiding the malaria elimination agenda.

61 IMPLICATION OF BIOCHEMICAL MARKERS AND ACE2 GENE MUTATION IN THE DISEASE SEVERITY IN MALARIA AND COVID-19 CO-INFECTED PATIENTS IN YAOUNDÉ, CAMEROON

M. Kameni Ngongang, E. Macdonald Bin, S. Kamdem, P. Masumbe Netongo, E. Tchoupe Kamoua*
1Research Laboratory, Molecular Dignostic Research Laboratory, Yaounde, Cameroon
2Medical Biochemistry, University of Yaounde1, Yaounde, Cameroon

Background: Since its first report in December 2019, coronavirus disease 2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), rapidly emerged as a pandemic affecting nearly all countries worldwide. Malaria remains a public health concern in many parts of the world especially in sub-Saharan Africa. Due to the similarity of symptoms between malaria and COVID-19, a malaria patient may be misdiagnosed as COVID-19 and vice versa in malaria endemic areas. The aim of this study was to establish the association between biochemical markers and genetic polymorphisms with disease severity in co-infected patients.

Methods: The study recruited 76 participants from 322 participants enrolled in the CCP project from March 2020 to December 2023. Participants presented with COVID-19 symptoms in Yaoundé, Cameroon. Blood samples were collected for malaria diagnosis using RDT, microscopy, and RT-PCR. Nasopharyngeal swabs were collected for SARS-CoV protein detection using RDT and RT-PCR. Disease severity was evaluated by measuring liver and kidney function markers. Genetic polymorphism was identified using mini Co-Dx qPCR. Data was analyzed using GraphPad Prism version 9 software.

Results: The study included 76 participants, with 32 males (44%) and 40 females (56%). The average age was 35.59 years, ranging from 15 to 66 years. Participants were divided into four groups: 20 with COVID-19, 20 with malaria, 16 with both infections, and 20 controls. The study found that co-infected patients had higher parasite levels (4,900 and 1,773 parasites/µL) compared to malaria mono-infected patients. Liver and kidney function biomarkers varied significantly among groups. Co-infected patients had higher ALAT and ASAT levels ($P = 0.014$ and $P = 0.034$), while COVID-19 patients had higher total Bilirubin levels ($P = 0.031$). Correlation was found between ACE2 gene polymorphism and disease severity.

Conclusion: Our study found that biochemical markers such as ALT, AST, Urea and creatinine levels, as well as genetic polymorphism in the ACE2 gene, were significantly associated with disease severity in malaria and COVID-19 co-infected patients. The combination of these biomarkers and genetic polymorphism allowed for accurate prediction of disease severity, which can inform treatment strategies and improve patient outcomes.

62 MODELING TICK INFECTION BY HAZARA AND DUGBE VIRUSES TO STUDY THE SURVIVAL AND SPREAD OF CRIMEAN-CONGO HEMORRHAGIC FEVER VIRUS IN THE ENVIRONMENT

S. Thibaudeau*1, A. Wu-Chuang1, H. Attoui1, L. Bell-Sakyi2, S. Rogee3, M. Sourisseau1, J. Richardson1, S. A. Lacour1
1UMR Virologie INRAE-Anses-ENVA, Maisons-Alfort, France
2Department of Infection Biology and Microbiomes, Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, 146 Brownlow Hill, Liverpool, United Kingdom
3DGA Maîtrise NRBC Département BioD, Vert-Le-Petit, France

Crimean-Congo hemorrhagic fever virus (CCHFV) is the etiological agent of a febrile syndrome in humans, characterised by hemorrhagic fever and mortality in 10 - 40% of cases. CCHFV is mainly transmitted by the bite of ticks of the genus Hyalomma, which are present in Corsica and the Mediterranean basin. In October 2023, the virus was isolated for the first time in France from Hyalomma marginatum ticks collected from cattle in the Pyrénées-Orientales region.

Because of its role in virus transmission and its importance in the viral cycle, the tick is both the vector and the reservoir of CCHFV. The thesis project therefore focuses on the molecular interactions between the virus and the tick allowing their cohabitation and the persistence of the virus in ticks.

CCHFV is a highly pathogenic virus and can only be handled in a biosafety level (BSL) 4 laboratory. The orthonairoviruses Hazara (HAZV) and Dugbe (DUGV) are both capable of infecting tick cells of the genus Hyalomma. We propose to use these viruses as BSL2 models of CCHFV, in order to map protein-protein and RNA-protein interactions between orthonairoviruses and Hyalomma tick cell lines. For the most robust interactors, their pro- or antiviral role will then be determined by gene-silencing experiments. These interactions will be confirmed on CCHFV replication in Hyalomma cell lines through collaboration with the Direction Générale de l'Armement.

Deciphering these interactions and their role will provide a better understanding of the molecular mechanisms that allow these viruses to persist in ticks.

63 DISSECTING THE VIRAL GENETIC DETERMINANTS OF DIFFERENTIAL MOSQUITO TRANSMISSIBILITY AND MOUSE PATHOGENICITY BETWEEN AFRICAN AND ASIAN LINEAGES OF ZIKA VIRUS

Shiho Torii1, Caroline Manet2, Jennifer S. Lord3, Morgane Lavina1, Ewa Pasquereau-Kotula2, Matthieu Prot4, Etienne Simon-Lorière4, Alicia Lecuyer1, Cheikh T. Diagne5, Oumar Faye5, Ousmane Faye5, Amadou A. Sall5, Michael B. Bonsall6, Xavier Montagutelli2, Louis Lambrechts1
1Institut Pasteur, Université Paris Cité, CNRS UMR2000, Insect-Virus Interactions Unit, Paris, France
2Mouse Genetics Laboratory, Institut Pasteur, Paris, France
3Department of Vector Biology, Liverpool School of Tropical Medicine, Liverpool, United Kingdom
4G5 Evolutionary Genomics of RNA Viruses, Institut Pasteur, Paris, France
5Arbovirus and Viral Hemorrhagic Fevers Unit, Institut Pasteur de Dakar
6Department of Biology, University of Oxford, Oxford, United Kingdom

Aim: Zika virus is a mosquito-borne flavivirus primarily transmitted among humans by Aedes aegypti. Over the past two decades, it has caused significant outbreaks associated with birth defects and neurological disorders. Phylogenetically, Zika virus is divided into two lineages: African and Asian, each exhibiting distinct biological properties. African lineage Zika virus strains are more transmissible by Aedes aegypti and more pathogenic to mice than their Asian counterparts, however the genetic determinants underlying these differences are unknown. The aim of the present study was to address this question.

Methods: We compared an African strain from Senegal and an Asian strain from Thailand by engineering a panel of chimeric viruses, in which segments of the parental genomes were swapped. We also developed a stochastic model of in vivo viral dynamics in mosquitoes.

Results: We found that the structural genes from the African strain enhanced viral internalization, while the non-structural genes improved genome replication and infectious particle production in mosquito cells. Comparing in vivo infection of Ifnar1 knockout mice revealed significant effects of both structural and non-structural genes on the clinical score and plasma viral load. In vivo mosquito transmission was most significantly influenced by the structural genes, although no single viral gene was solely responsible for this effect. The stochastic model of in vivo viral dynamics in mosquitoes showed that the primary difference between the African and Asian strains lied in their ability to cross mosquito salivary glands.

Conclusion: Natural Zika virus variation in mouse pathogenicity and mosquito transmissibility has a complex genetic basis that involves multiple regions of the viral genome.

Keywords: Zika virus, reverse genetics, mouse model, mosquito transmission, within-host dynamics.

64 IMPACT OF LACTOBACILLUS RHAMNOSUS AND BIFIDOBACTERIUM LONGUM ON ENTAMOEBA HISTOLYTICA INVASIVE PROCESS IN THE HUMAN COLON

T. Tréport*, JC. Olivo-Marin, E. Labruyère
Intistut Pasteur, Paris, France

Entamoeba histolytica is a human parasite and the causative agent of amoebiasis. This parasite colonizes the human colon and feed on bacterial microbiota. Amoebiasis emerges only in 20% of humans infected by E. histolytica. However, stimuli triggering the amoebiasis are still unknow. Our hypothesis is that the gut microbiota could influence the outcome of amoebiasis because (1) Studies highlight that bacterial microbiota can shape the virulence of E. histolytica, (2) In India, metagenomic studies in gut microbiota of symptomatic individuals infected with E. histolytica demonstrate a dysbiosis with for example a decrease of Lactobacillus and an increase of Bifidobacterium species compared to healthy patients.

It is still unclear whether this dysbiosis is the cause or effect of the presence of E. histolytica and the development of amoebiasis. To investigate this question, we chose to study the influence of L. rhamnosus and B. longum on E. histolytica's invasive process.

To find out if the phagocytosis of these bacteria could shape the virulence of the parasite, we quantified the activity of cysteine proteases in vitro. These enzymes are one the important virulence factors during the breakdown of the colonic barrier and can be secreted by E. histolytica. After phagocytosis of L. rhamnosus or B. longum, the activity of intracellular cysteine proteases increases, suggesting the implication of cysteine proteases in the phagocytosis process. In contrast, after phagocytosis of each bacterium, extracellular cysteine protease activity decreases, suggesting that the presence of bacteria may reduce the virulence of E. histolytica.

To investigate the impact of L. rhamnosus and B. longum's colonisation on E. histolytica's invasive process we used a human gut-on-a-chip device. We realized real time imaging and image quantification to examine the 3D architecture and the connectivity of the epithelium. Our preliminary results suggest that colonisation of the epithelium by the two bacteria may delay tissue degradation by E. histolytica.

Our further studies will be carried out to determine the mechanisms underlying the potentially protective effect of the two probiotics on the epithelium and/or the parasite.

Funding: Institut Pasteur/PTR 232./Unipharma program, Labex IBEID, France-BioImaging and HORIZON-HLTH-2021-DISEASE-04. The Biomaterials and Microfluidics core facilty was supported by a grant from Institut Carnot Pasteur Microbes & Santé. The Photonic BioImaging Platform was supported by France BioImaging; ANR-10–INBS–04; Investments for the Future.

65 ASSOCIATIONS BETWEEN INFLUENZA AND METEOROLOGICAL PARAMETERS IN FOUR CLIMATIC ZONES OF CAMEROON: IN THE GRASSLANDS, EQUATORIAL FOREST, SAHEL AND THE HIGHLANDS FROM 2017 TO 2022

D. Tsafack*1, C. Monamele1, F. Koro Koro2, N. Mohamadou Ripa1, C. Nsangou Yogne3, C. Ndongo Bilounga4, H. Munshili Njifon5, U. Tamoufe6, R. Perraut7, R. Njouom8
1Virology, Virology Department, Centre Pasteur Cameroon (CPC), 451, Street 2005, Yaoundé 2, PO BOX 1274, Yaoundé, Cameroon, Yaounde, Cameroon
2Research Laboratory, Department of Biochemistry, Faculty of Sciences, University of Douala, PO BOX 24157, Douala, Cameroon, Yaounde, Cameroon
3Virology, Garoua Annex, Centre Pasteur of Cameroon, Garoua, Cameroon, Garoua, Cameroon
4Research Laboratory, Department for the Control of Diseases, Epidemics and Pandemics (DLMEP), Ministry of Public Health, Yaounde, Cameroon, Yaounde, Cameroon
5Virology, Garoua Annex, Centre Pasteur of Cameroon, Garoua, Cameroon, Garoua, Cameroon
6Virology, Metabiota, Inc., PO Box 15939, Yaounde, Cameroon, Yaounde, Cameroon
7Virology, Garoua Annex, Centre Pasteur of Cameroon, Garoua, Cameroon,
Garoua, Cameroon 8Virology, Virology Department, Centre Pasteur Cameroon (CPC), 451, Street 2005, Yaoundé 2, PO BOX 1274, Yaoundé, Cameroon, Yaounde,
Cameroon 9Virology, Virology Department, Centre Pasteur Cameroon (CPC), 451, Street 2005, Yaoundé 2, PO BOX 1274, Yaoundé, Cameroon, Yaounde,
Cameroon 10Virology, Virology Department, Centre Pasteur Cameroon (CPC), 451, Street 2005, Yaoundé 2, PO BOX 1274, Yaoundé, Cameroon, Yaounde, Cameroon

Background: Numerous meteorological studies have attempted to relate climatological parameters to seasonal influenza. In this study we describe the relationship between meteorological parameters and influenza in four different climatic zones of Cameroon which have different climatic conditions.

Methods: This is a descriptive study conducted over a period of six years from January 2017 to December 2022 on 4263 nasopharyngeal samples. During this period, patients with influenza-like illness (ILI) and severe acute respiratory infection (SARI) were recruited from thirteen sentinel influenza surveillance sites in the Centre, Littoral, North and West regions of Cameroon. Monthly proportions of confirmed influenza cases were considered as dependent variables, while the monthly values of twelve meteorological parameters including temperature, humidity, precipitation, and solar radiation were considered as independent variables. SPSS Expert Modeller was used to determine associations between influenza activity and meteorological covariates in the different regions and to predict influenza activity during the last study year.

Results: Of the samples collected, 1175 were confirmed positive for influenza. Of the twelve candidate predictors included in the model in the Centre region, the expert modeller identified the maximum temperature at 2 meters as useful for predicting influenza B in 34.9% of cases. Meanwhile, the winter's additive model was the best for predicting total influenza and influenza A activity. According to the stationary R2, 30.8% and 36.9% of total influenza cases in the Littoral and North regions are explained by earth surface temperature and average corrected precipitation, respectively. In the West region, a simple seasonal model best described influenza activity at over 60%, with no identified climatic variable as a predictor.

Conclusions: These results will significantly contribute to reducing the burden of influenza in Cameroon through timely public health interventions.

Keywords: Influenza, meteorological parameters, forest zone, Sahelian zone, western highlandz

66 COMPARATIVE ANALYSIS OF RLR-SPECIFIC RNA LIGANDS DURING INFLUENZA VIRUS INFECTION

D. Uresin*1, S. Caglar1, V. Najburg2, R. Legendre3, C. Cassonet1, A. Di Gioacchino4, A. Barinov2, Y. Rahou2, S. Cocco4, S. Van Der Werf5, C. Demeret1, A. Komarova1
1Virology, Interactomics RNA and Immunity lab, Institut Pasteur, Paris, France
2Laboratoire Commun Institut Pasteur-Oncovita, Institut Pasteur, Paris, France
3Hub de Bioinformatique et Biostatistique, Institut Pasteur, Paris, France
4Laboratoire de Physique de l'Ecole Normale Supérieure, ENS, Paris, France
5Génétique Moléculaire des Virus à ARN, Institut Pasteur, Paris, France

Influenza viruses are members of the Orthomyxoviridae family with the genome consisting of segmented negative-sense single-strand RNA segments. They cause seasonal epidemics with a substantial burden on public health. RIG-I-like receptors (RLRs) play a major role in sensing RNA virus infection to initiate and modulate antiviral immunity. The RLR family consists of three members: RIG-I, MDA5, and LGP2. Several pieces of evidence indicate that RIG-I plays an important role in controlling of IAV infections. To this end, we first determined whether RIG-I and MDA5 were implicated in the immune response against the H1N1 pandemic strain from 2009 (WT H1N1pdm09) using knock-out (KO) respiratory cell lines. Both RIG-I and MDA5 were found to be implicated in the activation of the interferon (IFN) response upon H1N1pdm09 infection. Then, we used previously validated cell lines overexpressing One-STrEP tagged RLRs to purify RLR-specific RNA ligands from WT H1N1pdm09-infected cells by affinity chromatography followed by RNA extraction from RLR ribonucleoprotein complexes. Lastly, we used next-generation sequencing (NGS) to determine the RNA sequences of isolated RLR ligands. Overall, we isolated, characterized, and compared potential RLR ligands in IAVinfected cells.

67

MODELLING THE AIRR RESPONSE TO DENV1: A HUMAN CHALLENGE STUDY

T. Verdonckt*1, K.K. Ariën1, F. Van Nieuwerburgh2, A.S. Vermeersch2, C. Struyfs3, O. Lagatie3
1Unit of Virology, Department of Biomedical Sciences, Institute of Tropical Medicine, Antwerpen, Belgium
2Laboratory for Pharmaceutical Biotechnology/NXTGNT, Faculty of Pharmaceutical Sciences, Ghent University, Gent, Belgium
3Janssen Pharmaceutica NV, Beerse, Belgium

Dengue fever, caused by the dengue virus (DENV), is a vector-borne disease that poses a significant global health threat predominantly affecting tropical and subtropical regions. The incidence of dengue has dramatically increased over the past decades, with recent years witnessing historically high case numbers. Most DENV infections are asymptomatic or manifest as mild illness, but the disease can progress to severe forms, such as dengue hemorrhagic fever or dengue shock syndrome, which can be fatal. Severe dengue is particularly associated with secondary infections by different DENV serotypes, a phenomenon linked to antibody-dependent enhancement.
We hypothesize that severe dengue is an immunopathology, where severe clinical outcomes are influenced by aberrant immune responses. Our objective is to identify immunological markers of severe disease with prognostic value. To achieve this, we first aim to model the adaptive immune receptor repertoire (AIRR) response to dengue virus serotype 1 (DENV1) in healthy individuals and identify commonalities in the immune response.
To this end, we performed a retrospective study on clinical samples of a controlled human challenge study. In this study, nine healthy volunteers were infected with DENV1 under strictly controlled conditions. The participants were closely monitored, and blood samples were collected on days 0, 8, 10, 14, and 28 post infection. We analyzed the AIRR of these individuals on all timepoints using bulk B-cell receptor and T-cell receptor sequencing.
The poster will present the detailed results of these experiments, shedding light on the dynamics of the immune response to DENV1. By understanding these immune mechanisms in healthy subjects, we aim to establish a foundation for identifying immune markers predictive of severe dengue, which could inform future therapeutic and preventive strategies.

68 ANTILEISHMANIAL POTENTIAL AND IN SILICO PREDICTION OF PHARMACOKINETIC PROPERTIES OF SOME SYNTHETIC PHENOLIC COMPOUNDS

D. Wendji Monkam*1, C. Safeh1, R. Kemzeu1, C. Njanpa Ngansop1, M. Tchatat Tali1-2, D. Dize1, B. Pone1, L. Yamthe1, P. Tsouh1, F. Fekam Boyom1-2
1Biochemistry; Antimicrobial and Biocontrol Agents Unit, Laboratory of Phytobiochemistry and Medicinal Plants Study, University of Yaounde 1, Yaounde, Cameroon
2Malaria Drug Discovery, Advanced Research and Health Innovation Hub, Yaounde, Cameroon

Leishmaniasis is a Neglected Tropical Disease caused by flagellated protozoan parasites belonging to the Leishmania genus. The management of leishmaniasis mainly relies on chemotherapy through the use of Amphotericin B and its liposomal derivatives such as Miltefosine and Paromomycin. However, the effectiveness of the current treatment options is impeded by the toxicity, the development of resistance and their high cost, underlining the urgent need to search for new drug alternatives. Synthetic phenolic compounds, due to their wide spectrum of biological activity as highlighted in the literature, might be promising alternative for the discovery of potential antileishmanial drug candidate. The current study was designed to evaluate the antileishmanial potency with an emphasis on the pharmacokinetics and drug-likeness properties of potent compounds. Briefly, 17 synthetic compounds were tested for antileishmanial activity and in vitro toxicity respectively on the extracellular promastigote and on mammal cells using the resazurin based colorimetric assay. Active and non-toxic compounds were further tested for antileishmanial assay on the intracellular amastigote form and cytotoxicity on VERO cells. Active and selective compounds were selected for the kinetic study, then their pharmacokinetic properties were predicted using the SwissADME and pKCSM predictor tools. Of the 17 compounds tested, five showed very good activity on the promastigote form with IC50s ranging values ranging from 0.16 µg/mL to 5.88 µg/mL and only 4-isobutylvinylether B-pyranonaphthoquinone and 4- phenyl-B-pyranonaphthoquinone were selective on RAW cells (SI 1250 and 43.19 respectively). In addition, these 2 compounds showed very good activity on the intracellular amastigote form with IC50s of 1.25 and 1.16 µg/mL respectively and were selective toward VERO cells (IS of 21.68 and 47 .65 respectively). Inhibition kinetics studies showed that the compounds inhibited the growth of the promastigote form ofL eishmania donovani irreversibly within 4 hours and 24 hours respectively. The in silico analysis revealed that compounds, showed variable but promising pharmacokinetic properties with minimum toxicity. In conclusion, these two active compounds endowed with antileishmanial activity and favourable pharmacokinetics properties. However, In vitro and in vivo studies are recommended to validate the antileishmanial activity as well as the pharmacokinetics and toxicity profiles.

F.A.Q

Wondering how to prepare your presentation? In need of information about the conference location? Please read our F.A.Q. to explore the most frequently asked questions:

01 Congress Location

All the presentation, poster sessions and social events will take place in the Auditorium CIS and nearby rooms, at the Institut Pasteur of Paris. For this event the entrance of the Institut Pasteur will only be possible by the 205, rue de Vaugirard, 75015 Paris.

Please come with a valid ID document

You will have a unique badge for the entire event, please keep it visible all the time

02 Presentation Format

Each presentation has its own format, see the list below:

- **Keynote Lecture: 30 min + 15 min questions**
- **Invited Talk: 20 min + 10 min questions**
- **Selected Short Talk: 12 min + 3 min questions**

03 Poster Sessions

The posters will all be displayed at the same time during the whole event, just check your poster number on the lists in the poster room to set up your poster.
The presentation of your poster will be done by Even/Odd numbers to maximize space for each speaker. all the Even number will be presented during the Session 1 and all the odd numbered posters during the Session 2 (please refer to the conference program)

Recommend poster size: H x l 100cm x 70cm / 39” x 27”

04 Stay connected during the congress

Stay connected to your team and collaborators thanks to our free WI-FI accessible in the buildings. The QR code and password will be displayed in the audiotrium and nearby rooms.

Contact

ibeid-2024@conferences-pasteur.org

www.labexibeid.fr