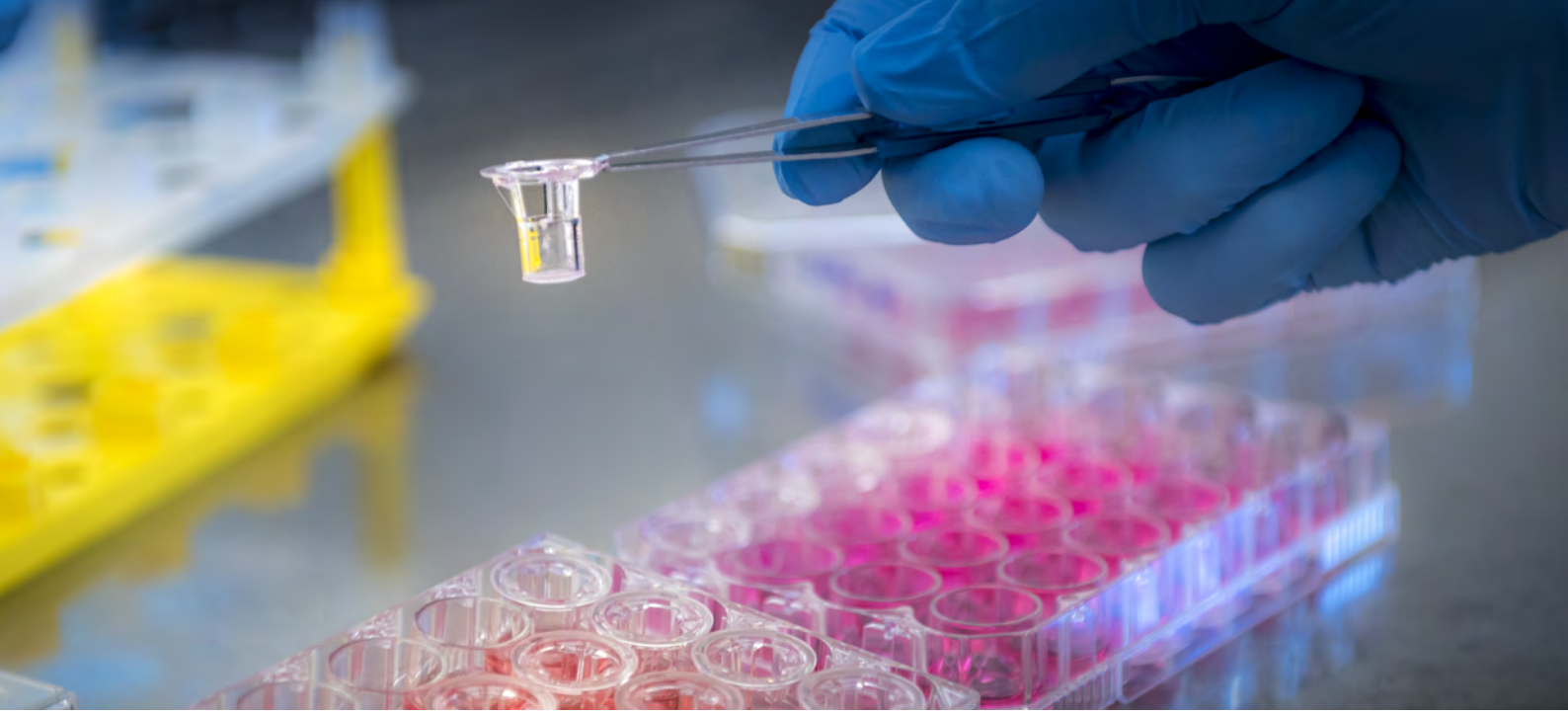

CIIL NewsLETTER

Jean Dubuisson

After the difficulties linked to the departure of several staff members of the administrative office, we begin 2024 more serenely. Indeed, the office has now been reinforced with the arrival of our new secretary-general, Sabine Blin. We took this opportunity to reorganize the administrative office in order to optimize its performances. The past year was also marked by the evaluation of the teams by the Institut Pasteur de Lille and 2024 will see the HCERES evaluation of the unit. In this issue, we continue with the presentation of researchers and engineers who actively contribute to the CIIL project. Here, we present Muriel Pichavant, Inserm researcher and Audrey Tarricone, CNRS engineer who joined the unit in January 2023 to work on the Virocrib program. We also congratulate Florent Sebbane who was granted an ERC Synergy grant and who is the coordinator of a PEPR program from ANRS-MIE on plague. In this issue, we also highlight the potential applications based on research programs developed by our scientists. Philip Supply presents his diagnostic kit for drug-resistant tuberculosis developed in collaboration with Genoscreen company and validated by the WHO. Nathalie Mielcarek and Jean-Claude Sirard present their work on nasal vaccines. Finally, a kit based on predictive markers of bovine health and developed by the team of Eric Viscogliosi has recently been licensed to the company Gènes Diffusion. I also take the opportunity of the newsletter to wish you all an excellent year for 2024.

Jean DUBUISSON

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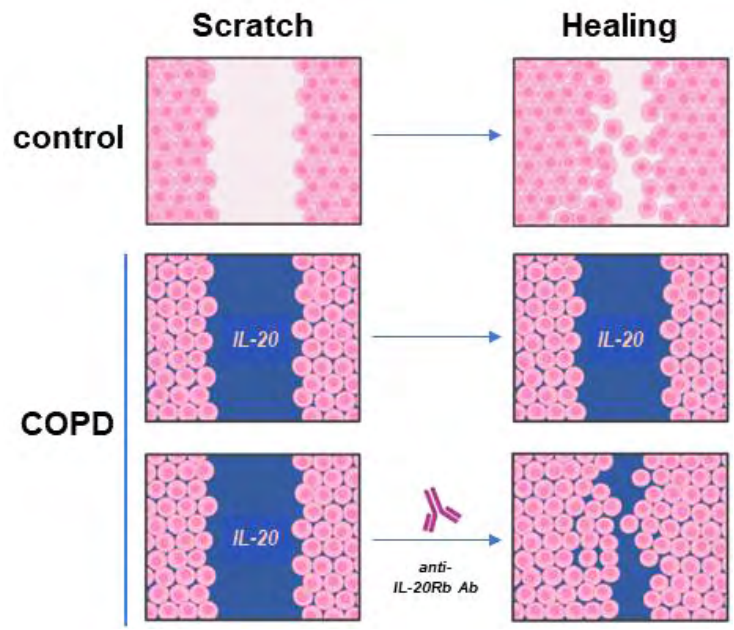
Muriel PICHAVANT
INSERM Researcher

I am Muriel Pichavant, Inserm Research Fellow and Co-Director of the «Opportunistic infections, immunity, environment and lung diseases» research team at the CIIL. I have always been interested in respiratory health, because it's a subject that touches me personally. That is why my entire research career, from my DEA (post-graduate diploma) to the present day, has always focused on lung diseases.

After training at the Université de Bretagne Occidentale (Brest, 29), I came to do my DEA and then my thesis on chronic respiratory diseases here at the Pasteur Institute in Lille, in the Inserm U416 Unit, under the supervision of Professor André-Bernard Tonnel. Dr Philippe Gosset shared his passion for the pulmonary immune system. During my thesis, I became interested in the close cross-talk between lung epithelial cells and dendritic cells, in homeostasis and also in the inappropriate response found in an asthmatic patient allergic to house dust mites. This translational research project enabled me to collaborate with pulmonologists at the Calmette Hospital of the Lille CHRU. It was also an opportunity to develop collaborations on the Campus, as well as with industry.

To expand my knowledge of the pulmonary immune system, I spent almost 5 years as a post-doctoral fellow at Childrens Hospital, Harvard Medical School in Boston, USA, in Professor D. Umetsu's laboratory. Dale put his trust in me as soon as I arrived and enabled me to develop new experimental models (mice and primates) as well as new tools useful for my projects. This is how I became interested in the immune mechanisms involved in the development of non-allergic asthma. I highlighted the pathogenic role of innate lymphoid cells (iNKT and ILC3) in neutrophilic asthma induced by an 'environmental' stress such as ozone, but also by a 'behavioural' stress such as a high-fat diet. This work has also enabled us to identify Th17 cytokines as potential therapeutic targets in these pathological contexts.

Still interested in the impact of environmental factors on chronic respiratory diseases, I returned to France as an Inserm CR in Dr François Trottein's team, just before the creation of the CIIL (2010), and then joined Dr Philippe Gosset's group. It was at this point that the theme of exacerbations of chronic lung disease emerged: Why do patients suffering from chronic lung disease experience a series of infectious episodes? Why are they more 'susceptible' to respiratory infections? Can we predict the onset of an exacerbation? These are the questions that have been at the heart of our research since then, with a particular focus on Chronic Obstructive Pulmonary Disease (COPD). This disease, whose main aetiological factor is cigarette smoke, is the 3rd leading cause of death in the world. COPD is an irreversible disease for which there is currently no cure. Only certain associated symptoms can be managed. There is therefore an urgent need for a better understanding of the disease, so that COPD patients can be better cared for. Thanks to local infrastructures and the active participation of lung specialists from the Lille CHRU (Olivier Le Rouzic, Stéphanie Lejeune, Cécile Chenivesse), we have been able to set up original experimental models, establish patient cohorts and develop unique tools. In mice and humans, we have shown that exposure to cigarettes alters the functional properties of dendritic cells and pulmonary macrophages, promotes an IL-17 response but impairs the IL-22 response, factors which could partly explain the increased susceptibility to pulmonary infections. In order to manipulate the host immune system and re-establish a competent immune response to pathogens, we have developed numerous intra-CIIL collaborations (Patricia de Nadai, Aurélie Tasiemski and Céline Wichlacz, Oleg Melnyk and Jerôme Vicogne, Camille Locht and Anne-Sophie Debrie, Priscille Brodin, Isabelle Wolowczuk) and on the IPL campus (Florence Pinet, David Hot), which have been financially supported by the CIIL (intraCIIL project), the CPER and the ANR.
Recently, the role of IL-20 cytokines, which, along with IL-22, belong to the IL-10 family, has emerged. Using a combination of murine and human approaches, we have shown that these cytokines are induced in COPD conditions and play a deleterious role in the control of lung infection and repair of the epithelial barrier (Figure). The monoclonal antibody that neutralises IL-20 cytokine



signalling, identified after screening a Display phage library, seems to us to be a promising therapeutic tool.

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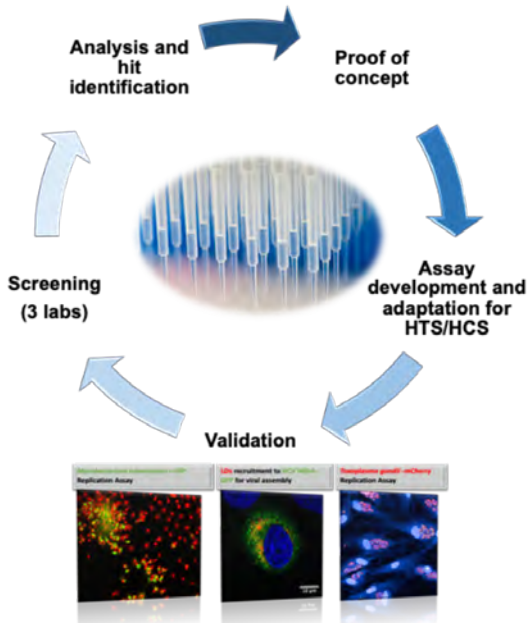
To find out more :

MOOC Université de Lille «Têtes chercheuses, les métiers de la recherche» :
www.my-mooc.com/fr/mooc/tetes-chercheuses-les-metiers-de-la-recherche/

Podcast «A pleins poumons» :
https://podcast.ausha.co/la-vie-institut-pasteur-de-lille/18-muriel-pichavant-a-pleins-poumons



Audrey TARRICONE
Research Engineer - CNRS

In 2015, after a Master 2 degree in Biological and Technological Sciences for Health from Jean Monnet University in Saint-Etienne, I joined the Bordeaux University Hospital and more specifically the Analytical Platform for Health Research in the Immunology and Immunogenetics Laboratory. After two years on the platform, I had the opportunity to become the operational manager. The aim was to ensure the £operation and technological development of the platform for the local, national and international scientific projects. With this experience, I discovered the clinical research in a hospital environment, I developed platform management skills and I worked on academic and industrial projects in various fields. Over these 5 years, I have been involved in the development of the 3 analytical fields of the platform: cell biology (flow cytometry, etc.), molecular biology (nCounter Flex a digital color-coded barcode technology for direct multiplexed measurement of gene expression, etc.) and serum biomarker assays (Bioplex 200).

In 2021, I joined the ARIADNE-Screening platform of the PLBS-UAR2014-US41 unit., as an engineer. This high-tech HCS-L2 platform is used to the high-content screening of biological disruptors such as siRNAs or small chemical molecules, potential drug candidates.
With this experience, I discovered the academic research and new technologies such as the acoustic nanodispenser and the automated confocal fluorescence microscope.

Since January 1, 2023, I'm working as an engineer in antiviral screening techniques in the MCV (Molecular and Cellular Virology) team, under the supervision of Dr Jean Dubuisson. I joined the VIROCRIB infrastructure, created by the CNRS, bringing together a consortium of virologists and biologists, research teams and technological platforms for screening molecules in several preclinical models (in vitro, ex-vivo, in vivo) with the aim of responding rapidly to the emergence of future pathogenic viruses that could lead to global health crises.
Today, the team is continuing its research to identify new antiviral molecules against coronaviruses on cell culture models in level 2 and 3 laboratories.

Nathalie MIELCAREK

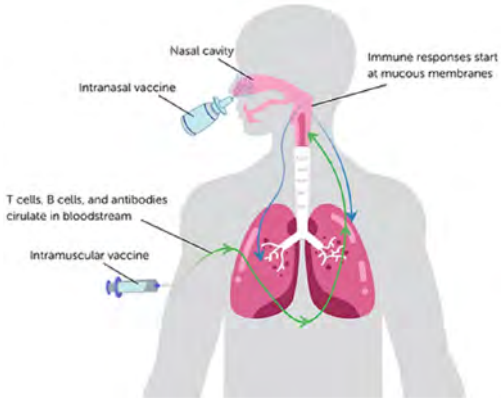
Jean-Claude SIRARD

NOSEVAC project: Leading the Frontier in Nasal Vaccine Development

The recent COVID-19 crisis has underscored the critical importance of large-scale vaccination in mitigating morbidity and mortality during pandemics, especially among the most vulnerable populations. However, one of the limitations of current vaccines is their limited ability, if not inability, to reduce pathogen transmission. This is even more obvious in the context of a respiratory infection, where the pathogen is transmitted by aerosol droplets expelled by an infected individual to an uninfected person.

CIIL is a pioneer and leader research center in the development of nasally delivered vaccines. These groundbreaking vaccines not only prevent disease, but also inhibit infection by a respiratory pathogen and transmission to a healthy person. Nasal vaccine administration allows for the local stimulation of the respiratory immunity to prevent infection or colonization by viruses or bacteria that use the nose as an entry point into the host. The induction of protective mucosal immunity, in particular through the production of secretory IgA and the activation and proliferation of tissue-resident memory T cells, proves highly effective in preventing pathogen entry and proliferation, and is primarily achievable through nasal vaccine administration.

At the CIIL, the team currently led by Nathalie Mielcarek, Inserm Research Director, and formerly by Camille Locht, Inserm Emeritus Director, has developed a live vaccine consisting of Bordetella pertussis, the bacterium responsible for whooping-cough, which has been genetically attenuated (Mielcarek et al. PLoS Pathogen 2006). Known as BPZE1, this vaccine strain, is deficient in the production of three major toxins and has been shown to be safe in several animal models before being evaluated in humans (Thorstensson et al. PLoS One 2014 ; Jahnmatz et al. Lancet Infect Dis 2020). Recent results from a phase 2b trial showed that BPZE1 induces broad, robust and durable nasal immunity (Keech et al. Lancet. 2023). BPZE1 therefore has the potential to achieve control of B. pertussis epidemic. These results should now be confirmed in a large phase 3 trial supported by ILIAD Biotechnologies, the licensee of BPZE1.



In parallel, a new European consortium, called NOSEVAC (Horizon Europe 2023-2028), has been launched in 2023 to develop innovative formulations to deliver nasal vaccines based on messenger RNA, self-amplifying RNA, and protein antigens technologies. NOSEVAC is focusing on bacterial and viral pathogens causing infections of the upper and lower respiratory tracts, including Streptococcus pneumoniae, SARS-CoV-2 and Influenza viruses. Two CIIL teams, led by Nathalie Mielcarek and Jean-Claude Sirard, actively participate in the NOSEVAC consortium coordinated by the European Vaccine Initiative which brings together 12 partners from 9 European countries. The NOSEVAC consortium's objective is to advance nasal vaccine platforms as an innovative approach to prevent infection at the earliest stage, thereby inhibiting upper respiratory tract infection by viruses and bacteria and preventing transmission and disease.

Additional informations are available at:
www.nosevac-project.eu/

The first-of-its-kind next generation sequencing-based kit for detection of drug resistant tuberculosis recommended by the World Health Organization

Philip SUPPLY

Drug resistant tuberculosis (TB) is the first cause of mortality due to antimicrobial resistance globally. Only 40% of the ~400,000 people who develop multidrug (MDR) TB each year are diagnosed and treated, far below targets of the World Health Organization's (WHO) End TB Strategy and the 2018 United Nations high-level meeting on TB. More than a dozen drug classes compose first and second line anti-TB treatment regimens. Due to the slow growth of Mycobacterium tuberculosis, drug susceptibility testing by culture can take up to two months, and conventional rapid molecular tests including one or few genetic targets only, resulting in treatment deficiencies and unsuccessful patient outcomes.

In order to overcome these limitations, I worked with GenoScreen on the IPL campus to develop novel molecular diagnostic tools, by leveraging the extraordinary progress of next generation sequencing (NGS) technologies and the accumulated knowledge on modes of action of anti-TB drugs and associated resistance mechanisms. As a part of this project, we teamed up with a world-wide consortium, called CRyPTIC, of which I chaired the steering committee, and which was funded by the Wellcome Trust and the Bill and Melinda Gates Foundation, and led by the University of Oxford with 30 world partners, including the WHO, the US and Chinese CDC. The overarching goal is to establish a comprehensive catalogue of genetic determinants of resistance in M. tuberculosis as a basis for the development of new molecular diagnostics, by whole genome sequencing (WGS) analysis of phenotypically resistant or phenotypically susceptible isolates collected worldwide. As of end 2023, more than 50,000 genomes have been analyzed, including 1,400 that were sequenced at GenoScreen. Different co-publications revealed new resistance determinants, and showed high performances of obtained catalogues to predict drug susceptibility or drug resistance. Two successive catalogues have been endorsed as a standard reference by the WHO, based on > 35,000 genomes in 2022 and expanded to > 50,000 genomes in 2023. However, in clinical routine conditions, WGS still requires a primary culture, taking usually 7-10 days, thereby delaying detection of resistance and treatment decisions.

Therefore, at GenoScreen and in the frame of the PathoNGenTrace SME-targeted Collaborative project supported by the EU FP7-HEALTH program, we conceived and developed an alternative culture-free approach, based on targeted next-generation sequencing (tNGS), which we finalized as the first-of-its-kind tNGS diagnostic assay of resistance to antimicrobials, called Deeplex® Myc-TB. This assay relies on a single 24-plex PCR, directly applicable on clinical specimens, including 18 main resistance associated gene targets, and followed by deep amplicon sequencing. The test can thereby simultaneously predict

Deeplex Myc-TB results, showing detection of a M. tuberculosis strain with an extensively drug resistant (XDR) mutation profile and with a Beijing/Lineage 2 genotype. Target gene regions (shown at the inner edge of the colored areas) are grouped into sectors according to the TB drug resistance with which they are associated. Red and green sectors indicate targets in which mutations associated with resistance are detected (in red around the circular map), and the regions in which no mutations or only mutations not associated with resistance (in grey around the map) are detected, respectively. ©GenoScreen, Lille.

resistance or susceptibility to 15 anti-TB drugs, genotype M. tuberculosis complex strains and identify more than 100 mycobacterial species, including non-tuberculous pathogens. We developed it as a ready-to-use molecular kit, coupled to a dedicated web app that integrates a mutation catalogue now based on the >50,000 genomes, included in the latest WHO catalogue. Time from clinical specimens to comprehensive diagnostic results can be reduced to 24-48h. As such, Deeplex Myc-TB is the most comprehensive rapid molecular diagnostic of drug resistant TB commercially available today, and the sole that can detect extensively resistant TB, as recently redefined by the WHO. This kit, which is produced by GenoScreen in Lille, has been marked for In Vitro Diagnostic in 2019.

We showed the high degree of accuracy of the assay to predict drug resistance or drug susceptibility based on data from > 4,000 isolates and 1,600 clinical specimens, and demonstrated that it could capture 97.1–99.3% of resistance phenotypes predicted by WGS. Our test was compared to a molecular "Swiss Army knife" as a result of its unprecedented versatility, by an editorial in the

European Respiratory Journal (doi: 10.1183/13993003.04077-2020). We used this new test to reveal a silent longitudinal outbreak of MDR-TB in South Africa (showcased in the 2018 annual report of CNRS Biology), and to show the national prevalence of zoonotic TB in a Middle East country, which were both undetectable by standard WHO-endorsed tests. The crucial need for such an extensive test for diagnosis and surveillance was further demonstrated by two large phylogenomics studies conducted with other international teams, showing the global spread and accumulation of resistance to up to 11 anti-TB drugs in major clones of M. tuberculosis. We also used Deeplex Myc-TB as a unique "reverse translational research" tool, to discover rare, evolutionarily early branching lineages of TB bacilli with outstanding biological and genomic features in East Africa.

Moreover, we participated to two large diagnostic trials to inform evaluation by WHO of tNGS as a novel diagnostic. After a successful pre-clinical phase, we implemented our test in TB reference centers in Benin and Rwanda in the H2020 EDCTP DIAMA project (including 9 African and 3 European countries), and in India, South Africa and Georgia in the UNITAID-funded Seq&Treat project led by the Geneva-based FIND foundation. Based on the obtained results, the WHO officially communicated in July 2023 that our assay was accurate - and the sole test meeting performance criteria for all 10 anti-TB drugs that were reviewed -, implementable in routine and cost-effective. As a result, the WHO now recommends Deeplex® Myc-TB to guide critical clinical decision-making for drug-resistant TB treatment.

A partnership has now also been concluded with the US company Illumina (world n°1 in sequencing), for worldwide distribution of the GenoScreen kit combined with sequencing consumables, under a Global Health Access initiative to support accelerated use in low- and middle-income countries. Deeplex Myc-TB is now used by the WHO and in >30 countries.

Our ongoing projects include the development of novel versions adapted to newly recommended treatment regimens for MDR-TB, and for detection of resistance in the causal agent of leprosy, M. leprae, and other pathogens.

These achievements are the results of ten years of common research efforts conducted with the R&D team at GenoScreen and with international teams. They have been recognized by the "Gardner Middlebrook Lifetime Achievement Award", received from the European Society of Mycobacteriology in 2022.

Cattle health prediction kit

Magali Chabé, et Eric Viscogliosi

Our ECOPHIP team focuses on the intestinal protozoa Cryptosporidium and Blastocystis, with major implications for public health, both in terms of health risk and health promotion. We aim to study these organisms using the «One Health» approach at the Human-Environment-Animal interface, through interdisciplinary and multi-species research, looking particularly at possible sources of transmission of these unicellular eukaryotes between human and animal populations, studying their biodiversity, life cycle, pathophysiology and impact on the gut microbiota.

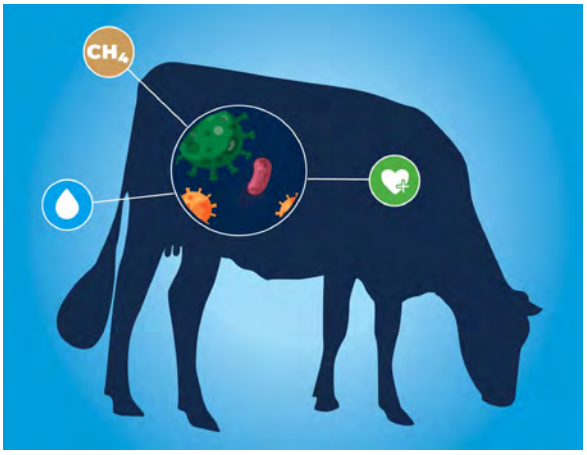
Back in 2016, as part of a collaboration with Christophe Audebert and Gaël Even, respectively R&D Director and Bioinformatics Data Scientist at GD Biotech / Gènes Diffusion, we highlighted the beneficial impact of Blastocystis on the gut bacterial microbiota in humans, both in terms of diversity and bacterial composition (Audebert et al., 2016). These results were confirmed by our group and other international teams, with Blastocystis now considered a member of a healthy gut microbiota. Our team has also joined the COST CA21105 Action - Blastocystis under One Health.

Collaboration with GD Biotech, a company specializing in biotechnologies for the agro, agri and environmental sectors, naturally continued in order to determine the prevalence of this protozoan in dairy cows in the Hauts-de-France region (Audebert et al., 2022), and of course to study its impact on the gut microbiota of dairy cows.

Following promising preliminary results, a co-maturation project led by Magali Chabé, with the bipartite agreement of SATT-Nord and GD Biotech, led to the filing of a European Patent (No. EP 22 212 049: Blastocystis sp. as a Predictive Biomarker of High Productive Longevity in Dairy Heifers), which is currently the subject of an international PCT application (PCT/EP2023/084652). An exclusive license has been signed between SATT-Nord and SAS Gènes Diffusion through its subsidiary GD Biotech, for the development of a detection kit for this biomarker predictive of health and productive longevity in cattle.

In fact, Blastocystis can be detected relatively early in heifers, where it is predictive of their ability to assume greater longevity in dairy production. In the animals included in the various studies carried out, it has been shown that young animals

with this biomarker have a greater longevity in dairy production (+25% longevity). If an animal carries this biomarker before the age of its first insemination, it will be able to produce more milk throughout its career. This improvement is made possible by animals that are more robust in the face of various infectious episodes. For example, biomarker-negative animals were found to have a much larger reservoir of potential pathogens.



Producing more during their dairy careers, these animals will also be more efficient in terms of their carbon footprint. Improving the longevity of dairy animals is in fact one of the levers for reducing the carbon impact of milk production, given that milk yields are not degraded for animals carrying the biomarker. This improvement in carbon footprint is currently estimated at around 15%.

Below, the additional information :

www.gdbiotech.eu/wp-content/uploads/2023/11/CP-GENES-DIFFUSION-FINAL-1-1.pdf

Florent SEBBANE

SYNERGY-PLAGUE : ERC Synergy project of the European Research Council

CIIL's plague and Yersinia pestis team, Nils Stenseth from the University of Oslo, Philip Slavin and Ulf Büntgen from the Universities of Stirling and Cambridge respectively, have been awarded funding from the European Research Council's ERC Synergy Grant. This funding will enable the implementation of a highly ambitious, interdisciplinary project entitled «Reconstructing the environmental, biological and societal factors of plague epidemics in Eurasia between 1300 and 1900 CE - Synergy-Plague». This project will address four main questions:

- How did the plague reappear in Europe in the 14th century?
- How did the plague reappear and spread in Eurasia after the Black Death?
- How did the clinical and demographic patterns of plague infection differ in space and time?
- Why did the plague disappear from Europe and the Middle East in the 18th and 19th centuries?

The project is based on the hypothesis that the waves of plague and the differences in reported clinical manifestations of plague between the second and third pandemics resulted from the unique alignment of multiple events: environmental (climatic and pedo-chemical), biological (from the individual to the ecosystem) and societal (demographic, socio-economic and political).To carry out this project, the four principal investigators (in the natural and human sciences), together with their team members and collaborators, are working together to identify the causes of the pandemic.

CIIL'S EVENTS

Third meeting of FHU RESPIRE, November 21- 2023

The "Fédération Hospitalo-Universitaire RESPIRE" project, coordinated by Claire ANDREJAK, Professor of Pneumology at the Amiens-Picardie University Hospital, is made up of the Amiens-Picardie, Caen, Lille and Rouen University Hospitals, INSERM and the main universities in the North-West inter-region. The FHU RESPIRE aims to strengthen hospital-university-research unit relationship in order to promote medical research about respiratory health and to improve the quality of care through more rapid dissemination of innovations. The central theme of this FHU is the impact of the environment on inflammatory and infectious lung diseases and their interactions.

FHU RESPIRE's 3rd meeting was held on 21 November in the IBL. After a progress report on the FHU RESPIRE project by Claire Andrejak, the coordinator, and Sandrine Dhenin-Pepin, the administrative manager, François Trottein has presented the latest advances on the theme of senescence and viral lung infections.
After this, the students who are leading the 3 FHU RESPIRE-accredited thesis projects, have reported their results:

* Elise Charrier (Amiens): Synthesis and biological evaluation of new antimycobacterials

* Daphné De Riols de Fonclar (Caen) EmerCoV: Evolutionary dynamics of Sarbecoviruses: mechanisms and conditions for the emergence of SARS-CoV-2

* Alice Michel (Rouen) MICROBIOSTHME: Study of the dynamics of upper and lower respiratory tract microbiomes associated with severe asthma in infants.

The morning has been concluded with a lecture by Nadia Haddad, Professor of Regulated Diseases, Zoonoses and Epidemiology at the Ecole Nationale Vétérinaire d'Alfort, who presented the latest and most worrying developments in avian influenza zoonoses.
Oral and poster presentations by researchers and student researchers from the various teams have given to everyone an opportunity to assess the wide range of topics covered by the FHU.
Then, two round tables provided an opportunity for participants to discuss «Organoids and epithelial cells», led by Audrey Vincent, and «Setting up population/environment projects», led by Luc Dauchet and Stephan Gabet.

Finally, we would like to congratulate Guillaume Pamart, currently a PhD student in the OpInfIELD team, who received the best poster award for his work on the role of quinolinic acid in modulating the inflammatory response to influenza virus infection. This will enable him to take part in a conference in his field in the near future.

Worth noting :

- The 4th FHU RESPIRE Day by video on Zoom on 05/14st/2024
- The 2nd FHU RESPIRE Congress in Cabourg city (Normandy), on 11/28st-29st/2024

Odile POULAIN

CIIL meets high school students in Lille

Over the past few years, several CIIL teams involved in the DECLICS program (Dialogue Entre Chercheurs et Lycéens) to interest them in the construction of knowledge:
www.cerclefser.org/fr/declics/
Established in 2014 by the Cercle FSER (Fondation Schlumberger pour l'Education et la Recherche), the DECLICS program aims to promote research, its approaches and its issues among young people and encourage the involvement of research staff in dialogue with the general public.

DECLICS Ambassadors» at Lycée Faidherbe, Lille (From left to right: Sylvia Viscogliosi, 3rd year Medical School / Master student; Jeremy Desramaut, Technician; Manon Ryckman, PhD student; Ruben Garcia Dominguez, PhD student; Constance Denoyelle, PhD student; Angéline Reboul, Post-doc; Magali Chabé, Assistant-professor, Gabriela Certad, Researcher; Nausicaa Gantois, Engineer; Eric Viscogliosi, DR CNRS).

Within this framework, and in collaboration with the Cercle FSER and teachers of Life and Earth Sciences (SVT), members of the CIIL teams meet scientifically-oriented students in their final year of high school. The meeting consists of two phases: a general presentation of the research professions and the visiting team's scientific activities by the «Captain DECLICS» followed by a speed-meeting with the high-school students and each team member (DECLICS ambassadors). During the speed-meeting, the ambassadors presented their careers (researcher, assistant-professor, post-doc, doctoral student, engineer, technician, medical student, master's student, bachelor's student, etc.) and replied to the high-school students' questions.
On December 15, the ECOPHIP (E. Viscogliosi) and Microbiology's Platypus (D. Devos) teams met with around sixty final-year students from the Lycée Faidherbe in Lille, together with SVT teacher Mme Henocq. Thanks to the diversity of the ambassadors' profiles, the operation was very successful and may have inspired new vocations.
Operation DECLICS takes place every year in November/December. All CIIL teams, as well as individual center staff, can apply by registering online via the link above. See you in 2024.

Eric VISCOGLIOSI

News in brief ...

New recruit

The CIIL welcomes Nassima AOUDJIT who has recently been recruited as a new account manager for the IBL building.

CNRS crystal medal

© Grégory Hau - CNRS_TALENTS_2023_DELEGATIONHAUTSDEFRANCE

At the CNRS Hauts-de-France Talents 2023 ceremony on December 12, Sébastien JANEL was awarded the CNRS Crystal Medal in recognition for his work on atomic force microscopy.

Preparatory meeting for the next CIIL's quinquennium

The year of 2024 will be marked by the five-year evaluation of our unit. On December 14, 2023, a CIIL General Meeting was held to prepare the HCERES dossier for the 2026-2030 term. Frank Lafont took the opportunity to present the results of the evaluation carried out by the Institut Pasteur's external Scientific Advisory Board. This evaluation provided the research teams with recommendations that will help them prepare the five-year dossier to be submitted to the HCERES in May 2024.

In addition, CIIL's Scientific Advisory Board will provide critical reading for any teams wishing to do so. In addition, a progress report was presented on the work of the Steering Committee for the next mandate, in particular the working groups on strategy, budget, communication & animation.

The infrastructure working group was introduced during the meeting, which ended with a question-and-answer session and open discussion.

Frank LAFONT

CIIL's general assembly of 2024

As at the beginning of each year, CIIL members gathered for a general meeting to review the events of the past year. It was followed by a moment of conviviality by sharing the traditional «galette».

Jean DUBUISSON

Contributors to this issue include :

- Muriel PICHAVANT
- Audrey TARRICONE
- Nathalie MIELCAREK
- Jean-Claude SIRARD
- Philip SUPPLY
- Magali CHABÉ
- Eric VISCOGLIOSI
- Florent SEBBANE
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