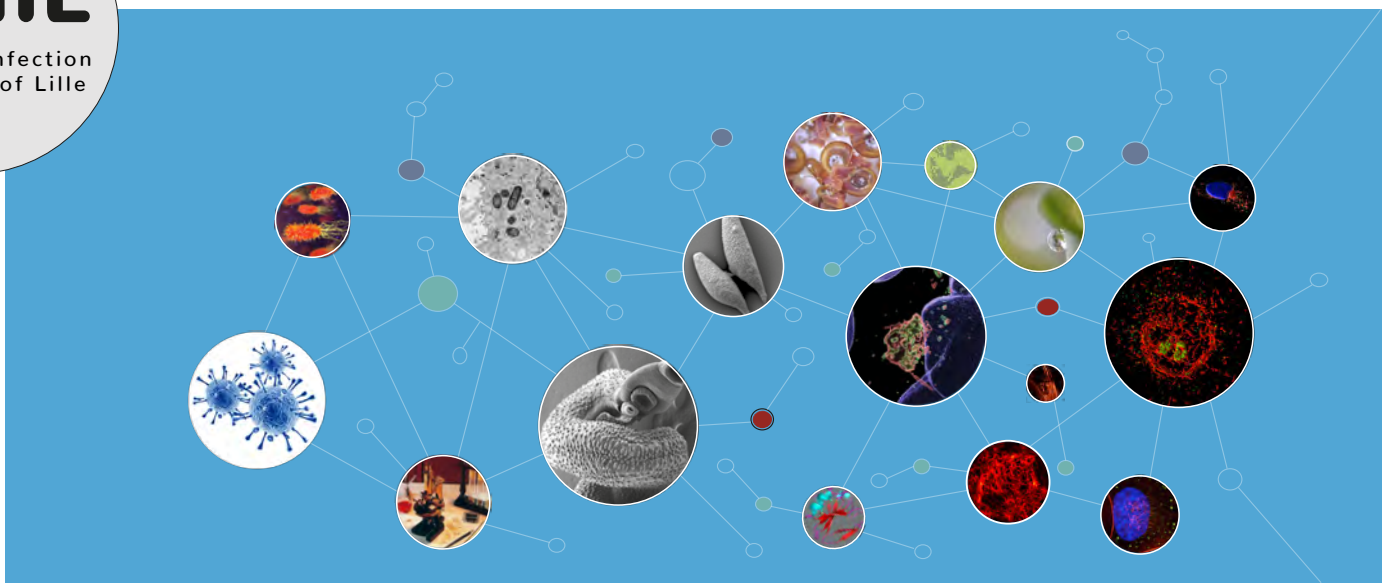
Newsletter

CIIL
Center for Infection & Immunity of Lille

N° | 14
October | 2024



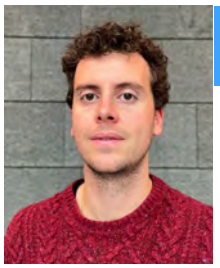
After the summer break, the activities of the teams have resumed at their highest level.

In this issue, we continue with the presentation of researchers and engineers who actively contribute to the CIIL project. Here, we present Ernesto Anoz-Carbonell who has recently been recruited as chargé de recherche at Inserm in the team Chemical Biology of Antibiotics, Cécile-Marie Aliouat-Denis recently promoted professor in the team Molecular & Cellular Virology, and Isabelle Wolowczuk, research director at CNRS in the team Influenza, Immunity & Metabolism. We also continue to present the engineers of the unit with the portrait of Muriel Lavie who works in the team Molecular & Cellular Virology and Thomas Mouveaux who works in the team Biology of Apicomplex Parasites. In this issue, we also highlight the MOSAIC research program coordinated by Alexandre Grassart and financially supported by the program of excellence of the University of Lille for interdisciplinary research involving several local experts in the fields of microfluidic, organoids and clinical research for the acceleration of innovation in new biomimetic models called “organ-on-chip”. October is also the month of the arrival of most new PhD students and, this year, they are 15 to join the CIIL. We wish them a warm welcome.

Jean DUBUISSON

Table of contents

Portraits of our scientists

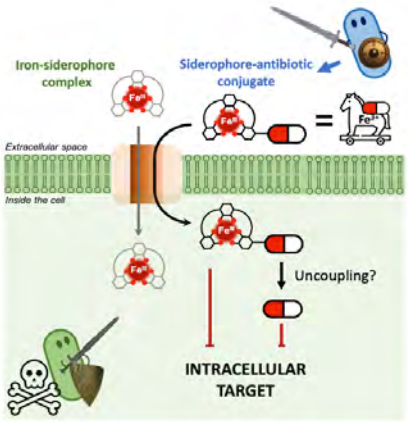


Ernesto Anoz-Carbonell
INSERM Researcher

I am Ernesto ANOZ-CARBONELL, and this October I start as CRCN at INSERM within the CBA team at CIIL. I have always been interested on the discovery and characterization of new bioactive compounds and their targets, combining both biochemical and microbiology approaches.

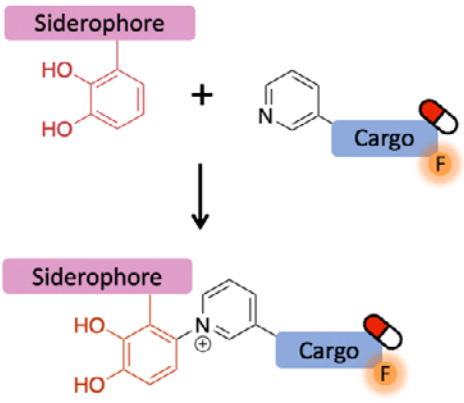
After my bachelor studies at the University of Zaragoza (Spain), I had the opportunity to carry out a 6-month research project at the group of René DE MOT at the Centre of Microbial and Plant Genetics (Leuven, Belgium). In this research stage, I focused on the study of antimicrobial proteins secreted by several strains of *Pseudomonas* (pyocins) and the identification and characterization of their targets, giving my first steps in the fields of microbiology and protein biochemistry.

In 2016, I initiated my Ph.D. studies within a multidisciplinary and collaborative research project between the groups of José Antonio AÍNSA CLAVER and Prof Milagros MEDINA at the University ofZaragoza and the Institute for Biocomputation and Physics of Complex (BIFI) (Spain). During my PhD thesis, I worked on the biochemical and spectroscopic characterization of several prokaryotic and eukaryotic flavoenzymes, proteins that contain flavin cofactors (mostly, FMN and FAD) or that synthetize them from riboflavin (vitamin B2). These proteins are involved in a wide range of biological processes, having a central role in metabolism through their ability to catalyze both one- and two-electron transfer reactions. Flavoenzymes are also associated with several human pathologies, including cancer development and progression, as well as neurodegenerative diseases. Thus, the detailed characterization of these enzymes contributed to the better understanding of their associated pathologies, and provided a framework for novel therapeutic strategies and the design of compounds targeting them.



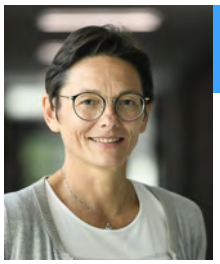
Additionally, I worked on the characterization of bacterial FADS synthases (FADS), bifunctional enzymes involved in the synthesis of the cofactors FMN and FAD in prokaryotes, specifically focusing on Mycobacterium tuberculosis FADS. During a stay at the laboratory of Riccardo MANGANELLI at the University of Padova (Italy), we demonstrated the essentiality of this mycobacterial enzyme, highlighting its potential as a target for antimicrobials. Furthermore, we showed that the inhibition of this target leads to the depletion of flavin cofactors (essential for other protein activity) and synergizes with some antituberculous compounds such as macozinone, which targets the flavoprotein DprE1. In order to identify inhibitors for this enzyme, we followed two different but complementary approaches: a wet-laboratory activity-based high-throughput screening and a docking-based virtual screening. Within both projects, we performed the first approximation for identification of inhibitors of the prokaryotic FADS that might contribute to exploit them as pharmacological antimicrobial drugs. However, for most of the hits we identified, we found low or no activity in bacteria despite of their good in protein activity. This lack of translatability between enzyme inhibition and antimicrobial activity heightened my interest on new approaches to facilitate the entry of compounds into bacteria.

After my PhD thesis, I joined the Chemical Biology of Antibiotics group, headed by Ruben HARTKOORN, at the CIIL. I worked in the framework of the project ANTIBIOCLICKS, that aims to improve compound penetration in bacteria through the coupling to siderophores and evaluate the potential of these conjugates in bacterial therapeutics and diagnostics. Initially, we discovered a novel natural siderophore-antibiotic conjugate produced by *Dactylosporangium fulvum*, and we found that this molecule can be generated synthetically through a Michael-type addition reaction between the catechol-containing siderophore and the 3-pyridyl antibiotic. In a next step, we are extrapolating this technology to other catechol-containing siderophores (such as enterobactin, acinetobactin and catechol-derivative of mycobactin) and other 3-pyridyl containing cargo-molecules (such as antibiotics or fluorophores) to generate a combinatorial library of siderophore-cargo conjugates. We have found that such novel biomimetic siderophore conjugates show facilitated bacterial uptake, and can be used to target clinically relevant Gram-negative bacteria (*Acinetobacter baumannii*, *Escherichia coli*, *Klebsiella pneumoniae and Pseudomonas aeruginosa*) and *M. tuberculosis*.



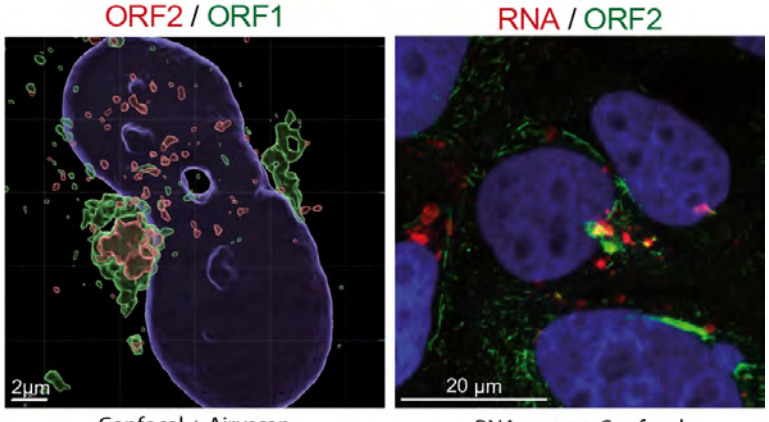
Siderophore conjugate

This October, I have started as CRCN at CBA team. In the team, our aim is to discover of new bioactive molecules and their development towards their clinical use to help in the fight against drug resistant bacterial infections. To do so, we are focused in the discovery of novel antibiotic molecules, as well as molecules and strategies to overcome both innate and adaptative antibiotic resistance of the main WHO classed priority pathogens.



Cécile-Marie Aliouat-Denis
Professor at University of Lille

I am Cécile-Marie Aliouat-Denis, Professor of Parasitology-Mycology at the Faculty of Pharmacy (UFR3S, University of Lille). I carry out my research in the Molecular & Cellular-Virology (MCV) team led by Jean Dubuisson at the CIIL. I am part of Laurence Cocquerel's group and I study the replication of the hepatitis E virus. I graduated from the Faculté Libre des Sciences of the Université Catholique de Lille, followed by a DEA in Parasitology (Univ. Lille). I then did my PhD thesis under the supe vision of Dr. Eduardo Dei-Cas (U42, Inserm), characterising the manganese-dependent superoxide dismutase of an opportunistic pulmonary microfungus: *Pneumocystis carinii*. After my thesis, I joined the laboratory of Prof. Ann Wakefield at the Weatherall Institute of Molecular Medicine (John Radcliffe Hospital, University of Oxford, UK) to study the function of the gene encoding the P. carinii manganese superoxide dismutase. I then took the opportunity to discover the pharmaceutical industry by accepting a 3-year position as a Principal Scientist at Johnson & Johnson Pharmaceuticals (Beerse, Belgium). There, I worked in the field of oncology and validated Chk2 as a potential drug target in the treatment of cancer.



Confocal + Airyscan — RNAscope + Confocal

In 2004, I was appointed Associate Professor (Faculty Dept of Pharmacy, University of Lille). I devote half of my time to teaching parasitology, medical mycology, animal biology and, more recently, virology to pharmacy and midwifery students. I also participate in courses that allow students to apply their skills by putting them into situations with simulated patients in the teaching pharmacy. To vary teaching methods, I have coordinated the development of a serious game which I propose to pharmacy students during their DE sessions.

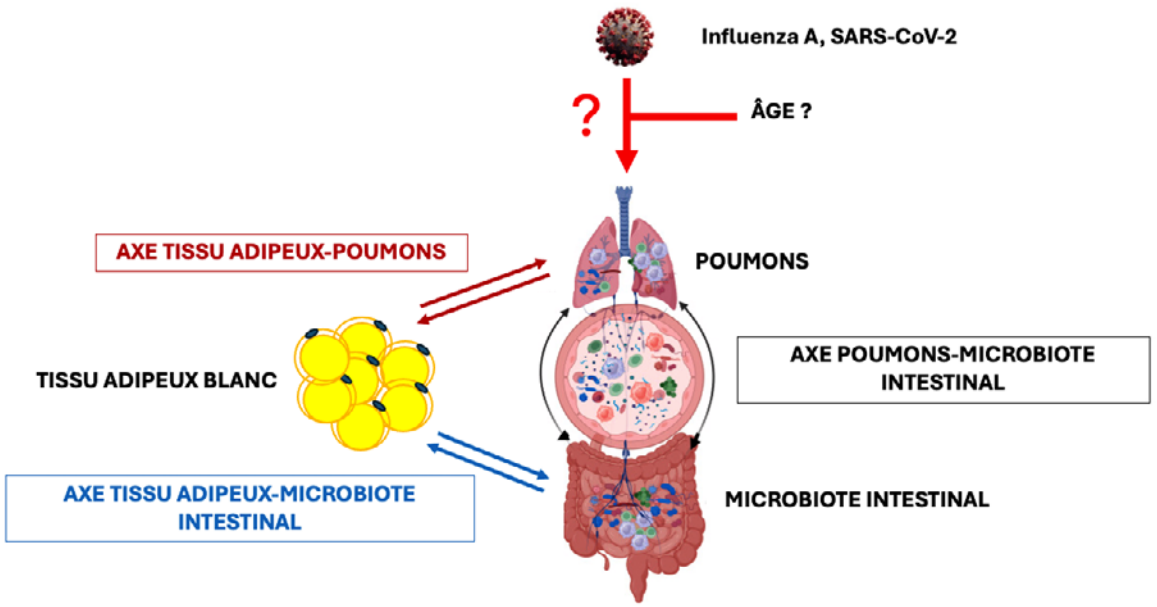
The first 10 years of my research career were devoted to studying the biological and cellular cycles of 0 and their value as phylogeographic markers. In the 1980s, Pneumocystis pneumonia was the most serious and common infection in AIDS patients. With the advent of triple antiretroviral therapy, support for research into opportunistic diseases declined. What's more, the existence of technological hurdles that slowed down the development of Pneumocystis research led me to turn my attention to virology in 2015.

When I joined Jean Dubuisson's team, Laurence Cocquerel wanted to develop a new line of research on hepatitis E virus (HEV), a major cause of acute hepatitis worldwide. It was a wonderful opportunity to help out at a time when a new topic was being introduced to the team. I have been involved in a new area of research, which is very motivating. I'm now working on the characterisation of ORF1 or HEV replicase, a high molecular weight polyprotein that is weakly expressed by the virus. Our first challenge was to detect the viral replicase in our HEV culture system. We then investigated its expression kinetics and subcellular localisation. In the host cell cytoplasm, ORF1 co-localises with other viral proteins (ORF2 viral capsid and ORF3 phosphoprotein) in perinuclear structures. We also detected markers of the endosomal recycling compartment (CD71 and Rab11) in these structures, suggesting that HEV hijacks this pathway to complete its viral c cle. We currently pursue the characterization of ORF1, focusing on the role of disordered linker regions in regulating ORF1 polymerase activity (in collaboration with Stéphane Bressanelli and his team at Institut de Biologie Intégrative de la Cellule, I2BC, Paris Saclay).

As there is no specific treatment for hepatitis E, I am also developing a project to identify extracts or natural molecules from plants that are active against HEV replication. Within the MCV team, Karin Séron is developing the antiviral axis for coronaviruses in collaboration with our colleagues working in pharmacognosy in the Dept of Pharmacy (Céline Rivière, Vincent Roumy, UMRT1158, BioEcoAgro). I'm extending this approach to HEV using two collections of extracts/molecules from (i) plants used in the Peruvian pharmacopoeia to treat liver diseases and (ii) regional or Moroccan extremophilic halophytes, which are natural reservoirs of rare bioactive compounds.

Isabelle Wolowczuk
CNRS research director

My name is Isabelle Wolowczuk, Research Director at CNRS, and I am part of the «Influenza, Immunity & Metabolism» team at CIIL. After obtaining my undergraduate and graduate degrees in immunogenetics at the Pierre and Marie Curie University (Paris 6), I joined the Pasteur Institute of Lille (IPL) to complete my DEA (Master's equivalent) and then my PhD under the supervision of Dr. Claude Auriault, in the laboratory of Prof. André Capron. During my PhD, I studied the immune response against the protein Sm28GST, a vaccine candidate against the parasite *Schistosoma mansoni*. This experience not only sparked my interest in this parasite but also allowed me to conduct part of my research in the field, in Kenya. I then undertook a postdoctoral fellowship in the laboratory of Prof. Klaus Rajewsky, a specialist in B lymphocytes, at the Institute of Genetics at the University of Cologne (Germany). My integration into CNRS in 1994 coincided with my return to the IPL campus, within the «Cellular Immunopathology of Infectious Diseases» team led by Dr. C. Auriault. My research focused on studying the cutaneous immune response induced by *S. mansoni* infection. Briefly, I demonstrated that interleukin 7 (IL-7) plays a key role in the development, growth, and lipid metabolism of the parasite, without contributing to the antiparasitic immune response. This original discovery gradually shifted my focus towards investigating the role of IL-7, and more broadly immunity, in the energy metabolism of more complex organisms than schistosomes, such as rodents and humans. Between 2006 and 2010, I led the «Neuroimmuno endocrinology» team at IPL, where we identified the metabolic tissue targeted by IL-7: the white adipose tissue. In 2010, I joined Prof. Philippe Froguel's team to work on the links between the immune system and alterations in white adipose tissue in humans (overweight, obesity, lipodystrophy). Since 2014, within the CIIL's «Influenza, Immunity & Metabolism» team, led by Dr. François Trottein, I have been focusing on studying the role of white adipose tissue in pulmonary inflammatory diseases, whether of viral origin (influenza, SARS-CoV-2) or environmental origin (chronic exposure to cigarette smoke, in collaboration with the OpInfIELD team at CIIL). The contribution of the white adipose tissue to the pathophysiology of respiratory diseases remains a largely unexplored field, as this tissue has long been seen only as an energy storage site. However, our studies, initially conducted in young-adult mice, reveal that the flu causes long-lasting disturbances in host metabolism, as well as transient changes in the inflammatory and metabolic properties of white adipose tissue, notably through the induction of thermogenesis in its subcutaneous depots (a process known as browning). The mechanisms responsible for this browning of white adipose tissue during influenza infection involve the activation of the PERK-ATF4 pathway in response to endoplasmic reticulum stress induced by the infection. Then, given that obesity and age are major risk factors for severe forms of influenza and COVID-19, and that both are associated with similar alterations in white adipose tissue, we studied the impact of SARS-CoV-2 infection in aged hamsters. Our research revealed that SARS-CoV-2 infection causes significant damage to this tissue, which is quickly repaired in young adults but worsens and persists in older subjects. This suggests that white adipose tissue could contribute to the severity of COVID-19 in the elderly. Currently, our work aims to analyze the interaction between the lungs, white adipose tissue, and the gut microbiota in young-adult and aged mice, as aging is also characterized by changes in the composition and function of the gut microbiota. The results reveal signatures specific to aged mice, reflecting changes induced by influenza infection in the lungs, white adipose tissue, and gut microbiota. Ultimately, this research could lead to innovative therapeutic strategies targeting white adipose tissue and/or the gut microbiota to reduce influenza-related damage in the elderly.



Adapted from Wed Eladham et al., Heliyon 10 (2024)

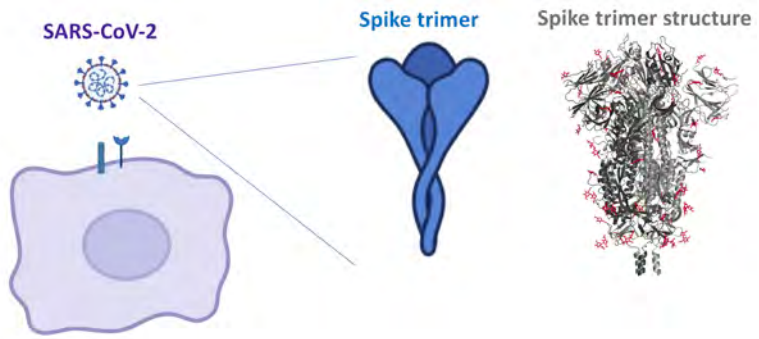
Muriel Lavie
INSERM research Engineer

After obtaining a degree in Biochemical and Food Engineering and Microbial Genetics from INSA Toulouse, I did my thesis in Dr Christian Boucher's team studying the pathogenic power of the plant pathogenic bacterium *Ralstonia solanacearum* at the Plant Microorganism Interactions Laboratory at INRA Auzeville Tolosanne. My work involved characterizing a family of bacterial virulence factors injected into the host cell via the type III injection secretion system.

Keen to broaden my experience of pathogen/eukaryotic cell interactions, in 2004 I joined Jean Dubuisson's Hepatitis C Virus (HCV) team (IBL, CNRS) for a three-year post-doctoral position. This change of theme gave me the opportunity to increase my knowledge of the cellular 'partner' of pathogens and to broaden my technical skills in virology, biochemistry, microscopy and cell biology. My work highlighted the antiviral effect of the serum amyloid A protein, a ligand of the HCV receptor, SR-BI, and enabled to characterize the mechanism of action of this inhibitor.

In 2008, my professional experience in the field of pathogen/eukaryotic cell interactions and my technical skills in cell biology, biochemistry and virology led me to apply for the position of IR2 in the U701 cancer virotherapy unit headed by Jean Rommelaere in Heidelberg. My assignments then included method development and research activities. The development activities were part of the implementation of the Parvoryx clinical trial aimed at evaluating the therapeutic potential of oncolytic murine parvovirus H-1PV in glioblastoma patients. In this context, I developed virus production protocols that complied with Good Manufacturing Practice, as well as virus analysis methods for monitoring the trial in vivo. In parallel, I took part in the research activities of Dr C. Dinsart's group, which is studying the sensitivity of different tumor models to the oncolytic effect of parvoviruses (PVs) and seeking to improve this potential by modifying parvoviral vectors with therapeutic genes. My work has enabled us to characterize the anti-angiogenic potential of wild-type parvovirus H1-PV and recombinant viruses expressing anti-angiogenic chemokines in a Kaposi's sarcoma model.

Following the closure of Unit U701 in 2012, I joined Dr Jean Dubuisson's Molecular and Cellular Virology team at the Centre for Infection and Immunity of Lille, which studies virus-host interactions in models of HCV, coronaviruses and hepatitis E virus. Between 2012 and 2019, I developed and supervised research projects concerning the characterization of HCV envelope proteins and viral entry into host cells. In 2019, I joined the Coronavirus group to develop a vaccine project against MERS coronavirus by generating subviral particles carrying chimeric MERS-CoV and Hepatitis B virus envelope proteins. Subsequently, the emergence of SARS-CoV-2 led us to use this approach to develop a vaccine against this new coronavirus. In parallel with these activities, I became interested in the role of the Spike (S) protein in virus entry and propagation via the cell-cell fusion mechanism. The S protein, which is anchored in the lipid envelope of the virus, is the major determinant of viral entry into the host cell by allowing fusion between the viral envelope and the cell membrane. It comprises the S1 domain, which interacts with the ACE2 receptor, and the S2 domain, which mediates fusion. Induction of the fusogenic activity of S requires two proteolytic cleavages at the S1/S2 site, located at the junction between the S1 and S2 subunits; and S2' located upstream of the fusion peptide In infected cells, a fraction of S reaches the plasma membrane and can induce fusion with the plasma membranes of neighboring cells expressing ACE2. The formation of these multi-nucleated giant cells contributes to the pathogenicity of SARS-CoV-2 by causing lesions within infected tissues and enhancing viral dissemination and escape from the immune system. Our work initially characterized the role of the different S cleavage sites and revealed that they modulate cell-cell entry and fusion in a host-dependent manner.



In addition, the S protein harbors 22 N-glycosylated sites that are important for its structure by contributing to its folding. Several glycosylation sites located in the vicinity of the S2' and S1/S2 cleavage sites are likely to influence the maturation of S, which is crucial for its ability to induce fusion, a key step in viral entry and an important process in viral pathogenesis. We recently undertook a functional characterization of the N-glycans located in the region of the cleavage sites of S for its entry and fusion functions. Our data revealed that these sites modulate the maturation of the protein, its intracellular trafficking and its ability to induce cell-cell fusion and entry. In the near future, these sites will be mutated in the context of the infectious clone in order to determine their importance for the viral cycle.

Thomas Mouveaux
CNRS engineer

It wouldn't be fair to introduce myself without telling you straight away that initially I didn't want to do research at all... I'm Thomas Mouveaux, a CNRS engineer and during my studies I intended to work in the agri-food industry on biological and microbiological risk. All my work placements have therefore been with companies such as Nestlé, Benedicta or Roquette Frère for my end-of-study placement. I got my Master 2 (professional, not research, of course) in 2008, the year of the sub-prime crisis, which brought hiring to a screeching halt, especially in private companies (as 'old-timers' may remember).

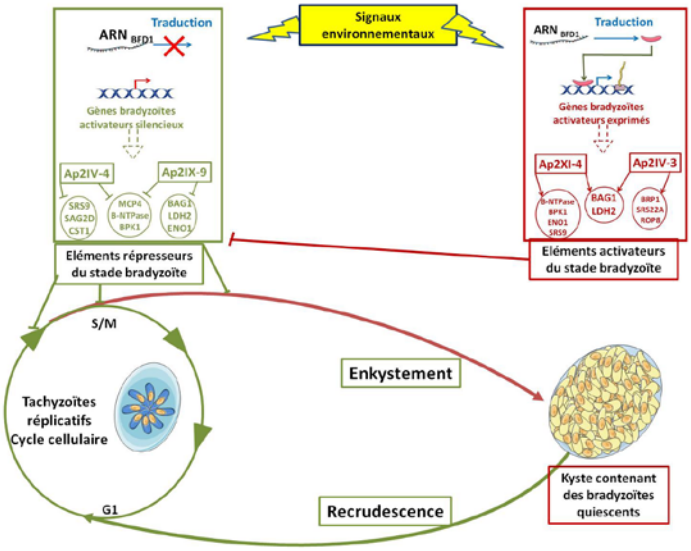
So life and the economic context redirected me towards a job as a research engineer. There I discovered a parasite responsible for a disease that kills almost no-one, that most people recover from without treatment and that is immune to any risk of future contamination: *Toxoplasma gondii*. In short, a seemingly harmless parasite of little interest. Well, that's its strength! The majority of patients are unaware of the contamination and survive the infection. They end up carrying living parasites in their brains for the rest of their lives. This makes *T. gondii* one of the most widespread parasites in the world. Every warm-blooded animal at sea, on land, in the air and in every type of climate is a potential host, with up to 60% of certain human populations seropositive for toxoplasmosis. So, to be successful, you have to be discreet.

I did a lot of work on the encysted form of the parasite. After 12 years of loyal service as a CNRS research engineer (which I'm still doing, by the way), I was offered the opportunity to do a PhD thesis, which I defended at the end of 2023. My primary motivation was to get out of my comfort zone and develop global analysis skills that weren't just technically based. Although I'm very happy to have had this opportunity and aware from the outset of the extra workload that it represented, I have to admit that it can be difficult for a 40-year-old working PhD student to reconcile family life, outside responsibilities and the obligations inherent in a PhD thesis (a little subliminal message to ITAs interested in a thesis: make sure that your partner is well informed about and in agreement with your project. At the age of 40, 2 people are needed to complete a thesis...).

My current research focuses on the regulation of parasite gene expression and the transition between the 2 human forms of the parasite, the actively proliferating form responsible for the acute phase of toxoplasmosis, the tachyzoite, and the encysted form resistant to the immune system and all existing treatments (for the moment...), the bradyzoite. I have developed a protocol for infecting rat brain cells with the parasite in order to study the changes that occur during encystment.

This model has enabled us to gain a better understanding of the mechanisms involved in cerebral infection on both the 'host brain' and 'parasite' sides, with, for the first time, evidence of a gradual conversion over time between proliferative and encysted forms.

This model is now an innovative tool for studying the action of inhibiting compounds on the latent form of the parasite, against which no treatment is effective.



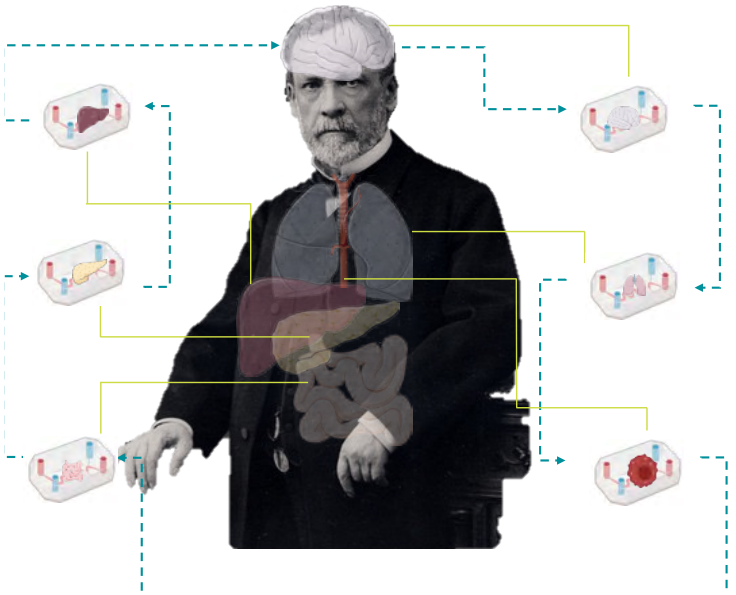
Mechanisms of interconversion between tachyzoite and bradyzoite forms

MOSAIC Project
Alexandre Grassart
INSERM researcher

The Initiative of Excellence of the University of Lille and its partners launched in 2023 a new program targeted to answer the challenges of contemporary transitions through interdisciplinarity research projects. After an evaluation process based on scientific excellence by the European Science Foundation and a prestigious international jury, the project MOSAIC has been recently awarded a 2,7M€ funding to better understand the mechanisms leading the transition from an acute infection to the establishment of chronicity. Coordinated by Alexandre Grassart head of the team MoHMI at the CIIL, the project gathers a consortium composed of 4 research units of the University of Lille (CIIL, U1067, U1011 and IEMN), 9 research teams (4 of which belongs to the CIIL: MoHMI, CVI, IIM, MCV), the Hospital of Tourcoing and the Museum of Natural Science of Lille. Encompassing expertise in microfluidics and microsystems engineering, human-induced pluripotent stem cell (hiPSC), infection, immunity, metabolism and medicine, the CDP MOSAIC aims to capitalize on this strong scientific environment in northern France to delineate the causative links between SARS-CoV-2 infection and its chronic complications known as Long-Covid. With an estimated prevalence of 4-5 % of previously infected persons, this emerging chronic disease is predicted to severely impact healthcare systems in the years to come and understanding the mechanisms leading to this condition is an urgent unmet need.

Covid and Long-Covid are known to be complex multifaceted diseases that are difficult to understand using current methodologies. On one side, conventional in vitro models poorly reproduce the complexity and variability of human physiology while on the other side animal models, frequently associated to ethical concerns, are inadequate to fully understand these human diseases. To tackle this technological bottleneck, following the national research strategy France 2030 roadmap for personalized medicine, the first objective of MOSAIC aims to develop the next generation of organ on chip technology (OoC), an emerging innovation bridging the gap between in vitro and vivo models. The new miniaturized microphysiological system developes by MOSAIC will support several key physiological features including a biomimetic vascularization to interconnect organoids derived from patients suffering from Long-Covid and eventually better understand the systemic interactions upon acute and chronic SARS-CoV-2 infection. Biological activities will be monitored through the integration of microsensors, biochemical assays, microscopy imaging, immune and metabolic responses will be analyzed and compared to clinical data to eventually improve the therapeutic strategies. The second objective aims to foster regional andnational capacities related to organ-on-chip (OoC) technologies. This will be achieved by the creation of hubs offering organoid and OoC technologies at biosafety level-2 and -3 through two facilities located at the Institut Pasteur de Lille and IEMN. This structuration will catalyze the innovation, harmonize technologies between research units and stimulate the creation of academic-industrial partnerships. Finally, the third objective aims to disseminate the technologies and methods herein developed. To do so, community outreach activities, training and education programs will be implemented within two graduate schools of University of Lille to increase the mass of highly skilled workforce in academia and industry at both regional and national scales. Finally, the Museum of Natural Sciences of Lille will support a strong dialogue between researchers and the society on scientific, technological and ethical topics addressed in this project through exhibitions, educational workshops, and participative research actions will be organized.

In conclusion, this project will open new avenues for modelling and understanding infection and chronic diseases. On a long-term basis, MOSAIC will shed light on the mechanisms behind the development of Long-Covid, a growing Public Health concern. Technologies developed in this program will lead to a better and faster prediction of the efficacy of pharmacological strategies and eventually support national and European policies for the development of alternatives to animal models.



Collective crystal award of the CNRS

Adeline Danneels (AI CNRS) and Audrey Tarricone (IE CNRS) from the team Molecular & Cellular Virology (MCV) of the CIIL have been awarded the collective crystal of the CNRS in the context of the Virocrib (https://www.virocrib.fr/) program. This consortium is a shared infrastructure of screening of antiviral molecules supported by CNRS-Biology and developed in the aftermath of the COVID-19 crisis. This collective crystal is shared with Nathalie Gros (IEHC CNRS) and Lisa Morichon (IE CNRS) of the CNRS unit CEMIPAI in Montpellier and with Aurélien Traversier (AI ULyon) and Emilie Laurent (IE ULyon) from the team VirPath at CIRI (UMR5308) in Lyon.

Virocrib gathers a consortium of virologists and biologists from research teams and technological platforms for antiviral screening in various complementary pre-clinical models with the objective of rapidly responding to the emergence of novel pathogens at high risk of leading to major sanitary crises. In the context of Virocrib, the MCV team uses its expertise in virology for the phenotypic screening of antivirals and to develop novel tools for these screenings. These tools are used for high content screening on the ARIADNE screening platform of PLBS unit located on IPL campus (https://ums-plbs.univ-lille.fr/les-plateformes-constitutives/ariadne-criblage).

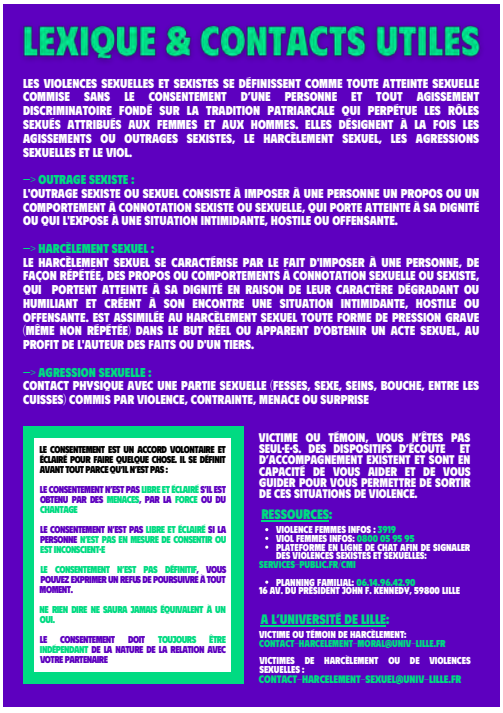
Since the beginning of Virocrib consortium, Adeline Danneels has been deeply involved in phenotypic screenings. Notably, she was involved in the IPL COVID-19 taskforce for the screening of a chemical library of medical compounds which led to the identification and characterization of the antiviral activity of clofoctol, an active antiviral compound against SARS-CoV-2.

In January 2023, Audrey Tarricone was recruited to work on the Virocrib consortium to perform phenotypic screenings of antiviral molecules in the context of coronavirus infections as well as other major viral infections. These approaches allow for the screening of nucleoside analogs generated in the context of the GAVO (Génération d'AntiViraux Originaux) consortium from CNRS-chimie as well as for the screening of SARS-CoV-2 protease inhibitors in the context of a local collaborative consortium.

Best Poster award

Congratulations to Joan FINE for receiving the award for the best poster at the 7th European Congress of Immunology, held in Dublin from September 1st to 4th, 2024! Joan FINE is a PhD student under the supervision of Dr. Arnaud Machelart and Dr. François Trottein at the Center for Infection and Immunity of Lille. Her research focuses on studying how infection with Mycobacterium tuberculosis affects the host's ability to control viral superinfection. Congratulations to her!

Violentometer poster



In 2023, the L'Oréal Foundation and IPSOS published an unprecedented international survey of the research community in 117 countries. The survey revealed that 1 in 2 women scientists had experienced sexual harassment in the workplace.

Based on this finding, the L'Oréal Foundation and the Gender - Intersectional Relations, Educational Relation (G-RIRE) team at the Universitý of Geneva proposed an adaptation of the Violentometer for the research world to raise awareness among people studying and/or working in these fields and enable them to assess their working environment.

This Violentometer has been posted at CIIL.

If you think you're in a "red" situation, don't hesitate to talk about it to others (family, friends, colleagues), and above all, to inform the CIIL Coregal. As CIIL's gender equality representatives, they are trained in gender-based and sexual violence (SGBV) and are there to listen to you in complete confidentiality, and to help you.

Elise	elise.delannoy@pasteur-lille.fr
Frank	frank.lafont@cnrs.fr
Isabelle	isabelle.wolowczuk@cnrs.fr
Karin	karin.seron@cnrs.fr

News in brief ...

Welcome to new students

Anaïs DARDAILLON,
Dir. F REAL
Team REAL

Clément BORDAS,
Dir. F TROTTEIN
Team TROTTEIN

Mahmoudou BA,
Dir. S MARION
Team KHALIFE

Agathe BOUR,
Dir. F REAL
Team REAL

Dima ABDALLAH,
Dir. G CERTAD
Team VISCOGLIOSI

Margot FRYDER,
Dir. L VAN MAELE
Team SIRARD

Axelle GRANDÉ
Dir. A MACHELART
Team BRODIN

Emeline DRIENCOURT,
Dir. M PICHAVANT
Team GOSSET

Maurane DEGARDIN,
Dir. S BONTEMPS-GALLO
Team SEBBANE

Carlos VIGIL-VASQUEZ,
Dir. D DEVOS
Team DEVOS

Emma LOUVET,
Dir. M LAVIE
Team DUBUISSON

Orane HUCHEZ,
Dir. S BELOUZARD
Team DUBUISSON

Quentin VANPEENE,
Dir. A GRASSART
Team GRASSART

Ruben GARCIA-DOMINGUEZ,
Dir. D DEVOS
Team DEVOS

Océane BONNINGUE
Dir. O. MELNYK
Team MELNYK

Contributors to this issue include:

- Cécile-Marie ALIOUAT-DENIS
- Ernesto ANOZ-CARBONELL
- Isabelle WOLOWCZUK
- Muriel LAVIE
- Thomas MOUVEAUX
- Alexandre GRASSART
- Karin SERON

Director and supervisor of the publication	:	Jean DUBUISSON
Editorial coordination	:	Sabine BLIN
Design	:	Sophana UNG
Proofreading	:	Orane HUCHEZ

CIIL - CNRS UMR9017 - INSERM U1019
1, rue du Professeur Calmette - 59000 Lille

https://www.ciil.fr