12TH OF MAY 2026

BOOKLET

STEERING COMMITTEE

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SPECIAL THANKS TO

Natacha Janiszewski, creator of the logo of this event

THANKS TO

RÉGION Nouvelle-Aquitaine

MICROBIO-NA
COMMUNAUTÉ DE MICROBIOLOGIE NOUVELLE AQUITAINE

université de BORDEAUX

Microbiology Day program

12th May 2026

8.30 am **Welcome**

9.00-9.05 am
Introduction, **Alexia Damour**

9.05-10.30 am **Session 1 : Host–Microbe Interactions, Cellular Hijacking, Infections and Immunity**

9.05 am: **Romain VILLÉGER, EBI-Poitiers (Scientist)**
L-serine promotes pro-carcinogenic effects of colibactin-producing E. coli

9.20 am: **Anaïs SCHNELLER, ImmunoConcept (PhD)**
Characterizing CMV-Specific Immune Signatures to Predict Post-Transplant Infection Risk

9.35 am: **Nathalie ARVY, BFP (Scientist)**
Lipid Droplets: Beyond Mere Energy Storage... Key Players in Viral Propagation

9.50 am: **Sandrine CLAUS, Starfish**
Leveraging high-resolution DNA sequencing and AI-based bioinformatics to identify next-generation biosolutions from soil microbiome for sustainable agriculture

10.05 am-11.05 am **Poster session I & Coffee break**

11.05 am-12.35 am **Session 2 : Microbial ecosystems, Genomic Diversity**

11.05 am: **Alejandro MANZANO MARÍN, Invited speaker**
Centre for Microbiology and Environmental Systems Science (CMESS), University of Vienna
Blood-feeding leeches: Bacterial solutions to a haematophagous diet

11.50 am: **Diego SANTOS GARCIA, INRAE Montpellier (Scientist)**
Whiteflies: a symbiosis puzzle

12.05 am: **Noé RENARD, LABCiS-Limoges (PhD)**
Proteomic characterization of extracellular vesicles derived from probiotic Lactobacillus strains

12.20 am: **Claire DA COSTA, EPOC (Postdoc)**
Linking sediment properties to microbial degradation of exopolymeric substances (EPS) in estuarine sediments

12.35 am-2.00 pm **Lunch break**

2.02 pm-3.00 pm **Session 3 : Microbial Cellular Machines, Survival and Adaptation Strategies**

2.00 pm: **Loïc RIVIÈRE, MFP (PR)**

African trypanosomes: the hidden face of lipid metabolism

2.15 pm: **Lélaud ESNAULT, ARNA (PhD)**

Engineering the Flagellar Type III Secretion System of Salmonella for Recombinant Therapeutic Protein Delivery

2.30 pm: **Emmeline PAOLI, EBI (PhD)**

Involvement of quorum sensing in the virulence of the Borrelia burgdorferi sensu lato complex

2.45 pm: **Martin LEFEUVRE, CBMN (PhD)**

Structure and interactions of RocS controlling chromosome segregation in Streptococcus pneumoniae

3.00 pm-4.00 pm **Poster session II & Coffee break**

4.00 pm-5.15 pm **Session 4 : Recent Advances and Emerging Perspectives in Biotechnology**

4.00 pm: **Audrey Gauthier, Damoclès diagnostic**

DAMOCLES Dx: Rapid phenotypic AST directly from urine samples using real-time bacterial profiling

4.15 pm: **Guillaume Goudounet, Kapsera**

Kapsera, une entreprise qui protègent l'avenir

4.30 pm: **Germain CHEVIGNON, ASIM-IFREMER (Scientist)**

Genomic Characterization of Marine Vibrio Species for the Development of Novel Diagnostic Tools

4.45 pm: **Axel PITARD, LIENSs (PhD)**

Exploring the antibiotic-like potential of plant extracts against multidrug-resistant pathogens

5.00 pm: **Arthur CHARAZAC, PHAR2-Poitiers (Master)**

Gallium Potentiates Cefiderocol Activity and Constrains Resistance in Stenotrophomonas maltophilia In Vitro

5.15 pm-5.30 pm **Awards and concluding**

HOST–MICROBE INTERACTIONS, CELLULAR HIJACKING, INFECTIONS AND IMMUNITY

Romain VILLÉGER, EBI-Poitiers

L-serine promotes pro-carcinogenic effects of colibactin-producing E. coli

A. Devaux, G. Roche, M. Rodrigues, N. Venisse, C. Juban, M. Lagrée, B. Diémé, C. Jousse, N. Barnich, D. Boucher, R. Villéger, M. Bonnet.

Colonic tissues are abnormally colonized by colibactin-producing Escherichia coli (CoPEC) in colorectal cancer (CRC) patients. CoPECs have been shown to promote colorectal carcinogenesis in several pre-clinical CRC mouse models. Here, we report that CoPEC reprograms the metabolism of colonic epithelial cells in a colibactin-dependent manner, leading to a Warburg-like effect, altered redox homeostasis, and disrupted amino acid metabolism. Among these metabolic modifications, we observed a significant decrease in both extracellular and intracellular serine levels. We found that CoPEC activates the L-serine-utilization operon during gut colonization, maximizing its competitive fitness advantage over a commensal strain. Moreover, an L-serine-depleted diet induces an early and transient decrease in CoPEC colonization of mice gut, associated with decrease of both DNA damages and tumor development. Finally, deletion of the bacterial tdcA gene involved in L-serine operon utilization reduces the competitive fitness of CoPEC, the in vitro adhesion and persistence within the epithelial cells and leads in CRC animal models to reduced carcinogenic activity of the pathobiont. This work highlights the interplay between intestinal microbiota factors, such as CoPEC, and nutritional factors, such as L-serine, in colorectal carcinogenesis.

Anaïs SCHNELLER, ImmunoConcept (PhD)

Characterizing CMV-Specific Immune Signatures to Predict Post-Transplant Infection Risk

Anaïs SCHNELLER, Pauline FRANCOIS, Emilie CAYSSIALS, Ludo THIRY, Kewreshini NAIDOO, Atika ZOUINE, Vincent PITARD, Julie DECHANET-MERVILLE, Hannah KAMINSKI

Cytomegalovirus (CMV) remains a major cause of opportunistic infection in solid organ transplant recipients even with preventive strategies, which mainly rely on donor(D)/recipient(R) serostatus. However, clinical studies have shown that combining serology with assays evaluating CMV-specific conventional cellular immunity (CMV-CMI, using either ELISA or ELISPOT measuring IFNγ after CMV-peptide stimulation of Peripheral Blood Mononuclear Cells (PBMCs)) can reduce unnecessary antiviral use in patients with positive ELISPOT results1. Yet, this approach remains imperfect. Approximately 20% of CMV-seropositive recipients (R^+) with positive CMV-CMI still develop infection2, suggesting cellular immune dysfunction. Conversely, 80% of R+ patients with negative CMV-CMI do not3 develop CMV disease, suggesting the involvement of others CMV-specific cellular actors, such as nonVd2Vg9 T cells and CD57NKG2C+ NK cells.

This study aims to comprehensively characterize CMV-specific immune components by combining spectral flow cytometry, together with ELISPOT.
PBMCs from 40 R^+ kidney transplant recipients were analyzed at three time points: pre-transplant baseline, an intermediate follow-up, and either at CMV infection onset (for infected patients) or a matched time point (for non-infected patients). Four dedicated spectral flow cytometry panels were used to profile immune

cell populations including αβ T cells, NK cells, and γδ T cells, and to assess dysfunction, activation markers together with transcription factors, cytokines and cytotoxicity. In parallel, ELISPOT assays were performed on the same samples to evaluate CMV-CMI.

Data analysis is ongoing, combining supervised (manual gating) and unsupervised (OMIQ software) approaches. At the end, we aim to define an immunological signature predictive of CMV infection risk, to guide the need and the duration of preventive strategy, thus minimize unnecessary antiviral cost and toxicity.

1 Kumar et al., American Journal of Transplantation 2019
2 Paez-Vega et al., Clinical Infectious Disease 2021
3 Kervella D et al., Kidney Int Rep 2025

Nathalie ARVY, BFP (Scientist)

Lipid Droplets: Beyond Mere Energy Storage… Key Players in Viral Propagation

Nathalie Arvy, Marguerite Batsale, Léna Jambou, Sara Shakir, Charlotte Quinteau, Luc Sofer, Vincent Simon, Marielle Cochet, Nathan Doner, Robert Mullen, Denis Coulon, Claire Bréhélin, Sylvie German Retana

Lipid droplets (LDs), which are dedicated to storing neutral lipids, are also dynamic organelles involved in numerous other functions including membrane remodeling during abiotic stress. While the hijacking of LDs by animal viruses is well documented, their role(s) in plant virus infection remains largely unexplored. Similar to animal viruses, potyviruses reroute host proteins, intracellular membranes, and lipids to create an optimized microenvironment for their efficient viral replication compartment (VRC) assembly and movement. We therefore investigated whether potyviruses can also exploit the LD machinery for their own benefit, akin to some animal viruses.

Utilizing lipid analyses, confocal and transmission electron microscopy, and viral propagation surveys in plants impaired in LD biogenesis, we show that potyvirus turnip mosaic virus (TuMV) infection induces a significant accumulation of neutral lipids and a proliferation of LDs in infected leaves, which are often located in close proximity to VRCs, suggesting a spatial and functional relationship between LDs and TuMV. We demonstrate also that two protein families crucial for LD biogenesis, namely the LIPID DROPLET-ASSOCIATED PROTEINs (LDAPs) and SEIPINs, facilitate TuMV propagation.

Taken together, our results indicate a pro-viral function of LDs in potyvirus-infected plants.

Sandrine CLAUS, Starfish

Leveraging high-resolution DNA sequencing and AI-based bioinformatics to identify next-generation biosolutions from soil microbiome for sustainable agriculture

Soils worldwide are progressively losing their vital functions, threatening agricultural productivity and ecosystem resilience. Soil microbiomes underpin these functions by mediating key biogeochemical and plant-associated processes, yet current understanding of microbial functional networks and interspecies interactions remains limited. To overcome this barrier, we developed KEYBIOMEAI, a patented discovery platform that combines high-resolution DNA sequencing with artificial intelligence–driven bioinformatics to identify keystone bacterial taxa within complex soil communities. Application of this approach to agricultural soils enabled the identification of bacterial strains contributing to plant growth promotion through a dual mechanism of auxin and lactic acid biosynthesis. These findings illustrate how integrating genomic resolution and AI analytics can accelerate the discovery of next-generation microbial biosolutions to enhance soil health and support a sustainable agriculture.

Alejandro MANZANO MARÍN, Invited speaker
Centre for Microbiology and Environmental Systems Science (CMESS), University of Vienna

Blood-feeding leeches: Bacterial solutions to a haematophagous diet

Symbiotic interactions with microbes are present across the eukaryotic tree of life. These symbioses can manifest in different ways, resulting in reproductive manipulation, feminisation, nutritional supplementation, microbiota control. Of strong evolutionary relevance are those inseparable associations, where the host and microbe have become so tightly linked that none can survive without the other. Blood-feeding leeches are confronted with a strong vitamin B deficiency, given their restricted diet. Consequently they have evolved symbiotic associations with not one, but several bacterial taxa. Most studied is the case glossiphoniid leeches with bacteriomes, where the leech host has evolved specialised organs to house these symbiotic bacteria. Less studied are the cases where symbionts occur across the alimentary canal. Using genomics and genome-based metabolic inference, we are shedding light onto the identity, metabolic potential, and evolution of these symbioses. In bacteriome-associated symbionts, we have uncovered processes of symbiont replacement, evolution of an alternative genetic code, and the recent evolution of Rhizobiaceae symbionts to complement the B vitamin deficiency of their leech hosts. On the other hand, symbionts associated to the alimentary canal in leeches lacking a bacteriome seem to have evolved a more complex consortium, where no one symbiont compensates for their host's B-vitamin deficiency. Furthermore, these symbionts are closely related and often monophyletic, suggesting a long history of association with leeches. Finally, while genomic reduction is evident in these symbionts, supporting long-term vertical transmission, retained pathways hint at an essential, and likely ancestral, role in maintaining an haematophagous lifestyle.

Diego SANTOS GARCIA, INRAE Montpellier (Scientist)

Whiteflies: a symbiosis puzzle

Diego SANTOS-GARCIA

The evolutionary history of whiteflies (Hemiptera: Sternorrhyncha: Aleyrodidae) is linked to their primary endosymbiont, Candidatus Portiera aleyrodidarum, which provides essential amino acids absent in their phloem diet. Yet, this essential relationship is only the tip of the iceberg. Unusual for a primary endosymbiont, the Portiera genome exhibits instability in certain lineages, a phenomenon linked to changes in whitefly development. Moreover, bacteria such as Hamiltonella and Arsenophonus have evolved from facultative to co-primary endosymbionts, compensating for essential functions lost from Portiera and becoming required for host development. This multi-layered system is further supplemented by a dynamic gut microbiota. The generalist herbivore Bemisia tabaci, for example, can acquire and maintain environmental bacteria with the potential to degrade plant defence compounds. Hence, gut microbiota may help whiteflies during the adaptation to non-suitable host plants.

Noé RENARD, LABCiS-Limoges (PhD)

Proteomic characterization of extracellular vesicles derived from probiotic Lactobacillus strains

Noé Renard (1), Tan-Sothea Ouk (1), Vincent Sol (1), Catherine Ouk (2), Emilie Pinault (2,3), Karine Grenier (1), Cornélia Landolt (1)

Introduction :

Extracellular vesicles (EVs) released by probiotic bacteria are emerging as promising postbiotic agents and natural nanocarriers[1], yet the impact of strain variability on their physical properties and proteomic cargo remains incompletely understood, particularly for Lactobacillus species envisioned for pulmonary delivery[2]. This study aimed to characterize the size, morphology, and protein composition of EVs secreted by five probiotic Lactobacillus strains to establish a foundational dataset for future therapeutic development.

Methods :

EVs were isolated from culture supernatants of Lactiplantibacillus plantarum 299V, L. plantarum ATCC 8014, Lacticaseibacillus rhamnosus GG, Limosilactobacillus reuteri CIP 101887^T, and Lactobacillus gasseri CIP 102991^T grown in MRS broth using differential centrifugation, filtration, and ultracentrifugation following MISEV2023 guidelines. Vesicle size and concentration were assessed by nanoparticle tracking analysis, morphology by transmission electron microscopy, and proteomes by LC–MS/MS (DDA- and DIA-PASEF on a timsTOF Pro 2), followed by bioinformatic annotation using UniProt, PSORTb, and KEGG Mapper.

Results :

All five strains secreted nanosized EVs with mean diameters ranging from approximately 70 to 100 nm, consistent with but slightly smaller than previously reported values for Lactobacillus-derived vesicles[2], suggesting both strain- and protocol-dependent effects on vesicle size distribution. After stringent filtering across biological replicates, 422, 489, 1325, 444 and 462 EV-associated proteins were retained for Lp299V, Lp8014, LrGG, LrCIP, and LgCIP, respectively, with subcellular localization analysis indicating a predominant cytoplasmic and cytoplasmic membrane origin and only minor contributions from cell wall and extracellular proteins. Functional annotation revealed a conserved core of metabolic, genetic information processing, and membrane transport pathways across strains, while strain-specific proteomic signatures highlighted differences in cell envelope remodeling, stress response, and regulatory functions.

Summary/Conclusions :

Probiotic Lactobacillus strains produce abundant nanoscale EVs that share a conserved functional proteomic core yet display distinct, strain-dependent signatures likely reflecting their physiology and ecological niches. These results provide a comprehensive reference framework for Lactobacillus-derived EVs and support their further exploration as safe, bioactive nanocarriers for targeted pulmonary drug delivery and other therapeutic applications.

References : [1] Xie J, Li Q, Nie S. Bacterial extracellular vesicles: An emerging postbiotic. Trends Food Sci Technol 2024;143:104275. https://doi.org/10.1016/j.tifs.2023.104275. [2] Lee B-H, Chen Y-Z, Shen T-L, Pan T-M, Hsu W-H. Proteomic characterization of extracellular vesicles derived from lactic acid bacteria. Food Chem 2023;427:136685. https://doi.org/10.1016/j.foodchem.2023.136685.

[3] Welsh JA, Goberdhan DCI, O'Driscoll L, Buzas EI, Blenkiron C, Bussolati B, et al. Minimal information for studies of extracellular vesicles (MISEV2023): From basic to advanced approaches. J Extracell Vesicles 2024;13. https://doi.org/10.1002/jev2.12404.

Claire DA COSTA, EPOC (Postdoc)

Linking sediment properties to microbial degradation of exopolymeric substances (EPS) in estuarine sediments

Claire Da Costa[1], Raphaël Bourillot[1], Isabelle Billy[1], Louise Monnier[1], Olivier Ther[1], Pieter Visscher[3], EXODIA Consortium, Olivier Braissant[2]

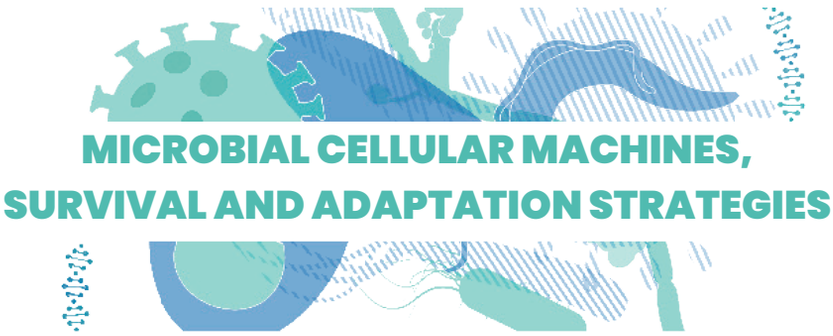
Microbial biofilms play a central role in sedimentary environments, notably through the production of exopolymeric substances (EPS). These complex matrices are fundamental for the establishment,

development, and persistence of microbial communities, as well as for organic matter cycling and biogeochemical processes. In estuarine sediments, EPS composition, production, and degradation dynamics are strongly influenced by environmental conditions, sedimentary substrate, and indigenous microbial communities.

This study focuses on two short sediment cores (~50 cm) collected from contrasted sandy and muddy zones of a point bar in the Gironde Estuary (France). The objective is to assess whether sedimentary conditions control EPS properties and their degradability by microbial communities. Sediments were characterized using sedimentological and geochemical approaches (facies description, grain size distribution, X-ray fluorescence spectroscopy), while the degradation dynamics of model EPS by sedimentary microbial communities at different depths were investigated using microcalorimetry, enabling continuous monitoring of microbial metabolic activity.

Results reveal a strong influence of sediment type on microbial activity associated with EPS degradation. Muddy sediments exhibit more intense and prolonged calorimetric signals than sandy sediments, indicating higher and more sustained microbial activity and suggesting greater efficiency in EPS models degradation under the tested conditions. This may reflect ecological adaptations to sedimentary constraints: in fine-grained, low permeability sediments, the complexation of EPS to clay mineral surfaces could limit the EPS degradability. The microbial community could have adapted by using more efficient degradation mechanisms. In contrast, sandy sediments, which are more permeable and retain less water, exhibit lower and more transient activity. Higher microbial biomass in muddy sediments may also contribute to these patterns.

Complementary analyses (Rock-Eval, sedimentary EPS characterization) are currently underway to link these activities to the intrinsic properties of organic matter and EPS. Ultimately, this integrated approach will provide new insights into the mechanisms coupling sediment structure, microbial activity, and EPS fate in estuarine environments.



Loïc RIVIÈRE, MFP (PR)

African trypanosomes: the hidden face of lipid metabolism

Loïc Riviere

African trypanosomes are major human and veterinary pathogens, but also highly divergent eukaryotic models with unusual metabolic features. While parasite metabolism has long been studied from a carbohydrate-centered perspective, lipid metabolism remains comparatively underexplored despite its central role in cellular organization and adaptation.

Here, we investigate the role of lipid droplets (LDs) and lipid mobilization pathways in trypanosomes, with a particular focus on a previously uncharacterized triglyceride lipase called TbPat. Using a combination of molecular genetics, advanced imaging (including expansion microscopy and immuno-electron microscopy), lipid analysis and proteomics, we demonstrate that TbPat localizes to lipid droplets in both insect and bloodstream forms.

Functional analyses reveal that TbPat is required for efficient triglyceride mobilization. Its disruption leads to a striking phenotype characterized by fewer but enlarged lipid droplets and intracellular triglyceride accumulation. Although global metabolic outputs remain relatively stable, proteomic data indicate significant remodeling of metabolic pathways, suggesting compensatory mechanisms and a potential regulatory role.

Altogether, our results identify TbPat as a key player in lipid droplet dynamics and uncover an unexpected level of complexity in trypanosome lipid metabolism. These findings highlight lipid droplets as important regulatory hubs and open new perspectives on parasite adaptation.

Lélaud ESNAULT, ARNA (PhD)

Engineering the Flagellar Type III Secretion System of Salmonella for Recombinant Therapeutic Protein Delivery

Lélaud Esnault[1], PI Thibaud T. Renault[1]

Over the last decades, a new paradigm has emerged: «living therapeutics», where natural or modified live organisms themselves become the medicine. Among the most promising agents is Salmonella enterica, whose natural tropism for tumor microenvironments makes it a compelling player in oncology. But what if we could go further, combining this natural ability of Salmonella to colonize tumors with the capacity to secrete therapeutic proteins directly on site? The flagellar Type III Secretion System (fT3SS) of Salmonella is a powerful nanomachine, naturally exporting proteins at remarkable speed: thousands of amino acids per second, roughly the equivalent of pumping out an entire protein the size of GFP in under a millisecond. During this PhD, we are working with an engineered fT3SS able to deliver recombinant proteins directly into the extracellular space. Our work pursues a dual ambition: first, to understand the fundamental «rules» underlying successful fT3SS-mediated secretion, and second, to use these rules to

enable secretion of functional therapeutic proteins. Through genetic engineering of protein constructs with diverse physicochemical properties, stability profiles, and length, we are currently characterizing key parameters determining secretion efficiency. These results are being used to design therapeutically relevant protein constructs, from immunotherapeutics based on single-domain antibodies (VHHs) to more complex self-assembling constructs forming nanoparticles. Together, this work builds a framework for engineering Salmonella as a programmable protein delivery platform, opening perspectives for future living therapeutic applications.

Emmeline PAOLI, EBI (PhD)

Involvement of quorum sensing in the virulence of the Borrelia burgdorferi sensu lato complex

Emmeline Paoli1, Jean-François Jégou2, Laurent Cronier3, Willy Aucher1 and Julien Verdon1

Lyme disease is the most common vector-borne disease in the Northern Hemisphere. Its etiological agents belong to the Borrelia burgdorferi sensu lato complex, which are transmitted to humans by bites from Ixodes ricinus tick. Among pathogenic species, B. afzelii is the predominant species involved in Lyme borreliosis in Europe. Successful transmission and infection require tightly controlled gene regulation that allows physiological adaptation of the bacteria while switching from the tick vector to the mammalian host. Quorum sensing, a bacterial cell-to-cell communication mechanism, is known to modulate virulence and physiological processes in many pathogens. Previously, in our laboratory, a putative AI-2-dependent quorum sensing system has been identified in B. afzelii, yet its functional role remains poorly understood. We thus explore the functionality and the role of this system in the virulence of B. afzelii. A luxS deletion mutant (ΔluxS), targeting the gene responsible for AI-2 synthesis, was generated and its phenotype was characterized via in vitro studies prior to in vivo investigations. In particular, AI-2 production was quantified and confirmed to be abolished in the ΔluxS strain. Transcriptomic profiling (RNA-seq) comparing wild-type and ΔluxS strains uncovered significant differential expression of genes associated with virulence and host adaptation, including the sigma factor rpoS, known to control expression of several key virulence factors such as OspC and DbpA, required during early mammalian infection. Interestingly, ospC transcription was strongly reduced in the mutant strain. These findings were validated by quantitative reverse transcription PCR and protein analyses, including SDS-PAGE and LC-MS/MS, confirming the reduced OspC production in the absence of luxS. Our results suggest that AI-2-dependent quorum sensing contributes to the regulation of virulence-associated pathways in B. afzelii, highlighting a potential role for luxS in the modulation of host-pathogen interactions. Ongoing in vivo studies aim at further elucidating the impact of this system on infectivity and transmission dynamics.

Martin LEFEUVRE, CBMN (PhD)

Structure and interactions of RocS controlling chromosome segregation in Streptococcus

Martin Lefeuvre, Ana Álvarez-Mena, Estelle Morvan, Clara Lambert, Anagha Kallisseri Parambil, Zeren Xu, Nadia El Mammeri, Florian Malard, Erick J. Dufourc, Cécile Feuillie, Christophe Grangeasse, Birgit

Accurate chromosome segregation is a fundamental process for bacterial viability, yet its molecular mechanisms remain poorly understood. In Streptococcus pneumoniae, an opportunistic pathogen responsible for severe invasive diseases, the growing resistance to antibiotics represents a major public health challenge and highlights the urgent need for novel therapeutic targets. In this context, the protein RocS (Regulator of Chromosome Segregation) has recently been identified as a key player in chromosome segregation and its coupling to cell division. RocS combines a DNA-binding domain (N-terminal HtH domain) and a predicted amphipathic helix (C-terminal AH domain) involved in membrane anchoring. Despite its

central role, mechanistic insights into RocS's simultaneous interactions with DNA and the membrane remain largely unknown. We aim to elucidate the conformations and interaction mechanisms of RocS with both the lipid membrane and DNA by combining solid-state and solution NMR spectroscopy in conjunction with complementary biophysical approaches. The overall objective is to understand how RocS ensures the proper positioning and segregation of chromosomes during the bacterial cell cycle. Preliminary work has focused on the predicted amphipathic helix of RocS, the key element for membrane anchoring. Using static and MAS solid-state NMR, combined with AFM, we showed how the small membrane anchor confers interactions with liposomes, inserting in a kink-helix conformation into lipid domains. Conservation analysis over different kingdoms of life suggests our results to reflect a more general membrane-targeting mechanism. In a divide and conquer approach, we further prepared the HtH domain using a denaturation–renaturation strategy, and characterized the domain by solution-state NMR. We will further present the production and purification of recombinant RocS, paving the way for the preparation of isotopically labeled samples. In the long term, the project will provide a structural understanding of a central process in the chromosome segregation and could open perspectives for the development of antibacterial strategies targeting the division and propagation of S. pneumoniae.

Audrey Gauthier, Damoclès diagnostic

DAMOCLES Dx: Rapid phenotypic AST directly from urine samples using real-time bacterial

Urinary tract infections (UTIs) are among the most common bacterial infections and are frequently treated empirically, contributing to antimicrobial resistance. Current microbiology workflows still require centralized laboratories and long turnaround times before obtaining antimicrobial susceptibility testing (AST) results.
DAMOCLES Dx is developing a rapid phenotypic AST platform capable of monitoring early bacterial response to antibiotics directly from urine samples. The technology combines automated fluidic analysis, real-time signal acquisition and morphological profiling to rapidly characterize bacterial susceptibility patterns.
This presentation will introduce the DAMOCLES Dx approach, the underlying technology, and preliminary results obtained on borated urine samples, highlighting the potential for rapid decentralized microbiology and faster therapeutic decision-making.

Germain CHEVIGNON, ASIM-IFREMER (Scientist)

Genomic Characterization of Marine Vibrio Species for the Development of Novel Diagnostic Toolspneumoniae

Moreau Yannis, Jacquot Maude, Garcia Céline, Canier Lydie, Travers Marie-Agnes, Tourbiez Delphine, Chevignon Germain

The genus Vibrio comprises numerous marine bacteria, including several species recognised as important pathogens with significant implications for both human health and aquaculture. In particular, marine molluscs are highly susceptible to infections caused by specific Vibrio taxa. The development of accurate species-level diagnostic tools remains a major challenge, largely due to the substantial intraspecific genetic diversity and the limited availability of complete and curated genome assemblies in public repositories. This taxonomic complexity hinders both pathogen identification and disease management strategies in marine ecosystems. To date, various methodologies are currently used for bacterial identification, including sequence-based approaches and MALDI-TOF mass spectrometry.
To develop new diagnostic tools, we sequenced and assembled 115 complete genomes from strains representing 42 distinct Vibrio species. The genomes were obtained by long-read sequencing and assembled using a dedicated pipeline optimised for long-read data, ensuring high contiguity and completeness. Notably, eight of these genomes represent the first complete assemblies available for their respective species.
In this study, we compared the performance of MALDI-TOF, MLSA, and whole genome sequencing for the identification of Vibrio species. Using comparative genomics, we delineated the Vibrio core genome and identified a set of candidate species-specific genomic markers. These loci were systematically validated

against a comprehensive dataset of 7000 publicly available Vibrio genomes from 47 species, with particular emphasis on clades containing invertebrate pathogens. Our analysis revealed novel markers with high discriminatory power and interspecies specificity, enabling robust taxonomic resolution across the genus. We propose novel single-gene diagnostic markers that allow accurate and consistent identification of Vibrio species, offering a streamlined alternative to current multi-locus approaches. In addition to its diagnostic potential, this marker provides a strong phylogenetic signal, supporting more accurate classification within the genus. This work also allowed us to formulate recommendations for the identification and diagnosis of Vibrio bacteria, contributing to the development of next-generation molecular tools for monitoring Vibrio diversity in marine ecosystems.

Axel PITARD, LIENSs (PhD)

Exploring the antibiotic-like potential of plant extracts against multidrug-resistant pathogenspneumoniae

Pitard Axel 1, Parizadeh Leila 1, Iorfida Ophélie 1, Achour Oussama 1,2, Sopena Valérie 1, Lanneluc Isabelle 1, Le Joubioux Florian 1,3, Sirvent Pascal 3, Maugard Thierry 1, Sablé Sophie 1

Plant-derived bioactive molecules represent a promising source of natural alternatives to conventional antibiotics. These compounds display a high diversity of chemical structures and mechanisms of action, enabling them to target multiple bacterial processes while potentially limiting the emergence of resistance. This PhD research focuses on the antimicrobial potential of plant extracts against multidrug-resistant (MDR) bacterial strains, including clinically relevant pathogens such as Staphylococcus aureus (including methicillin-resistant phenotypes) and Pseudomonas aeruginosa, among others. The main objective is to characterize their antibacterial activity, elucidate their molecular and cellular mechanisms of action, and evaluate their potential as innovative antibiotic-like anti-infective agents.

A panel of medicinal and aromatic plants traditionally used to treat infectious diseases was selected. Hydroalcoholic extracts were prepared and first screened using broth microdilution assays to determine minimum inhibitory concentrations (MICs). Minimum bactericidal concentrations (MBCs) were subsequently assessed by subculturing on agar plates. Several extracts display low MIC values, ranging from 0.3125mg/mL to 5mg/mL, together with relatively low MBCs and MBC/MIC ratios consistent with bactericidal activity. These findings demonstrate a pronounced antibiotic-like effect against resistant bacterial strains. To further enhance antibacterial efficacy and explore combination strategies, selected extracts were tested in binary mixtures against priority pathogens. These experiments reveal additive effects and, in some cases, synergistic interactions, characterized by significant reductions in MIC and/or MBC values compared to individual extracts.

Overall, this work identifies plant extracts and extract combinations with bactericidal profiles, additive or synergistic interactions, and characterized modes of action. These results highlight promising plant-derived candidates and combination strategies for the development of next-generation therapies targeting infections caused by multidrug-resistant bacteria.

Arthur CHARAZAC, PHAR2-Poitiers (Master)

Gallium Potentiates Cefiderocol Activity and Constrains Resistance in Stenotrophomonas maltophilia In Vitropneumoniae

Arthur CHARAZAC (1,2,3), Jérémy MOREAU (1), Julie Crémiter (1,2,3), Frédéric Tewes (1,2)

Introduction

Stenotrophomonas maltophilia is an opportunistic Gram-negative pathogen responsible for difficult-to-treat hospital-acquired infections due to its intrinsic multidrug resistance. Cefiderocol, a last-resort siderophore cephalosporin, represents a valuable treatment option; however, emergent resistance threatens its efficacy. Gallium, an iron-mimetic metal that disrupts bacterial iron metabolism and has shown

antimicrobial activity in recent clinical trials, may potentiate cefiderocol activity and suppress resistance. This study evaluated the in vitro efficacy of the cefiderocol–gallium combination and its impact on the emergence of cefiderocol resistance in S. maltophilia.

Methods

Twenty clinical S. maltophilia isolates from French university hospitals were tested. Minimum inhibitory concentrations (MICs) of cefiderocol and gallium nitrate were determined in iron-depleted cation-adjusted Mueller–Hinton broth (ID-CAMHB). Drug interactions were assessed using checkerboard assays. Resistance evolution was examined through serial MIC determinations during repeated exposure to cefiderocol alone or combined with gallium (molar ratio 1:179) in three representative isolates with distinct baseline susceptibilities.

Results

Baseline cefiderocol MICs ranged from 0.06 to 2 mg/L (all within EUCAST susceptibility breakpoints). In combination with gallium (0.25–128 mg/L), cefiderocol MICs decreased 2- to 32-fold (range: 0.016–0.25 mg/L). Checkerboard assays frequently displayed a U-shaped interaction profile, indicating an optimal cefiderocol–gallium ratio; at higher gallium concentrations, activity declined, likely due to competition between free gallium and the cefiderocol–gallium complex for bacterial uptake.

Serial passage with cefiderocol alone rapidly selected for high-level resistance (64- to 512-fold MIC increases within 2–4 passages). In contrast, the combination markedly suppressed resistance emergence: MICs remained at or below the susceptibility breakpoint in two isolates and only modestly increased in one. Resistance stability after five drug-free passages (≤4-fold MIC decrease) suggested underlying genetic adaptation. Notably, the combination restored activity against cefiderocol-resistant isolates selected during serial passages, with impressive MIC reductions of 64- to 2048-fold.

Conclusions

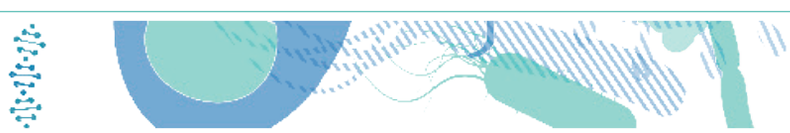
Gallium markedly enhances cefiderocol activity against S. maltophilia, constrains resistance development, and restores susceptibility in resistant strains. The ratio-dependent interaction implies competition for bacterial iron uptake pathways, emphasizing the need for dosing optimization. These findings suggest that combining cefiderocol with gallium could extend cefiderocol's clinical utility and represents a promising strategy for treating infections with limited therapeutic options.

Guillaume Goudounet, Responsable Microbiologie R&D Kapsera

Kapsera, une entreprise qui protègent l'avenir

Kapsera est une biotech française spécialisée dans la microencapsulation d'actifs naturels grâce à une technologie de microfluidique brevetée. L'entreprise développe des solutions biodégradables pour l'agriculture, la nutrition et la santé animale. Son objectif est d'améliorer l'efficacité et la stabilité des ingrédients tout en réduisant leur impact environnemental.

POSTER



SESSION 1 : RESISTANCE AND MOLECULAR MECHANISMS OF MICROORGANISMS

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29	Autin	Michel	Disassembly of the HIV-1 integration complex: a role for TAR RNA
31	Souffleur	Elsa	Hijacking the remodeler: how post-translational modifications of TAF-1ß shape human adenovirus infection
33	Vilatte	Mila	Structure-function characterization of Gtwin endogenous retrovirus integration
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1 - Méline Laborde, PhD student

Microbiologie Fondamentale et Pathogénicité - MFP - UMR 5234 – CNRS, Université de Bordeaux

Structural and functional studies of the accessory protein Bet from the Prototype Foamy Virus.

Larobe M, Calmels C., Guillon E, Lindemann D, Munk C, Parissi V, Lesbats P.

Foamy viruses belong to the retrovirus family but are classified as a distinct group, the Spumaretroviruses. They display several atypical features compared to other studied retroviruses : they are considered non-pathogenic, and they carry out reverse transcription late in their replication cycle, resulting in the production of viral particles containing DNA rather than RNA. These viruses are endemic in several animal species, including non-human primates, cats, equines, and bovines, and can also be found in humans, where they are referred to as Prototype Foamy Virus (PFV).

The Prototype Foamy Virus (PFV) encodes the viral accessory protein Bet, one of the most enigmatic accessory proteins among retroviruses, which may be responsible for some of the atypical characteristics of this virus, as it is not found in other retroviruses. Although Bet is known to antagonize members of the APOBEC3 restriction factor family, its broader structure and functions during the viral cycle remain largely unexplored.

Our preliminary results highlighted the presence, within Bet, of a conserved CCCH zinc finger pattern, suggesting the existence of structural determinants essential to its activity. The mutation of this motif leads to an alteration in viral replication as well as a loss of antagonism towards APOBEC3, highlighting its functional importance.

Furthermore, our first crystallization assays provided promising results, paving the way for the first high-resolution structural determination of a foamy virus accessory protein. Such a structure would constitute a major advance, Bet presenting no known viral or cellular homologue and its low conservation between the different foamy virus lines suggesting a unique structural flexibility, possibly involved in host adaptation.

3 - Pauline Marchal, PhD student

Microbiologie Fondamentale et Pathogénicité - MFP - UMR 5234 – CNRS, Université de Bordeaux

SARS-CoV-2 and GCN2, a strange relationship

Pauline MARCHAL, Patricia PINSON, Floriane LAGADEC, Marie-Line ANDREOLA, Mathieu METIFIOT

Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) is a highly transmissible pathogen responsible for a global health crisis. A deeper understanding of its replication strategies and interactions with host cells remains essential, particularly in the context of long COVID and the continuous emergence of viral variants.

To counter viral infection, host cells activate multiple defence mechanisms, including the Integrated Stress Response (ISR). The ISR is a conserved cellular pathway that temporarily halts protein synthesis in response to stimuli such as nutrient deprivation, viral infection, or oxidative damage. The ISR promotes cellular adaptation by modulating translation and activating specific stress transcription factors.

GCN2, a key kinase in this pathway and the only one conserved through evolution (from yeast to human). It plays a role in several human diseases, including cancer, Alzheimer's disease, and obesity. Recent studies have also highlighted its role in innate immunity, where it acts as a restriction factor against retroviruses such as HIV and other RNA viruses. However, several RNA viruses, including HIV, SARS-CoV-2, and ZIKV, have evolved strategies to manipulate the ISR to favour their own replication under stress conditions.

Our data suggest that SARS-CoV-2 may also escape ISR. Notably, after 48 hours of infection, we observe a decrease in GCN2 protein level. Appelberg et al. reported that infection leads to over-activation of the mTORC1 complex, resulting in a robust inflammatory cytokine response and metabolic reprogramming that favours viral replication. Together, these findings indicate that SARS-CoV-2 actively modulates host cellular stress responses. Elucidating the interplay between the ISR and viral infection may therefore reveal novel therapeutic targets.

5 - Juliette Villagomez, PhD student

Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

Exploring Adenovirus Chromatin Dynamics and Associated Proteins During the Viral Cycle

Juliette Villagomez, Fabienne Rayne, Muriel Faure, Jessica Ragues, Nicolas Landrein, Benoit Roger, Axel Imhof and Harald Wodrich

The adenovirus genome consists of double-stranded DNA organized in a chromatin-like structure, where it interacts with the pVII protein in a nucleosome-like complex known as the adenosome. This structure remains tightly compacted within the viral capsid. Upon nuclear entry, adenoviral chromatin undergoes dynamic remodeling, coordinating early and late gene expression as well as viral genome replication. While cellular factors such as histones and chromatin remodelers are thought to be involved in these processes, the underlying mechanisms remain poorly understood.

In this study, we aim to establish an antibody-mediated proximity biotinylation system targeting pVII to identify viral and cellular factors involved in adenoviral chromatin dynamics. By identifying these factors via mass spectrometry, we seek to unravel the molecular mechanisms governing adenoviral genome accessibility and regulation throughout the infection cycle.

7 - Mathilde Lartigau, PhD student

Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

Exploring pVI release in vitro: insights into adenoviral endosomal escape

Mathilde Lartigau, Nicolas Landrein, Fabienne Rayne, Benoit Roger, Muriel Faure, Jessica Ragues and Harald Wodrich

Adenoviruses enter host cells via receptor-mediated endocytosis, followed by escape into the cytosol – a critical step mediated by the viral protein pVI. This lytic protein is released from the viral capsid inside the endosome, where it disrupts the membrane through its N-terminal amphipathic helix, allowing the viral capsid to escape and continue its infection cycle. pVI release is preceded by a series of well-orchestrated events: binding of the virus to cellular receptors (Integrins and CAR receptor) that destabilizes the capsid, followed by endocytosis of the bound viral particle, which ultimately leads to pVI release. Once released, pVI interacts with endosomal membranes via its amphipathic helix, facilitating membrane disruption. In this study, we investigate the molecular triggers required for pVI release using fluorescent microscopy and live-imaging. We aim to mimic the cellular environment during adenoviral infection and define the conditions necessary to observe this process in vitro. Ultimately, this approach could provide a novel framework for studying viral membrane disruption and the mechanisms of adenoviral endosomal escape.

9 - Nicolas Sola, PhD student

Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

ClpV ATPase: Structure and Role in Type VI Secretion System recycling

Nicolas SOLA, Julien GIRAUD, Denis PTCHELKINE, Rémi FRONZES, Éric CASCALÈS, Esther MARZA

Type VI Secretion Systems (T6SS) are contractile bacterial nanomachines that mediate interbacterial competition and virulence in Gram-negative bacteria. Following contraction and toxin delivery, the T6SS sheath must be disassembled by the AAA+ ATPase ClpV to enable component recycling and system reactivation. However, the late stages of T6SS function, particularly sheath disassembly and recycling mechanisms, remain poorly characterized. ClpV is recruited specifically to contracted sheaths, where TssC N-terminal helices become accessible for interaction, but the structural basis for this process is largely unknown. Here, we present the first cryo-EM structural analysis of ClpV from enteropathogenic E. coli. Our structure reveals ClpV adopts a hexameric open-ring conformation with flexible N-terminal domains that enable binding to TssC subunits of the contracted sheath. This architecture provides initial insights into how ClpV recognizes its substrate and positions itself for disassembly. These findings represent a first step toward understanding the molecular mechanisms underlying T6SS recycling and regulation of this important bacterial weapon system.

11 - Nathanael Benoit, PhD student

Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

A ubiquitin- like protein controls assembly of a bacterial type VIIb secretion system

Nathanaël Benoit, Gabriel U. Oka, Nathanaël Benoit, Axel Siroy, Francesca Gubellini, Esther Marza , Rémi Fronzes

Type VII secretion systems (T7SS) are protein translocation machines crucial for virulence and bacterial competi- tion in Gram- positive bacteria. Despite their importance, the structural basis for assembly of type VIIb secretion systems (T7SSb), a widely distributed variant in Firmicutes, remains poorly understood. We present the cryo–electron microscopy structure of the T7SSb core complex from Bacillus subtilis, revealing how the ubiquitin- like protein YukD, coordinates assembly of the secretion machinery. YukD interacts extensively with the central channel component YukB and facilitates its association with the pseudokinase YukC, forming a stable building block for channel assembly. Time- lapse microscopy and competition assays demonstrate that YukD is essential for proper T7SSb complex formation and contact- dependent bacterial killing. Our findings reveal how bacteria have adapted a ubiquitin- like protein as a structural regulator for assembling a large secretion complex.

13 - Sabine Pereyre, Lecturer/Researcher

Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

Spread of a dual resistant Mycoplasma genitalium clone harboring an A2058T substitution in 23S rRNA in men in France

Sabine Pereyre, Cécile Laurier-Nadalié, Carla Balcon, Nadège Hénin, Amandine Dolzy, Marie Gardette, Jennifer Guiraud, Cécile Bébéar

Background

Macrolide resistance has been rapidly increasing worldwide in Mycoplasma genitalium. The spread of macrolide resistance has been reported to be polyclonal. However, a few resistant clones may be circulating, particularly in men. To search for the potential spread of M. genitalium macrolide-resistant clones in men in France, we performed a nationwide survey to investigate the mgpB type of macrolide-resistant strains.

Methods

A one-month systematic prospective collection of M. genitalium-positive specimens in men was performed between 15 Sept. and 15 Oct. 2021 and 2022 in French diagnostic laboratories. Resistance-associated mutations were detected using 23S rRNA, parC, and gyrA gene sequencing. Typing was performed using SNP analysis of the mgpB adhesin gene on all macrolide-resistant strains.

Results

M. genitalium-positive specimens were collected from 229 and 191 male patients from 38 and 37 French laboratories in 2021 and 2022, respectively. The overall prevalence of macrolide-resistance associated mutations was 53.2% (95%CI 47.9-58.3%) and the percentage of fluoroquinolone resistance-associated mutations was 25.2% (95%CI 20.8%-30.1%). The most frequent macrolide-resistance associated mutation was A2059G (Escherichia coli numbering) (46.6%) followed by the A2058T substitution (33.5%) and the A2058G mutation (19.5%). The proportion of A2058T transversion increased significantly compared to a similar previous study in 2018 (18.8% in 2018 vs 34.2% in 2022, p=0.02). MgpB typing of macrolide-resistant strains revealed 47 distinct sequence types (STs), including 16 new STs. ST159 was the most frequent ST representing 20.2%. All ST159 strains harbored both the A2058T transversion in 23S rRNA and the S83I fluoroquinolone-resistance associated mutation in ParC. Moreover, 94.1% of ST159 were from bisexual or men who have sex with men, and 63.6% were from the Paris region.

Conclusion

We report the emergence of the A2058T transversion among macrolide-resistant strains in France and the spread of a dual resistant A2058T-S83I ST159 clone more likely circulating in MSM from Paris.

15 - Marine Baraquin, PhD student

Acides nucléiques : Régulations naturelles et artificielles -ARNA - U1212 - INSERM - UMR5320 – CNRS, Université de Bordeaux

Plasmid detox: how bacteria let go of hok/Sok?

Marine Baraquin, Andrés Escalera-Maurer, Adriana Messineo and Anaïs Le Rhun

The hok/Sok locus is a type I toxin-antitoxin system commonly found in Enterobacteriaceae. Hok is a toxic protein that targets the bacterial inner membrane and triggers bacterial death. Hok expression is regulated by Sok, an antisense RNA that binds to the hok mRNA to prevent its translation. When encoded on plasmids, Hok kills its host upon plasmid loss, thereby maintaining the plasmid in the population. This mechanism is known as post-segregational killing (PSK). Understanding PSK and bacterial survival strategies could guide novel antibiotic development. Although PSK by hok/Sok has been studied in detail and was shown to rely on a difference of stability between the hok and the Sok RNA, the parameters influencing PSK efficiency and how bacteria escape killing are yet to be described. Here, we investigated the effect of the Hok peptide sequence and the hok mRNA abundance on PSK efficiency in Escherichia coli and Salmonella Typhimurium. We artificially triggered plasmid loss and monitored PSK using bacterial growth and time-lapse fluorescence imaging. We compared the activity of Hok sequences and determined that the most efficient hok/Sok sequence to mediate PSK is the one of the multidrug-resistant plasmid R1. We visualized PSK escapers and determined the effect of varying amount of hok mRNA on this phenotype. Taken together, our results uncover key parameters influencing PSK efficiency providing a deeper understanding of the molecular determinants governing plasmid maintenance.

17 - Léa Bientz, Lecturer/Researcher

Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

Unexpected isolation of carbapenemase DIM-1 in Enterobacterales in France

Léa Bientz, Saoussen Oueslati, Sabine Pereyre, Bogdan I. Iorga, Laure Coulange-Mayonnove, Cécile Bébéar, Delphine Girlich, Véronique Dubois, Thierry Naas

Background

The DIM-1 metallo-β-lactamase is mainly described in Pseudomonas (P. stutzeri, P. aeruginosa, P. putida, P. guguanensis) in the Netherlands, Poland, Africa and Asia, and its gene is found on plasmids or on the chromosome. Retrospective analysis of 280 carbapenemase-producing Enterobacterales strains isolated at Bordeaux University Hospital in France between 2014 and 2024 revealed the blaDIM-1 gene in Enterobacterales for the first time. This strain was isolated in 2023 from a rectal swab from a patient repatriated from Africa.

Methods

The genetic support of the blaDIM-1 gene was studied by plasmid extraction using Kieser's method, followed by electroporation in Escherichia coli TOP10 and conjugation experiments in E. coli J53. The minimum inhibitory concentrations of β-lactams were determined on the transformants and transconjugants.

Results

A strain identified by MALDI-TOF (Bruker) as belonging to the Enterobacter cloacae complex and producing carbapenemase OXA-48 via an immunochromatographic test (RESIST-5, CORIS) was reclassified by NGS as Enterobacter hormaechei xiangfangensis carried not only the blaOXA-48 gene, but also blaCTX-M-15 and, unexpectedly, the blaDIM-1 gene. The blaDIM-1 gene was located on a plasmid between 66 kb and 154 kb upstream of an ant(2»)-Ia gene. The introduction of this plasmid into E. coli TOP10 led to a significant decrease in susceptibility to β-lactams, demonstrating the functionality and resistance conferred by DIM-1. The conjugation rate was very low (<10-8 per donor); however, interestingly, the resulting transconjugants harboured a hybrid plasmid of approximately 154 kb carrying both blaDIM-1 and blaOXA-48. Furthermore, DIM-1 enzyme was not detected by commonly used immunochromatographic tests (RESIST-5, CORIS; CARBA-5, NG-Biotech), but only by the CARBA NP biochemical test, highlighting a possible underestimation of its prevalence by current standard methods.

Conclusion

Plasmid-mediated carbapenemase DIM-1 in Enterobacterales presents a significant potential risk of rapid spread between species. Its low detectability by conventional immunochromatographic tests highlights the need for biochemical methods to ensure effective surveillance.

19 - Lisa Scillia, Post doc

Microbiologie Fondamentale et Pathogénicité - MFP - UMR 5234 – CNRS, Université de Bordeaux

Potential of Lipid AntiSense Oligonucleotides to overcome antibiotic resistance in extended-spectrum β-lactamase-producing Escherichia coli

L. Scillia, H. Barry, D. Bégu, L. Béven, L. Varlet, M. Mondin, T. Kauss, C. Arpin

Background

To combat antimicrobial resistance, the Word Health Organization has established that Escherichia coli resistant to third-generation cephalosporins (3GC) is a critical priority for Research & Development of new antibiotics. One promising approach, is to restore the efficacity of existing antibiotics using antisense oligonucleotides (ASOs). We have developed chemically modified ASOs targeting blaCTX-M-15 the most prevalent extended-spectrum β-lactamases in E. coli. To overcome the major obstacle of bacterial uptake, the ASOs were conjugated to a nucleolipid, generating LASOs (lipid–antisense oligonucleotides). The goal of this interdisciplinary project was to evaluate the effect of LASOs on reducing ceftriaxone (3GC) resistance in CTX-M-15-producing E. coli by deciphering LASOs action mode.

Methods

LASOα (25-mer) designed to target the beginning of the blaCTX-M-15 mRNA were tested by minimal inhibitory concentration (MIC) assay to evaluate the effect of phosphorothioate (PTO)-modified LASOα (5µM) on different E. coli strains (5 x 105 bacteria/mL) on ceftriaxone (MICCFX) resistance. The mode of action of LASO was then investigated by quantitative Reverse-Transcription PCR (RTqPCR) and Western blotting experiences using the same ratio bacteria/LASO than MIC. Flow cytometry and microscopy experiments such as confocal and super-resolution (stochastic optical reconstruction microscopy) were performed to decipher the localization of LASO.

Results

PTO-modified LASOα targeting blaCTX-M-15 mRNA was able to decrease by up to 26-fold, the MICCFX in resistant laboratory and clinical E. coli strains, without affecting bacterial viability.
Transcriptional analyses (RT-qPCR) showed no decrease in target mRNA levels, suggesting that LASOα PTO acts through a steric hindrance mechanism. However, analyses by Western blot revealed the CTX-M-15 translation inhibition at least 2-fold. Flow cytometry analyses indicated that nearly one-third of the bacterial cells interacted with LASOα PTO. However, it remains difficult to determine their precise intracellular localization by the used microscopy techniques. Beyond their sequence-specific antisense activity, additional effects were explored suggesting that LASO may reduce the activity of purified β-lactamase on nitrocefin, a chromogenic cephalosporin substrate.

Conclusions

These promising results pave the way for future therapeutic applications of LASOs in the fight against antimicrobial resistance.

21 - Audrey Toirot, PhD student

Microbiologie Fondamentale et Pathogénicité - MFP - UMR 5234 – CNRS, Université de Bordeaux

Carriage of colistin-resistant Klebsiella pneumoniae in intensive care and oncohematology units in Nouvelle-Aquitaine: resistance mechanisms and transmission risk

Audrey TOIROT, Jeanne Begue, Laure Mayonnove, Sabine Aillerie, Cécile Bébéar, Véronique Dubois

Colistin is a last-resort antibiotic against multidrug-resistant bacteria, including carbapenemase-producing Enterobacterales (CPE). Its antimicrobial activity is based on electrostatic interactions with lipid A, outermembrane component of Gram negative bacilli. The emergence of pan-resistant strains has renewed interest in studying colistin resistance mechanisms (CR). Among bacterial species of concern, Klebsiella pneumoniae stands as a top priority pathogen with high prevalence in healthcare associated infections and wide spread of multiresistant clones, such as ST147 carbapenem resistant strains. As part of the RESCO study, rectal screenings for isolates that had acquired CR were conducted between 2019 and 2021 in intensive care and oncohematology patients in Nouvelle-Aquitaine. Eleven colistin-resistant K. pneumoniae isolates were collected, with five isolates producing CTX-M-15 ESBL and six remaining susceptible to cephalosporins. Until now, the mechanism of CR in fecal carriage K. pneumoniae strains remained undetermined.
All K. pneumoniae isolates were sequenced by NGS (MiSeq, Illumina®), and their genomes were assembled de novo (SPAdes). Six genes were analyzed (mgrB, crrB, phoP/Q, pmrA/B),

and plasmid-mediated resistance genes were searched using nBLAST and ResFinder. Complementation assays, introducing wild-type genes on the pTOPO plasmid (Invitrogen®), confirmed the involvement of mutated genes.
Six isolates carried inactivating mutations in mgrB, including two start codon deletion and four with a complete gene deletion. Colistin susceptibility was restored by mgrB complementation for all six strains. Novel mutations were identified in crrB (Q239H, T276A). Multiple mutations were identified in two-component system phoP/phoQ and pmrA/pmrB, with a still unresolved role in CR, regarding complementation assays.
No plasmid-mediated colistin resistance genes were detected. Among the 11 isolates studied, MLST analysis identified two predominant sequence types : ST37 and ST147, previously associated with carbapenemase production. This study elucidated the genetic basis of CR in K. pneumoniae from colonization, primarily mediated by chromosomal mutations, thereby limiting the risk of CR dissemination and its distribution among different STs.

23 - Vincent Parissi, Lecturer/Researcher
Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

Cellular subversion of retroviral integrases chromatin binding function for optimal host invasion

D. Lapaillerie, Y. Zgadzay, C. Tumiotto, P. Lesbats, S. Sousa, M. Ruff, V. Parissi

Our work aims to understand the molecular and cellular determinants for chromatin invasion by retroelements. This process relies on the integration of the viral genome into host DNA by the intasome complex. Retroviral integration is profoundly influenced by the chromatin environment that determine whether the provirus will undergo efficient expression or remain latent. The selection of insertion sites is a complex, multi-faceted process that involves the successive targeting of the viral capsid and intasome by cellular factors such as CPSF6 and LEDGF/p75 in the case of lentiviruses as HIV-1.
Preference for specific chromatin structures ultimately modulates the interaction between the retroviral intasome and nucleosomes, thereby serving as an additional regulatory parameter in site selection. To better define the functional interfaces engaged in chromatin integration, we require structural data regarding the HIV-1 intasome/nucleosome interaction and the nucleosomal strand transfer complex (Nuc-STC). In our previous, and ongoing, ANRS-funded project (INterfaces&StructurIN), we employed a combination of biochemical techniques and structural docking methodologies to elucidate the functional interfaces between the intasome and its nucleosomal substrate across various retroviral models, including HIV-1 and the human foamy prototype virus PFV.
Our findings demonstrate how chromatin compaction affects accessibility to these interfaces and provide the first molecular insights into the regulatory role of chromatin structures in integration. Additionally, we reveal that LEDGF/p75 and histone H3K36me3 modifications contribute to the proper structuring of optimal nucleosomal templates, addressing long-standing questions regarding the role of this cellular factor during integration (Lapaillerie et al., NAR 2021, Lapaillerie et al., in revision). Our work also identified local chromatin R-loop structures generated during transcription along with the Aquarius helicase involved in their resolution, as novel determinants influencing the selection of HIV-1 integration sites (Penzo et al., Nature Microbiology 2025). Significantly, we discovered that HIV-1 integrase (IN) can recognize and bind to specific histone modifications, suggesting a novel chromatin reader function within the SH3-folded C-terminal domain (CTD) of IN. Further structure-function analyses indicate that this recognition is modulated by LEDGF/p75 both in vitro and in infected cells. Selection of IN mutations and drugs targeting this chromodomain—capable of inhibiting and redirecting integration—highlights their potential as therapeutic targets and tools for controlled gene transfer (Mauro et al., NAR 2019, Mauro et al., mBio 2023). Comparative studies with other retroelements including yeast retrotransposon and endogenous retroviruses imply that retroviral INs act as multifunctional chromatin binders, scanners, and potential «readers»— playing a critical role in chromatin invasion. Our data also reflect a co-evolutionary strategy for regulating and balancing genome invasion, ensuring a controlled integration process.

25 - Delphine Lapaillerie, ITA

Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

Early detection of retroviral genomes by DNA repair machineries

Delphine Lapaillerie, Camille Tumiotto, Viviana Scoca, Suzanne Figueiredo, Mathieu Maisch, Carole Bertinetti, Marylene Mougel, Fabrice Fleury, Paul Lesbats, Olivier Delelis, Jacques Dutrieux, Francesca Di Nunzio, Vincent Parissi

HIV-1 infection triggers multiple cellular pathways that modulate viral replication and may promote latency. Central to this process is the reverse transcription of the viral RNA into DNA and its integration into host chromatin, both steps being regulated by the cell. Emerging evidence suggests that homologous recombination (HR) proteins, especially RAD51, may influence both pre- and post-integration stages. In this study, we show that HIV-1 induces the rapid formation of RAD51 nuclear foci in a BRCA1/2-dependent manner, with RAD51 loading onto viral DNA immediately during reverse transcription. Using ChIP, imaging, and biochemical assays, we demonstrate that this process enhances viral infectivity and reverse transcription efficiency. Our findings reveal a novel cellular response that recruits repair factors to viral DNA, regulating reverse transcription and influencing viral DNA fate. Especially, our study on the stability of non-integrated viral DNA under conditions of BRCA1/2 pathway inhibition reveals increased persistence. Our results highlight a new cellular response to infection involving the recruitment of these repair factors to the viral DNA, modulating the reverse transcription step and influencing the fate of different populations of viral DNA. This process may contribute to the persistence of viral genomes in infected cells and the establishment of latent virus reservoirs. This work uncovers a new role for RAD51 in modulating early HIV-1 replication stages, providing insights into host-virus interactions and potential therapeutic strategies.

27 - Emylie Salle, Master 2 student

Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

Study of a potential role of Penton cleavage in the early stages of adenovirus infection

Emylie Salle, Jean-Baptise Vergnes, Benoit Roger, Harald Wodrich

Adenovirus is a non-enveloped linear double-stranded DNA virus. Following internalization by endocytosis, the adenovirus capsid undergoes a partial disassembly within the endosome, triggering the release of internal capsid protein VI, which destabilizes the endosomal membrane allowing viral escape into the cytosol. This disassembly step must be precisely timed: occurring too early dilutes protein VI and impairs infectivity, while occurring too late leads to viral degradation via the endolysosomal pathway. The nature of the trigger of this event in the endosome is still not clear. During the assembly of new adenoviral particles, structural protein precursors undergo a maturation process mediated by the Adenovirus Protease (AVP). AVP cleaves several structural proteins (pIIIa, pVI, pVII, pVIII and pTP) converting hyperstable immature particles into metastable mature virions competent for infection. Recently, the lab identified the capsid protein Penton (one of the three major capsid proteins, not known to be a substrate for AVP) as a potential new target for the protease, whose processing could play a role in the early steps of infection. Our current hypothesis is that AVP could be reactivated within the endosome to cleave the Penton protein, thereby promoting partial disassembly leading to protein VI release and endosomal escape. This newly identified potential AVP cleavage site in penton protein is conserved in C-specie adenoviruses, like type 5 adenovirus (Ad5), that are described to escape from early endosomal compartment, and is not found in B-specie adenoviruses, like type 7 adenovirus (Ad7), which are believed to exit from late endosomes. To assess the functional role of Penton processing during viral infection, and investigate if this could play a role in the timing of endosomal escape, we mutated penton's potential AVP cleavage sites in Ad5 (generating the Ad5-PM3 mutant) in order to prevent its cleavage by AVP. Plaque assays on HEK 293 αvβ5 cells adressed the replication capacity of Ad5-PM3 compared to Ad5-WT. U2OS cells were also infected with GFP-expressing vectors (WT and PM3) to assess infectivity by flow cytometry. Localization of endosomal escape (early vs late endosomal compartments) was evaluated by immunofluorescence, tracking co-localization of viral protein VI release with endosomal markers (EEA1 = early endosomes or Rab7 = late endosomes) over infection time courses comparing Ad5-WT, Ad5-PM3 as well as Ad7-WT particles. Finally, the kinetics of viral genome delivery to the nucleus was quantified over time with these 3 viruses by monitoring the nuclear appearance of protein VII, a viral chromatin-associated protein.

29 - Michel Autin, PhD student

Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

Disassembly of the HIV-1 integration complex: a role for TAR RNA

Autin M., Bertinetti C., Zgadzay Y., Lapaillerie D., Munier-Lehmann H., Bonomi M., Ruff M., Lesbats P. and Parissi V.

Host chromatin invasion by retroviruses relies on their stable integration into the chromosomes of infected cells. Integration is catalyzed by the integrase protein (IN) within the Strand Transfer Complex (STC). Completion of the integration process requires then the disassembly of the STC and the DNA damage repair at the insertion site. These post-integration disassembly steps remain poorly known.

IN protein carries additional functions including binding to the genomic viral RNA, especially to the trans-activator response (TAR) region. Mutations in the IN carboxyl-terminal domain known to bind RNA affect both IN stability at the integration site and transcription of viral genes (Winans and Goff, 2020). Furthermore, recent findings demonstrate that the binding of IN to TAR RNA induces structural changes in both IN and TAR in addition to enhance Tat binding to TAR potentially optimizing the viral transactivation (Rocchi et al., 2022).

Based on these data, we proposed that the binding of TAR to IN may occur just after integration, leading to STC destabilization and promoting its dissociation from the nucleosomal site. The in vitro dissociation assays revealed that RNA, but not DNA, efficiently promotes STC disassembly on nucleosomal templates. Among the nucleic acid structures tested, the HIV-1 TAR RNA exhibited the strongest dissociation activity, selectively releasing integrase and LEDGF/p75 from the integrated nucleosomal product without altering chromatin integrity. TAR mutants defective in integrase interaction failed to promote STC disassembly. Furthermore, we performed in cell kinetics analyses of key steps of the viral life cycle as reverse transcription, integration and transcription in K562 cells. For the first time, we monitored STC disassembly kinetics in cells by quantifying integrase–viral DNA interactions using ChIP-qPCR and with a TAR mutant virus, we observed a delay in integrase disassembly compared to the wild-type virus. Although additional conditions need to be tested to further clarify post-integration events as well as pharmacological approaches targeting this process.

Our work highlights a novel functional interplay between HIV-1 integration and transcription, which requires precise coordination to ensure the optimal invasion of host chromatin by the virus. If the disassembly of the HIV integration complex by TAR RNA proves to be critical in the viral life cycle, the pharmacological approach could lead to the discovery of a new antiviral drug.

31 - Elsa Souffleur, Master 2 Student

Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

Hijacking the remodeler: how post-translational modifications of TAF-1ß shape human adenovirus infection

Elsa SOUFFLEUR, Fabienne RAYNE, Juliette VILLAGOMEZ, Harald WODRICH

Human adenovirus (HAdV) possesses a double-stranded DNA genome that assembles into a chromatin-like structure via the viral protein VII (pVII) within the viral capsid. Upon virus entry, HAdV escapes from the endosomal compartment and virus particles traffick to the nucleus where they release the viral genome for nuclear import. Inside the nucleus, viral gene expression must be initiated to ensure a productive replication cycle. To do so, the highly condensed incoming viral chromatin selectively recruits host chromatin remodelling factors, which remodel it into a more accessible conformation, allowing access to key promoters of immediate early genes, such as E1A, and driving viral gene expression. Among these remodelling factors, the histone chaperone TAF-1ß has been shown to associate with viral chromatin via pVII, facilitating the accessibility of immediate early genes and supporting efficient HAdV replication. How HAdV selectively recruits TAF-1ß is still unknown. TAF-1ß is subject to post-translational modifications (PTMs) that may regulate its recruitment to viral chromatin, a mechanism that remains largely unexplored.

This study investigates the functional impact of PTM-targeted regions of TAF-1ß on its interaction with HAdV chromatin and on viral replication.

Stable U2OS cell lines depleted of endogenous TAF-1ß and reconstituted with TAF-1ß deletion mutants lacking putative PTM sites were successfully generated and validated by immunofluorescence microscopy and western blot analyses. Using protein pull-down assays combined with HAdV infection, we aim to determine whether these PTM-targeted domains are required for TAF-1ß recruitment to adenoviral chromatin and for its ability to remodel it during

infection.
These results will decipher the role of PTMs in TAF-1ß-mediated chromatin remodelling during HAdV infection, ultimately enlarging our understanding of the host-virus interplay at the chromatin level.

33 - Mila Vilatte

Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

Structure-function characterization of Gtwin endogenous retrovirus integration

Mila Villatte, Maelys Lemoine, Yury Zgadzay, Delphine Lapaillerie, Bruno Mugat, Paul Lesbats, Charlotte Grimaud, Marc Ruff, Severine Chambeyron and Vincent Parissi.

The human genome is under constant threat from invasion by mobile genetic elements, such as retroviruses and retrotransposons. The majority of eukaryotic genomes contain numerous transposable elements (TEs). If these elements are activated, they can relocate within the host genome or even multiply, significantly increasing the risk of harmful genetic changes. One might expect that natural selection would have eliminated these genomic intruders. Surprisingly, they are prevalent in eukaryotic genomes, suggesting a coexistence between host and parasite that can sometimes resemble a symbiotic relationship. Examining how a host genome responds when these parasites invade, including identifying where they insert themselves and the regions where they become active while maintaining host survival, represents a fundamental question in biology. Indeed, answering this question is vital for comprehending the true impact of TE insertions on the function of the host genome. Our RehosTE project seeks to elucidate the functional relationships between host genomes and endogenous retrovirus (ERV) integration, using Drosophila as a model system in collaboration with the Institut de Génétique Humaine (IGH) in Montpellier. Our focus is on the Gtwin ERV integrase (IN), a key viral enzyme responsible for inserting retroviral DNA into the host genome. Through structural and functional characterization, we have uncovered critical insights into Gtwin IN's integration mechanics and chromatin-binding properties. X-ray crystallography revealed that the putative catalytic domain of Gtwin IN adopts a fold characteristic of the DDE retroviral integrase family, confirming its evolutionary and functional kinship with other retroviral INs. In vitro integration assays using reconstituted nucleosomes demonstrated that Gtwin IN efficiently catalyzes the insertion of viral sequences into both naked DNA and nucleosomal templates. This allowed us to define its chromatin structure preferences and map the functional interfaces through which Gtwin IN associates with the nucleosome surface. To further probe its chromatin engagement, we employed a direct Chromosome Binding Assay (diCBA) setup in our team, which confirmed Gtwin IN's intrinsic chromatin-binding function. Preliminary proteomic analyses led us to propose Pontin, a cellular AAA+ ATPase, as a putative chromatin-targeting factor for the Gtwin intasome complex. Its role in Gtwin chromatin targeting and integration is currently under investigation. By comparing this new integration model with other retroviral systems studied in our team, we reinforce the concept that able of interpreting chromatin cues to optimize integration. Intriguingly, our findings suggest that host cells may co-opt these viral mechanisms to regulate and balance genome invasion, ensuring a controlled integration process. ANR-24-CE12-5869-02 RehosTE "Functional Relationship between the drosophila Host genome and ERV integration"

35 - Dina Alezzi, PhD student

Acides nucléiques : Régulations naturelles et artificielles -ARNA - U1212 - INSERM - UMR5320 – CNRS, Université de Bordeaux

Rho-dependent transcription termination widely shapes the transcriptome of Helicobacter pylori

Dina Alezzi, Nicolas J Tourasse, Fabien Darfeuille, Isabelle Iost

The ε-proteobacterium Helicobacter pylori colonizes the stomach of nearly half of the human population and is associated with severe diseases, including gastric cancer. Its ability to adapt to this unique and hostile environment is supported by complex transcriptional activity, the regulation of which remains largely unexplored. In particular, while transcription start sites have been extensively mapped, transcription termination sites and their regulatory roles remain largely unknown. In bacteria, transcription termination occurs mainly through intrinsic mechanisms or Rho-dependent transcription termination (RDTT). RDTT plays a central role in gene regulation in many bacterial species, but its contribution in H.pylori is still poorly understood.

Previous work from our laboratory suggests that the Rho factor contributes to the biogenesis of some small regulatory RNAs, suggesting a potential link between transcription termination and RNA-mediated regulation. Here, we aim to identify RDTT sites at the genome-wide level. Using Nanopore direct RNA sequencing, we mapped RNA 3' ends in the presence or absence of the Rho inhibitor bicyclomycin. Preliminary analyses indicate that most non-coding RNAs exhibit Rho-dependent transcription termination. In addition, several RDTT events were identified within 5' untranslated regions, suggesting a potential regulatory role of RDTT in controlling gene expression. These results provide new insights into how Rho-dependent termination shapes the H.pylori transcriptome.

37 - Simon Ferrer, Intern in master's degree

Qualyse

Multiplex digital PCR for discrimination and quantification of the four mycoplasmas causing Caprine Contagious Agalactia

Simon FERRER-GOYENECHE, David SCHIKORSKI, Fabien LABROUSSAA, Michaël TREILLES

Contagious Caprine Agalactia (CCA) is a disease listed by the World Organisation for Animal Health and is caused by four closely related mollicutes : Mycoplasma agalactiae (Ma), M. mycoides subsp. capri (Mmc), M. capricolum subsp. capricolum (Mcc), and M. putrefaciens (Mp). CCA is a major cause of mastitis, arthritis and keratoconjunctivitis in goats, resulting in substantial economic losses in the Mediterranean regions, Asia, North Africa and in the Middle East. However, the disease remains under-diagnosed due to limitations of conventional molecular tests. Current commercial real-time Polymerase Chain Reaction (PCR) assay can differentiate Ma from the three others mycoplasmas but fails to identify the specific causal agent among Mmc, Mcc and Mp. In addition, pathogen load in milk samples fluctuates considerably over the course of an infection, complicating accurate clinical monitoring. This project aims to develop and validate a digital PCR (dPCR) assay enabling the species-specific detection and quantification of all four CCA agents in a single reaction. The first aim was to establish a dPCR workflow on reference strains using novel primers and probes targeting specific mycoplasma genes. This will be performed on pure material (genomic DNA and cultures), and subsequently on spiked milk. The second objective is to validate the assay using clinical caprine milk samples from infected herds. Beta-actin is included as an endogenous positive control to identify potential false-positive results. This assay will provide a routine diagnostic tool for CCA, delivering absolute quantification of the pathogens, resolving the specificity gaps of current PCR tests, and enabling veterinarians to adapt their disease control strategies for caprine mycoplasmoses.

Keywords : Mycoplasmas ; Contagious Caprine Agalactia; multiplex digital PCR ; diagnostic tool.

39 - Ana luzia Lacerda, Post doc

LIttoral ENvironnement et Sociétés - LIENSs - UMR 7266 – CNRS, Université de La Rochelle

Approches intégrées pour évaluer l'exposition microbienne et virale des chevaux en Nouvelle-Aquitaine dans une perspective One Health

Ana Luzia Lacerda; Jérémy Grondin; Dânia Vieira Gois Fernandes; Gaëlle Gonzalez; Sonia Burrel; Baptiste Defaye; Hélène Agogué; Denis Malvy; Laurence Delhaes

Le programme EMERG a étudié l'exposome microbien et viral des chevaux en Nouvelle-Aquitaine dans une perspective « One Health », visant à caractériser la diversité des micromycètes et des bactéries, ainsi que la présence du virus West Nile (WNV) dans les haras. Des échantillons ont été collectés à l'aide de pièges à poussière, analysés par culture sur géloses Sabouraud, avec identification des colonies par spectrométrie de masse MALDI-TOF et quantification (CFU/mL). Parallèlement, l'ADN extrait des pièges a été soumis à des analyses de shotgun sequencing (NGS : ITS pour les champignons et 16S pour les bactéries), permettant de comparer les résultats obtenus par NGS avec ceux issus de la culture. La détection du WNV a été réalisée par sérologie et qPCR, en collaboration avec le Laboratoire National de Référence d'encéphalopathies équines et le service de Virologie du CHU de Bordeaux. Les cultures ont révélé une prédominance d'Aspergillus spp., principalement A. fumigatus (n=13, moyenne 2782 CFU/mL), A. nidulans (n=11, 2694 CFU/mL) et A. terreus (n=8, 2400 CFU/mL). Parmi les levures, Sarocladium strictum (n=1, 1667 CFU/mL) et Rhodotorula mucilaginosa (n=2, 1333 CFU/mL) ont été identifiées, ainsi que quatre autres levures non identifiées au rang d'espèce par MALDI-TOF. Les analyses d'amplicons (short reads, Illumina) n'ont pas révélé de différences significatives dans la structure globale des

communautés de micro-champignons ou de bactéries entre les pièges provenant de groupes de chevaux WNV séropositifs ou séronégatifs. Toutefois, les échantillons provenant de groupes avec des animaux séropositifs présentaient des abondances plus élevées de certains groupes des micro-champignons et des bacteries, notamment Aspergillus spp et Staphylococcus spp. Ces résultats soulignent l'intérêt d'une approche intégrée combinant culture, sérologie et analyses moleculaire pour caractériser l'exposome équin et détecter précocement les pathogènes. L'application du metabarcoding pourrait constituer un outil diagnostique rapide et fiable pour la surveillance des haras et, plus largement, des biocénoses, illustrant ainsi la complémentarité des méthodes classiques et innovantes pour mieux comprendre la diversité microbienne et virale affectant les chevaux et contribuer à la mise en place de stratégies de prévention et de suivi adaptées.

41 - Cynthia Cavaillon, PhD student

Laboratoire Inflammation, Tissus Epithéliaux et Cytokines - LITEC - UR15560, Université de Poitiers

Impact of hypoxia and HIF-1α expression on the infection of human keratinocytes by the Usutu virus

Cynthia Cavillon, Sonia Lacourt, Nicolas Leveque, Hamid-Reza Rezvani, Charles Bodet, Magali Garcia

Usutu virus (USUV) is an emerging arbovirus in Europe. Although generally asymptomatic in humans, infection can lead to severe neurological manifestations, particularly in immunocompromised patients. Following its inoculation mainly in the extravascular space of the dermis and the epidermis during the blood meal of the infected mosquito, USUV replicates notably in the keratinocytes of the epidermis.

Recent data shows that hypoxia and activation of the Hypoxia Inducible Factors (HIFs) pathway, transcription factors whose expression is regulated according to the level of oxygenation, can impact viral replication by modulating in particular the immune response and cellular metabolism. This study aims to evaluate (i) the impact of hypoxia and (ii) HIF-1α expression on USUV infection in human keratinocytes. In hypoxia (ppO2 at 1%) as well as in normoxia (ppO2 at 21%), a decrease in viral replication was observed in HIF-1α under-expressing keratinocytes (HIF1KD) compared to control cells, as well as a significant increase in antiviral response, both at the basal level and during infection. In order to overcome the biases related to viral replication, stimulation by poly(I:C), a synthetic analogue of double-stranded RNA mimicking a viral infection, of HIF1KD keratinocytes led to a significantly increased antiviral response compared to control cells. These results suggest a facilitating role of HIF-1α expression on USUV replication and inhibition of the antiviral response during human keratinocyte infection. Given the impact of HIF-1α expression on cellular metabolism, studies are ongoing to determine the metabolic modulations induced outside and during viral infection.

43 - Séphora Theresine-Augustine, PhD student

Microbiologie Fondamentale et Pathogénicité - MFP - UMR 5234 – CNRS, Université de Bordeaux

Optimization of a human gut-on-chip to study the pathogenicity of Candida albicans

Sephora THERESINE-AUGUSTINE, Fernanda LOPEZ-GARCIA, Karine DEMENTHON

Commensal Candida albicans yeasts, can become pathogenic and resistant to treatments when the host immune system is compromised, leading to severe infections. Current biological models fail to accurately replicate the complexity of the human body. Organs-on-chips (OOCs) are an innovative alternative to model organ functionality and recapitulate some of their physiological or pathological features in-vitro. Building on previous results demonstrating the successful differentiation of caco-2 cells into a healthy intestinal epithelium layer, we propose to enhance the currently developed gut-on-a-chip by vascularizing it and making it immunocompetent. Resulting in a physiologically realistic microenvironment to study intestinal Candida infections. In this project, we managed to obtain a differentiated endothelial monolayer where the cells align in the direction of flow. We showed that circulating immune cells of the THP-1 type are able to migrate between the microfluidic channels responding to the inflammation triggered by the infection of C. albicans, also it was possible to observed the yeast being phagocytized by the THP-1 cells. These findings demonstrate the potential of the gut-on-a-chip as a powerful tool to study the dynamics of Candida infections and immune responses.

SESSION 2 : ENVIRONMENT, MICROBIOLOGICAL ECOLOGY AND BIOTECHNOLOGIES

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8	Arnould	Kathyanna	A protozoan Seipin orchestrates cell division through lipid droplet biogenesis
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SESSION 2 : ENVIRONMENT, MICROBIOLOGICAL ECOLOGY AND BIOTECHNOLOGIES

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2 - Elorri Garcia, PhD student

Chimie et Biologie des Membranes et des Nano-objets - CBMN - UMR 5248 - CNRS - Bx INP – BSA, Université de Bordeaux

Deciphering microalgae-nanoplastics interactions by Atomic Force Microscopy and confocal microscopy

Elorri GARCIA, Anthony VIAL, Michael MOLINARI, Audrey BEAUSSART

With the rising anthropisation, several pollutants, such as nanoparticles, are disseminated in the environment, potentially affecting living organisms. Microalgae have the capacity to absorb and accumulate various toxic pollutants, making them good candidates for bioremediation, but also key players in contaminants transfer as they are at the lowest trophic level of the food chains. However, the molecular mechanisms leading to the adhesion of nanoparticles to microalgae are still poorly understood.

The objective of this study is to decipher these interactions at the molecular scale. The originality of the approach relies on the use of a combination of biophysical tools, namely Atomic Force Microscopy (AFM) and confocal microscopy, applied to the model green microalgae Chlorella vulgaris and fluorescent polystyrene nanoparticles decorated by amine functional groups.

Our approach revealed that nanoplastics adhere more at the surface of microalgae harvested in the exponential phase as compared to the stationary phase. We also demonstrated that the pH of the surrounding solution plays a key role in the adsorption, with the highest amount of nanoplastics attached to the biosurfaces in acidic conditions. For cells harvested in the stationary phase, AFM imaging revealed the appearance of fibrils network at the cell surface, identified as chitin-like fibers by confocal microscopy using fluorescent-lectin staining of the N-acetyl-D-glucosamine units. Altogether, our results bring new light on the parameters influencing the adsorption of nanoplastics to biological surfaces and open promising perspectives to optimize conditions that would favor large-scale exploitation of the algal bioresource, for instance in bioremediation processes.

4 - Louis Rouillan, PhD student

Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

Structural study of the type VIIb secretion system (T7SSb) of Bacillus subtilis involved in bacterial competition

Louis Rouillan, Axel Siroy, Rémi Fronzes

Type VII secretion systems (T7SS) are crucial mechanisms and intricate protein complexes that enable Gram-positive bacteria to survive and cause disease. These systems allow bacteria to outcompete by killing their rivals. While the mycobacterial T7SSa subtype has been extensively studied, the structural organization of the T7SSb subtype, which is widely distributed in Firmicutes, has remained largely unknown.

In this study, we present the cryo-electron microscopy structure of the Bacillus subtilis T7SSb core complex. We discovered that this machinery is composed of three key proteins: YukB, YukC, and YukD. Remarkably, we successfully obtained the complete hexameric structure of the core complex under native conditions in Bacillus subtilis

6 - Sara Basiglio, PhD student

Department of Food, Environmental and Nutritional Sciences (DeFENS), University of Milan (Milan, Italy)

Assessing the impact of chemical pollutants on the gut microbiome of wild pollinators

S. Basiglio, F. Patriarca, R. Ali, E. Holzer, L. Cabiddu, S. Casini, F. Sgolastra, D. Lupi, F. Mapelli, E. Crotti

Pollinators play a crucial role in sustaining agricultural ecosystems, yet their populations have been declining worldwide in recent decades. Chemical pollutants have been recognized as one of the primary causes of this decline, potentially affecting insect health by altering their gut microbiome. To date, research on the impact of chemical exposure on pollinators microbiome has largely focused on a limited number of species (Apis mellifera, Bombus spp.) primarily investigating insecticides and herbicides at field application levels. Little is known about how residual concentrations of different categories of chemicals influence the gut microbiome of other pollinators, such as wild pollinators. Thus, the objective of this study was to evaluate the impact of different categories of chemical pollutants on the gut microbiome of two highly efficient wild pollinators, Osmia bicornis and Eristalis tenax. Individuals of both species were exposed in laboratory trials to residual doses of four chemicals (boscalid, copper chloride, glyphosate, and ivermectin) administered singularly and in mixture, to test potential synergistic effects. These

compounds occur as residues in pollen and nectar, providing an ecologically relevant context for assessing their effects on pollinator health. Quantitative PCR was used to measure bacterial and fungal abundance, and Illumina sequencing of the bacterial 16S rRNA gene and the fungal ITS2 region were performed to investigate microbial taxonomy. In O. bicornis, exposure to copper chloride and boscalid resulted in significant reductions in gut bacterial abundance. Additionally, the composition and diversity of the gut microbiome were affected by all tested chemicals. In E. tenax, exposure to the tested chemicals did not affect overall bacterial and fungal abundance. However, bacterial community composition shifted in response to the exposure to copper chloride, ivermectin, and the mixture of glyphosate and ivermectin. The results obtained suggest that residual doses of chemical pollutants can differentially disrupt the gut microbiome of wild pollinators, potentially affecting their health and, consequently, the ecosystem services they provide.

8 - Kathyanna Arnould, PhD student

Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

A protozoan Seipin orchestrates cell division through lipid droplet biogenesis

Kathyanna Arnould, Perrine Hervé, Yoshiki Yamaryo-Botté, Stéphane Claverol, Frédéric Bringaud, Cyrille Botté et Loïc Rivière

Lipid droplets (LDs) are conserved organelles present in all eukaryotes, where they play key roles in lipid storage and mobilization. Their biogenesis depends on the endoplasmic reticulum (ER) protein Seipin, which is highly conserved and has been extensively characterized in model eukaryotic systems. However, its role in parasitic organisms such as Trypanosoma brucei remains unexplored.

In this study, we identified and characterized a Seipin ortholog in Trypanosoma brucei, named TbSeipin. In silico structural analyses revealed a high degree of structural conservation with Seipin proteins from other organisms. Functional conservation was further supported by heterologous complementation in Saccharomyces cerevisiae, where TbSeipin was able to rescue lipid droplet defects in a Seipin-deficient strain.

Using a CRISPR/Cas9 genome editing technology, recently optimized in our team, we generated endogenously tagged and knock-in cell lines. Localization studies showed that TbSeipin is enriched in ER subdomains and at ER–LD contact sites. Functional analyses revealed that TbSeipin is essential for LD biogenesis. Its loss leads to altered LD size distribution, increased LD number, and dysregulated neutral lipid metabolism.

Unexpectedly, we observed severe cellular phenotypes. TbSeipin-deficient parasites exhibit impaired cell cycle progression, resulting in multinucleated cells and defects during the final stages of cytokinesis. Together, our findings reveal an unexpected link between lipid droplet biogenesis and cytokinesis in T. brucei, highlighting TbSeipin as a central coordinator of parasite cellular organization.

10 - Yoann Fautras, PhD student

Chimie et Biologie des Membranes et des Nano-objets - CBMN - UMR 5248 - CNRS - Bx INP – BSA, Université de Bordeaux

Study of aerobic and anaerobic cultivable sedimentary microbiota -Capability of isolates to produce and degrade extracellular polymeric substances and possible use in biotechnology

FAUTRAS Yoann (speaker), VITTU Lauriane, LE SENECHAL Caroline, BOURILLOT Raphael, CARIO Anaïs, VILAIN Sébastien

This study is part of a larger project aiming to analyze the Extracellular Polymeric Substances (EPS) contents of sediments from modern and ancient estuaries (ANR “EXODIA”). EXODIA aims to better define the composition and function of EPS in modern and ancient estuaries, and their interaction with clay and metals through diagenesis. The aim of this study is to isolate, characterize and identify the culturable microorganisms potentially involved in the estuarine sediment EPS cycle (anaerobic and aerobic bacteria), in particular strains able to produce high quantities of EPS and/or able to degrade EPS. A maximum of microorganisms from the most representative sediment horizons on 6-m deep cores were isolated by a culturomics strategy that relies on using 16 media and 2 temperatures of incubation, and in aerobic and anaerobic conditions, as well as enrichment strategies to focus on EPS degrading and biofilm-forming strains. After isolation and constitution of a strain’s library, each

strain is grown as planktonic and sessile pure culture and their ability to produce EPS (mucoid character), to form biofilms and to produce EPS-modifying enzymes (DNAses, proteases, hydrolases, lyases) are assayed. Antibiosis and antibiofilm activities of isolates against bacterial reference strains in biofilm research (Escherichia coli, Pseudomonas aeruginosa, Staphylococcus aureus, Acinetobacter baumannii) are carried out. All the information relative to the isolates will be listed in a publicly available database. The identification of isolates will be performed in first intention by mass spectrometry. In parallel, genomic identification of the microbiome in sediment samples will be performed. This will allow us to estimate how isolates are representative of the global community.

12 - Jean-etienne Porcheron, PhD student

Ecologie et Biologie des Interactions - EBI - UMR 7267 – CNRS, Université de Poitiers

Malassezia sympodialis, une levure à s'arracher les cheveux

Jean-Etienne PORCHERON, Louise NALET, Stéphanie CRAPART, Marion GIRARDOT, Christine IMBERT et Estelle PERRAUD-CATEAU

Les levures du genre Malassezia font partie intégrante du microbiote cutané, en particulier au niveau du cuir chevelu où elles jouent un rôle clé dans la formation des pellicules. Malassezia se distingue des autres genres de levures habituellement rencontrés chez l'Homme par sa lipodépendance, son caractère agglutinant caractéristique, et sa vitesse de croissance lente. Le travail présenté concerne l'espèce Malassezia sympodialis dont les modalités de croissance sont encore assez peu décrites dans la littérature en particulier en condition biofilm. L'objectif était de développer des modèles standardisés de croissance de M. sympodialis, en conditions à la fois planctonique et sessile (biofilm).

Les expériences ont été réalisées en milieu Dixon, gélosé et liquide, en microplaques de 96 puits et en utilisant des souches cliniques (CHU de Poitiers). La cinétique de la croissance planctonique a été suivie par mesure de l'absorbance à 600nm pendant 72 heures. Les biofilms ont été suivis pendant 7 jours ; ils ont été préparés en respectant une phase d'adhérence de 24 heures puis une phase de maturation de 6 jours. La biomasse et l'activité métabolique fongiques ont été évaluées par des tests au Cristal Violet (CV) et aux sels de tétrazolium (XTT), respectivement. En condition planctonique, M. sympodialis présente une croissance lente, avec un temps de génération d'environ 7 heures et une phase exponentielle se stabilisant vers 25 heures. En condition sessile, la croissance est lente et reste stable durant les 24 premières heures. Une augmentation significative de la biomasse (75%, $p<0.0001$) et de l'activité métabolique (76%, $p<0.0001$) est observée entre 48 et 96 heures, suivie d'une stabilisation. L'évolution superposable des approches CV et XTT démontre que l'augmentation de l'activité métabolique au cours du temps témoigne d'une augmentation de la biomasse fongique.

Des observations macroscopiques et microscopiques mettent en évidence la présence d'inclusions caractéristiques de cette espèce au sein de la gélose, possiblement liées à la composition lipidique du milieu Dixon. Des travaux sont en cours pour mieux comprendre l'origine de ces inclusions dont la nature n'a jamais été analysée dans la littérature.

En conclusion, ce travail de modélisation de la croissance de M. sympodialis planctonique et en biofilm, constitue une base solide pour aborder la dynamique de cette levure au sein du microbiote cutané. Des modèles polymicrobiens, inter-règnes, sont en cours de mise au point et permettront de mieux comprendre le rôle de M. sympodialis dans le développement de l'état pelliculaire du cuir chevelu et de rechercher de nouvelles approches préventives ou curatives ciblant Malassezia spp.

14 - Aurélie Touya, PhD student

Mycologie et Sécurité Alimentaire - MycSA - UR 1264 – INRAE, Université de Bordeaux

Intraspecific variability in secondary metabolites production across F. avenaceum isolates

Aurélie TOUYA , Carmen HICKS , Tom WITTE , Stéphane BERNILLON , Nadia PONTS , Vessela ATANASOVA , David P. OVERY , Florence RICHARD-FORGET

Abstract:

Fusarium avenaceum is a cosmopolitan pathogen infecting a broad range of hosts (1), although its presence is mainly associated with Fusarium Head Blight (FHB), a devastating disease having great economic repercussions (2) as well as posing health issues with the production of mycotoxins (3). Several of these toxins are tightly regulated as food and feed contaminants, as

it is the case for deoxynivalenol or fumonisins (4). Meanwhile, F. avenaceum produces enniatins, emerging mycotoxins that are currently neither routinely detected nor regulated, and whose effects on health are poorly studied despite being regularly found in FHB-contaminated matrices (5). However, F. avenaceum potential to yield specialized metabolites production extends well beyond enniatins, and various studies have highlighted the wide array of compounds this species can produce (1, 6). These small molecules, which are often associated with ecological functions and adaptation within an organism, are synthesized via several genes organized into biosynthetic gene clusters (BGCs) that are co-localized and co-regulated (7). Over the years, studies have highlighted the great potential of Fusarium fungi in producing secondary metabolites, especially F. avenaceum whose genome is enriched in BGCs compared to other species (1, 8).
Currently, very few Fusarium specialized metabolites have been associated with their BGC, let alone in F. avenaceum, a species on which knowledge remains scarce. Given the considerable intraspecific diversity within this species (9), assessing its capacity and intraspecific variability in specialized metabolites production could help better predict its contribution to FHB.
To fill this knowledge gap, we investigated the potential in secondary metabolites production across 10 F. avenaceum isolates. Strains were cultivated for 14 days in 3 different culture media, and mycelia was separated from the culture broth prior to extraction and injection through UHPLC-HRMS. A consensus secondary metabolite profile was obtained for each of the 10 isolates by combining all media conditions, showing a great conservation of signals while strain-specific ones were still observed. Media as well as sample type (mycelium or broth) were responsible for the separation of samples, emphasizing the importance of cultivating organisms in several conditions to better capture the diversity of secondary metabolites production.
In addition, a preliminary work has been conducted using the genomes of 3 strains showing differences in their metabolomic profiles. Number in BGCs were fairly comparable, with around 90 clusters per genome. A focused analysis on polyketide synthases (PKS) and non-ribosomal peptide synthases (NRPS) showed a large proportion of conserved enzymes among the 3 genomes, consistent with metabolomics results.
Understanding the full potential of secondary metabolites production in Fusarium fungi, as well as their functions, is essential to get a more complete picture of Fusarium ecology, and could lead to developing new strategies for disease management.

References
1. Lysøe E, Harris LJ, Walkowiak S, Subramaniam R, Divon HH, Riiser ES, Llorens C, Gabaldón T, Kistler HC, Jonkers W, Kolseth A-K, Nielsen KF, Thrane U, Frandsen RJN. 2014. The genome of the generalist plant pathogen Fusarium avenaceum is enriched with genes involved in redox, signaling and secondary metabolism. PloS One 9:e112703.
2. Chai Y, Senay S, Horvath D, Pardey P. 2022. Multi-peril pathogen risks to global wheat production: A probabilistic loss and investment assessment. Front Plant Sci 13.
3. Ekwomadu TI, Akinola SA, Mwanza M. 2021. Fusarium Mycotoxins, Their Metabolites (Free, Emerging, and Masked), Food Safety Concerns, and Health Impacts. Int J Environ Res Public Health 18:11741.
4. 2006. Règlement (CE) n o 1881/2006 de la Commission du 19 décembre 2006 portant fixation de teneurs maximales pour certains contaminants dans les denrées alimentaires (Texte présentant de l'intérêt pour l'EEE)OJ L.
5. Coulet F, Hymery N, Coton E, Coton M. 2025. Enniatin Mycotoxins in Food: A Systematic Review of Global Occurrence, Biosynthesis, and Toxicological Impacts on In Vitro Human Cell Models. Compr Rev Food Sci Food Saf 24:e70270.
6. Witte TE, Hermans A, Sproule A, Hicks C, Talhouni T, Schneiderman D, Harris LJ, Eranthodi A, Foroud NA, Chatterton S, Overy DP. 2024. Identification and Confirmation of Virulence Factor Production from Fusarium avenaceum, a Causal Agent of Root Rot in Pulses. J Fungi 10:821.
7. Eagan JL, Keller NP. 2025. Fungal secondary metabolism. Curr Biol 35:R503–R508.
8. Lin C, Feng X, Liu Y, Li Z, Li X-Z, Qi J. 2023. Bioinformatic Analysis of Secondary
Metabolite Biosynthetic Potential in Pathogenic Fusarium. 8. J Fungi 9:850.
9. Yli-Mattila T, Abbas A, Gavrilova O, Gagkaeva T. 2022. Molecular Variation and Phylogeny within Fusarium avenaceum and Related Species. Diversity 14:574.

16 - Irène Valenti, PhD student

Mycologie et Sécurité Alimentaire - MycSA - UR 1264 - INRAE

Screening wheat microbiota isolates for mycotoxin control leads to the identification of potential new species.

Irene Valenti, Fatima Aqeel, Louis Carles, Florence Richard-Forget, Marco Saracchi, Daniela Bulgari, Andrea Kunova, Paolo Cortesi and Matias Pasquali

Co-occurence of different mycotoxins in the same cereal field is very common. Particularly, the combination deoxynivalenol (DON) – enniatin B (ENB) obtained a significant attention due to its potential synergistic effects on different biological systems [1]. The wheat microbiota may

host microorganisms able to promote plant health contrasting pathogens and their secondary metabolites, like mycotoxins.
This work aimed to screen strains isolated from wheat microbiota, to select new sustainable candidates able to contrast DON-ENB accumulation in grains. Approximately 50 microorganisms, both bacteria and fungi, were isolated in selective media with the purpose of collecting the widest microbial diversity. The microorganisms were isolated from wheat spikes (i) affected by Fusarium head blight in experimental field sites and (ii) treated with DON and ENB in laboratory. Subsequently, genomic DNA was extracted and sequenced by Illumina NovaSeq X and only non-pathogens were retained for screening. Whole genomes were assembled using Galaxy platforms while Microscope or Helixer and Eggnog Mapper, were used to annotate bacterial and fungal strains, respectively. Bacterial phylogenetic was based on whole-genome data by combining TYGS, PubMLST and ANI results. Fungal classification combined ANI with MLST analysis based on concatenated strain-specific nucleotide sequences.
This study revealed a total of 34 species, with different ecological roles, including pathogens (Pantoea agglomerans), novel potential plant-growth-promoting bacteria (Kosakonia cowanii), and saprophytic species like Peniophora lycii and Trametes versicolor. We identified both rare taxa (Acrodontium sp.) and ubiquitous genera (Penicillium spp.), and 3 new potential species belonging to the genera Clavibacter, Achromobacter and Mortierella. Considering the new species, genome completeness is estimated at 99.5% for bacteria (CheckM) and 96.5% for Mortierella (BUSCO). To fill the remaining gaps in the fungal genome, integration of long-read sequencing data is scheduled.
Overall, these results highlight the complexity of plant microbiota and suggest the presence of still unexplored biodiversity, with potential implications for future research.
[1] Valenti, I., Tini, F., Sevarika, M., Agazzi, A., Beccari, G., Bellezza, I., Ederli, L., Grottelli, S., Pasquali, M., Romani, R., Saracchi, M., & Covarelli, L. (2023). Impact of Enniatin and Deoxynivalenol Co-Occurrence on Plant, Microbial, Insect, Animal and Human Systems: Current Knowledge and Future Perspectives. Toxins, 15(4), 271. https://doi.org/10.3390/toxins15040271

18 - Lila Moussaoui

Microbiologie Fondamentale et Pathogénicite - MFP - UMR 5234 – CNRS, Université de Bordeaux

Characterization of the protein Atlastin in Trypanosoma brucei brucei

Lila Moussaoui, Ophélie Cosnefroy, Mélanie Bonhivers and Eloïse Bertiaux

The African trypanosome, Trypanosoma brucei, is a flagellated protozoan responsible for sleeping sickness. In this parasite, the flagellum is anchored to the cell body by a specialized cytoskeletal structure called the Flagellum Attachment Zone (FAZ), which includes a microtubule quartet (MTQ), a unique structure of kinetoplastid parasites. Despite the electron microscopy description of the MTQ, which reveals a close association with the ER, its protein composition remains largely unknown and its function poorly characterized.
Atlastins are conserved proteins across eukaryotes (mammals, plants, yeasts) involved in ER tubule fusion and microtubule-ER interactions. An ortholog, TbAtlastin (Tb927.10.14510), is present in T. brucei, suggesting that similar mechanisms may exist in this parasite. The aim of this internship was to characterize TbAtlastin to test its involvement in MTQ-ER coupling.
We confirmed its localization in the ER and along the MTQ by immunofluorescence and U-ExM, with specific enrichment at the distal end of the MTQ after detergent extraction. Its functional characterization by CRISPR-Cas9 knockout is underway. In parallel, the study of TbReticulon, another ER protein involved in the shaping of membrane tubules, is also integrated into this analysis. In mammals and plants, Atlastin and Reticulon cooperate within the same functional complex to organize the tubular ER, suggesting that an analogous complex could exist in T. brucei. Depletion of TbReticulon leads to severe defects in morphogenesis and cell division, highlighting the functional importance of this MTQ-ER interface. The identification of protein interactions of the Atlastin protein is a first step towards describing interaction complexes between MTQ and the ER.
Thus, these results support the existence of molecular coupling between the ER and MTQ, the complete characterization of which constitutes the central focus of this work.

20 - Florine Girard-Blanc, PhD student

Ecologie et Biologie des Interactions - EBI - UMR 7267 – CNRS, Université de Poitiers

Conservation of undA within the genus Pseudomonas and its regulation.

Florine GIRARD-BLANC, Vincent DELAFONT, Charly DUPONT, Annabelle MERIEAU, Alexandre CREPIN, Julien VERDON

The bacterial genus Pseudomonas releases large amounts of volatile organic compounds (VOCs) that play important roles in their ecology. Among these, 1-undecene has been identified as a key chemical signal in several mechanisms along with strong antifungal activity. In P. aeruginosa, for example, this compound acts as a pathogen-associated molecular pattern (PAMP), inducing a 'fight-or-flight' response from Caenorhabditis elegans, including behavioural aversion and the activation of immune genes (Prakash et al., 2021). In P. fluorescens MFE01, 1-undecene is synthesised by the UndA enzyme and exhibits antibacterial activity by inhibiting the growth of Legionella pneumophila via long-distance signalling (Corre et al., 2021). It is also described as an intraspecific airborne communication molecule, notably involved in biofilm maturation (Dupont et al., 2023). Furthermore, in the absence of a classical quorum sensing system such as PQS or Las systems in this strain, 1-undecene could thus play a similar role in cellular communication. In this context, the aim of our study is to determine whether this system is conserved within the genus Pseudomonas and to investigate its regulation in order to understand its role as a communication system.

To assess this genetic conservation, 803 genomes representative of 14,000 genomes within the genus Pseudomonas, selected from the Genome Taxonomy Database (GTDB), were aligned using BLAST against the nucleotide sequence of the undA gene from the P. fluorescens strain MFE01. The results show 99.9% conservation of the gene, suggesting strong functional constraints within Pseudomonas. To determine whether different Pseudomonas species are capable of producing 1-undecene, a collection of clinical and environmental strains was screened by measuring their anti-Legionella activity. Our data show that 26 out of 54 strains exhibit growth-inhibitory activity. The volatilome of the strains was then analysed by solid-phase microextraction (SPME) coupled with gas chromatography and mass spectrometry (GC-MS) to detect the presence of 1-undecene. Our analyses revealed the presence of this metabolite in 77% of the strains, indicating that the amount emitted varies between strains under our experimental conditions.

Thus, the undA gene, which enables the synthesis of 1-undecene, is a highly conserved gene within the genus Pseudomonas. This suggests that it has remained stable despite being under strong selective pressure. An analysis of the regulation of this gene in MFE01 strain is therefore currently underway, involving the creation of mutants of the rbdA and gacS genes, as well as the investigation of other biological activities.

22 - Régis Grimaud, Lecturer/Researcher

Institut des Sciences Analytiques et de Physico-Chimie pour l'Environnement et les Matériaux - IPREM - UMR 5254 – CNRS, Université de Pau et des Pays de l'Adour

Marinobacter nauticus SP17 uses siderophore-dependent and -independent pathway to acquire iron in seawater

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In seawater, iron exhibits a very complex speciation and its concentration is characteristically very low (i.e., 0.02 to 1 nM). The low availability combined to a high microbial uptake rates, make iron a potential limiting micronutrient for the growth of heterotrophic bacteria in the Ocean. To acquire this essential element, bacteria employ various mechanisms like siderophore production or Fe^{3+} ABC transporters. To better understand iron acquisition in the ocean by marine heterotrophic bacteria, we used the bacterium Marinobacter nauticus SP17, which is known to produce the siderophore petrobactin. We identified two genes encoding TonB-dependent transporters for petrobactin: OptA, located near the petrobactin biosynthetic gene cluster, and OptB, situated elsewhere on the chromosome. A petrobactin-deficient mutant revealed that, while petrobactin contributes to iron acquisition, it is not essential for growth under iron-limited conditions. This suggests the presence of alternative petrobactin-independent iron uptake pathways. One such pathway involves the ferric ion-binding protein FbpA which is the substrate binding protein of an Fe^{3+} ABC transporters. A ΔfbpA mutant exhibited impaired growth on all tested substrates under iron limitation, demonstrating

the importance of this Fe^{3} ABC transporters in iron acquisition. Strikingly, the double mutant ΔasbABF ΔfbpA was unable to grow, indicating that petrobactin and FbpA mediate two distinct, complementary and partially redundant iron acquisition systems. The presence of multiple iron uptake systems likely reflects an evolutionary adaptation to the chemical complexity and dynamic nature of iron speciation in ocean environments.

24 - Lauriane Vittu

Chimie et Biologie des Membranes et des Nano-objets - CBMN - UMR 5248 - CNRS - Bx INP – BSA, Université de Bordeaux

Study of the aerobic sedimentary bacteriobiota

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This study is based on a part of the EXODIA project (ANR "EXODIA"), which investigates estuarine sedimentary extracellular polymeric substances (EPS) and their interaction with metals during diagenesis.

The goal here is to isolate, characterize, and identify all cultivable microorganisms derived from the sediments in the Garonne River, and their ability to produce or degrade EPS, as well as their antibacterial and/or anti-biofilm activity. To this end, microorganisms are isolated using a culturomics strategy including 14 media and two different incubation temperatures, as well as sample enrichment phases targeting EPS production or degradation properties.

A library of all isolates is constructed, and each isolate will be individually analyzed using phenotypic tests under both planktonic and sessile conditions. Their ability to produce EPS (mucoid character), form biofilms, or produce EPS-degrading enzymes (DNases, proteases, hydrolases, lyases) is examined with those tests. Their antibacterial and anti-biofilm activity against reference strains of the ESKAPEE group (Escherichia coli, Pseudomonas aeruginosa, Staphylococcus aureus, Acinetobacter baumannii) will also be analyzed. All data obtained will be published in a publicly accessible database.

The identification of isolates will initially be performed using mass spectrometry. At the same time, a genomic analysis of the samples' microbiome will be conducted. Taken together, these results will provide an overall picture of the diversity of the isolates and their geological, medical, or biotechnological significance.

26 - Laura Bernard, PhD student

LIttoral ENvironnement et Sociétés - LIENSs - UMR 7266 – CNRS, Université de La Rochelle

Marine bacteria-derived pigments : a promising approach to discover new antimicrobial molecules.

Bernard Laura, Garrabos Margot, Sopena Valérie, Bodet Pierre-Edouard, Sablé Sophie, Chevrot Romain, Picot Laurent, Valérie Thiéry and Colin Béatrice

The rise of multidrug-resistant bacteria, therapy-refractory cancers, and immune-evading viruses underscores the critical need for molecules with novel mechanisms of action, as these pathologies remain leading causes of global morbidity and mortality (1–3). Among these threats, multidrug-resistant bacteria (MRB) pose an escalating challenge. While antibiotics once revolutionised infectious disease treatment, their extensive and inappropriate use has accelerated the spread of bacterial resistance. Projections suggest that by 2050, bacterial infections could become the leading cause of death worldwide, highlighting the urgent need to discover effective compounds as alternatives to conventional antibiotic therapies (4,5). This situation underscores the urgent need to discover and develop novel compounds with high efficacy and original modes of antibacterial action. In this context, marine bacterial metabolites emerge as a promising reservoir of bioactive molecules, combining strong antimicrobial potential with the prospect of inspiring innovative therapeutic strategies (6–8). Fortunately, marine environments hold immense potential with their wealth of unexplored bioactive molecules, including halogenated furanones, pigments, and antimicrobial peptides. The aim of this project is to explore the antimicrobial properties of natural pigments produced by specific marine bacteria isolated from the Atlantic coast (La Rochelle, France). This project is organised into several main stages. First, marine bacteria from the Atlantic coast were collected and isolated. Second, the pigments produced by these bacteria isolates are extracted and characterised in order to assess their diversity and potential biological properties. Third, the biological properties of these pigments

are investigated through the evaluation of their antimicrobial and antibiofilm activities. These analyses are intended to determine whether the compounds could serve as promising candidates for therapeutic development against infections. At this stage, a collection of 28 marine bacterial strains have already been collected and the construction of a natural pigment library is underway. Regarding two pigmented extracts, initial results show antimicrobial activity against pathogenic targets bacterial strains. In conclusion, the project embodies an innovative and promising approach to addressing major public health issues. We anticipate the discovery of novel marine-derived bioactive molecules, the development of new therapies to combat multidrug-resistant bacterial infections and the effective valorisation of marine resources from Charente-Maritime.

1. Qiao, Y. et al. Phototherapy and Mechanism Exploration of Biofilm and Multidrug-Resistant Helicobacter pylori by Bacteria-Targeted NIR Photosensitizer. Small Weinh. Bergstr. Ger. 19, e2205248 (2023).
2. Wei, G. et al. Phototherapy-based combination strategies for bacterial infection treatment. Theranostics 10, 12241–12262 (2020).
3. Banday, A. H. et al. Exploring the potential of marine natural products in drug development: A comprehensive review. Phytochem. Lett. 59, 124–135 (2024).
4. Maharramov, E. et al. Exploring the principles behind antibiotics with limited resistance. Nat. Commun. 16, 1842 (2025).
5. Naghavi, M. et al. Global burden of bacterial antimicrobial resistance 1990–2021: a systematic analysis with forecasts to 2050. The Lancet 404, 1199–1226 (2024).
6. Srinivasan, R., Kannappan, A., Shi, C. & Lin, X. Marine Bacterial Secondary Metabolites: A Treasure House for Structurally Unique and Effective Antimicrobial Compounds. Mar. Drugs 19, 530 (2021).
7. Barzkar, N., Sukhikh, S. & Babich, O. Study of marine microorganism metabolites: new resources for bioactive natural products. Front. Microbiol. 14, (2024).
8. Grivard, A. et al. Archaea Carotenoids: Natural Pigments with Unexplored Innovative Potential. Mar. Drugs 20, (2022).

28 - Fojan Agahi, Post doc

Mycologie et Sécurité Alimentaire - MycSA - UR 1264 – INRAE

Interaction of Enniatin B and B1 with Wheat-Associated Bacillus Strains: Growth Inhibition and Biodegradation

Fojan Agahi, Vessela Atanasova, Marie-Noëlle Verdal-Bonnin, Florence Forget, Louis Carles

Enniatin B (ENNB) and enniatin B1 (ENNB1) are among the most prevalent emerging Fusarium mycotoxins, commonly co-occurring in cereals and derived foods as structurally related cyclic hexadepsipeptides. Their ionophoric activity disrupts membrane integrity and cellular homeostasis, raising concerns regarding their biological effects and combined toxicity. The wheat microbiota represents the first microbial community exposed following infection by the pathogen. This microbiota is known to play a key role in agricultural systems; however, limited information is available on how its composition and functionality are affected by exposure to Fusarium-produced enniatins (ENNs). The aim of this study was to evaluate the sensitivity of representative wheat-associated bacterial strains towards ENNB and ENNB1, both individually and in combination, and to investigate their capacity to degrade these mycotoxins.

From an initial collection of wheat-associated bacteria, two strains, Bacillus pumilus DSM27 and Bacillus atrophaeus DSM7264, were selected as representative models to evaluate the sensitivity to ENNB and ENNB1, as well as the biodegradation potential of ENNs. To evaluate sensitivity, each strain was exposed in vitro to a range of ENNB and ENNB1 concentrations (0, 10, 15, 25, 35, 45, and 50 µM), both individually and in combination, and growth was monitored hourly by measuring optical density at 600 nm over 48 h. Growth parameters were used to estimate the half-maximal effective concentration (EC50) through dose–response analysis. Biodegradation kinetics of ENNB and ENNB1 (15 µM) were assessed over 48h and quantified using high-performance liquid chromatography with diode-array detection (HPLC-DAD).

Dose–response analysis revealed a markedly higher sensitivity to ENNB1 compared to ENNB in both strains, with EC50 values of ~15 µM for ENNB1, while ENNB showed no significant inhibitory effect up to 50 µM. The mixture exhibited intermediate toxicity, with EC50 values of 22.31 µM for B. pumilus DSM27 and 25.46 µM for B. atrophaeus DSM7264, suggesting an antagonistic effect of ENNB. Kinetic analysis demonstrated rapid biodegradation of ENNB by both strains, reaching complete depletion within 24 h. Notably, ENNB1, showing higher toxicity, was also degraded over time, supporting the potential of these strains to cope with the most biologically active enniatin forms.

This study provides first quantitative toxicity data of ENNs on the wheat-associated microorganisms and first evidence of ENN-degrading potential by these microorganisms, which will help to clarify the role of these mycotoxins in the interaction between Fusarium and the wheat microbiota, and anticipate the potential consequences of microbial shifts caused by ENNs on interactions among Fusarium species during infection and plant fitness.

30 - Chaima Hakkach, M2 Intern / Stagiaire

LIttoral ENvironnement et Sociétés - LIENSs - UMR 7266 – CNRS, Université de La Rochelle

Anti-Adhesion potential of marine bacterial metabolites on breast cancer

Chaima Hakkach, Émile Bonnenfant, Rachida Mersni-Achour, Kevin Baranger, Jennifer Saliba, Béatrice Colin, Pierre-Édouard Bodet, Benjamin Musnier, Valérie Sopena, Sophie Sablé, Isabelle Lanneluc and Ingrid Arnaudin

Introduction: Microorganisms exhibit notable similarities to cancer cells. Bacterial biofilms are heterogenous communities organized into microenvironements that are low in oxygen and nutriments, and often acidic, conditions reminiscent of solid tumors that limit treatment efficacy. Moreover, bacterial dissemination from mature biofilm mirrors certain aspects of metastasic cancer cell migration and invasion. In both cases, cells detach from a primary site, circulate through the vascular system, adhere to and colonize secondary sites, suggesting the existence of common chemical mediators1,2. Thus, some microbial molecules could be repurposed for therapeutic use to target metastasic progression, a mechanism responsible for nearly 90% of cancer-related deaths3. In this context, marine bacteria, rich in bioactive secondary metabolites, represent a promising source of novel anticancer compounds4.

Objectives: This study aims to optimize experimental protocols for evaluating the anti-adhesion potential of a marine bacterial consortium on breast cancer cells, and to identify the targets and cellular mechanisms involved. Methods: The bacterial consortium was cultured on solid medium to produce a secretome, which was tested in vitro on two cell lines : MDA-MB-231 (triple-negative breast cancer) and HSK-MEC (healthy endothelial cells). MTT cell viability assays were performed to determine non-cytotoxic concentrations containing sufficient levels of bioactive compounds. Experimental parameters were then optimized, including cell seeding density, bacterial secretome pre-treatment duration, and cells/matrix and cell interaction times. Matrix adhesion assays were conducted using fibronectin or poly-D-lysine (control) pre-coating, to investigate specific interactions between cells and integrins. Interactions between tumor cells and endothelial cells were assessed through fluorescent cell labeling, enabling quantification of anti-adhesion potential ot the secretome. Results: Preliminary results suggest a non-specific anti-adhesion effect of the bacterial secretome on the HSK-MEC cell line after 1.5 hours of cells/matrix contact. Cells/cells interaction conditions require further optimization. Pre-treatment of endothelial cells with the bacterial secretome appears necessary, and a longer contact time with tumor cells may help to better reveal morphological alterations.

1. Ivanenko, N. BIOFILM AND TUMOR: INTERPRETATION OF INTERACTION AND TREATMENT STRATEGIES. Review. Med. Sci. of Ukr. 17, 104–120 (2021).

2. Russo, M., Sogari, A. & Bardelli, A. Adaptive Evolution: How Bacteria and Cancer Cells Survive Stressful Conditions and Drug Treatment. Cancer Discovery 11, 1886–1895 (2021).

3. Kilmister, E. J., Koh, S. P., Weth, F. R., Gray, C. & Tan, S. T. Cancer Metastasis and Treatment Resistance: Mechanistic Insights and Therapeutic Targeting of Cancer Stem Cells and the Tumor Microenvironment. Biomedicines 10, 2988 (2022).

4. Khalifa, S. A. M. et al. Marine Natural Products: A Source of Novel Anticancer Drugs. Marine Drugs 17, 491 (2019).

32 - Ophélie Iorfida, Intern

LIttoral ENvironnement et Sociétés - LIENSs - UMR 7266 – CNRS, Université de La Rochelle

Exploration of plant extracts and marine bacterial secretomes as sources of antibacterial compounds against resistant pathogens

Iorfida Ophélie, Pitard Axel, Parizadeh Leila, Sopena Valérie, Achour Oussama, Lanneluc Isabelle, Le Joubioux Florian, Sirvent Pascal, Maugard Thierry, Sablé Sophie

Antimicrobial resistance is a major global challenge of the 21st century(1), driven by the emergence of bacterial strains capable of surviving and proliferating despite antibiotic treatments(2). This alarming situation underscores the urgent need to identify novel bioactive compounds with antibacterial properties. In this context, the present study explores natural resources as potential reservoirs of new antimicrobial agents, focusing on both plant-derived compounds and marine bacterial metabolites.

Plant extracts were produced and characterized, leading to the obtainment of phenolic compounds and other bioactive molecules exhibiting antibacterial properties. Notably, these extracts demonstrated significant inhibitory effects against pathogenic bacteria, with minimum inhibitory concentration (MIC) values ranging from 0.3125 to 5 mg/mL against a methicillin-

resistant Staphylococcus aureus (MRSA) strain.
In parallel, the antibacterial potential of secondary metabolites derived from the secretomes of marine bacteria was investigated. These secretomes showed measurable activity in agar diffusion assays, indicating the presence of diffusible antibacterial compounds.
Overall, these initial findings highlight the promising potential of plant extracts and marine bacterial secretomes as alternative sources of antimicrobial agents. Their exploitation through bioproduction approaches could contribute to the development of new therapeutic strategies to combat antibiotic-resistant pathogens.
1. Mohsen Naghavi and others, 'Global Burden of Bacterial Antimicrobial Resistance 1990–2021: A Systematic Analysis with Forecasts to 2050', The Lancet, 404.10459 (2024), pp. 1199–226, doi:10.1016/S0140-6736(24)01867-1.
2. 'Résistance Aux Antibiotiques : Symptômes, Traitement, Prévention - Institut Pasteur', n.d. <https://www.pasteur.fr/fr/centre-medical/fiches-maladies/resistance-aux-antibiotiques> [accessed 2 April 2026].

34 - Emma Vasseur, M2 Intern / Stagiaire

LIttoral ENvironnement et Sociétés - LIENSs - UMR 7266 – CNRS, Université de La Rochelle

Marine biocalcifying bacteria and carbonic anhydrase: a biological approach for the consolidation of limestone built heritage

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Keywords: biocalcification, marine bacteria, built heritage, calcium carbonate, carbonic anhydrase
Context and objectives
Limestone built heritage progressively deteriorates under the effects of climatic, biological and pollution-related factors. Current consolidation methods rely mainly on chemical treatments, which are often short-lived and may alter the stone. In this context, biocalcification emerges as a promising and innovative biological alternative.
This work explores the potential of marine biocalcifying bacteria capable of precipitating calcium carbonate to consolidate limestone. Unlike approaches based on urea hydrolysis, which generate ammonia that is harmful to calcareous materials, our strategy targets the carbonic anhydrase (CA) pathway in the studied biocalcifying bacteria. This enzyme catalyses the conversion of CO_2 into bicarbonate ions, thereby promoting the precipitation of calcium carbonate. The aim of this work is therefore to optimise the bioprecipitation conditions of marine bacteria in order to favour material consolidation.
Experimental approach and preliminary results Five marine bacterial strains selected for their biocalcifying potential were studied in vitro. Optimisation of bioprecipitation conditions to maximise calcium carbonate precipitation focused on the composition of the cementation medium (carbon and calcium sources) as well as physicochemical conditions (pH, salinity). Initial results allowed the identification of favourable growth and $CaCO_3$ precipitation conditions specific to each bacterium.
Furthermore, the presence of genes encoding carbonic anhydrase was investigated by PCR gene amplification. Specific primers were designed and amplification conditions were optimised. This work will form the basis for gene expression analyses by RT-qPCR, in order to confirm the involvement of this enzymatic pathway in the selected bacterial strains under biocalcification conditions.
This project thus opens up promising prospects for the development of sustainable restoration solutions compatible with calcareous materials, combining consolidation efficacy with preservation of the integrity of architectural heritage.

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Exploring the role of the microbiota-gut-brain axis in glioblastoma

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The microbiota–gut–brain axis (MGBA) is increasingly recognized as a key regulator of brain homeostasis through its control of immune tone, metabolic signaling, and neuroactive compound production. However, its contribution to brain tumor biology, particularly glioblastoma, remains

largely unexplored. Glioblastoma is a highly aggressive tumor characterized by profound local and systemic immunosuppression, metabolic rewiring, and resistance to standard-of-care therapies. We hypothesized that GB progression is influenced by bidirectional interactions with the gut microbiota. Using syngeneic and xenograft mouse models, we show that glioblastoma implantation induces dysbiosis, marked by shifts in specific bacterial taxa associated with tumor burden. Importantly, treatment with the Stupp protocol (the therapeutic regimen for glioblastoma) partially restores microbiota composition, suggesting that therapeutic efficacy may be linked to microbiota remodeling. Mechanistically, we identify a role for microbiota-dependent metabolic pathways in tumor progression. Tryptophan hydroxylase 1 knockout mice, which exhibit impaired peripheral serotonin production, develop larger tumors, supporting a functional link between gut-derived metabolites and glioblastoma growth. Consistently, metabolomic analyses reveal alterations in circulating metabolites associated with tumor presence. In parallel, we observe that glioblastoma-induced dysbiosis correlates with systemic and tumor-associated inflammatory changes, highlighting a microbiota-driven modulation of the immune microenvironment.
Altogether, our findings uncover a bidirectional interaction between glioblastoma and the gut microbiota, involving metabolic and immune pathways. This work supports the MGBA as a novel component of glioblastoma biology.

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Engineering a bacterial secretion platform for the export of recombinant proteins

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The biobased production of recombinant proteins has great potential for future applications and circular economies. In recent years synthetic biology toolboxes have been developed for the use of Gram-negative bacteria as production chassis. However, a cell lysis step is often required due to the protein production taking place intracellularly. While a variety of conventional methods exist, many cause impurities and could damage the product. This makes production expensive and time-consuming.
The flagellar Type III Secretion System (fT3SS) is a bacterial secretion system found in both Gram-positive and -negative bacteria. The fT3SS naturally secretes flagellin at a high rate (1), which is subsequently assembled outside the cell to form the flagella. Unlike the injectisome, the fT3SS is non-pathogenic. Together with its ability to secrete recombinant proteins (2-3), this allows for continuous production and harvesting, as well as simplified downstream processing. While much is known about the fT3SS, it is tightly regulated, and poorly characterized regarding the export of recombinant proteins. Here we have developed the fT3SS into an efficient secretion platform by characterizing and optimizing secretion signals.
Combined with engineering strains which can synthesize and export recombinant proteins during their growth, the engineered fT3SS creates a high-yield low-cost bacterial production platform. It supports lysis-free production with reduced cellular contaminants and improved process scalability. This lowers barriers for protein production and accelerates the development of a quick affordable pipeline for new industrial and therapeutic solutions.

References

1) Renault, T. T., Abraham, A. O., Bergmiller, T., Paradis, G., Rainville, S., Charpentier, E., Guet, C. C., Tu, Y., Namba, K., Keener, J. P., Minamino, T., & Erhardt, M. (2017). Bacterial flagella grow through an injection-diffusion mechanism. eLife, 6, e23136. https://doi.org/10.7554/eLife.23136
2) Green, C. A., Kamble, N. S., Court, E. K., Bryant, O. J., Hicks, M. G., Lennon, C., Fraser, G. M., Wright, P. C., & Stafford, G. P. (2019). Engineering the flagellar type III secretion system: improving capacity for secretion of recombinant protein. Microbial cell factories, 18(1), 10. https://doi.org/10.1186/s12934-019-1058-4
3) Singer, H. M., Erhardt, M., Steiner, A. M., Zhang, M. M., Yoshikami, D., Bulaj, G., Olivera, B. M., & Hughes, K. T. (2012). Selective purification of recombinant neuroactive peptides using the flagellar type III secretion system. mBio, 3(3), e00115-12. https://doi.org/10.1128/mBio.00115-12

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Integration of ATP synthase into respiratory supercomplexes redefines mitochondrial bioenergetic organization

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Kinetoplastids are divergent, unicellular eukaryotic parasites responsible for major human

(e.g., Chagas disease, Sleeping Sickness and Leishmaniasis) and livestock diseases and possess a single, highly specialized mitochondrion. The ATP synthase (CV) polymers have been characterized and it has been demonstrated that they strongly contribute to shaping of the inner mitochondrial membrane (IMM). However, the electron transport chain complexes (ETCs) are yet to be structurally characterized in kinetoplastids. More globally, any direct structural coupling between CV and the ETCs has never been demonstrated, in spite of the tight functional coupling owing to the formation of the proton gradient across the IMM leading to driving the CV to synthesize ATP. Here, using cryo-electron microscopy and biochemical characterization, we resolve multiple CV-containing assemblies that physically link CII, CIII and CIV to CV, together with CV dimers and monomers captured in distinct functional conformations. These include CV–CII–CIV2, CV2–CII2–CIV2, and CV2–CII2–CIV2–CIII4 architectures. Integration of CV into these supercomplexes is driven by a noncanonical heterodimeric module of two ATPg orthologs (ATPg1 and ATPg2) and extensive phospholipids (notably cardiolipins) interactions, which repurpose the canonical CV dimer interface to favor CV–ETC contacts. These assemblies remodel the IMM and likely confer functional advantages enabling rapid bioenergetic remodeling as kinetoplastids transition between respiring and non-respiring life stages. Our results provide the first structural demonstration of direct ETC–CV supercomplexes in kinetoplastids and link lineage-specific molecular innovation to organelle architecture and function

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Identification de bactéries impliquées dans le transfert de plasmides de résistance le long d'un continuum One-Health

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Les bactéries résistantes aux antibiotiques représentent une menace majeure pour la santé humaine. Un facteur clé de leur émergence est le transfert horizontal de gènes entre bactéries appartenant aux différents écosystèmes — animal, humain et environnemental. Ce transfert est largement médié par des plasmides, éléments génétiques mobiles capables de disséminer rapidement des gènes de résistance entre espèces bactériennes, jouant ainsi un rôle central dans la propagation de l'antibiorésistance. Ce travail vise à identifier les souches bactériennes clés contribuant de manière disproportionnée à la propagation de plasmides de résistance entre écosystèmes.

Pour cela, des campagnes d'échantillonnage ont été réalisées le long d'un continuum environnemental, incluant des prélèvements chez des animaux de ferme (fèces, cavités buccales et nasales) ainsi que dans leur environnement direct (foin, eau de boisson, poussières de surface). Plusieurs genres bactériens généralistes et connus pour porter des plasmides de résistance ont été sélectionnés par pré-enrichissement en milieux sélectifs, suivi d'un ensemencement sur des milieux spécifiques. Les souches isolées ont été identifiées par spectrométrie de masse afin de confirmer leur appartenance taxonomique. Des concentrations minimales inhibitrices (CMI) ont ensuite été déterminées pour sélectionner des clones multirésistants.

Au total, 840 souches ont été isolées, dont 409 bactéries à Gram négatif : 31 Acinetobacter spp., 8 Aeromonas spp., 31 Klebsiella spp., 52 Pseudomonas spp., 41 Escherichia coli, 38 Enterobacter spp. et 51 Serratia spp. Le criblage des souches d'E. coli a révélé que 39 présentaient une résistance à au moins trois antibiotiques, dont environ la moitié (n = 24) portaient des plasmides. Les niveaux de résistance observés sont plus élevés dans les souches issues des environnements de foin et de poussières que dans les autres milieux étudiés. Parmi les Klebsiella spp., 14 souches présentaient également un profil multirésistant. Le séquençage des génomes et des plasmides de ces souches par technologie Nanopore est en cours et permettra d'identifier les plasmides impliqués dans ces résistances. L'étude de ces souches apportera des éléments clés pour mieux comprendre les mécanismes et processus impliqués dans la propagation de l'antibiorésistance entre réservoirs environnementaux et animaux, et le rôle central des plasmides dans ces dynamiques.

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Single and Combined Effects of Nanoplastics and Metals on Marine Phytoplankton:

Focus on Thalassiosira pseudonana

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Over the past few decades, overpopulation and new technologies have led to an increase in resource consumption and waste production, causing diverse forms of environmental damage such as water pollution by plastics and metals including cadmium (Cd). This element is a non-essential metal for primary producers such as marine diatoms, which are the basis of marine food webs. Nanoplastics (NPs) are also a serious threat to marine microalgae. They mainly come from the slow and incomplete degradation of macroplastics, but they are also directly found in products such as cosmetics. Previous studies have shown the effects of Cd and NPs as single contaminants on algal physiology. However, little is known about their combined effects on marine microalgae and T. pseudonana specifically.

This study aimed at characterizing both the physiological and intracellular responses of Thalassiosira pseudonana to increasing free Cd2+ concentrations (6.6 – 4332 nM) and negatively-charged polystyrene (PS-COOH: 409 ± 29 nm) concentrations (50 – 250 mg/L). A combination of growth and subcellular assays was applied with measurements by flow cytometry.

While no effects on growth have been observed when exposed to PS-COOH, a growth inhibition was detected above 737 nM of free Cd2+, with EC50 of 1104 ± 146 nM. Exposure to increasing free Cd2+ induced subcellular damages: chlorophyll a content remained unchanged while cell size slightly decreased at 329 nM before increasing from 418 nM. Cellular granularity increased up to 1029 nM, suggesting algal adaptations.

Further experiments will be conducted on the effects of the mixture of Cd and NPs based on the value of the EC50 for Cd and varying concentrations of NPs.

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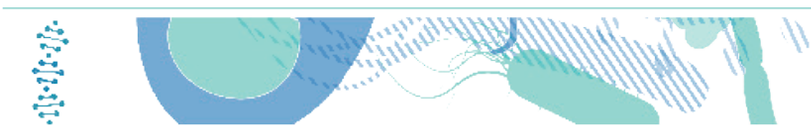

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