Thank you !

Doc'J Symposium 2024

Abstract Booklet

16th May 2024 – Jouy-en-Josas

Abstract n°1

Thanh-Julie Nguyen[1]

[1]Dynenvie – MaIAGE

Impact of pesticides on wild pollinators

Keywords : Pesticides, Wild Pollinators, Landscape Context, Impacts

In Europe, one in ten bee and butterfly species are threatened, and populations are declining for 37% of bees and 31% of butterflies. The massive use of pesticides is one of the factors contributing to the decline in wild pollinator populations. While the harmful effect of these pesticides has been demonstrated for the domestic bee, it is still difficult to understand the effects on wild pollinators, given the wide diversity of diets, lifestyles and sizes within these different groups.

The composition and structure of landscapes can modify the exposure of wild pollinators to pesticides, either by barrier effects or by amplification in the case of landscapes with few floral resources. This raises the question of the impact of pesticides on wild pollinators, and the extent to which landscape elements can reduce or increase these effects. The aim of my thesis is therefore double: to identify the landscape variables affecting the exposure and impact of pesticides on wild pollinators in order to address the current lack of knowledge. The outcome of my work will be to understand the relationships between the diversity and abundance of wild pollinator species and pesticide exposure, to highlight variations in the sensitivity of different pollinator species to pesticides, and to assess the impact of the landscape context on the presence of pesticides and their effect on wild pollinator populations.

Thematic identifiers

- Microorganisms, Health & Environment
- Animal Sciences, Diversity, Adaptation & Health

Acknowledgements

Organisers:
Laura OBRY (BaPS – Micalis)
Léa WAGNER (SyBER – Micalis)
Delphine POLVE (FInE – Micalis)
Marie STOSSKOPF (PIMs – Micalis)
Ronan SOUDY (ProbiHote – Micalis)
Constance PATIN (PhylHom – Micalis)
Armand BERNARD (Cosynus – Micalis)
Matthieu BERTRAND (EpiMic – Micalis)
Amrita RAJA-RAVI-SHANKAR (MECP2 – BREED)

Financial supports:
The Centre Presidency and its team: Nathalie TOUZE, Isabelle FOUCADE, Nadine ROGER, Anne LAGUILLEZ, Sylvie INIZAN
The DESSE
MTS unit (Medicines and Technologies for Health)

Logistical supports:
Valérie DAVANT for Doc'J's communications and graphic charter
Véronique MARRACCI for badges and goodies
Fabienne DUCLUZEAU for poster printing
L'ADAS (Stéphane GAUBERT) for lending poster grids

Poster n°9

Giovany RUBIO[1]
[1]PROSE

Exploring microbial dynamics based on the microbial transition state thermokinetic theory

Keywords : Microbial growth, thermokinetic modeling, oleaginous yeast, environmental factors.

The Microbial Transition State (MTS) model, employing a thermokinetic approach rooted in statistical physics, establishes a link between growth kinetics and the energy balance of cell metabolism (Desmond-Le Quéméner & Bouchez, 2014). This model has demonstrated success in simulating both microbial communities and pure cultures (Delattre et al., 2019).
Further exploration of the MTS theory is essential to understand the impact of environmental conditions (i.e. temperature, pH, salinity) on growth dynamics. It is possible to apply first principles from non-equilibrium thermodynamics to predictively integrate the effect of this parameters into the MTS model.
The oleaginous yeast *Yarrowia lipolytica*, which has shown its potential for multiple industrial applications, is used to perform microbial cultures at different environmental conditions for the study of microbial growth rate. Ongoing research is focused on studying the microbial growth dynamics in microplates. The next phase of this study will center on advancing the MTS model.

Thematic identifier

- Microorganisms, Health & Environment
- Digital Sciences & Systems Modelling

Abstract n°2

Gabriel Costa Monteiro Moreira[1], Hélène Kiefer[1], Hélène Jammes[1]
[1]MECP2 – BREED

Epigenetic processes of adaptation in ruminants

Keywords : Epigenetics, Ruminants, Immune system, DNA methylation, Functional annotation

There is an increasing demand to produce healthier food using fewer natural resources, reducing environmental impact and preserving biodiversity. Thus, it is crucial to understand the molecular basis of genotype vs environment interactions in the expression of phenotypes. Epigenetic processes are of great importance driving the phenotypes, also serving as a memory of the animal's trajectories. By applying and integrating cutting-edge technology/epigenetic assays (e.g., assays to profile DNA methylation, open chromatin and histone marks) we are working towards the identification of biomarkers to diagnostic the individual health and performance. Investigating the epigenome of dairy cows exposed to contrasting temperatures (heat-stress conditions), we have highlighted DNA methylation variations induced by heat stress which may affect cattle's immune system. Profiling the methylome of bovine blood immune cells and integrating with functional annotation, we have highlithed cell-subtype specific regulatory regions (e.g., enhancers) which may regulate the expression of a gene known to play a role on host response to infection and immune system homeostasis. Selected biomarkers will also feed into the epigenotyping tool under development (https://rumigen.eu) allowing large-scale/large-cohort genotyping. Taken all the tools and knowledge together, our research will contribute to better understand the genome function on ruminant's adaptation to the different environments.

Thematic identifier

- Animal Sciences, Diversity, Adaptation & Health

Abstract n°3

Henri Lagarde[1], Pauline Martin[1], Didier Boichard[1]

[1]G2B – GABI

Designing breakthrough cattle breeding programs to keep pace with changes in the sector over the next 20 years

Keywords : Genetics, cattle breeding systems, forecasting

The French suckler and dairy cattle industries will face numerous challenges over the next 20 years. These include, but are not limited to, falling beef consumption, volatile input costs, rising temperatures, the sensitivity of forage crops to water shortages, possible future regulations targeting methane production by cattle, the emergence of pathogens and a decline in the number of farmers. Genetic improvement through selection is one way of adapting to these changes.

This post-doctorate is organised in two stages. Firstly, it will involve leading an interdisciplinary group of experts on the cattle industry, in order to determine the scenarios for changes in cattle farming in France over the next 20 years, and the appropriate cattle genetics to go with them. Links will also be established with comparable scientific and professional initiatives. In a second phase, the aim will be to use simulations to determine the optimum selection schemes for producing these cattle genetics.

The work carried out as part of this post-doctorate will be the subject of a forward-looking report on the development of French cattle farming over the next 20 years, and will also contribute to the GA and PHASE bi-departmental working group on "Experimentation to co-design and evaluate sustainable cattle farming systems", as well as being used in the writing of scientific articles.

This 3.5-year post-doctorate is funded by the PEPR agroecology and digital research programme as part of the CoBreeding project.

Thematic identifier

- Animal Sciences, Diversity, Adaptation & Health

Poster n°8

Mélanie Mathis[1], Maria Ciobanu, Chrystelle Bureau, Angeline Guenne, Ludwig Jardillier, Ariane Bize

[1]PROSE

Identification of methanogenic archaea viruses in anaerobic digesters using a flow cytometric archaea cell sorting approach

Keywords : Methanogenic archea, Cytochrome F420, Flow cytometry, Provirus, Nanopore sequencing

Archaeal viruses play a fundamental role in microbial ecology by influencing biological processes and directly affecting and regulating archaeal communities. However, to date, only around ten methanogenic archaeal viruses have been isolated and partially characterised. Methanogenic archaea develop in a wide range of anaerobic biotopes and are distributed in ten distinct orders, representing a high degree of phylogenetic diversity. They play a major role in the biochemical carbon cycle through the production of methane. In addition, they are involved in the methanisation of bio-waste, a process that is essential for the ecological transition. Knowing more about their viruses and understanding them better has a double interest, both fundamental and applied. The aim of my internship project is to identify the proviruses or viruses of methanogenic archaea in anaerobic digesters, in order to characterise their diversity. To do this, methanogenic archaea cells will be sorted by flow cytometry in collaboration with IDEEV DEEM, followed by sequencing of the DNA extracted and amplified from the sorted cells, using Oxford Nanopore technology. This sorting is based on the presence of cytochrome F420 from methanogenic archaea, which is autofluorescent in its oxidised form, and is particularly abundant in hydrogen-trophic methanogenic archaea. The sequences obtained will be used for genomic analysis. Various bioinformatics tools will be used to detect viral sequences within metagenomes and predict their hosts. The functional content of the viruses will then be studied, in particular to look for the presence of metabolic helper genes.

Thematic identifier

- Microorganisms, Health & Environment

Poster n°7

Delphine Polvé[1], Sandy Ribes, Claudia Bevilacqua, Florence Castelli, Céline Henry, Julie Cadiou, Nicolas Lapaque, Véronique Douard, Pierre Larraufie
[1]FInE – Micalis

Modulation of enteroendocrine cells by intestinal microbiota

Keywords : Intestinal microbiota, intestinal hormones, enteroendocrine cells

Enteroendocrine cells (EECs) are key players in the intestinal epithelium due to their ability to produce and secrete intestinal hormones in response to changes in their environment. These hormones play a crucial role in energy metabolism, digestion and intestinal transit, functions which are impaired in many pathologies also associated with an imbalance of the intestinal microbiota. Different populations of EECs can be distinguished along the intestinal tract, linked to variations in the microbial environment. A strong link between gut microbiota and EECs is highlighted by the dysregulation of circulating levels of some gut hormones in axenic mice. To understand the role of the microbiota in EECs regulation, mice with an unaltered microbiota were compared with mice treated with broad-spectrum antibiotics. The presence of microbiota led to a significant decrease in circulating GLP-1 levels, as well as changes in gene expression of certain gut hormones in specific intestinal regions. To distinguish the specific response of EECs, these cells were sorted using mice expressing a fluorescent protein in EECs. In addition to variations in the expression of genes encoding gut hormones, transcriptomic analysis revealed alterations in the energy metabolism of these cells, particularly in oxidative phosphorylation by the gut microbiota. These observations suggest that, beyond the known mechanisms, the intrinsic metabolic regulation of EECs could impact their functions, thus opening up new strategies to regulate EEC functions.

Thematic identifier

- Microorganisms, Health & Environment
- Animal Sciences, Diversity, Adaptation & Health

Abstract n°4

Solène Fresco[1]

[1]G2B – GABI

Can we genetically select dairy cows that produce less methane?

Keywords : Methane, Genetics, Dairy cows, Predictions

Cattle's ability to value forage is a major advantage. However, by degrading the plant compounds consumed by cows, ruminant micro-organisms produce methane. Since methane is a greenhouse gas that is a major contributor to climate change, agriculture, and cattle farming in particular, is often singled out for its enteric methane emissions. However, it has been shown that for the same milk production and feed consumption, some cows produce less methane than others, revealing a potential for selecting animals that emit less. Genetic and genomic selection of low-emission cows is therefore a strategy for mitigating climate change.

Setting up such a selection requires fairly accurate measurements in large numbers, but the direct measurement tools available to date do not allow this. Several indirect measurement tools have been developed, in particular equations for predicting methane emissions based on the mid-infrared (MIR) spectra of milk. This is based on rumen fermentation, which influences both the production of fatty acids found in milk (and therefore in the MIR spectrum) and methane production.

These equations can then be applied to the MIR spectra routinely collected from cows at milk recording, providing a very large number of phenotypes. Thanks to them, it is then possible to study the genetic determinism of methane emissions and develop a genetic evaluation to identify the least methane-emitting animals.

Thematic identifiers

- Animal Sciences, Diversity, Adaptation & Health
- Agroecosystems & Environment

Abstract n°5

Dylan Saunier[1], Eric Venot[1], Estelle Rathahao-Paris[1]

[1]Drugs and Technologies for Health Department (DMTS) – CEA / INRAE

Automatic search for markers of exposure to dietary chemical contaminants in perinatal biological matrices to characterize the chemical exposome

Keywords : Bioinformatics, Chemistry, Exposome

Detecting and characterising xenobiotics or exposure markers in complex matrices is a major challenge in analytical chemistry. The development of increasingly sensitive analytical tools such as liquid chromatography coupled to high-resolution mass spectrometry (LC-HRMS) has made it possible to detect a large number of compounds per analysis. However, the resulting increase in data produced as part of ever more ambitious projects makes this exercise impossible to carry out manually.

In our laboratory, we are working on automated approaches to data processing based on suspect screening and non-targeted.

The first approach consists of searching for exposure markers from a predefined list of chemical compounds by means of *in-silico* prediction of their metabolites and the generation of signals detectable by mass spectrometry.

The non-targeted approach aims to extract signals that meet criteria ensuring their reliability as well as the characteristics of xenobiotics, and involves applying different filters to identify signal clusters corresponding to the presence of specific isotopes (C, Cl, Br, S) and/or known biotransformations (glucuronidation, sulphation, glutathione conjugation), as well as selecting signals on the basis of their frequency of presence in several samples. Finally, annotation proposals are made on the Pubchem database to identify possible xenobiotics.

Thematic identifiers

- Microorganisms, Health & Environment
- Digital Sciences & Systems Modelling

Poster n°6

Alexandre Lecomte[1], Aurélie Derre-Bobillot[1], Nicolas Trainel[2], Anne-Marie Cassard[2], Pascale Serror[1] and Cristel Archambaud

[1]CPE – Micalis, [2]INSERM (U996) Paris-Saclay University

Lipid droplets in hepatocytes support *Enterococcus faecalis* intracellular multiplication

Keywords : *Enterococcus faecalis*, hepatocytes, intracellular-multiplication, lipid droplets

Enterococcus faecalis is an opportunistic Gram-positive pathogen responsible for hospital- and community-acquired infections. To date, *E. faecalis* is also one of the rare bacteria for which a link between intestinal overgrowth and the severity of alcohol-related liver damage has been demonstrated. Severity and mortality of alcoholic hepatitis are consistent with the presence of *E. faecalis* expressing cytolysin, a toxin capable of lysing bacteria and cells. In the mouse liver, *E. faecalis* are recognised by the resident macrophages, leading to inflammation and hepatic lesions. We have recently shown that *E. faecalis* multiplies and survives in hepatocytes. This intracellular lifestyle is associated with the appearance of intracellular microcolonies, indicating that hepatocytes may serve as a niche for *E. faecalis*. Whether the intracellular lifestyle of *E. faecalis* in hepatocytes contributes to liver injury remains to be investigated. Combining cellular models of infection, bacterial genetic screening and pharmacological agents to modulate host-signalling pathways, we identified bacterial candidates involved in invasion or intracellular multiplication of *E. faecalis* in hepatocytes. We also showed that lipid droplets support *E. faecalis* intracellular multiplication in hepatocytes. Finally, we identified an *E. faecalis* transcriptional regulator involved in regulating the level of lipid droplets. We anticipate this work will provide insights into the contribution of intracellular *E. faecalis* growth in liver injury.

Thematic identifier

- Microorganisms, Health & Environment

Poster n°5

Lindsay Goulet, Florian Plaza Oñate, Pauline Barbet, Edi Prifti, Eugeni Belda, Emmanuelle Le Chatelier, Guillaume Gautreau
[1]IBS - MetaGenoPolis

CroCoDeEl: automatic detection of cross-contamination in metagenomic data

Samples submitted for metagenomic sequencing may be contaminated during laboratory steps by DNA from an external source (i.e. laboratory reagents) or from other samples processed simultaneously (cross-contamination). Such contamination can distort results and, if undetected, lead to erroneous conclusions. Despite being a critical issue, cross-contamination remains little studied. A few tools have been developed, but they suffer from a number of limitations, notably a lack of sensitivity.
By inspecting species abundance profiles in public cohort samples, we have identified patterns specific to this contamination. Here we present CroCoDeEL, a tool that automatically searches for these patterns to identify contaminated samples. CroCoDeEL is based on a pre-trained supervised model with semi-simulated data. Our approach requires no negative controls, works with related samples (natural sharing of strains such as mother and child), discriminates between sources of contamination and contaminated samples, and estimates contamination rates. Comparative analysis of two public cohorts fully curated by expert eyes revealed that CroCoDeEL identifies contaminated samples and their respective sources of contamination, even at low rates (down to 0.1%) if sequencing depth allows. The use of CroCoDeEL on 13 cohorts focusing on human colorectal cancer revealed that contamination is a widespread problem. We believe that our work underlines the urgency of systematically addressing cross-contamination to ensure the robustness of studies based on metagenomic data.

Thematic identifier

- Microorganisms, Health & Environment

Abstract n°6

Arthur Lequertier[1]

[1]MaIAGE

Transmission of information through a metabolic network

Keywords : Bacteria, metabolic networks, information theory

Bacterial metabolism can be represented mathematically as a vast network of chemical reactions. In such networks, propagated disturbances can carry information about environmental disturbances. To quantify this information, we need to study the responses of system components in the presence of noise. Here we study the response of the system to disturbances according to probability distributions. The mutual information between the variables in the model is used to quantify their dependencies in the form of information transfer. We expect this work to help us understand the signal processing capabilities of bacteria, while taking account of internal and environmental noise as well as uncertainties.

Thematic identifier

- Microorganisms, Health & Environment
- Digital Sciences & Systems Modelling

Abstract n°7

Mathilde Sola[1], Camille Champion[1], Raphaëlle Momal[1], Emmanuelle Le Chatelier[1], Adrien Paravel[1], Sandrine Auger[1], Jean-Marc Chatel[1], Mahendra Mariadassou[1], Magali Berland
[1]IBS – MGP

In silico reconstruction of an ecological niche: towards the design of new-generation probiotic consortia

Keywords : Gut microbiota, interaction networks, network inference, ecological niche, New Generation Probiotics

In recent years, researchers have increasingly focused their research on the role of microbiota bacteria in health. Alterations to its structure, known as dysbiosis, could explain the susceptibility of individuals to developing certain pathologies. To restore balance to the ecosystem, many strategies involve discovering and using bacterial species as new preventive and therapeutic tools: new-generation probiotics. The intestinal microbiota comprises a multitude of bacteria from different species, interacting in different ways. Interaction networks are mathematical tools used to study the dependencies and associations between entities within a biological system. Using abundance data, it is possible to reconstruct graphs, including the nodes of which represent bacterial species and the edges the co-occurrence between these species. Two methods have recently been developed at MGP using different approaches to find out more about the neighbourhood of a species of interest. The 'GuildOmics' project, the collaboration result between MGP and MICALIS, is a perfect example of the application of this approach. Centred around *Faecalibacterium prausnitzii*, the aim of this project is to develop new-generation consortia in which the bacteria interact with each other in a cooperative manner, to promote the protective effect of the species of interest recognised as active in the intestinal ecosystem. The in silico phase, based on data from several large public cohorts, has identified a number of companion species. The experimental validation phase is currently underway.

Thematic identifier

- Microorganisms, Health & Environment
- Digital Sciences & Systems Modelling

Poster n°4

Nathan Gérard[1], Angeline Guenne, Ariane Bize, Miguel Iniesto
[1]PROSE

Study of the bio-industrial potential of cyanobacteria in wastewater treatment

Keywords : wastewater, cyanobacteria, biomarkers, microbial mat, 16S metabarcoding

Cyanobacteria, found in aquatic environments, are photosynthetic organisms that, in association with other microorganisms, can form complex structures known as “microbial mats”. These mats are capable of recycling organic matter and decomposing pollutants. Their sensitivity to alterations induced by human activities makes them valuable indicators of the health of aquatic ecosystems. To observe the impact of human activities on microbial mats, microcosms have been set up in the laboratory where a microbial mat from a hypersaline environment will be exposed for 3 to 4 months to three different wastewaters resulting from human activity (urban wastewater, agricultural water, and a pesticide-doped synthetic water). Longitudinal monitoring of microbial community composition and key physico-chemical parameters will be carried out. Following this exposure, the V4V5 regions of the 16S rDNA will be sequenced using Illumina MiSeq technology. A bioinformatics analysis will identify the cyanobacteria in the various microbial mats. By studying the dynamics of these communities under controlled conditions, we aim to create a “reference table” and identify potential biomarkers for early detection of pollution effects. In addition, this research could lead to the identification of organisms capable of degrading or eliminating these contaminants. A better understanding of these communities could, in the longer term, enable us to better preserve aquatic ecosystems from anthropogenic disturbance.

Thematic identifier

- Microorganisms, Health & Environment

Poster n°3

Antoine Daussin[1*], Pauline Barbet[1*], Mathieu Almeida[1] , Aurélie Caille[2] ,Claire Cherbuy[3] , Nathalie Meunier[2] , Nicolas Pons[1] , Victoria Meslier[1]
[1]MetaGenoPolis, [2] UNH (Human Nutrition Unit) Clermont Auvergne University, [3]Micalis
*Equal contribution

MetaNutriDB, a collection of public cohorts with curated metagenomic and nutritional data

Keywords : Shotgun metagenomics, Human gut microbiome, Nutrition, Fiber, Database

With the constant evidence of the gut microbiota role in many pathologies, there is a need for more robust and comprehensive meta-analysis of the link between gut microbiota and health. Publicly available shotgun metagenomic data give the opportunity for hypothesis testing on the factors driving the intestinal balance in health and disease. Notably, diet is among the main factor shaping the gut microbiota and is intrinsically linked to the intestinal microbiota balance. In this context, we developed MetaNutriDB, the first publicly available shotgun metagenomics collection of human gut microbiome associated with host nutritional data. We collected metagenomic data from public studies with their corresponding metadata (host health, study type, study objectives, sequencing tools and depth, demographic, clinical and nutritional data). Nutritional data were collected with a particular interest for diet, fiber intake, and the presence of nutritional intake information. Fourteen cohorts have been collected from observational or interventional studies published after 2015 on human adults with available metagenomic samples and at least one nutritional information. MetaNutriDB comprised 4040 samples, including 2911 healthy and 66 sick individuals from 14 different countries. We also developed a user-friendly interface for the scientific community to find and classify the MetaNutriDB samples in specific categories, such as available macronutrients and micronutrients intakes, studies or individual specificities. MetaNutriDB will be completed with additional publicly available cohorts to further contribute to the boarder picture on the relation between the gut microbiota and diet.

Thematic identifiers

- Microorganisms, Health & Environment
- Food Science & Engineering

Abstract n°8

Léa Wagner[1], An Hoang[2], Olivier Borkowski[1], Matthieu Jules[1]

[1]SyBER – Micalis ; [2]BioRetroSynth – Micalis

Development of a cell-free system for bacterial genomes expression

Keywords : cell-free, genome, transcriptomic, *E. coli*

Lysate-based cell-free systems are complex mixtures of enzymes and small molecules that can perform *in vitro* biological processes, such as transcription, translation, and biochemical reaction cascades. They are generated by extracting cellular machinery through cell lysis and then enriching the resulting lysate with a buffer. This buffer supplies ribonucleosides, amino acids, an ATP regeneration system, and several biochemical cofactors, making it possible to express any DNA of interest. Due to their simplified biochemical composition and the absence of cellular membranes, cell-free systems are invaluable tools for unraveling cellular processes, as demonstrated by the seminal work of Nirenberg and Matthaei (1960's) in deciphering the genetic code. Nowadays, these systems find widespread applications in protein production, biosensing, and the development of genetic circuits in biotechnology.
My doctoral project aims to develop an *Escherichia coli* lysate-based cell-free system that allows for the expression of an entire bacterial genome, resulting in a transcriptome that can be sequenced by RNA-seq. Only requiring a genome (extracted or synthetized), such a system will allow to deepen our understanding of non-cultivable bacteria (for instance it constitutes 70% of the human gut microbiota) by revealing transcriptional landscapes and testing regulatory mechanisms at the genomic level in different biochemical conditions.

Thematic identifiers

- Microorganisms, Health & Environment
- Digital Sciences & Systems Modelling

Abstract n°9

Tania Kamwouo[1], Sylvie Bouttier[1], Séverine Domenichini[1], Claire Janoir[1]
[1]BaPS – Micalis

Characterization of the network structure of the extracellular matrix of *Clostridioides difficile* biofilm

Keywords : Biofilm, matrix, *Clostridioides difficile*, extracellular DNA

Clostridioides difficile is a Gram-positive, strictly anaerobic, and spore-forming bacterium responsible for nosocomial and community intestinal infections. The major problem of *C. difficile* infections is the occurrence of recurrences, in 15 to 30% of cases after a first episode, more than half of which are relapses, related to the same strain. These relapses occur because of the ability of the bacteria to persist in the digestive tract in its forms of resistance: spores and perhaps also in the form of biofilm. Although no formal evidence of biofilm formation in vivo exists to date, arguments support this hypothesis. *C. difficile* is capable of forming biofilms in vitro. Depending on the strains, the biomasses of these biofilms are more or less important and cohesive. We have shown by different techniques, including imaging by confocal laser scanning microscopy, that extracellular DNA (eDNA) is the central component of the matrix, which ensures the cohesion of the biofilm. This role is related to the presence of a network of fine filaments, which binds bacteria together. In the absence of this eDNA, the biofilm disperses, but the dispersion effect on the biofilm is more or less important depending on the strains. Other components such as certain proteins or polysaccharides have also been identified within the matrix, including polysaccharide II, an essential component of the surface of *C. difficile*, which seems to be a component of this filamentous network.

Thematic identifier

- Microorganisms, Health & Environment

Poster n°2

Philippine Coeugnet[1], Julie Labatut, Sophie Hooge
[1]GABI & LISI – GIBBS team

Innovation for the agroecological transition in animal and plant breeding: analysis and support for co-design processes and systems

Keywords : Co-design, Participatory breeding, Agro-ecology

The agro-ecological transition calls for a review of research practices, and in particular for research to be opened up to non-scientific stakeholders. Animal and plant breeding are often hermetically sealed, whereas the agroecological transition requires links to be made between the different biological processes involved in agricultural systems. It is therefore necessary to develop new ways of recoupling design processes in animal and plant breeding, and to revise innovation processes by including non-scientific stakeholders. In this context, my post doc aims to answer the following research question: **What properties are essential to the functioning of a mechanism for co-designing breeding schemes for agroecological transition, mobilizing a heterogeneity of knowledge and stakeholders?** In order to answer this question, the postdoc aims to observe and support colleagues in the COBREEDING project, who are in charge of implementing concrete cases of co-design on various species: (i) the introduction of local breeds of chicken into cropping systems, (ii) the design of disruptive bovine breeding schemes to meet the constraints of climate change, and (iii) the redesign of the Versailles Saclay experimental unit towards agroecology.

Thematic identifier

- Territory, Governance and Innovation in Society

Poster n°1

Auneau Camille[1], Xiaojun Liu, Joel Awinzure Agumah, André Pauss, Laura André, Thierry Ribeiro, Sabrina Guérin-Rechdaoui, Vincent Rocher, Carlyne Lacroix, Olivier Chapleur, Ariane Bize, Céline Roose-Amsaleg
[1]PROSE

Effect of propionate on microbial communities in methanization, in semi-continuous pilots

Keywords : Methanization, Micro-organisms, Biostatistics, Metabarcoding

Methanization is a natural anaerobic biological process that converts organic matter into biogas, rich in methane and carbon dioxide. It involves bacteria and archaea, and proceeds in four successive stages: hydrolysis, acidogenesis, acetogenesis and methanogenesis. This last stage is carried out exclusively by methanogenic archaea. These microbial communities are sensitive to environmental changes, which can lead to inhibition and reduced biogas production. For example, propionate, a volatile fatty acid produced during acidogenesis, can inhibit methanogenic archaea when present in high concentrations. Despite this, studies on the inhibition of methanization by propionate are still few and far between. In order to identify biomarkers likely to prevent this inhibition, four semi-continuous pilots, methanizing urban sewage sludge, were exposed to different concentrations of sodium propionate (NaPro, from 0 to 13g/L). 16S rDNA metabarcoding data were generated to study the response of microbial communities to the inhibitor. As part of my internship, I am currently analyzing these data using supervised and unsupervised bioinformatics and statistical methods. The results revealed inhibition in reactors with higher NaPro levels, as well as a marked temporal effect on microbial communities. In addition, a supervised analysis identified taxonomic groups impacted by high NaPro concentration. However, the abundances of these taxonomic groups were relatively low. Further statistical methods will be applied to refine the results, and the focus will also be on biological interpretation.

Thematic identifier

- Microorganisms, Health & Environment

Abstract n°10

Paola RAMIREZ[1]
[1]PROSE

Gas-liquid transfer dynamics in a three-phase biofiltration pilot plant

Keywords : Aeration, Biofiltration, Gas-liquid transfer, Modelling

Biofiltration is an intensive urban wastewater treatment process based on a fixed-bed reactor that combines filtration of suspended matter and biological treatment. Nitrifying biofilters emit N_2O, a powerful greenhouse gas. It is essential to understand the gas-liquid interactions of nitrifying biofilters because of their influence on aeration and emissions of this gas. To do this, an experimental and modelling method was used. We set up a biofiltration pilot plant with similar height as an industrial biofilter, with polystyrene beads as the fixed bed. The pilot is equipped with sensors to measure liquid and gaseous flow rates, as well as oxygen levels. Various experimental methods were used to study oxygen transfer dynamics under abiotic conditions, and were modelled using several reactors in series. According to the results, disparities in behaviour between the different zones of the reactor are observed, and are influenced by the specific transfer coefficients and oxygen fluxes generated by the ascending liquid phase. The modelling takes into account the consequences of pressure and gas depletion caused by the height of the system. Using this method, it is possible to evaluate the transfer coefficients and gas concentrations in the biofiltration process. In addition, long-term monitoring under biotic conditions was carried out to analyse transfer dynamics during nitrification.

Thematic identifier

- Microorganisms, Health & Environment

Abstract n°11

Léa Huet[1]

[1]BaPS – Micalis

Are *Clostridioides difficile* surface polysaccharide synthesis enzymes new therapeutic targets?

Keywords : cell wall, polysaccharides, *Clostridioides difficile*, surface structures, essentiality

Clostridioides difficile is a pathogenic, gram-positive bacterium that is strictly anaerobic, spore-forming, motile and toxigenic. *C. difficile* infections (CDIs) cause symptoms ranging from simple diarrhea to pseudomembranous colitis, which in some cases can lead to death. CDIs are treated with antibiotics, but resistance is emerging. This is why it is important to look for new therapeutic targets against *C. difficile*. The surface of *C. difficile* comprises lipoteichoic acid (LTA), a peptidoglycan to which polysaccharide II (PSII) is attached and an essential S-layer, composed of SlpA protein, non-covalently linked to PSII.
A locus predicted to be essential, containing all the genes encoding the PSII and LTA synthesis proteins, has been identified. The project focuses on the study of two genes at this locus, CD2783 involved in the synthesis of PSII and *tuaG* predicted to be involved in the synthesis of LTA. As part of the study of the essentiality of PSII, two mutants constructed before my arrival in the laboratory were characterised via proteomics and different phenotypes were tested. My work confirms that PSII is the support for all CWPs proteins. The second objective is to verify the essentiality of the *tuaG* gene and its involvement via the construction of a conditional lethal mutant. The *tuaG* gene is essential for bacterial survival, which could imply that LTA is also essential for bacterial survival.

Thematic identifier

- Microorganisms, Health & Environment

Abstract n°12

Victor Lecoeuche[1], Yannick Fayolle[1], Eleftheria Ntagia[1], Théodore Bouchez[1]

[1]PROSE

Gas Diffusion Electrode for improving the Microbial Electrosynthesis process.

Keywords : Microbial Electrosynthesis , Process Engineering, Mass transfert, Bioelectrochemical systems, Gas diffusion electrodes

Finding sustainable chemical compound synthesis methods and carbon dioxide mitigation and removal technologies are two challenges that must be met to ensure successful transitions. As a potential solution, microbial electrosynthesis is a biological process aiming to convert carbon dioxide and electrons obtained from biomass oxidation into chemical compounds. The bioelectrochemical cell consists of two chambers between which only ions and electrons are exchanged. The biomass oxidation occurs in one of these compartments, called the anode, whereas the conversion of carbon dioxide into added-value components occurs at the cathode. The interface between microorganisms and electrodes has to be studied and improved to achieve better productivity, decreased costs, and scalability of the process. The gas diffusion electrode is a promising technology that could be deployed at the cathode to deliver electrons and carbon dioxide at the exact same spot, creating an ideal growth area for the CO2-reducing microorganisms. In recent years, few studies coupling Microbial electrosynthesis and the gas diffusion electrode have been published. Each of these studies presents positive results obtained from this coupling, but the deconvolution of the various parameters involved in these systems makes system evaluation complex. Further research efforts should be devoted to understanding the interactions between the gas diffusion electrode and the microbial communities involved in the process. Experiments and modeling are two approaches that could be combined to build and apply this knowledge to improve the electrode/microbes interfaces and the performances of the microbial electrosynthesis process.

Thematic identifiers

- Microorganisms, Health & Environment
- Agroecosystems & Environment