IJPB Symposium 2026

Chemical interactions between plants and their environment: from the molecule to the field

Institute Jean-Pierre Bourgin for Plant Sciences, Versailles

23-25 September 2026

Abstract Book

https://ijpb-plant-sciences-2026.symposium.inrae.fr/

WELCOME

We are pleased to welcome you to The IJPB Symposium 2026 edition, dedicated to ***chemical interactions between plants and their environment: from the molecule to the field.***

The symposium includes an **opening lecture and four thematic sessions**, each involving **an international and an IJPB keynote speaker as well as presentations from participants** selected from submitted abstracts. The themes of each session are outlined below:

1 - Chemical signals involved in plant response to their environment.

2 - Perception and transduction of chemical signals.

3 - Integration of chemical interactions in ecological communities and agroecosystems.

4 - Agroecological innovations derived from studies of plant-environment interactions.

The aim of this exciting meeting is to **foster collaborations and facilitate knowledge exchange among participants** by bringing together renowned specialists in the field and a high level of interdisciplinarity.

The symposium will also feature **a tour of the IJPB Plant Observatory (PO), a large and unique cluster of integrated facilities dedicated to multi-level phenotyping of plants.**

Scientific organising committee

B. Alunni, S. Jasinski, E. King, O. Loudet, A. Marmagne, A. Voxeur

Logistical and administrative support

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Many thanks to all the IJPB members who helped and supported us continuously throughout the organisation of this event.

Many thanks to the INRAE Île-de-France – Versailles-Saclay Research Center for making their facilities available and helping us to organise this event.

Thanks to our sponsors and partners

The organisation of the symposium would not have been possible without the help of our sponsors, and we sincerely thank them for their financial support.

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GPS coordinates: Latitude 48.80210, Longitude 2.08723
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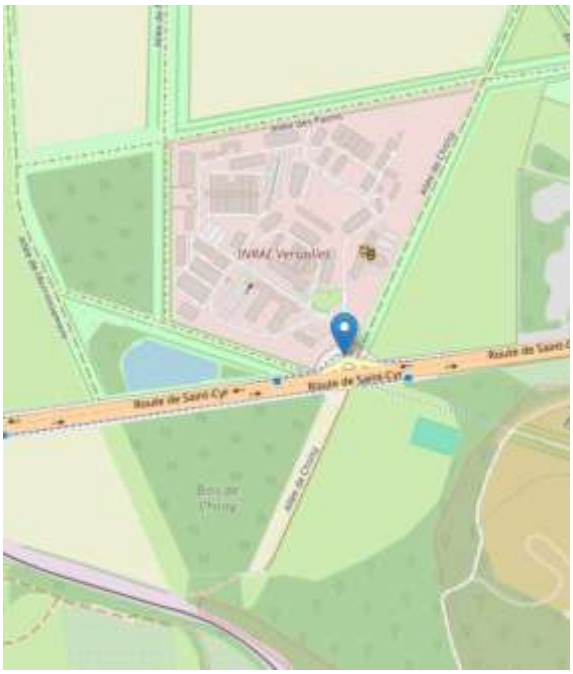

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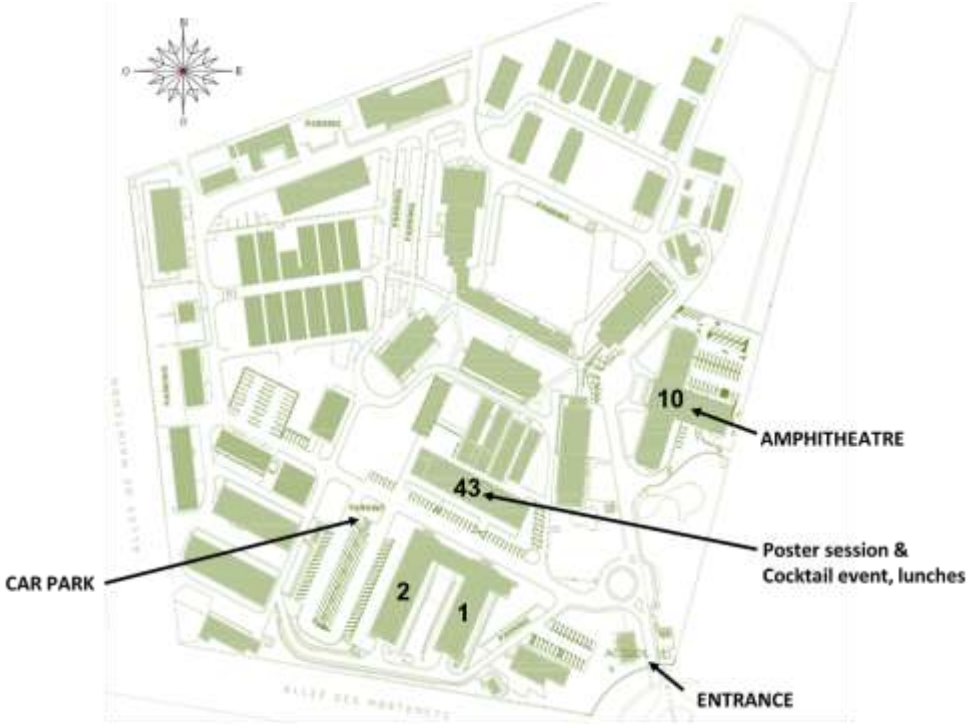

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Soak the seed-coated paper in water overnight

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Programme Overview

	Wednesday, 23 September	Thursday, 24 September	Friday, 25 September
9:00 am		**Session II** (9:00 - 10:20 am)	**Visits** (9:00 - 11:00 am)
10:00 am			
		Coffee break	**Coffee break**
11:00 am	**Registration** (10:30 am - 1:30 pm)	**Session II** (10:50 - 11:55 am)	**Session IV** (11:20 am - 12:40 pm)
12:00 pm		**Lunch**	
1:00 pm			**Lunch**
	Welcoming (1:30 - 2:00 pm)	**Session III** (1:30 - 2:50 pm)	
2:00 pm	**Introductory session** (2:00 - 2:50 pm)		**Session IV** (2:10 - 3:15 pm)
3:00 pm	**Session I** (2:50 - 4:10 pm)	**Coffee break**	**Closing Ceremony (Prizes)**
		Session III (3:20 - 4:35 pm)	
4:00 pm	**Coffee break**		End at 3:35 pm
5:00 pm	**Session I** (4:40 - 6:00 pm)	**Free Time**	
6:00 pm	**Break**		
7:00 pm	**Poster session & Cocktail event** (6:15 - 9 pm)	**Gala Dinner** (7:00 - 10 pm)	
8:00 pm			
9:00 pm			

Programme

Wednesday, 23 September

10:30 am - 1:30 pm	Registration (lunch not included)
1:30 - 2:00 pm	Welcome
2:00 -2:50 pm	**Keynote: Marnix Medema**, Deciphering the Chemical Language of Plant-Microbiome Interactions using Computational Omics
2:50 - 6:00 pm	**Session I. Chemical signals involved in plant response to their environment** *Chairs: S. JASINSKI, H. NORTH, S. SOUNDIRAMOURTTY*
2:50 - 3:20 pm	**Keynote: J. C. D'AURIA**, Chemical Warfare in the Field: Unraveling the Biosynthetic Logic of Gramine and Hordenine
3:20 - 3:40 pm	**Early career: L. LECLERC**, A multilateral dialogue: how biotic complexity shapes plant immunity
3:40 - 3:55 pm	**S. HUIZINGA**, How do lettuce root exudates affect *Fusarium oxysporum*?
3:55 - 4:10 pm	**T. BARRIT**, A GWAS-based study of iron nutrition, coumarins and plant defense using the Arabidopsis/*Dickeya spp.* Pathosystem
4:10 - 4:40 pm	**Coffee break**
4:40 - 5:15 pm	**IJPB keynote: A. VOXEUR, F. PERREAU, S. BOUTET, J. C TOTOZAFY**, The use of molecular profiling approaches to improve our understanding of interactions between plants and their environment
5:15 - 5:30 pm	**S. FIRMIN**, MicroRNAs in root rhizodeposits: the missing piece of plant holobiont communication plasticity under abiotic stress
5:30 - 5:45 pm	**K. BAUDRY**, A shared genetic network links p-coumaric acid, lignin traits, and water deficit responses in maize
5:45 - 6:00 pm	**V. BEAUDOUX**, Induced allelopathy in rye: weed-specific root exudate signaling and benzoxazinoid-mediated responses
6:00 - 6:05 pm	**COLASSE SA Company,** Flash talk
6:05 - 6:15 pm	**Break**
6:15 - 9:00 pm	Poster session & Cocktail event at IJPB (building 43)

Thursday, 24 September

9:00 - 11:55 am	**Session II. Perception and transduction of chemical signals** *Chairs: C. GILLOTEAU, A. MARMAGNE, A. VOXEUR*
09:00 - 09:30 am	**Keynote: C. SANCHEZ-RODRIGUEZ**, Decoding the Cell Wall: How Plants Translate Extracellular Information into Growth and Defense Responses
09:30 - 09:50 am	**Early career: A. DARD**, Glow with the flow: PersIcPLANT a new genetically encoded fluorescent biosensor to visualize hydropersulfides in plant cells
09:50 - 10:05 am	**G. PANDHARIKAR**, Tree-Fungi Mutualistic Interactions: The Roles of Poplar Terpenes
10:05 - 10:20 am	**A. BOO**, Programmable bacteria-to-plant chemical communication using HSL and peptide-gated gene circuits
10:20 - 10:50 am	**Coffee break**
10:50 - 11:10 am	**IJPB keynote: S. BONHOMME**, Bioynthesis and perception of strigolactones in a bryophyte, the moss *Physcomitrium patens*
11:10 - 11:25 am	**S. SOUNDIRAMOURTTY**, Inositol Phospho Glycans, a mere by-product of membrane remodeling or key signaling molecule that mediate responses to biotic stress?

11:25 - 11:40 am	**L. MONTICELLI**, Establishing *Physcomitrium patens* as a model to investigate chemical interactions with nitrogen-fixing cyanobacteria
11:40 - 11:55 am	**A. DAVIERE**, The pectic part of the cell wall as an important source of signals for plant response to the environment
11:55 am - 1:30 pm	**Lunch (Building 43)**
1:30 - 4:25 pm	**Session III. Integration of chemical interactions in ecological communities and agroecosystems** *Chairs: B. ALUNNI, D. FUSTER, O. LOUDET*
1:30 - 2:00 pm	**Keynote: R. SAWERS**, Host factors promoting benefit from arbuscular mycorrhizal symbiosis
2:00 - 2:20 pm	**Early career: P. KROHN**, Periderm integrity gates spatial chemical defence and fungal community assembly in roots
2:20 - 2:35 pm	**K. SCHLAEPPI**, Soil iron and root immune components mediate microbiome feedbacks in Arabidopsis
2:35 - 2:50 pm	**U. HOECKER**, Response of *Arabidopsis thaliana* to plant-plant competition
2:50 - 3:20 pm	**Coffee break**
3:20 - 3:40 pm	**IJPB keynote: A. DELLAGI**, Metabolic Reprogramming Drives Microbe-Mediated Nitrogen Acquisition
3:40 - 3:55 pm	**C. VENEAULT-FOURREY**, Microbiota profoundly impact poplar host plant metabolites and root exudate content and composition
3:55 - 4:10 pm	**S. CHOPRA**, Maize specialized metabolites: their genetic regulation and ecological function in plant herbivory
4:10 - 4:25 pm	**A. IHNATOWICZ**, Linking metabolism and environment: discovery of novel enzymes in coumarin biosynthesis shaping stress responses in Arabidopsis
4:25 - 4:35 pm	**G. MOUILLE,** Peer Community In Plant
4:35 - 7:00 pm	**free time**
7:00 - 10:00 pm	Gala dinner at “La Flotille”

Friday, 25 September

9:00 - 11:00 am	Visits
11:00 - 11:20 am	**Coffee break**
11:20 am - 12:30 pm	**Session IV. Agroecological innovations derived from the study of how plants interact with their environment** *Chairs: S. BONHOMME, E. KING, J. MANGONI-MPAY*
11:20 - 11:50 am	**Keynote: S. GOORMACHTIG**, Decoding beneficial Plant–Microbe interactions: Citizen science and Omics-Driven Pathways to Sustainable Legume Production
11:50 am - 12:10 pm	**Early career: P. HOMOBONO**, Phenomic prediction to integrate plant-environment interactions in a cross-year framework for steviol glycosides assessment in *Stevia rebaudiana*
12:10 - 12:30 pm	**IJPB keynote: M. CORSO**, How seeds reshape their specialized metabolome for stress response and adaptation
12:30 - 2:00 pm	**Lunch (Building 43)**
2:00 - 2:15 pm	**J. FERREIRA DE CARVALHO**, Designing resistant and durable agroecological apple orchards
2:15 - 2:30 pm	**L. ANDRUSZKOW**, Deciphering mechanisms of service plants involved in the disruption of host plant recognition by a specialist insect herbivore using complementary volatolomic approaches
2:30 - 2:45 pm	**C. BENEZECH**, 1 + 1 ≠ 2? Combined Biosolutions Reshape Durum Wheat Responses to Multiple Stresses
2:45 - 3:00 pm	**G. GIANNELLI**, Exploring below-ground metabolomic signatures of perennialism in New Perennial Grain lines
3:00 - 3:15 pm	**A. KEBIECHE**, From defence-related transcripts to metabolomic signatures: chemical modulation of carrot response to biocontrol under heat stress
3:15 - 3:35 pm	**Closing ceremony** (Poster/Talk prizes)

Talk Abstracts

Deciphering the Chemical Language of Plant-Microbiome Interactions using Computational Omics

Marnix H. MEDEMA

Bioinformatics Group, Wageningen University & Research, Wageningen, The Netherlands

Plants and microbes produce a wealth of specialized metabolites, which play important roles in ecology and are key mediators of plant-microbiome interactions. Genome sequence data has revealed that only a tiny fraction of the chemical diversity of these metabolites has been unearthed. Here, I will highlight recent work performed in my research group and with the wider community on developing and applying computational and artificial intelligence approaches to chart biosynthetic diversity, and to predict chemical (sub)structures and functions of metabolites directly from sequence data. Specifically, I will provide examples of how we are applying these methods to identify gene and gene clusters from plant microbiomes responsible for rhizosphere competence and plant protection. From the host side, I will show how paired omics data can facilitate discovery of molecules that mediate defence and microbiome recruitment. All in all, these computational approaches will facilitate smarter and more targeted automated genome mining of natural products to uncover the hidden chemical language of life that drives antagonism and collaboration between plants and microbes.

Chemical Warfare in the Field: Unraveling the Biosynthetic Logic of Gramine and Hordenine

John Charles D'AURIA

Leibniz Institute of Crop Plant Genetics and Crop Plant Research (IPK) OT Gatersleben, Seeland 06466, Germany

In the *Poaceae*, the indole alkaloid gramine and the phenethylamine hordenine form a coordinated allelochemical defense system shaped by distinct metabolic origins and sharply partitioned tissue accumulation. Their ecological significance has long been recognized, yet the biochemical basis that governs their formation and deployment has remained incomplete, particularly the early steps of the gramine pathway.

A multi year research program has now resolved the full biosynthetic route for gramine through the combined use of barley pan genomics, comparative transcriptomics, and targeted metabolomics. This work identifies the cytochrome P450 monooxygenase CYP76M57, also known as AMI synthase or HvAMIS, as the catalyst that converts tryptophan to aminomethylindole. Mechanistic studies show that HvAMIS performs a cryptic oxidative rearrangement involving carbon–carbon bond cleavage and carbon–nitrogen bond formation. This reaction represents the first enzymatically observed Hofmann rearrangement in nature.

The project also reveals how gramine and hordenine are deployed through contrasting spatial strategies within the plant. Hordenine, derived from tyrosine, accumulates predominantly in roots and rhizosphere proximal tissues. Gramine, in contrast, is concentrated in leaves. A high sensitivity RP UPLC FLD platform has been used to map the distribution of these metabolites across twenty two barley accessions and multiple Lupinus species, which exposes lineage specific patterns of allelochemical allocation.

Synthetic biology approaches that include modular cloning, CRISPR Cas9, and heterologous expression systems allow the de novo reconstruction of both pathways in microbial and plant hosts. This includes the successful engineering of gramine biosynthesis in buckwheat, a pseudocereal within the genus *Fagopyrum*. Together, these advances establish a precise biochemical foundation for the strategic use of natural allelopathy in crop improvement. The work provides a route toward chemically self reliant germplasm that supports sustainable alternatives to synthetic pesticides.

A multilateral dialogue: how biotic complexity shapes plant immunity

Laëtitia LECLERC[1], Antony CHAMPION[2], Sophie GAUDRIAULT[3], Jean-Benoît MOREL[1], Annette MORVAN-BERTRAND[4], Nicolas NÈGRE[3], Marie-Pascale PRUD'HOMME[4]

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[4]UMR EVA, Université de Caen Normandie, Caen, France.

When a plant mounts an immune response, it does not respond to a single attacker, it integrates signals from a complex biotic environment. My research has dissected the successive layers of this complexity. I first showed that fructan exohydrolases, enzymes involved in carbohydrate metabolism, are upregulated by salicylic acid alongside canonical defense genes in non-fructan accumulating plants, revealing unexpected metabolic nodes of immune regulation [1]. I then demonstrated that the oral microbiota of the lepidopteran pest *Spodoptera frugiperda* suppresses jasmonate-dependent defenses in rice during feeding. Using antibiotic-treated larvae to deplete the oral microbiome, combined with RNA-seq, phytohormone quantification, and CRISPR knockout mutants, I established that the insect microbiome actively manipulates plant immunity during attack, the plant response is shaped not only by the insect, but by the microbial community it carries [2]. I then explored the plant side of this equation: a leaf-associated bacterial symbiont produces metabolites with potent insecticidal activity against *Spodoptera* species across a broad host range, demonstrating that plant-associated microorganisms can also act as allies in plant defense. I am currently extending this framework to the community level, investigating whether the immune response of a focal plant to biotic stress is modulated by the identity of its conspecific neighbors, a concept of social immunity. To first establish whether this phenomenon exists across the plant kingdom, I am surveying diverse angiosperm families. I then focus on wild *Poaceae* species from contrasting ecosystems to disentangle the ecological and evolutionary drivers of social immunity, asking whether domestication, life history traits, or habitat shape this neighbor-dependent immune response. Collectively, these results reveal that the plant immune response is not a bilateral dialogue, it is a multilateral conversation, and we have only just begun to identify all the speakers.

References

[1] Nguyen et al. (2023) Fructan exohydrolases (FEHs) are upregulated by salicylic acid together with defense-related genes in non-fructan accumulating plants. Physiologia Plantarum

[2] Leclerc, L. et al. (2024) Early transcriptomic responses of rice leaves to herbivory by Spodoptera frugiperda. Scientific Reports

How do lettuce root exudates affect *Fusarium oxysporum*?

Sjors HUIZINGA[1], Gertjan KRAMER[2], Martijn REP[3], Harro BOUWMEESTER[1], Anna HEINTZ-BUSCHART[4], Lemeng DONG[1]

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[2]Mass-Spectrometry of Biomolecules, Swammerdam Institute for Life Sciences, University of Amsterdam.
[3]Molecular Plant Pathology, Swammerdam Institute for Life Sciences, University of Amsterdam.
[4]Biosystems Data Analysis, Swammerdam Institute for Life Sciences, University of Amsterdam.

Plants spend up to a third of their energy on the production of metabolites that are exuded from the roots. Composition of these root exudates can be adjusted depending on growth and stress conditions to shape the rhizosphere microbiome to the needs of the plant. Root colonizing fungi are an important part of the root microbiome. Some species benefit the plant by facilitating nutrient uptake and ward off attacking pathogens, whereas others are pathogenic and can lead to devastating agricultural losses. Here, we study lettuce root exudate composition under different nutrient treatments, and how the pathogenic fungus *Fusarium oxysporum* perceives and reacts to it. Using ANOVA simultaneous component analysis (ASCA) on untargeted LC-MS/MS data, it was demonstrated that the composition of the exudate differs between control, nitrogen-deficient, and phosphate-deficient lettuce plants, and that this difference develops over time. In particular, lettuce root exudates were found to contain a wide diversity of sesquiterpene lactones, some of which were strongly regulated in response to nutrient treatment. Next, in an *in vitro* assay, these same lettuce root exudates caused nutrient treatment dependent growth responses in *F. oxysporum*. Growth effects of selected sesquiterpene lactones were confirmed using pure compounds. Together, these results suggest that sesquiterpene lactones are important active components of lettuce root exudate, which could be involved in altering plant-fungus interactions in response to nutrient deficiency. Production and exudation of these compounds could be leveraged in selective breeding to develop crops that can shape more advantageous root microbiomes.

A GWAS-based study of iron nutrition, coumarins and plant defense using the Arabidopsis/*Dickeya spp*. pathosystem

Thibault BARRIT[1], Alicja DOBEK[1], Marta POTRYKUS1, Weronika BABINSKA-WENSIERSKA[1], Jérémy GROSJEAN[2], Magdalena MACKE[1], Izabela PERKOWSKA[1], Aleksandra TUNSKA[1], Arthur KORTE[3], Manus CAREY[4], Paul WILLIAMS[4], Alexandre OLRY[2], Ewa LOJKOWSKA[1], Anna IHNATOWICZ[1]

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As shown previously by our research group, *Arabidopsis thaliana* is an excellent model to study the coumarin biosynthetic pathway and the natural variability of coumarin accumulation in different environments. To better understand the link between maintenance of iron (Fe) homeostasis, biosynthesis and accumulation of coumarins, and plant immunity, we exploit genetic variability among natural Arabidopsis populations and study their differential susceptibility to plant pathogens of the genus *Dickeya spp*. under various Fe availability. Bacteria belonging to *Dickeya* genus cause soft rot, which destroys potato crops and many other economically important plants.

In this study, we cultivated a set of 105 Arabidopsis accessions in hydroponic cultures under Fe-deficient conditions both with and without pathogen inoculation. We collected a phenotypic dataset focusing on traits such as root and shoot fresh weight, pigments quantity, photosynthetic activity, disease severity index, and systemic response at different time points. In parallel, we performed targeted metabolic profiling to quantify coumarins in roots and root exudates, as well as ionomics to determine Fe and other nutrients levels in shoots. To identify the genetic variation associated with these traits, Genome-Wide Association Studies (GWAS) are underway. First significant associations and candidate genes have been detected. Ongoing multi-trait analyses aim to uncover additional loci and novel genetic factors underlying broader phenotypic variation.

Our goal is to identify and characterize new genes associated with the observed phenotypic variability, revealing previously undescribed components of the coumarin synthesis pathway involved in the 'battle for iron' between plants and pathogens.

Funding: NCN grant UMO-2022/47/B/NZ2/01835 (AI)

The use of molecular profiling approaches to improve our understanding of interactions between plants and their environment

Stéphanie BOUTET, Sylvie CITERNE Frédérique TELLIER, Jean-Chrisologue TOTOZAFY, François PERREAU, Aline VOXEUR

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Plants continuously acclimate to changing biotic and abiotic environments through complex molecular responses involving metabolites, lipids, phytohormones and cell wall-derived oligosaccharides. Deciphering these responses requires integrated molecular profiling approaches capable of capturing this chemical complexity.

The Plant Observatory-Chemistry/Metabolism at the Jean-Pierre Bourgin Institute for Plant Sciences (PO-Chem) provides state-of-the-art analytical expertise based on mass spectrometry for the quantification, characterisation and identification of small plant molecules such as phytohormones, primary and specialised metabolites, lipids and oligosaccharides. Beyond analytical services, PO-Chem collaborates closely with plant researchers to design innovative molecular profiling strategies that address fundamental biological questions.

Through selected collaborative case studies, we will illustrate how these complementary molecular profiling approaches have contributed to generating new biological knowledge and how PO-Chem continues to foster interdisciplinary research aimed at improving our understanding of plant–environment interactions and thus at uncovering actionable levers to modulate them.

MicroRNAs in root rhizodeposits: the missing piece of plant holobiont communication plasticity under abiotic stress

Maroua ALAOUI[1], Mélanie BRESSAN[2], Céline ROISIN[1], Léa JAFEU[1], Mathilde BOUTEILLER[2], Michel Pierre FAUCON[1], Etienne YERGEAU[3], Isabelle TRINSOUTROT-GATTIN[2], Stéphane FIRMIN[1]

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Plants can cope with environmental stresses by regulating the rhizodeposition of diverse bioactive compounds [1]. Recent evidence has revealed that roots of plants grown on contaminated soils actively release microRNAs into the rhizosphere via extracellular vesicles (EVs), opening a new dimension in our understanding of plant–soil chemical communication [2]. However, whether these root-derived microRNAs contribute to shaping root-associated microbial interactions and enhancing plant survival and performance remains poorly understood. therefore, we isolated EVs from two phylogenetically distant species, *Triticum aestivum* and *Brassica napus*, exposed to perfluorooctanoic acid (PFOA)-contaminated soil and drought stress. New wheat plants treated with wheat EVs exhibited a marked increase in resistance to chemical stress, an effect associated with shifts in bacterial community abundance and carbon use efficiency in the rhizosphere. EV molecular profiling and computational analyses identified microRNAs enriched in rhizodeposits under abiotic stress conditions, which were predicted to target plant-associated bacterial genomes, including *Bacillus subtilis* and *Pseudomonas fluorescens*. Using root-derived EVs or synthetic microRNA, we demonstrated significant effects on bacterial growth and metabolic activity, accompanied by inhibition of biofilm formation in *B. subtilis*. Taken together, our findings demonstrate that microRNAs associated with root-derived EVs are commonly secreted by plants and act as cross-kingdom signaling molecules modulating rhizospheric bacteria, suggesting a novel adaptive mechanism by which plants harness their microbiome to cope with abiotic stress. These results open new perspectives for the development of microbiome-based agroecological strategies to improve crop resilience under climate change.

References

[1] Haskar Jyoti Parasar, Indrani Sharma, Niraj Agarwala, Root exudation drives abiotic stress tolerance in plants by recruiting beneficial microbes, Applied Soil Ecology, Volume 198, 2024, 105351.
[2] Firmin S., Houben D., Fontaine J., Lounès-Hadj Sahraoui A., Trinsoutrot- Gattin I., Faucon M-P., MicroRNAs: an emerging class of root exudate component of wheat response to polluted soil, 2024. Water air and soil pollution. 235 (9), 564

A shared genetic network links p-coumaric acid, lignin traits, and water deficit responses in maize

Kevin BAUDRY[1,2,3], Sandrine CHAIGNON[4], Nerea BRASERO PARDOW[2,3,4], Marie-Pierre JACQUEMOT[4], Christine PAYSANT-LE ROUX[2,3], Sébastien BEAUBIAT[4], Stéphanie PATEYRON[2,3,] François TARDIEU[5], Claude WELCKER[5], Olivier TURC[5], Clémentine VITTE[1], Johann JOETS[1], Llorenç CABRERA-BOSQUET[5], Valérie MECHIN[4], Marie-Laure MARTIN[2,3,6], Sylvie COURSOL[4]

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Water deficit strongly affects forage maize performance by reducing biomass production and altering digestibility. This stress induces major shifts in cell wall composition, including phenolic compounds such as p-coumaric acid, with strong genotype dependence reflecting contrasting biochemical adaptations affecting both stress response and forage quality [1-2]. However, the molecular links between water deficit, cell wall remodelling and digestibility remain poorly understood. To address this, seven contrasting maize genotypes were characterized under well-watered and moderate water deficit conditions using indoor high- throughput plant phenotyping (HTP) platforms. HTP traits were combined with measurements of digestibility, cell wall composition and transcriptomic profiles collected from three stem internodes per plant. Linear mixed models were used to identify genes associated with genotype × water condition interactions across HTP, digestibility and cell wall traits. Integrative analysis identified 260 candidate genes associated with water deficit- responsive traits. Network analysis revealed a highly interconnected genetic architecture comprising 16,294 trait-sharing interactions, with a dominant module linking p-coumaric acid, S-unit content and β-O-4 yield, accounting for 90.8% of all interactions. Fifteen hub and connector genes were further identified, including a master hub connecting multiple trait- associated modules. These results uncover key components of the genetic basis underlying cell wall remodelling under water deficit and highlight candidate genes for improving forage digestible yield under water deficit conditions.

References

[1] López-Malvar, A et al. (2025) Front Plant Sci. doi: 10.3389/fpls.2025.1571407.
[2] Main, O. et al. (2025) PLoS One. doi: 10.1371/journal.pone.0338077.

Induced allelopathy in rye: weed-specific root exudate signaling and benzoxazinoid-mediated responses

Victoria BEAUDOUX[1], Manon GENVA[1], Pierre DELAPLACE[2], Caroline DE CLERCK[2], Frédéric BOUCHÉ[3], Marie-Laure FAUCONNIER[1]

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Agriculture faces the challenge of maintaining crop productivity while reducing reliance on synthetic herbicides, whose environmental impacts and the emergence of resistant weeds threaten long-term sustainability. Allelopathy, defined as the inhibition of one plant by another through the release of allelochemicals, represents a promising alternative for sustainable weed management. In cereals, allelopathic responses can be induced by neighboring weeds, allowing plants to optimize the balance between growth and defense. However, the mechanisms underlying weed recognition and induced allelopathy remain poorly understood. This study investigates induced allelopathic responses in rye exposed to six weed species differing in phylogeny and ecology: three monocotyledons (*Alopecurus myosuroides*, *Avena fatua*, and *Lolium perenne*) and three dicotyledons (*Galium aparine*, *Papaver rhoeas*, and *Matricaria chamomilla*). Co-culture systems were established using solid-phase extraction (SPE) tubes to enable controlled root interactions and root exudate collection. Weed root exudates are being analyzed for their ability to trigger allelopathic responses in rye. The production of benzoxazinoids (BXs), major rye allelochemicals, is quantified both in collected root exudates and in root tissues to assess metabolic responses to weed presence. In parallel, plants are phenotyped through root architecture analysis as well as shoot and root biomass measurements to investigate biomass allocation associated with induced allelopathy. By comparing the responses induced by monocotyledonous and dicotyledonous weeds, this work aims to identify differential induction patterns and improve our understanding of belowground chemical communication involved in crop–weed interactions.

Decoding the Cell Wall: How Plants Translate Extracellular Information into Growth and Defense Responses

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Plants continuously monitor their extracellular environment and respond to developmental, environmental, and biotic stimuli. Increasing evidence indicates that the plant cell wall is not only a structural component but also a dynamic compartment whose composition and organization influence cellular signaling and plant responses to stress and disease.

Our work aims to understand how changes in cell wall properties are linked to signaling processes that coordinate growth, defense, and adaptation. Using cell biological, genetic, and biochemical approaches, we have investigated how perturbations in cell wall assembly and remodeling affect plant behavior across different contexts. Studies on cellulose synthesis and cell wall dynamics have revealed close connections between cell wall organization, cellular growth, and adaptive responses to environmental challenges [1-3].

Studies on plant-pathogen interactions has further shown that changes in cell wall composition and architecture are associated with disease resistance and defense activation [4,5]. In particular, modifications in pectin methylesterification and other wall properties accompany interactions between plants and vascular pathogens, highlighting the dynamic nature of the extracellular matrix during stress and infection. We have also explored how infection-induced responses are linked to developmental plasticity, revealing extensive remodeling of root vascular tissues together with changes in cell wall organization during disease progression [5].

Together, these studies illustrate how cell wall dynamics are integrated with signaling networks that coordinate plant growth, immunity, and adaptation, providing new insights into how plants translate environmental information into physiological and developmental responses.

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Glow with the flow: PersIcPLANT a new genetically encoded fluorescent biosensor to visualize hydropersulfides in plant cells

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Hydroxyl radicals (•OH) are highly reactive molecules that can cause severe cellular damage. Plants rely on a range of redox-based protective systems to limit oxidative stress, but how these processes are organized in living tissues remains poorly understood. One emerging component of cellular sulfur chemistry involves hydropersulfides (RSSH), small and highly reactive sulfur-containing molecules that are part of conserved sulfur redox networks present across all domains of life. To investigate their dynamics in living plants, we developed PersIc (PERSulfide IndiCator), a genetically encoded fluorescent biosensor that specifically reports hydropersulfide dynamics in real time with high spatial resolution. After validation in mammalian cells, we adapted the sensor for plants (PersIcPlant), enabling visualization of hydropersulfide changes from cellular to organ scale. Using this tool, we aim to determine how environmental stresses influence hydropersulfide dynamics and how these changes relate to plant stress responses and adaptation. In parallel, we are developing complementary biosensors with distinct spectral properties to investigate how plant interactions with pathogens and symbionts affect redox processes associated with oxidative stress, including hydroxyl radical formation. Together, this work will provide a dynamic view of sulfur-based redox chemistry in living plants and its role in stress resilience, building on deeply conserved biochemical systems that are fundamental to cellular life.

Tree-Fungi Mutualistic Interactions: The Roles of Poplar Terpenes

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Plant terpenes are important organic compounds and secondary metabolites that play key roles in plant development and plant-microbe interactions. Among them, triterpenes are recognized as a component of plant defence mechanisms. However, its role in balancing plant defence and symbiotic interactions remains poorly understood. In our study, we investigated the function of triterpene (β-amyrin) in ectomycorrhizal and endophytic symbiosis. Transgenic poplar lines with enhanced (OE) or suppressed (KO) expression of the β-amyrin synthase gene were generated. Root growth and development, as well as root colonization by the ectomycorrhizal fungus *Laccaria bicolor* and the endophytic fungus *Hyaloscypha* (*Cadophora*) *finlandica*, were evaluated. Our results showed that elevated β-amyrin production did not affect root growth nor development. However, β-amyrin overproduction significantly reduced ectomycorrhization rates and decreased *in planta* colonization by *L. bicolor*. Furthermore, high β-amyrin levels inhibited the formation of intracellular coils by *H. finlandica*. These findings suggest that higher β-amyrin concentrations restrict endophytic fungal penetration and confine fungal colonization primarily to the root apoplast. This study provides new insights into the role of triterpene (β-amyrin) in symbiotic interactions. Our findings help to understand the role of triterpenes regulating both ectomycorrhizal and endophytic associations, highlighting β-amyrin as a potential mediator of the balance between plant defence and beneficial microbial colonization.

Programmable bacteria-to-plant chemical communication using HSL and peptide-gated gene circuits

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Plants live in chemically rich environments where microbial signals, nutrients, pollutants, and stress cues are integrated into developmental and immune decisions. However, tools to program and read these interactions in a predictable way remain limited. Here, we develop synthetic communication modules that connect microbial chemical sensing to controllable gene expression in plants. Building on p-coumaroyl-homoserine lactone signaling, we implement inducible plant NOT gates using a panel of ten phage repressors, creating orthogonal regulatory parts that can invert and tune plant transcriptional outputs. We further extend this framework with arbitrium-inspired peptide regulators, aiming to establish peptide-based channels for bacteria-to-plant communication. To reduce construct-to-construct variability, these regulatory systems are paired with CRISPR-based targeted integration, enabling more predictable expression than random T-DNA insertion. Together, these components provide a modular route to engineer plant cells that respond to microbial or environmental chemical signals with defined transcriptional programs. Although current implementations focus on single-layer logic, they establish a foundation for multi-input circuits that could record, report, or reshape plant–microbe interactions. This work offers a synthetic biology platform for dissecting chemical communication in ecological communities and for developing future agroecological tools that couple microbial sensing with plant responses.

Bioynthesis and perception of strigolactones in a bryophyte, the moss *Physcomitrium patens*

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Strigolactones (SLs) are a fascinating class of apocarotenoid specialised metabolites produced by all land plants. SLs act as allelochemical signals in the soil, inducing the germination of seeds from root-parasitic plants and promoting symbiosis with arbuscular mycorrhizal fungi. Remarkably, they also function as phytohormones in seed plants and in mosses. We have been studying SL perception and signalling in *Physcomitrium patens* for several years. As with parasitic plants, *P. patens* has a much higher number of genes encoding potential SL receptors than most seed plants. These genes may encode receptors not only for SLs, but also for other yet unidentified allelochemicals. I will present our ongoing work to characterize these proteins as well as to identify the ligands of these receptors. By combining genetic, biochemical and chemical approaches, we hope to elucidate the structures of novel signalling molecules in a bryophyte model.

Inositol Phospho Glycans, a mere by-product of membrane remodeling or key signaling molecule that mediate responses to biotic stress?

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The plasma membrane and cell wall constitute the first barrier against external threats. Although this continuum is essential for understanding plant stress adaptation, the dialogue between these two compartments remains poorly understood. In this study, we focus specifically on the communication between pectins (major components of cell wall) and Glycosyl Inositol Phosphoryl Ceramides (GIPCs, major sphingolipids of plasma membrane [1]). Our preliminary results show that defective GIPC glycosylation is associated with biochemical changes in pectins, including increased cleavage by glycosyl hydrolases, leading to the release of pectic oligosaccharides into the apoplast. Similarly, pectic defects are associated with the accumulation of sugar-containing polar head groups, known as inositol phosphoglycans (IPGs), derived from GIPCs. Although the role of cell wall-derived oligosaccharides has been extensively studied, particularly in plant immunity [2], little is known about oligosaccharides-like originating from plasma membrane. Are they merely by-products of membrane remodeling, or are they genuine signaling molecules involved in acclimation processes? Upon incubation of Arabidopsis with *B. cinerea*, increased GIPC cleavage and accumulation of IPGs were observed, consistent with phospholipase C activity from *B. cinerea*. [3]. To investigate the role of polar head groups released from GIPC cleavage, tested defense properties against *Botrytis cinerea* in *Arabidopsis thaliana* leaves. Pretreatment with these IPG-enriched extracts appears significantly reduce the rate of *B. cinerea* infection over a one- week time course. Moreover, hormone quantification was performed 24 hours post- infection to further investigate the deployment of this defense mechanism and determine whether these previously overlooked oligosaccharides could coordinate responses to biotic stress.

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Establishing *Physcomitrium patens* as a model to investigate chemical interactions with nitrogen-fixing cyanobacteria

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Diazotrophic cyanobacteria are promising natural biofertilizing partners, yet the molecular mechanisms governing their interaction with plants remain poorly understood. While feather mosses have been shown to recruit nitrogen-fixing cyanobacteria through diffusible chemical cues [1], the identity of the molecules underlying this communication remains unknown. Because strigolactones act as signaling molecules during other beneficial plant symbioses, they represent plausible candidates for investigating whether similar signaling pathways contribute to bryophyte-cyanobacteria interactions. The model moss *Physcomitrium patens*, with its well-established genetic toolkit, provides a genetically tractable model to test this hypothesis.[2] To address this question, we implemented a workflow integrating controlled co-culture experiments, fluorescence microscopy, phycocyanin quantification, SL-like phenotypic bioassays and untargeted metabolomics. Following growth optimization of *Anabaena flos-aquae* under moss-compatible culture conditions, preliminary co-cultures with wild-type and the strigolactone-deficient Ppccd8 P. patens mutant were established. Fluorescence microscopy suggests reproducible cyanobacterial colonization, with filaments remaining associated with moss tissues. In parallel, cyanobacterial culture filtrates are being evaluated using a *Physcomitrium patens* phenotypic assay to assess SL-like biological activity [3]. Meanwhile, comparative untargeted metabolomic profiling of moss controls, cyanobacterial cultures and co-cultures has been initiated to identify candidate metabolites associated with interaction establishment, including metabolites potentially associated with strigolactone signaling. Overall, this work provides a framework for identifying candidate metabolites underlying bryophyte-cyanobacteria interactions and advances our understanding of the chemical mechanisms governing their establishment, with potential implications for the development of sustainable cyanobacterial biofertilizers.

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The pectic part of the cell wall as an important source of signals for plant response to the environment

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The correct response of the plant to changes in the pectic part of the cell wall is essential for its interactions with the environment. Pectin modifications affect the mechanical properties of the cell wall but can also lead to the production of chemical signals. We found that depending on characteristics such as the size, the degree of esterification and the reducing end, pectin fragments called oligogalacturonides (OGs) produced during pathogen infection can activate or repress plant defense activation [1]. Upon wounding, plants can activate defense mechanisms but can also repair tissues and regenerate new organs or even a whole plant. The ETHYLENE RESPONSE FACTOR 114 (ERF114) and ERF115 play a paramount role in regeneration enabling for example callus formation, de novo root regeneration and root meristem regeneration [2, 3]. However, the upstream signals linking wounding to ERF114/ERF115 induction and regeneration are still unknown. Through the combination of metabolomic analysis, pharmacological and genetic approaches, we found that ERF114/ERF115 expression is linked with pectin modifications in *Arabidopsis thaliana*. Thereby, we investigated the role of OGs as wound signals during regeneration. OG treatment could induce ERF115/ERF114 expression as well as their target genes and promote a faster root organogenesis from leaf explants in an ERF115/ERF114-dependent manner. This positive effect was dependent on the size but not on the degree of esterification of OGs. Lastly, we found that OGs act additively with auxin treatment in promoting root regeneration, revealing a promising tool to achieve regeneration in recalcitrant plant species.

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Host factors promoting benefit from arbuscular mycorrhizal symbiosis

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Arbuscular mycorrhizal fungi are ubiquitous in cultivated soils, forming symbiotic relationships with the roots of major crop species. Studies in controlled conditions have demonstrated the potential of the symbiosis to enhance the growth and nutrient efficiency of host plants. It is difficult, however, to estimate the benefit in the field, not least because of the lack of suitable AMF-free controls. We report the use of maize genetic mutants to generate AMF incompatible sentinel plants to be used as a baseline against which to evaluate the impact of the symbiosis. To estimate the overall effect of AMF and characterise the impact of plant genetics on symbiotic outcome, we have selectively incorporated AMF-incompatibility into maize genetic mapping populations. Using high resolution soil maps, we have shown response to AMF to vary dramatically within a single field, reflecting heterogeneity in nutrient availability. We have used QTL analysis to identify regions of the genome linked to differential performance in the presence or absence of arbuscular mycorrhizal symbiosis. In combination with allele-specific expression analysis, we are identifying candidate genes associated with different aspects of host response to AMF. The genetic architecture of host response indicates that there are trade-offs between growth with or without AMF. As such, as we pursue efforts to reduce agricultural inputs and make better use of AMF in the efficient use of soil resources, we may need to consider not only changes to management practices but also to the genetic make-up of the crops themselves.

Periderm integrity gates spatial chemical defence and fungal community assembly in roots

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Plants live in microbially complex soils, where chemical interactions determine whether surrounding organisms become partners, passengers or pathogens. To manage these interactions, roots deploy physical barriers together with specialized metabolites, which shape microbial access, growth and community assembly. However, it remains poorly understood how these defence layers are spatially coordinated from local metabolite deployment to ecological outcomes in soil, particularly in mature, periderm (cork)-containing root tissues undergoing secondary growth. Here, we investigate how integrity of the periderm controls spatial chemical defence and plant–fungal interactions in *Arabidopsis thaliana*. Combining section-resolved transcriptomics, spatial metabolite profiling, exudate analysis, fungal infection assays and soil mycobiome profiling, we reveal a pronounced chemical zonation along the longitudinal root axis with mature, periderm-containing root regions being enriched in tryptophan-derived defence metabolites. Strikingly, disruption of periderm formation enhances accumulation and release of chemical defences. Functionally, we find that these tryptophan-derived metabolites restrict fungal overcolonization of the periderm in mono-association assays and contribute to spatial fungal community assembly in natural soil. Consistently, plants impaired in either periderm integrity or tryptophan-derived defence metabolism show moderate growth defects, whereas simultaneous disruption of both defences causes a pronounced fitness penalty. Together, our findings identify the periderm as a dynamic chemical interface that links physical and chemical barrier integrity, fungal colonization and plant performance. This establishes mature root tissues as active regulators of plant–environment interactions from the molecule to the field and highlights spatially targeted root chemistry as a potential route to fine-tune crop resilience in soil.

Soil iron and root immune components mediate microbiome feedbacks in Arabidopsis

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Soil microbiomes affect growth and health of plants growing in complex soils. While the agro-ecological impact of such microbiome feedbacks is well established, their variability by soil context and plant varieties remain unresolved issues. We have established a model system with *Arabidopsis thaliana* to work on these problems. Microbial feedbacks of Arabidopsis vary strongly with soil batches and plant genotype. Using multivariate, correlation and modelling approaches, we identified plant-available iron to explain large parts of the variation of microbiome feedbacks on plants. We demonstrate that beneficial microbiome feedbacks occur mainly at low levels of plant-available iron, i.e. when plants grow in suboptimal soil. The main purpose of Arabidopsis is to learn how plants perceive soil microbiomes and how they modulate their performance in response to complex soil microbiomes. Based on natural variation among Arabidopsis accessions and a screen for genome-wide associations, we found several gene candidates to be associated with microbiome feedbacks. Most advanced is our work on a TNL receptor termed Mediator of Microbiome Feedbacks 1 (MMF1). An update on recent results that point towards the importance of root immune components as genetic determinants for microbiome feedbacks in Arabidopsis will be presented.

Response of *Arabidopsis thaliana* to plant-plant competition

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In natural environments, plants compete with neighboring plants for resources such as light, water and nutrients. To detect neighbors, plants have evolved mechanisms which are poorly understood at the molecular-genetic level. We therefore examine the impact of competition on the growth and reproductive success of *Arabidopsis thaliana* grown in crowded settings together with conspecifics or with the grass *Lolium perenne*. Intraspecific and interspecific competition resulted in strongly reduced shoot branching and silique production. Fertilization did not overcome the inhibitory effect of competition, showing that plants under competition did not experience a lack of mineral nutrients. The reduction in shoot branching correlated with greatly altered gene expression in lateral buds, in particular of hormone- and defense- related genes, while it was independent of the hub transcription factor BRANCHED1. Mutants defective in strigolactone signaling or biosynthesis retained a response to competition. In contrast, mutants in jasmonic acid signalling exhibited a reduced response to competition. We further propose that below-ground communication together with a sensing of soil volume participates in the response to competition.

Metabolic Reprogramming Drives Microbe-Mediated Nitrogen Acquisition

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Plants require substantial amounts of nitrogen (N) to grow and thrive, with N accounting for approximately 3–4% of plant dry matter. To acquire this essential nutrient, plants rely on both direct uptake from the soil and microbe-mediated uptake pathways. Our central hypothesis is that plant metabolism plays a pivotal role in regulating microbe-mediated N acquisition and utilization. First, plants must adjust their N metabolism when interacting with mutualistic symbionts to optimize these beneficial associations. Establishing and maintaining symbiosis requires coordinated changes in carbon (C) and N metabolism, ensuring that both partners benefit from the interaction. Second, the composition of root-associated microbial communities is strongly influenced by plant metabolic dynamics. Our group has demonstrated that the root exudate composition of mycorrhizal maize plants is profoundly altered under N deficiency, indicating that mycorrhization under low-N conditions induces the release of specific "cry-for-help" metabolites that are likely involved in recruiting beneficial microorganisms. We further investigate these metabolites and their functions in shaping the rhizosphere and hyphosphere microbiome. In parallel, we use multi-omics and metabolic modeling approaches to show that arbuscular mycorrhizal fungi colonization under low-N conditions triggers a profound reorganization of both root and leaf metabolism. These metabolic adjustments support the establishment and functioning of the symbiosis while improving plant adaptation to N limitation. This research is expected to provide fundamental insights that will contribute to the development of more sustainable and agroecological cropping systems.

Microbiota profoundly impact poplar host plant metabolites and root exudate content and composition

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Trees are associated with a wide variety of microorganisms that colonize the different tissues of their host. In this study, we examined the establishment of fungal and bacterial communities from roots to shoots in poplar cuttings (*Populus tremula* × *tremuloides*) over a period of 30 days, and the subsequent shaping of plant chemistry by this colonization. Poplar cuttings were planted in either natural or gamma-irradiated soil. We tracked microbial communities across bulk soil, the rhizosphere, roots and shoots using DNA metabarcoding, while we analyzed root exudates and tissue metabolites using gas chromatography-mass spectrometry. Our results showed that the *Populus* microbiome originates in the rhizosphere and evolves over time. The composition of poplar root exudates is also dynamic, and the associated microorganisms greatly reduce the abundance of metabolites in these exudates. Over 70 metabolites, particularly lipid-related compounds and defense molecules, appeared at high abundances exclusively in microbe-free conditions, suggesting that microbes actively modify or consume these secretions early in colonization. Microbial colonization alters the composition of organ metabolites differentially; primary metabolism is predominantly affected in roots and defense metabolism in leaves. Specific poplar metabolites correlate with the abundance of specific microbial taxa. Overall, this study highlights the profound impact of microbial interactions on the metabolic pathways of plants. It demonstrates that commonly observed plant exudate profiles likely reflect metabolites that are not readily consumed and/or highlight the presence of negative feedback following colonization. This study of poplar trees sheds light on the intricate interplay between plants and their associated microbial communities.

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Maize specialized metabolites: their genetic regulation and ecological function in plant herbivory

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Modern crop production relies on synthetic pesticides to protect crops from insect pests, yet widespread pesticide use has significant environmental, economic, and evolutionary costs. Although crop breeding has dramatically improved yield, agronomic performance, and adaptation to modern production systems, it has largely overlooked ecological traits that enable crops to actively participate in self-defense through preformed and herbivore-induced volatile signaling, and recruitment of natural enemies. We are leveraging into plant primary metabolism that leads to the formation of specialized metabolites through multiple metabolic pathways. These include lignins, flavonoids, phenolics, and volatile organic compounds. To characterize their beneficial effects, we have developed and used near-isogenic lines (NILs) to understand the cause of insect mortality when larvae are exposed to maize specialized metabolite overproducer NILs. To fine-tune spatiotemporal biosynthesis and regulation of specialized metabolites in desirable tissues, role of a master regulator required for genetic modifications in plant primary and specialized metabolites will be discussed. By integrating chemical ecology, plant genetics, insect behavior, this research is providing the foundation for breeding cultivars that not only produce high yields but also support ecosystem services and sustainable pest management.

Linking metabolism and environment: discovery of novel enzymes in coumarin biosynthesis shaping stress responses in Arabidopsis

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Coumarins act as important chemical signals in plant responses to environmental challenges, linking specialized metabolism to stress adaptation. Despite their established roles in iron (Fe) acquisition, environmental stress responses, and shaping the root microbiome, the biosynthetic network underlying coumarin production and exudation in *Arabidopsis thaliana* remains incompletely understood. Here, we combine in silico analyses with natural variation, mutant analyses, and multi-omics approaches to uncover new components of coumarin biosynthesis. In a first approach, QTL mapping followed by candidate prioritization identified a UDP-glycosyltransferase (UGT) likely involved in the synthesis of scopolin, the glucosylated form of the major Arabidopsis coumarin scopoletin. Mutant analysis supported by metabolomics under Fe deficiency and osmotic stress revealed UGT-dependent changes in coumarin-related and broader metabolic profiles, linking this gene to glucosyltransferase-mediated adjustment in roots and exudates during stress. In a second, independent approach, phylogenetic and in silico analyses identified candidate enzymes within 2-oxoglutarate- and Fe(II)-dependent dioxygenase (2OGD) family. Selected 2OGDs were functionally characterized through biochemical assays in vitro and mutant analysis in planta, confirming their role in a long-sought step in esculetin biosynthesis. We identify the first O-demethylation reaction in Arabidopsis specialized metabolism and show that enzymes designated as S6OD convert scopoletin to esculetin, contributing to plant performance under limited Fe availability. Together, these complementary strategies uncover new enzymatic components of Fe-responsive coumarin metabolism and connect metabolic diversity to environmental stress responses, providing new insight into the molecular basis of plant–environment interactions.

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Decoding beneficial Plant–Microbe interactions: Citizen science and Omics-Driven Pathways to Sustainable Legume Production

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Our citizen science initiative “Soy in 1000 Gardens” demonstrates how participatory research can accelerate biotechnological innovation in agriculture. By identifying soybean nodulators adapted to local soils, we uncovered nitrogen-fixing strains that excel commercial strains to nodulate soybean when grown in our region. This project highlights how community engagement, industry collaboration, and fundamental science can converge to deliver climate-resilient protein crops for Europe, strengthening agricultural independence in a shifting climate and geopolitical landscape.

Our lab further applies advanced in-field GWAS and integrated plant omics to decode the molecular basis of high-performing soybean–*Bradyrhizobium* partnerships adapted to North-Western European environments.

By bridging fundamental science and applied biotechnology, we seek to find crop solutions that optimize nutrient efficiency and transform molecular knowledge into scalable agricultural innovations.

Phenomic prediction to integrate plant-environment interactions in a cross-year framework for steviol glycosides assessment in *Stevia rebaudiana*

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Breeding of *Stevia rebaudiana* is challenged by the genetic and environmental regulation of steviol glycoside accumulation, requiring extensive phenotyping across genotypes, environments, and growing seasons to identify superior cultivars. Because these traits emerge from plant-environment interactions, developing rapid, scalable phenotyping approaches that capture environmentally responsive biochemical variation is essential for sustainable crop improvement. Near-infrared spectroscopy (NIRS) offers a promising solution, as spectral signatures integrate information on plant metabolism, physiological status, and environmental responses, providing high-dimensional endophenotypes for phenomic prediction (PP). We evaluated a NIRS phenomic prediction-based [1,2] approach for key sweetener-related traits, including stevioside, rebaudioside A, total steviol glycosides, and sweetness-associated compounds. Fifteen spectral preprocessing strategies and five predictive models were assessed using multi-genotype field trials conducted across two growing seasons in Liposthey, France (2017–2018). Model performance was evaluated through repeated within-year validation and independent temporal validation across years. Substantial differences were observed among preprocessing and modeling strategies. Within- year validation highlighted RR-BLUP, GLMNET, and Bayesian Ridge Regression (BRR) as the most promising predictive approaches. Temporal validation revealed lower predictive ability, emphasizing the influence of environmental variation on model transferability. Despite this challenge, some traits and spectral preprocessing strategies remained robust across years. The main findings and their implications for PP under contrasting environmental conditions will be presented. Overall, NIRS PP exploits biochemical signatures arising from plant-environment interactions to accelerate stevia breeding, reduce dependence on destructive analyses, and support the identification of promising elite genotypes across environments. This approach also provides a foundation for future integration with genomic selection and prediction of more complex breeding targets, including yield.

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Designing resistant and durable agroecological apple orchards

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Environmental and health constraints demand agro-ecological orchards that can tolerate a broad spectrum of pests and pathogens while relying on sustainable alternatives to phytosanitary chemicals. Commercial varieties currently offer genetic resistance through a single major allele, a strategy that is rapidly broken down by pathogen evolution. Durable, long-term resistance therefore requires pyramiding complete and partial genetic resistances that engage complementary molecular pathways against multiple threats. We combined mapping populations and diverse germplasm panels to uncover novel resistance sources. Integrating metabolomics, transcriptomics and comparative genomics, we pinpointed candidate genes and metabolites linked to apple resistance. Selected genotypes carrying distinct resistance loci were evaluated in greenhouse trials and experimental orchards combining agroecological levers. Our genetic analyses revealed several new loci conferring genetic resistance to apple scab, fire-blight and rosy aphid. For a subset of these loci, we documented the accumulation of specific triterpenes with putative antifungal activity. Ongoing untargeted metabolomic profiling now extends to a collection of 330 cider-type and heirloom apple varieties. The project will deliver timely insights into the molecular determinants of multi-pest resistance. These results will feed directly into breeding programmes by defining ideotypes, identifying elite progenitors and providing robust genetic- and biochemical markers for selection.

Deciphering mechanisms of service plants involved in the disruption of host plant recognition by a specialist insect herbivore using complementary volatolomic approaches

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Plant volatolome is a very diverse chemical universe which is deeply explored for fragrance and organoleptic applications but also for chemical ecology purposes because of its proven role as mediator in biotic interactions. Especially, olfaction plays a fundamental role in key insect behaviors, such as the search for a suitable host plant. However, these mechanisms are complex and require exhaustive qualitative and quantitative characterization of the volatolome. Crop diversification strategies, including the use of service plants, offer promising tools to manipulate pest behavior by disrupting host recognition. For instance, field experiments have demonstrated that *Calendula officinalis* can disrupt the oviposition behavior of the cabbage root fly, *Delia radicum*, a major specialist pest of brassica crops during their early growth stages. This study aimed to unravel the volatile compounds involved in this disruption. In order to analyze the impact of the interaction between the two species on the characteristics of their volatolome, Volatile Organic Compounds (VOCs) from the service plant, *C. officinalis* and a host plant, *Brassica oleracea* were both trapped in Dynamic Headspace and extracted under vacuum using Vacuum Assisted Sorbent Extraction (VASE) followed by thermal desorption coupled with GC-MS. These two complementary approaches allowed us to largely explore plant volatolome through the collection of naturally emitted VOCS and the exploration of the full emission potential thanks to VASE. Furthermore, only VASE extraction strength allowed us to identify numerous VOCs from *Brassica oleracea* cocultivated with *Calendula officinalis*, which gave us new elements to understand the possible mechanisms underlying this disruption mechanism.

How seeds reshape their specialized metabolome for stress response and adaptation

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Specialized metabolites (SMs) play essential roles in seed quality by modulating developmental processes and enhancing tolerance to environmental stresses. In seeds, SM composition is highly dynamic and responsive to environmental conditions, contributing to protection against desiccation, heat stress, pathogens, and other environmental challenges.

Our research investigates how environmental stresses and nutrient availability reshape the seed specialized metabolome and how these metabolic changes contribute to stress adaptation. Using multi-omics approaches combined with functional genetics, we have shown that seeds of several Brassicaceae species (*Arabidopsis thaliana*, *Camelina sativa*, and *Brassica napus*) exhibit remarkable metabolic plasticity by adjusting their SM profiles in response to changing environmental conditions.

A major focus of our work has been the characterization of seed glucosinolate (GSL) diversity and its functional significance. Published and preliminary data from our groups have identified genes and enzymes involved in GSL side-chain elongation, substantially advancing our understanding of GSL diversity and its ecological function. We have demonstrated that environmental conditions strongly influence seed GSL accumulation and the production of their degradation products. Furthermore, we identified and characterized the gene network responsible for the biosynthesis of newly discovered acylated GSLs under both optimal and heat-stress conditions. These metabolic changes were associated with altered antioxidant capacity and reduced seed performance under stress.

Our results reveal both conserved metabolic responses to environmental stress and genotype-specific regulatory mechanisms that shape seed specialized metabolism. These findings provide new insights into the adaptive significance of GSL diversity and the molecular mechanisms underlying seed quality, stress resilience, and plant defense.

1 + 1 ≠ 2? Combined Biosolutions Reshape Durum Wheat Responses to Multiple Stresses

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Reducing chemical inputs while maintaining crop productivity is a major challenge for sustainable agriculture. Biosolutions, including biostimulants and biocontrol agents, are increasingly considered promising alternatives to improve plant resilience against environmental constraints. However, little is known about their combined effects under multiple simultaneous stresses. This study evaluated the impact of a biostimulant and a biocontrol agent, applied individually or in combination, on durum wheat exposed to *Septoria tritici* blotch (*Zymoseptoria tritici*) and water deficit. Plant phenotypic traits and gene expression profiles were monitored throughout the experiment. Applied separately, both biosolutions enhanced plant performance through distinct mechanisms. The biostimulant promoted early vegetative growth, whereas the biocontrol agent improved chlorophyll content and nitrogen status during later developmental stages. Surprisingly, their combined application did not produce additive phenotypic effects and even reduced several growth-related traits compared with individual treatments, suggesting complex physiological interactions between the two biosolutions. Transcriptomic analyses revealed that the combined treatment specifically induced genes associated with growth, photosynthesis, and defense pathways. This coordinated molecular response indicates a physiological reprogramming that was not fully reflected at the phenotypic level under the tested multi-stress conditions. Overall, our results demonstrate that combining biosolutions generates responses that cannot be predicted from their individual effects. These findings provide new insights into the mechanisms underlying biosolution interactions and highlight the importance of integrating both physiological and molecular approaches to better understand plant adaptation to complex environmental constraints.

Exploring below-ground metabolomic signatures of perennialism in New Perennial Grain lines

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This study [1] investigates the specialized metabolome of roots and the rhizosphere in New Perennial Grains, an area still largely neglected despite the important role of specialized metabolites in plant growth, stress resistance, environmental adaptation, nutrient acquisition, and interactions with microorganisms. New Perennial Grains can regrow for several years and develop an increasingly extensive root system, thus representing a valuable model for studying long-term root–soil dynamics. The research compared four New Perennial Grain lines, 235a, 280b, 11955, and OK72, over four years of growth in a field trail. These were also compared with the annual durum wheat cultivar Ardente and an 11-year-old perennial *Thinopyrum intermedium*. Using an untargeted metabolomic approach, the study identified 2,529 metabolites. In the first year, New Perennial Grain lines showed higher levels of adenine, pseudouridine, and syringic acid than Ardente. These compounds may support improved nitrogen management, while syringic acid is also linked to fungal pathogens resistance. The OK72 line stood out from the other genotypes from the first year, showing higher abundance of metabolites involved in root architecture, systemic resistance, and herbivore defense, such as glutathione, serotonin, and compounds related to α-linolenic acid metabolism. By the fourth year, OK72 remained distinct from the other New Perennial Grain lines and shared with *Thinopyrum intermedium* high levels of purine nucleosides and diazanaphthalenes, compounds with antimicrobial activity. Overall, OK72 showed below-ground traits closer to perennial species, greater pathogen resistance, and a stronger ability to attract beneficial rhizosphere microorganisms, making it a promising parental candidate for breeding programs.

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From defence-related transcripts to metabolomic signatures: chemical modulation of carrot response to biocontrol under heat stress

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Climate change is increasing the frequency and intensity of heat episodes, with potential consequences for plant defence metabolism and the performance of biocontrol strategies. Understanding how elevated temperature interacts with plant defence stimulators is therefore essential for developing sustainable crop protection approaches. Here, we investigated the response of carrot to a bacterial biocontrol product, characterised as a plant defence stimulator, against carrot leaf blight caused by *Alternaria dauci*. An initial screening of 40 cultivated genotypes revealed contrasted levels of protection, highlighting a strong influence of plant genetic background. Based on phenotypic and transcriptomic data, six responsive genotypes were selected for further investigation under optimal and elevated temperature regimes. Transcriptomic analyses identified distinct gene expression profiles associated with heat exposure, treatment response and their interaction, suggesting that thermal conditions reshape induced resistance processes rather than simply attenuating them. To explore the downstream chemical consequences of these transcriptional changes, we integrated UHPLC-HRMS-based metabolomics. Metabolic profiling of treated and untreated plants revealed extensive chemical reprogramming shaped by temperature regime, genotype and treatment. Candidate metabolic features were associated with contrasted protection levels depending on the thermal context, indicating that the chemical expression of induced defence varies according to both plant genetic background and environmental conditions. By connecting transcriptomic and metabolomic layers, this study provides mechanistic insight into heat-dependent chemical signals underlying carrot response to biocontrol and opens perspectives for optimizing crop protection strategies under warming climatic conditions.

Poster Abstracts

P1

Generation of *Botrytis cinerea* Mutants Affected in Putative Pectin-Degrading Enzyme Genes

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Our research focuses on the role of oligosaccharides in the signaling pathways that regulate plant adaptation and immunity in *Arabidopsis thaliana*. To decipher the biological functions of these signaling molecules, we aim to generate highly specific oligosaccharides, particularly oligogalacturonides (OGs) derived from pectin degradation, with defined structural features such as the degree of polymerization and the degree of acetylation. Access to well-characterized Ogs is essential for understanding how their structural diversity influences their biological activity.

To achieve this goal, we seek to establish efficient methods for the production of tailor-made OGs by identifying and characterizing novel carbohydrate-active enzymes. As a source of pectinolytic enzymes, we use *Botrytis cinerea*, a necrotrophic fungal pathogen responsible for gray mold disease. We are expressing selected *Botrytis* proteins that target pectins to determine their enzymatic activities in collaboration of the team of Jérôme Pelloux (BIOPI, Amiens). In parallel, we generate *Botrytis cinerea* mutants carrying deletions in genes encoding these enzymes. These mutants are used to investigate the contribution of the corresponding enzymes to fungal virulence on *Arabidopsis thaliana* and to assess their growth and behavior on pectin-based media. In this poster, we will present the strategy to generate and identify the *Botrytis cinerea* mutants.

Ultimately, this work will provide new enzymatic tools for the controlled production of structurally defined oligosaccharides and improve our understanding of their roles in plant immunity while shedding light on the molecular mechanisms underlying *Botrytis* pathogenicity.

P2

Unveiling rhizosphere chemical interactions through metabolomics: From anoxic stress to pathogen suppression in agricultural systems

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This work summarizes the application of metabolomics as a primary tool to characterize the chemical landscape of the rhizosphere and soil water across different environmental challenges and cropping systems. Understanding these signals is crucial for developing sustainable agricultural practices. We employed advanced analytical workflows, including liquid chromatography coupled with high-resolution mass spectrometry (LC-HRMS), to perform both targeted and untargeted metabolite profiling.

Key findings and examples

- Cover crop bioactivity: In studies of ribwort plantain (*Plantago lanceolata*), we quantified bioactive iridoid glycosides (aucubin, catalpol) and phenylethanoid glycosides (acteoside), identifying their temporal dynamics and potential for suppressing soilborne pathogens like *Rhizoctonia solani*.
- Rhizosphere dynamics: Within the *Cropdrive* project, untargeted soil metabolomics identified over 700 biochemicals in cover crop amended soils with carrot. We observed significant upregulation of benzoxazinones in rye-amended soils and distinct dipeptide profiles in soils challenged with *Sclerotinia* pathogens, suggesting these molecules play roles in microbial signaling or nutrient uptake under stress.
- Environmental stress responses: Soil water metabolomics was used to identify metabolic shifts in ice-encased, anoxic soils. Significant changes in organic acids (e.g. citric and malic acids) and amino acids (e.g. adenine) were detected, reflecting the interplay between plant roots and soil microorganisms in oxygen-depleted environments.

Conclusions: These activities demonstrate that metabolomics provides unprecedented insights into the "chemical language" of the soil-plant system. By linking specific metabolites to soil health and plant protection, we can identify agroecological solutions that reduce dependency on synthetic pesticides and enhance crop resilience in a changing environment.

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[2] Icebreaker (2020-2023) - Reducing the agronomic and economic impact of ice damage on golf courses and other grasslands. Read more at www.nibio.no

P3

Investigating early defensive chemical mechanisms against *Aphanomyces euteiches* in pea and faba bean

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The oomycete *Aphanomyces euteiches* is a major pathogen of legumes, especially pea, causing root rot and that can significantly reduce crop yields. QTL (Quantitative Trait Loci) associated with partial and high levels of resistance have been identified in pea and faba bean, respectively, but the underlying defense mechanisms remain unknown, notably in the early steps of interactions between the plant and *A. euteiches* spores possibly mediated by root exudates. We aimed at characterizing the metabolic profiles of root extracts and exudates from susceptible and partially resistant pea genotypes carrying or not the QTL, as well as from a resistant faba bean genotype. Root tissues and root exudates were sampled from plants grown in a hydroponic device. An untargeted metabolomics approach using UHPLC-Orbitrap mass spectrometry was developed to identify molecular signatures and potential biomarkers for resistance. Multivariate statistical analyses were used to identify differential chemical family compounds produced and/or exuded by the roots. Initial annotation of genotype-discriminating metabolites revealed the presence of peptides, flavones and triterpenoids associated with resistance. Root exudate fractions containing the identified potential biomarkers are being tested on *A. euteiches* mycelium growth on Petri dishes and zoospore motility through a chemotaxis assay using a dedicated microfluidic chip. This study will improve our understanding of the defense mechanisms associated with plant resistance to *A. euteiches*, and will help to identify breeding and biocontrol targets for legume protection against this very damaging disease.

P4

Chemical interactions in Lichens, Bryophytes and non-flowering plants: endophytic fungi as sources of bioactive metabolites

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Ecological interactions influencing the production of bioactive metabolites in plants and their symbiotic partners have been extensively studied, particularly in aromatic and medicinal species. These interactions involve the co-regulation of biosynthetic gene clusters, signaling exchange, and coordinated defensive responses, all of which contribute to the metabolic rewiring of endophytes and highlight plants as reservoirs of ecologically driven chemical diversity. Endophytic fungi, which colonize plant tissues asymptomatically, not only regulate host metabolic networks affecting transcriptional, enzymatic, and signaling pathways linked to primary and secondary metabolism, but also actively contribute metabolites, enzymes, and intermediates to host biosynthetic pathways. This evidence has led to the concept of “hybrid metabolic systems”, where fungal and plant enzymes cooperate to produce structurally novel compounds, or “eco-metabolites,” not synthesized independently by either partner.

Bryophytes, lichens, and other non-flowering plants host highly diverse fungal endophyte communities involved in host physiology, ecological interactions, and natural product biosynthesis. As early colonizers of terrestrial ecosystems, these organisms evolved under intense biotic and abiotic pressures, including pathogens, herbivory, and environmental stress, driving the development of remarkable chemodiversity rich in specialized metabolites associated with defense and stress adaptation. Current evidence suggests that fungal secondary metabolism in symbiotic systems should be interpreted through a microbiome-centered perspective, where long-term co-evolution, ecological specialization, and regulatory plasticity generate chemical novelty. This framework supports the exploration of host-associated fungi as promising sources of new bioactive compounds for pharmaceutical and biotechnological applications [1].

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P5

Versailles Arabidopsis Stock Center (VASC)

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Arabidopsis thaliana is a powerful plant model for functional biology, genetics and, more recently, population genomics. For nearly 30 years, the Versailles Arabidopsis Stock Center (VASC) has been collecting, producing, preserving, characterizing and distributing various Arabidopsis biological resources [1]. Besides large collections of mutants, including homozygous mutant lines, which are used to investigate gene functions, VASC offers numerous natural genotypes collected worldwide, as well as resources resulting from crosses between these variants, which allow the analysis of diversity's impact, particularly on complex plant traits. Most of the resources are unique. They are accompanied by molecular characterization, genotyping or sequencing data, and can be useful to a wide range of users, ensuring cumulative characterization of the same material over time. The collections are made easily and reliably available through an information system comprising a database and a web portal for description and distribution (https://publiclines.versailles.inrae.fr/). Several thousand seed lots are provided each year to the international scientific community, of which around one-third in France and two-thirds abroad. VASC achieved ISO9001 certification in 2024.

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P6

Biosynthesis of fragrant terpenoids from plants you normally disregard

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Bryophytes are the pillows in the forest with numerous ecological functions, and they produce a huge variety of specialized metabolites. Liverworts in particularly produce interesting fragrant terpenoids, which attract microarthropods to help with sperm cell distribution. The knowledge about the production of fragrances among bryophytes is scarce, thus we have embarked on projects to identify novel terpene synthases and other enzymes part of the terpenoid profiles. In liverworts microbial-like terpene synthases plays a crucial role in the synthesis of smaller terpenoids. We have established the biosynthesis of several fragrant terpenoids from *Frullania tamariscii*, *Nardia scalaris,* and *Lophocolea bidentata*. In *F. tamarisci* we established the biosynthesis of tamariscol, a fragrance that was patented for the use in perfumes in 1985 [1,2]. We have established several fragrant *Physcomitrium patents* lines, expressing these enzymes to study the *in-planta* function along with transient expression in *N. benthamiana*. The aim is to show elucidate terpene biosynthesis in bryophytes and identify the crucial ecological functions.

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P7

Hydropriming of tomato seeds with *Ribes nigrum* and *Juniperus communis* extracts promotes plant growth and modulates metabolism

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The increase in demand for sustainable crop management has found in plant-based biostimulants a promising alternative to classical agrochemicals. Seed priming technology by using phytoextracts from aromatic and medicinal plants offers a strategy to improve seedling performance and tolerance under stress conditions, even though the mechanism underlying their activity remains poorly understood. In this study we investigated the effect of hydropriming on tomato seeds (*Solanum lycorpersicum* cv Sailor) with *Ribes nigrum* (blackcurrant) and *Juniperus communis* (juniper) hydroalcoholic extracts: morphological development, stress molecular markers and fruit parameters have been evaluated, by combining in vitro, phytotron and greenhouse trials. Hydropriming with both extracts promoted vegetative growth, with distinct morphological responses. Transcriptomic profiling by RNA-seq was conducted at two different developmental stages on plants grown from hydroprimed seeds, to identify changes in gene expression associated with the exposure to extracts. Biochemical analyses were performed on early germination stages, under salt stress conditions, to assess the impact of priming in stress resilience: this approach revealed treatment-dependent modulation of malondialdehyde (MDA) and antioxidant enzyme pattern (SOD, POD, CAT). To pinpoint the constituents/fractions mainly responsible for the bioactivity, different fractions obtained by separating the two extracts with HPLC were tested independently. Obtained results support the potential of phytoextracts as holistic and sustainable tools for crop management.

P8

Unravelling the molecular network involving microRNA in seed dormancy and leaf senescence in response to temperature

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Seeds are at the core of agriculture and biodiversity, with germination and seedling emergence strongly influencing crop productivity. However, the global climatic changes adversely affects gemination physiology and agroecosystem performance. In parallel, leaf senescence significantly contributes to seed filling and plant productivity by ensuring efficient nutrient remobilization, primarily nitrogen (N), from aging leaves to developing organs including young leaves, flowers and seeds. However, despite the well-documented role of microRNAs (miRNAs) in various plant developmental processes, their involvement in coordinating leaf senescence with seed quality traits remains largely unexplored. The analysis of transcriptome and small RNA-sequencing data libraries from *Arabidopsis thaliana* seeds produced at different maternal temperatures identified ten candidate miRNAs showing differential expression in dry and imbibed seeds. Overexpression (OE lines) and knockdown (STTM lines) mutant lines of the selected miRNAs were generated in Arabidopsis for functional characterization. Notably, OE lines of two miRNAs (miR-I and miR-II) displayed premature leaf senescence, whereas their knockdown (STTM lines) results in delayed senescence. Dry seeds of these lines also showed variation in N and C content. Additionally, 15N labelling followed by assessment of 15N revealed a significant difference in biomass, N and 15N allocation which ultimately accounted for differential N remobilization efficiency and N use efficiency between the OE and STTM lines of miR-II. Future work includes characterization of molecular functions of miR-I and miR-II in leaf senescence and seed traits and cross-talk with environmental factors. This study aims to uncover regulatory mechanisms linking senescence and seed maturation/dormancy, providing insights for improving crop productivity.

P9

Identification of RD29 as a new cargo of autophagy using proteomic and artificial intelligence

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Macro-autophagy is a conserved eukaryotic mechanism that degrades cytoplasmic components via autophagosomes, recycling nutrients and maintaining cellular homeostasis. In plants, autophagy is essential for nutrient remobilization, stress adaptation, and organelle turnover, with the ATG5-ATG12 conjugation system and ATG8-PE complex playing pivotal roles in autophagosome formation and cargo targeting. This study investigated proteomic changes in *Arabidopsis thaliana* wild-type (WT) and atg5 mutant leaves subjected to dark stress, mimicking senescence. Dark treatment induces autophagy gene expression and led to a decline in chlorophyll and protein concentrations in both genotypes. Proteomic analyses identified 2,297 differentially abundant proteins, revealing similar metabolic shifts in WT and atg5: decreased primary metabolism (carbon, amino acid, and energy pathways) and increased water transport proteins (e.g., aquaporins). However, atg5 mutants exhibited exacerbated accumulation of proteins linked to translation machinery, stress responses, and endoplasmic reticulum (ER) proteins, suggesting defective ribophagy and ER-stress management. Clustering of proteomic data highlighted genotype-specific responses. As atg5 mutants are impaired in protein recycling we found many proteins over-accumulated in atg5, amongst which were hypothesized autophagy cargoes. Using AlphaFold2 simulations, we identified high-confidence interactions (iPTM > 0.65) for several proteins amongst which RD29A. Yeast two-hybrid (Y2H) and bimolecular fluorescence complementation (BiFC) assays confirmed interactions between RD29A and ATG8h/i. We showed that interaction with ATG8i is dependent of the LDS and UDS sites, thus validating the stress-responsive RD29A protein as a selective autophagy cargo.

P10

Herbivory and Plant–Plant Signaling Shape Volatile Emissions and Oviposition Responses in Tomato

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In a previous study, we demonstrated that wild and cultivated tomatoes release markedly different volatile profiles, and these differences may play a crucial role in the oviposition preference of the insect herbivore *Tuta absoluta*, which tends to favor cultivated plants. In the present research, our first objective was to evaluate whether herbivory by *T. absoluta* larvae modulates the volatile composition of wild (*Solanum habrochaites*) and cultivated tomato (*S. lycopersicum* cv. Santa Clara), and whether these herbivory-induced changes influence the oviposition preference of *T. absoluta*. Our results showed that damage by *T. absoluta* increased the total amount of volatiles released and altered the abundance of specific compounds in both *S. habrochaites* and *S. lycopersicum*. In terms of oviposition, *T. absoluta* consistently preferred healthy plants over infested ones, and cultivated *S. lycopersicum* over *S. habrochaites*. Since herbivory-induced volatiles may serve not only as cues for herbivores but also as airborne signals perceived by neighboring plants, we next investigated whether volatiles emitted by infested and non-infested *S. habrochaites* and *S. lycopersicum* could modify the volatile phenotype of neighboring healthy *S. lycopersicum* plants through aerial exposure in paired chambers, and subsequently influence *T. absoluta* oviposition behavior. We found that exposure to volatiles from non-infested *S. lycopersicum* altered the volatile profile of neighboring healthy plants and increased *T. absoluta* oviposition. Together, these findings indicate that direct herbivory and volatile exposure can both shape plant volatile emissions, with contrasting consequences for *T. absoluta* oviposition behavior.

P11

Uncovering the molecular basis of allelopathy in *Arabidopsis thaliana* using an innovative phenotyping assay and Genome-Wide Association mapping

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Pesticides have been extensively used for weed and pest management to boost agricultural productivity, resulting in serious environmental and health concerns. Therefore, there is an urgent need to transition towards sustainable, agroecological strategies. Among the environmentally friendly alternatives is allelopathy, a natural process referring to the direct or indirect, positive or negative effects of one plant on another, through the release of chemical compounds (allelochemicals) into the environment [1]. While research on allelopathy has primarily focused on the isolation, identification, release pathways, and mode of action of allelochemicals, comparatively little attention has been given to the genetic basis underlying allelopathic interactions [2].

In this study, we aimed to determine the genetic architecture underlying rhizospheric allelopathic interactions in *Arabidopsis thaliana*. In order to phenotype the allelopathic effects, we first developed a robust plant-soil feedback (PSF) assay, leveraging a high-throughput phenotyping robot [3] to precisely quantify allelopathic interactions. Using this PSF assay combined with a GWA mapping using a mixed linear model, coupled with a local score approach, we identified QTLs involved in allelopathic effects at the gene level. This strategy enabled us to highlight specialised metabolites as key factors in rhizospheric allelopathic interactions in Arabidopsis. The role of one candidate locus, encoding an allantoate amidohydrolase has been explored more deeply.

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P12

Modeling *Dickeya dadantii* organ-specific infection and defense response activation in tomato via signal transduction networks

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In the current agricultural context, it is more than necessary to develop sustainable solutions to protect the cultures whilst limiting the use of chemicals. Among the crops affected by these challenges, tomato (*Solanum lycopersicum*) is a high-value crop highly susceptible to *Dickeya dadantii*, a versatile pathogen causing soft rot through tissue decay, capable of infecting stems, leaves, and roots, growing anaerobically, and establishing asymptomatic infections that act as silent contamination reservoirs [1]. However, the molecular mechanisms underlying this host-pathogen interaction remain poorly understood, limiting the development of targeted solutions. To overcome this challenge, the development of regulatory networks now represents a significant advance among innovative *in silico* approaches [2], offering the possibility of studying the complex interactions between the plant and its pathogens. During this PhD project, three regulatory networks will be developed: i) a module regulating organ development and growth cycle such as stem and root elongation, leaf and lateral roots initiation, flowering time; ii) a regulatory network of the plant immune's system incorporating hormonal signaling pathways; and finally iii) *Dickeya dadantii*'s virulence regulatory network. All modules will be connected to represent organ-specific infection, hormonal crosstalk, and growth/defense trade-off. Dual RNA-seq data from both bacterial and plant transcriptomes during infection will be used to validate the predicted networks. This will be a key tool in understanding how *Dickeya dadantii*'s infection is perceived by the plant and impacts the plant growth and health in an organ-specific manner.

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P13

Investigating the role of continuous cell wall remodelling in hydathode immunity and microbiome composition

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Hydathodes are specialized leaf-margin glands that exude xylem sap as droplets when its influx exceeds the evapotranspiration rate, a phenomenon known as guttation. Hydathodes consist of tracheids supplying a specialized tissue of small, thin-walled cells—the epithem—connected to permanently open water pores, forming a direct interface between the vascular system and the environment. Because guttation fluid provides favourable conditions for microbial growth, hydathodes are privileged entry points for vascular pathogens causing systemic diseases, such as *Xanthomonas* (*Xcc*). In response, plants have evolved defence mechanisms to limit pathogen colonisation and invasion through hydathodes, although the underlying immune processes remain poorly understood. We hypothesise that continuous cell wall remodelling in the epithem generates cell wall–derived elicitors (oligosaccharides,OS) that may shape the hydathode microbiome by promoting beneficial microorganisms and restricting pathogen development. We are analysing the OS composition of guttation fluid using oligoglycomic LC–MS approaches to investigate their potential roles in triggering defence responses or affecting microbial growth. We will also characterise associated signalling pathways involving receptors and pectin methylesterases (PMEs) localised in *Arabidopsis thaliana* hydathodes. This should allow us to determine whether PME-mediated pectin demethylesterification promotes pectin degradation in the epithem, generating oligogalacturonides that could keep the hydathodes defenses continuously activated.

P14

Production of bioactive molecules via microbial conversion of plant biomass to improve plant resilience

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The use of plant protection products has boosted agricultural production over the past 70 years, but it also entails risks for human health and the environment. Pesticides harm biodiversity and the sustainability of agricultural systems, while nitrogen fertilizers pollute air and water. To meet these challenges, the agricultural sector is turning to sustainable practices such as integrated crop protection, supported by initiatives like the EU's ECOPHYTO plan, aimed at reducing pesticide use while maintaining optimum production. The search for environmentally-friendly biosourced compounds is thus becoming crucial to improving plant resilience. In this context, the main ambition of the RAMBO project is to produce biocontrol and biostimulation molecules, and thus reduce the use of pesticides and fertilizers, thanks to the microbiological bioconversion of plant biomass (BM). Fungi and nitrifying bacteria from endogenous flora will be used as versatile cellular factories to convert plant BM - a renewable, abundant and local source of carbon and nitrogen - into high value-added molecules. The BM used will be *Miscanthus*, a plant with a short growing cycle, requiring no pesticides or fertilizers, mainly used for non-food purposes, and whose industry is highly structured at national level. By exploring fungal biodiversity, RAMBO will identify fungal strains with the strongest capacity to grow on *Miscanthus* mulch and produce cocktails of molecules enriched in bioactive compounds such as oligosaccharides (OS), secondary metabolites (MS) and peptides (Pept). These cocktails will be tested for their ability to stimulate growth and/or resistance to pathogens in maize, a plant of major agronomic interest in France. The approach and results obtained in RAMBO could subsequently be extended to other crops.

BM : biomass, OS : oligosaccharides, MS : specialized metabolites, Pept : peptides, BC : Biocontrol BS : Biostimulation

P15

The genus of *Lasiodiplodia*, a rich source of bioactive secondary metabolites, involved in plant and environmental interactions

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Lasiodiplodia is a well-known phytopathogen from the family *Botryosphaeriaceae* associated with numerous plant diseases on a wide variety of hosts. Before the introduction of DNA sequence-based methods, this genus was treated as monotypic and characterized only by *L. theobromae* [1]. The widespread use of biomolecular markers for fungal identification has led to the proliferation of new species belonging to the genus, such as *Lasiodiplodia pseudotheobromae*, *Lasiodiplodia mediterranea*, *Lasiodiplodia exigua*, *Lasiodiplodia venezuelensis* and *Lasiodiplodia brasiliensis* [2,3]. Fungi of this genus are great producers of secondary metabolites originated from different pathway of secondary metabolism. The production of these compounds is related to their involvement in the virulence of the fungus, in mediating biochemical communication or in nutrient acquisition. Investigations on the biosynthetic potential of these fungal species pursue two different aims: 1) a better understanding the interaction between host and pathogen to fight diseases caused by these fungi; 2) the identification of new compounds for applied field. In this regard, *Lasiodiplodia* spp. have been recognized as a good source of promising compounds (over 270 compounds) including both low and high molecular weight compounds such as cyclopeptides, depsidones, exopolysaccharides, jasmonates, and preussomerins with a broad spectrum of biological activities (i.e., anticancer, antimicrobial, anti-inflammatory, cytotoxic, and phytotoxicity) that attracted the attention of researchers for their potential biotechnological applications [4-6]. In the present communication, a comprehensive description of most relevant secondary metabolites produced by *Lasiodiplodia* spp. will be reported.

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P16

Quantifying load and taxonomy of arbuscular mycorrhizal fungi in plant roots by long-read sequencing

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Root colonization by arbuscular mycorrhizal fungi is commonly assessed in studies investigating the relationships between mycorrhizae and root exudates of colonized plants. This assessment is generally time-consuming, as it involves a staining protocol followed by manual counting under a microscope. Although inexpensive, this method requires the trained eye of an expert and is therefore subject to observer bias. Moreover, in the absence of automation and standardization, it remains difficult to conduct large-scale experiments within a reasonable timeframe. More limitingly, microscopy lacks taxonomic resolution, constraining our ability to link variation in root exudates with changes in mycorrhizal community composition.

To overcome these limitations, we are developing host-associated microbial PCR (*hamPCR* [1]) with long-read sequencing to study arbuscular mycorrhizal fungi. *hamPCR* is based on the co-amplification of a single-copy host gene and the SSU–LSU region of the ribosomal DNA for the fungi in complex DNA samples of colonized plant roots. This co-amplification enables estimation of fungal load relative to host DNA abundance. Further, the sequence of the fungal amplicon is then used for the taxonomic identification of mycorrhizal fungi within the host. The principle of the method, its main challenges, and its potential applications in chemical ecology will be presented in the context of studying mycorrhizal colonization across different maize genotypes.

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P17

Exploring the role of volatile organic compounds from aromatic plants to disrupt interactions between grapevines and *Scaphoideus titanus*

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Flavescence dorée (FD) is a phytoplasma disease threatening European grapevines. The leafhopper *Scaphoideus titanus* is the primary vector of FD, and its management relies only on pesticides. To reduce this reliance, I aim to understand how volatile organic compounds (VOCs) from aromatic plants mediate plant defences and disrupt vector behaviour. I will investigate how different thyme chemotypes influence behavioural and physiological interactions between grapevine cultivars and *S. titanus*. Thyme chemotypes synthesise large amounts of VOCs that may prime neighbouring plants or directly affect pest behaviour. First, I will compare the host suitability of four grapevine cultivars differing in their susceptibilities to FD. Short-term host preference of *S. titanus* will be evaluated using two-choice assays on whole plants and leaf discs. Long-term acceptance and host suitability will be evaluated in cages by measuring fitness proxies (e.g. survival, development). Second, feeding behaviour of *S. titanus* is a key step in phytoplasma transmission; therefore, I will use electropenetrography (EPG) to assess phloem access and ingestion on four cultivars, characterising resistance to the pest. Third, I will assess the effects of thyme VOCs on *S. titanus* behaviour and performance. The most and least susceptible cultivars to FD will be pre-exposed to different thyme chemotypes. EPG and performance assays will then determine whether thyme VOCs induce resistance in grapevine, altering feeding behaviour or reducing pest performance. This aims to identify cultivar x chemotype combinations capable of improving pest management of *S. titanus*, contributing to sustainable agricultural solutions.

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P18

Possible interactions of Water Lettuce (*Pistia stratiotes*) with aquatic photoautotrophs

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This study has been undertaken to investigate the allelopathic potential of *Pistia stratiotes* spent medium on isolated eukaryotic algae strains. The tested green algae isolates were *Chlorella sorokiniana*, *Chlorella vulgaris*, *Monoraphidium griffithii*, *Monoraphidium pusillum*, *Coelastrum sphaericum*, *Desmodesmus communis*, *Scenedesmus obtusus* and *Tetradesmus obliquus*. Control green algae cultures in Jaworski's medium, *Pistia* Spent Medium (PSM) and *Pistia* Spent Medium supplemented with nutrients (PSM+N) were inoculated with the isolated strains to investigate the allelopathic effect. From the experimental results, all isolates were able to grow in *Pistia* spent medium, but growth was inhibited in all cases compared to control cultures. The results showed that *Pistia* spent medium contains algistatic compounds. The inhibitory effect appears to be strongly species-specific, as there are significant differences even between closely related species. The present study aimed to evaluate the algae strains growth and algae strains physiology (chlorophyll-carotenoid ratio). The growth of the cultures was followed microscopically by counting the individual numbers with Neubauer counting chamber. Algal strains of *Chlorella vulgaris*, *Monoraphidium pusillum* and *Chlorella sorokiniana* showed clear growth inhibition in PSM medium compared to the Control, suggesting that *Pistia* contains allelopathic compounds. The Chlorophyll carotenoid ratios were measured by Spectrophotometry. In the algal strains physiology of the experiment *Chlorella sorokiniana*, *Chlorella vulgaris* of the strains of inhibited and non-inhibited algal strains of *Desmodesmus communis*, *Monoraphidium griffithii* showed inhibition by chlorophyll-carotenoid ratio. The study reveals that *Pistia* spent medium holds the capacity to alter algal community structures even if the physical plant is no longer present. It can directly suppress specific isolated algal strains. Thus, allelopathic compounds present could be a reason for inhibition.

Keywords: *Pistia stratiotes*, Allelopathic compounds, Algal strains, *Pistia* spent medium

P19

Screening of the interactions between phytobeneficial bacteria and rapeseed cultivars with contrasting degrees of sensitivity to broomrape

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Branched broomrape (*Phelipanche ramosa* L.) is a parasitic plant that infests many crops of agricultural importance, including rapeseed (*Brassica napus* L.) [1]. It causes significant yield losses worldwide, yet there is currently no effective control method [2]. Some existing commercial rapeseed cultivars are highly sensitive to the parasite, while others are more tolerant. The criteria influencing the degree of sensitivity are not fully understood. Thus, it is unclear whether sensitivity is strictly linked to genotype or if the soil microbiome plays a role as well. In this study, a screening of the interactions between a plant-beneficial bacterial strain, that can naturally occur in the rapeseed rhizosphere, and rapeseed cultivars was conducted. In total, sixteen cultivars with contrasting degrees of sensitivity to broomrape were cultivated *in vitro* for two weeks, inoculated or not with the strain. Potential germination-inducing factors (GIFs), which are documented in the literature as stimulating the germination of broomrape seeds, were extracted from the roots of rapeseed plantlets and quantified using gas chromatography and mass spectrometry. Furthermore, the colonization of the roots by the strain, that was transformed to constitutively express red fluorescence, was estimated. The study aimed to assess the strain's ability to regulate the quantity of GIFs in the roots and whether the quantity of GIFs and colonization are linked to the degree of cultivar sensitivity to broomrape. Overall, we observe that bacterial-driven GIF production and bacterial colonization intensity do not correlate with the cultivars' sensitivity to *P. ramosa*.

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P20

Role of microbiota and mycorrhizal fungi in *Zea mays* L. performance under low nitrogen condition.

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Maize (*Zea mays* L.), the world's most produced crop, requires nutrients, particularly nitrogen, to grow. To achieve target crop yields, farmers use large amounts of nitrogen fertilizers that are detrimental to the environment. Moreover, fertilizer prices are increasing, stressing the urgent need to innovate toward more sustainable agriculture and change agricultural practices. Maize is able to establish symbioses with arbuscular mycorrhizal fungi (AMF), which can provide water, phosphate, and nitrogen to the plant while also protecting it from (a)biotic stresses. In exchange, maize provides photosynthates. Maize is also colonized by a diverse microbiota comprising bacteria and fungi, which structure is strongly influenced by keystone taxa such as AMF. Root-associated microbes can enhance plant growth through different mechanisms. A promising approach is to exploit beneficial interactions between plants and their microbiota as an agroecological lever to reduce inputs. By analyzing the natural root-associated microbiota of a wild type maize genotype and its mycorrhiza-deficient mutant, combined with the isolation and screening of a maize root-associated bacterial collection, we are able to select bacteria that are associated with mycorrhizal fungi and have beneficial effects on the plant. The assembly of these bacteria into synthetic bacterial communities (SynCom) and their inoculation on plants is our main strategy to engineer maize microbiota. In this poster, the analysis of the natural microbiota by metabarcoding (bacterial 16S and fungal ITS) and the screening of the bacterial collection are presented and the next step of the project are discussed.

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PARSADA METASERV project

Development of Generic Resources and Tools for the Selection and Deployment of Service Plants Against Pests and Diseases

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The gradual withdrawal of active phytopharmaceutical substances across Europe places several French agricultural sectors in situations of technical deadlock regarding pest and disease management. Among the available alternatives, service plants (SPs) are attracting increasing interest due to their ability to regulate pests and diseases. However, their mechanisms of action, performance under varying pedoclimatic and agronomic conditions, and deployment requirements remain insufficiently characterized and poorly standardized across sectors. In this context, the METASERV project, a PARSADA awardee funded by FranceAgriMer, aims to develop generic resources, methods, and tools for the evaluation and deployment of service plants against pests and diseases. Building on the achievements of the PS-CREA network, the project seeks to strengthen connections between fundamental knowledge, agronomic evaluation, and practical applications. Over a five-year period, METASERV brings together a cross-sector consortium to study a preselection of 26 service plant species across diverse cropping systems, targeting the regulation of root-knot nematodes, soil-borne and airborne fungal pathogens, insect pests, and weeds. The project is based on an integrative traits-functions-services approach. Three complementary levels of investigation are implemented: (i) controlled-environment experiments aimed at identifying and quantifying the biological mechanisms involved in pest and disease regulation; (ii) field experiments simultaneously assessing both services and disservices in contrasting cropping systems; and (iii) omics approaches to characterize the molecular determinants associated with functions of interest. Special attention is given to potential disservices linked to service plant use (nutrient competition and visuses reservoirs). By its end, METASERV aims to deliver a harmonized methodological framework for service plant evaluation, open and interoperable knowledge bases, and operational resources for stakeholders across agricultural sectors (technical guidelines, decision-support tools). More broadly, the project seeks to improve understanding of the biological and agronomic determinants governing the use of service plants as a lever for pest and disease regulation.

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From Seed Exudates to Agroecological Innovation: Harnessing Common Bean Spermosphere Peptides for Biocontrol

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Seeds are critical for plant reproduction, dispersal, and agricultural productivity, with seed quality and vigour determining germination and early seedling establishment. During germination, seeds release a complex mixture of compounds into the spermosphere, a dynamic microenvironment mediating interactions with soil microbial communities. Among these, peptides are increasingly recognized for their potential roles in plant–microbe interactions. While plant-derived peptides can influence microbial diversity and exhibit antimicrobial properties, the contribution of seed-exuded peptides remains largely unexplored. In this study, we present the first characterization of the spermosphere peptidome, using seeds from eight genotypes of common bean (*Phaseolus vulgaris* L.) cultivated in two contrasting production regions. The protein-rich nature of common bean seeds provides an ideal model for investigating peptide diversity released during germination. Through untargeted LC-MS/MS-based peptidomic analysis, we identified 3,258 peptides derived from 414 precursor proteins, offering novel insights into the peptide composition of the spermosphere and laying the foundation for understanding their roles in biotic interactions during this critical phase. To explore their functional potential, we used the CAMP (Collection of Anti-Microbial Peptides) prediction platform alongside an in-house AI-based classifier to screen the identified peptides. We selected 20 candidate antimicrobial peptides (AMPs) with the highest predicted activity scores for validation. In-vitro assays demonstrated antimicrobial activity of several peptides against bacterial and fungal plant pathogens, including seed-infecting species. These findings shed light on the previously uncharacterized spermosphere peptidome and reveal a novel reservoir of naturally exuded bioactive peptides as promising sustainable alternatives to synthetic pesticides in agriculture.

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Role of the arbuscular mycorrhizal fungi and its hyphospheric microbiota in maize nitrogen nutrition: an agroecological lever for reducing the inputs

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The world population is expected to approach 10 billion by 2050, increasing the pressure on agriculture to sustain crop production while reducing its dependence on nitrogen fertilizers and their environmental impacts. Harnessing plant-associated microbiota to improve nitrogen use efficiency (NUE) represents a promising strategy to address this challenge. Arbuscular mycorrhizal fungi (AMF), which colonize the roots of most terrestrial plants, including maize (*Zea mays*), can enhance plant nutrient acquisition through their extensive extraradical mycelium (ERM). In particular, inoculation with *Rhizophagus irregularis* has been shown to improve maize nitrogen nutrition. However, the metabolic capacities of AMF alone are limited for mobilizing key soil nutrients, suggesting that their contribution to plant nutrition may also rely on microorganisms inhabiting the hyphosphere, the soil niche directly influenced by the ERM. Hyphosphere-associated bacteria (HABs) can perform functions involved in nutrient mobilization that complement those of the fungus. This project aims to determine whether *R. irregularis*, in association with maize under low-nitrogen conditions, recruits specific bacterial taxa and nitrogen-related functions within the hyphosphere. By comparing hyphosphere bacterial communities across three soils with distinct agricultural histories, we will investigate whether AMF-associated microbial recruitment is conserved across different soil microbiomes or is soil-dependent. Ultimately, this work will identify bacterial candidates and functions that could be assembled into a synthetic microbial community designed as a biostimulant to improve maize nitrogen nutrition while reducing fertilizer inputs.

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Use of lipid nanocapsules for the formulation of an antimicrobial peptide as an alternative to conventional pesticides for seed treatments on rapeseed

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Seed lots for agricultural use must meet strict physiological and sanitary quality criteria. For several decades, maintaining seed vigour has relied largely on the direct application of synthetic pesticides, particularly to control damping-off during germination and seedling establishment. Due to their adverse environmental impact, many active substances have already been withdrawn from the market. Within the framework of the SUCSEED research project, biodegradable molecules with low persistence have been identified. These molecules possess antimicrobial properties and are promising candidates for the agricultural transition towards progressively reducing synthetic plant protection products derived using conventional chemistry. Nevertheless, identifying these active and biodegradable molecules represents only a first step. A major technological bottleneck remains regarding the preservation of their biological activity during, and following, application to seeds. One strategy explored to address this challenge relies on the use of lipid nanocapsules: oil nanodroplets that are able to encapsulate and deliver active compounds with a wide range of physicochemical properties. Lipid nanocapsules promote interaction with biological surfaces and regulate the release of transported molecules over time. Results of particle size and surface charge characterization highlight the existence of a stable association between the lipid nanocapsules and molecular actives tested. Furthermore, nephelometry analyses of the *in vitro* biological activity of active molecules against the necrotrophic fungus *Alternaria brassicicola* were found to be enhanced when they formulated with lipid nanocapsules. These findings confirm, therefore, the strong potential of lipid nanocapsules to contribute to the next generation of seed treatments.

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