SPS
Saclay Plant Sciences

université
PARIS-SACLAY

CEPLAS
Cluster of Excellence on Plant Sciences

SPS-CEPLAS Summer School 2024

« Plant science to tackle climate change »

June 16-21, 2024
Saint-Lambert-des-Bois, France

Participant's guide

Contents

Organizers / Sponsors 2

Venue / Hotel 3

Important information 4

Travel instructions 5

Planning at a glance 6

Program 7

Abstracts 14

Speakers and Organizers 34

Organizers

SPS Saclay Plant Sciences | université PARIS-SACLAY

CEPLAS Cluster of Excellence on Plant Sciences

Sponsors

université PARIS-SACLAY | GRADUATE SCHOOL Biosphera

Sciences Université Paris Cité

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Venue

Centre Port-Royal
Chemin du Charme et du Carrosse
78470 Saint-Lambert-des-Bois
Tel: +33 (0)1 30 12 17 12
accueil@centreportroyal.com

Contact person

Michael Hodges: + 33 (0)6 89 26 71 67

Important information

Arrival of the participants - Sunday June 16

A bus will take you from the RER B station «St Rémy-lès-Chevreuse» to the Centre Port-Royal at 3 PM. To take the bus, wait in front of the station.

Do not be late for the bus.

The Summer School will begin at 4 PM.

Do not forget to bring a laptop (and the corresponding charger).

Activities on site

Please note that the Summer School location is in the countryside, isolated from any town. Be sure to take with you any item you need as well as casual clothes, comfortable shoes and a raincoat.

There may be a lot of mosquitoes so you might want to bring repellent sprays.

End of the Summer School - Friday June 21

On the last day of the Summer School, the rooms have to be vacated after breakfast. Make sure your things are packed and ready on time. Your luggage will be stored in a dedicated room close to the reception desk.

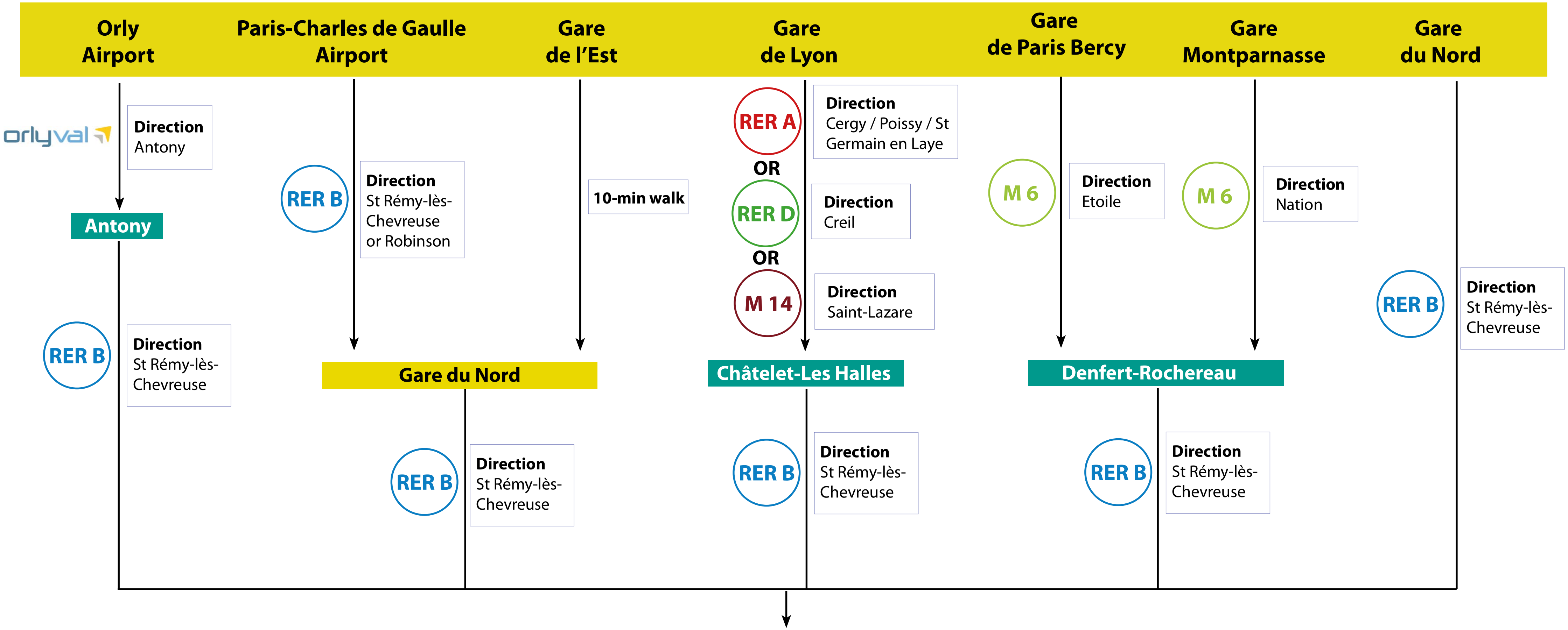
The Summer School will end around 4:30 PM.
A bus will also take you back to the RER B station «Saint-Rémy-lès-Chevreuse» after the Summer School. The bus will leave at 5 PM sharp.

Those of you who have their flight / train a little early in the evening of June 21 might want to leave earlier and take a taxi to Saint-Rémy-lès-Chevreuse (you can carpool). If so, you can ask the reception staff of the Centre Port-Royal to make a taxi reservation for you. But you will have to pay for the taxi and get reimbursed by your lab.

Travel instructions
> RER B station «Saint-Rémy-lès-Chevreuse»

Transports in Paris area

https://www.ratp.fr/en/
https://www.iledefrance-mobilites.fr/en



Saint-Rémy-lès-Chevreuse

A bus will take you:

- **from the «Saint-Rémy-lès-Chevreuse» station to the Summer School location at 3PM on June 16**
- **from the Summer School location to the «Saint-Rémy-lès-Chevreuse» station at 5PM on June 21**

!! Warning !!
> Make sure the train or RER you take stops at the station you need to get off at (stops are indicated on screens or light panels).
> There might be construction works on the different metro or RER lines indicated above, which may perturb traffic.

Planning at a glance

	Sunday June 16	Monday June 17	Tuesday June 18	Wednesday June 19	Thursday June 20	Friday June 21
8 AM				8:30 AM Bus		
9 AM		9 AM Session « Reducing N inputs & improving NUE »	9 AM Session « Carbon: capture & sequestration »		9 AM Session « Plant resilience to climate change»	9 AM Session « Future research practices & opportunities »
10 AM				10 AM Visit to the Fontainebleau Palace & Gardens Packed lunch		
11 AM						
12 PM		12:30 PM Lunch	12:30 PM Lunch		12:30 PM Lunch	12:30 PM Lunch
1 PM						
2 PM		2 PM Workshop « Communication & outreach »	2 PM Workshop « Communication & outreach »	2 PM Bus 2:30 PM Visit to the Barbeau Forest Field Station	2 PM Workshop « Communication & outreach »	2 PM Workshop Presentations
3 PM						3 PM Break 3:30 PM Closing discussion Round table
4 PM	4 PM Welcome Climate change & agriculture talks	4 PM Break 4:30 PM Poster sessions Poster prize Discussions « Apéro »	4 PM Break 4:30 PM Climate Fresk	4 PM Bus	4 PM Break 4:30 PM Session « Plant resilience to climate change»	4:30 PM End of the school
5 PM						
6 PM	6 PM Flash talks: Getting to know each other			6 PM Using the field station data	6 PM Pétanque Tournament	
7 PM				7 PM Bus 7:30 PM Dinner at a restaurant		
8 PM	8 PM Dinner	8 PM Dinner	8 PM Dinner		8 PM Dinner	
9 PM						

Program

Sunday June 16

4 PM – 4:15 PM: Welcome introduction

4:15 PM – 6 PM: Opening talks

Andreas Weber (Institute of Plant Biochemistry, Heinrich Heine University Düsseldorf - Düsseldorf, Germany)
"The role of plants in the global carbon cycle and in climate change mitigation" - *In this talk, I will highlight the urgent need to address anthropogenic carbon emissions and achieve net zero emissions to mitigate the impacts of climate change. I will emphasise the crucial role of plants and agriculture in carbon capture and sequestration, as well as the importance of sustainable practices such as agroforestry and carbon farming. The presentation will discuss strategies to avoid, adapt and mitigate greenhouse gas emissions from different sources, including methane, nitrous oxide and carbon dioxide. I will highlight the importance of increasing crop yields per unit area to avoid land use change and the need for sustainable intensification of agriculture. The presentation calls for interdisciplinary research and collective action in plant sciences to address the challenges of climate change and to align crop production with carbon farming goals.*

Heribert Hirt (King Abdullah University of Science and Technology - Saudi Arabia)
"PlantACT!: A global think tank for plant science-based solution to the climate crisis" - *Current agriculture and land use contributes to up to 25 % of total GHG emissions. Therefore, plant scientists are at center stage to find possible solutions to a transition to sustainable agriculture and land use. The PlantACT! initiative lays out a road map in which areas and how plant scientists can contribute to find plant science-based solutions to turn agriculture from a GHG emitter to an ecologically sustainable GHG sequesterer.*

6 PM – 8 PM: Flash-talks of the participants' research - Getting to know each other

8 PM: Dinner

Monday June 17

9 AM – 10 AM: Session « Reducing N inputs & improving NUE »

Jacques Le Gouis (UMR Génétique Diversité Ecophysiologie des Céréales - Clermont-Ferrand, France)
"Breeding for Nitrogen Use Efficiency in the context of climate change" - *Nitrogen fertilisers used on arable crops represent a growing cost for farmers and they can cause nitrate pollution in water tables and rivers. In addition, they are major contributors to greenhouse gases emission both during their production and if not absorbed by the plant as nitrous oxide. In this context, breeding varieties that use nitrogen more efficiently, to produce high grain yield and protein concentration, is becoming an important objective for plant breeding.*

10 AM – 10:30 AM: Break

10:30 AM – 12 PM: Session « Reducing N inputs & improving NUE »

Anne Krapp (Institut Jean-Pierre Bourgin for Plant Sciences – Versailles, France)
"Nitrogen signalling in a changing environment" - *Plant responses to nitrate availability are controlled by a large gene regulatory network that is governed by several transcription factors. The transcription factor family NLP (NIN-like Protein) are top-tier players in this network. Abiotic factors that interfere with the responses to nitrogen will be discussed from the perspective of a changing environment.*

Fabien Chardon (Institut Jean-Pierre Bourgin for Plant Sciences – Versailles, France)
"Decoding the nitrogen flux dynamics in plants under changing climate" - Plants absorb nutrients from the soil for growth, with nitrogen uptake and remobilization being crucial for seed development. The balance of nitrogen from these sources, regulated by internal processes and environmental factors, determines seed composition. While cellular responses to environmental changes are well understood, the impact of environmental stress on nitrogen balance remains underexplored. This presentation will examine how biotic and abiotic stresses significantly influence nitrogen use efficiency (NUE) in plants, creating various bottlenecks in nitrogen flux dynamics during seed filling.

Benoît Alunni (Institut Jean-Pierre Bourgin for Plant Sciences – Versailles, France)
"Improving crop N nutrition by manipulating root-associated microbes" - *Plants attract beneficial microbes in the rhizosphere by providing them with carbon sources secreted within root exudates. In turn, microbes like arbuscular mycorrhizal fungi or plant growth promoting bacteria facilitate plant nutrition. In this lecture, we will detail some recent advances ranging from molecular mechanisms to field trials and discuss how these interactions can be exploited to improve agricultural sustainability and how these may be impacted by climate change.*

12 PM – 12:30 PM: Session « Reducing N inputs & improving NUE » - Discussions

12:30 PM – 2 PM: Lunch

2 PM – 4 PM: Workshop « Communication & outreach »

Isabel Mendoza (Global Plant Council)
"Workshop on outreach and communication" - *Dive into the world of science communication, including the social media platforms, in this 7-hour workshop. Participants will have to collaborate in groups, where they will be provided with a hot-topic paper centered around plants and climate change. Their task? Craft compelling communications tailored for the general public. Don't miss out on this chance to sharpen your communication skills and make a meaningful impact.*

4 PM – 4:30 PM: Break

4:30 PM – 8 PM: Poster session / Poster prize

8 PM: Dinner

Tuesday June 18

9 AM – 10 AM: Session « Carbon: capture & sequestration »

Amanda Cavanagh (University of Essex - Colchester, UK)
"Optimising photosynthesis to future-proof crops" - *Adapting crops to warmer growing season temperatures is a major challenge in mitigating the impacts of climate change on crop production. While nearly all processes in plants are impacted by above-optimum temperatures, the impact of heat stress on photosynthetic processes stand out for their centrality. Therefore, understanding and improving photosynthetic responses to changing environmental conditions is crucial in developing high-yielding resilient crops. This talk provides an update on transgenic strategies that show promise in improving the high-temperature tolerance of photosynthesis.*

10 AM – 10:30 AM: Break

10:30 AM – 12 PM: Session « Carbon: capture & sequestration »

Sylvie Dinant (Institut Jean-Pierre Bourgin for Plant Sciences – Versailles, France)
"Source-Sink Relationships in Crop Plants and their resilience to changing environment" - *Plant growth and development under optimal growing conditions depends primarily on two factors: the efficiency of photosynthesis in its photosynthetic organs (source organs), and its ability to transport photoassimilates to the harvested ones (usually sink organs). Significant advancements have been made in understanding how source-sink relationships influence both yield and nutritional quality, particularly in response to environmental changes. I will delve into the mechanisms behind these source-sink relations.*

Philippe Ciais (Laboratoire des Sciences du Climat et de l'Environnement - Saint-Aubin, France)
"Mapping forest structure and biomass at high resolution from trees to globe using high resolution satellite imagery and deep learning" - *Dr. Ciais will address how high-resolution satellite data enable tree level carbon monitoring at national and global scales. Moreover, he will discuss how machine learning models allow the fusion of satellite data into maps of forest attributes and how these can be used with ground data to attribute forest disturbances to driving factors. He will summarize the most relevant advances highlighting their application towards consistent tree biomass monitoring systems, monitoring carbon losses and carbon gains from restoration and forest degradation, ultimately supporting the mitigation of climate change.*

Cornelia Rumpel (Institut d'Ecologie et des Sciences de l'Environnement Paris, France) (in videoconference)
"The role of plants in soil carbon sequestration" - *Soil organic carbon sequestration is one of the natural based solutions able to mitigate climate change, while providing multiple benefits. Indeed, soils store more carbon than the biosphere and the atmosphere combined in different forms. The soil carbon pool is dynamic and can be influenced by human activity. Soil carbon sequestration can be enhanced by increasing organic matter inputs and is largely dependent on vegetation types and landuse. Indeed, plants are the main actors in soil biogeochemical cycles, determining the amount and forms of carbon sequestered in soil. In this presentation, I will highlight the plants' effects on soil carbon storage and the management strategies to be applied to increase soil carbon sequestration and limit trade offs.*

12 PM – 12:30 PM: Session « Carbon: capture & sequestration » - Discussions

12:30 PM – 2 PM: Lunch

2 PM – 4 PM: Workshop « Communication & outreach »

4 PM – 4:30 PM: Break

4:30 PM – 8 PM: Climate Fresk

Elise Colcombet and Marie Grovel (Climate Fresk animators)
In just 3 hours, the collaborative Climate Fresk workshop will teach you the fundamental science behind climate change. By activating the group's collective intelligence, Climate Fresk workshops enable participants to take ownership of the subject matter. The Climate Fresk methodology doesn't involve an expert presenting information to the group ; instead, it requires all participants to take an active role in the building-up of the Fresk, becoming participative learners. As participants link the causes and effects of climate change, they are able to take a step back and understand the systemic nature of the challenges.

8 PM: Dinner

Wednesday June 19

8:30 AM – 10 AM: Bus trip to Fontainebleau

10 AM – 12:30 AM: Visit to the Fontainebleau Palace & Gardens (https://www.chateaudefontainebleau.fr/en/)
ATTENTION: You have to be at 11:20 AM at the welcome desk for the groups, in order to be on time for the guided tour (your guide will be Mathias). Don't be late !!

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12:30 PM – 2 PM: Packed lunch (in the « Galerie des Fleurs » in case of rain)

2 PM – 2:30 PM: Bus trip to the Barbeau Forest

2:30 PM – 4:30 PM: Visit to the Barbeau Forest Field Station (http://www.barbeau.universite-paris-saclay.fr/index.html)

Daniel Berveiller (Laboratoire Écologie Systématique & Évolution - Gif-sur-Yvette, France)
"Visit of Barbeau forest research station" - *The Barbeau forest research station is located near Fontainebleau forest, 50 km South-East of Paris. It is the place of several research projects in various domains, especially in forest ecosystem functioning, bio-climatology and ecophysiology. The Barbeau station is also engaged in the European Research Infrastructure ICOS (Integrated Carbon Observation System) as Class 1 station, the highest level of sensor/instrumentation deployment and data supply of the infrastructure. After introducing the scientific context of such an experimental station, the visit will focus on the technical aspects of the forest station, the instruments deployed in the soil, on the trees and at the top of the 35m high tower which overlooks the forest canopy by up to 6m.*

4 PM – 5:30 PM: Bus trip to the Centre Port-Royal

6 PM – 6:45 PM: Using the field station data

Nicolas Delpierre (Laboratoire Écologie Systématique & Évolution - Gif-sur-Yvette, France) (in videoconference)
"Measuring the breath of forests" - *I will first give an overview of the methods used to measure the exchange of gases (CO_2 and H_2O) between ecosystems and the atmosphere. Then I'll look at what these measurements can tell us about how forests are functioning in an era of climate change.*

7 PM – 7:30 PM: Bus trip to Montigny le Bretonneux

7:30 PM – 9:30 PM: Dinner at the restaurant LE TABLIER (31 avenue du Lycée, La Mare Caillon, 78180 Montigny le Bretonneux)

9:30 PM : Bus trip back to the Centre Port-Royal

Thursday June 20

9 AM – 10 AM: Session « Plant resilience to climate change »

Antoine Martin (Institut des Sciences des Plantes de Montpellier - Montpellier, France)
“Nutrient signaling networks in plants under elevated CO_2” - *The elevation of CO_2 leads to major modifications of plant growth and physiology. We explore in Arabidopsis how high CO_2 regulates plant growth and nutrient signaling, by combining molecular physiology, gene regulatory networks and quantitative genetics. I will present here our latest findings on these topics revealing signaling, molecular and genetic mechanisms by which plants adapt to a changing environment.*

10 AM – 10:30 AM: Break

10:30 AM – 12 PM: Session « Plant resilience to climate change »

Hannes Kollist (Institute of Plant Sciences Paris-Saclay - Gif-sur-Yvette, France / University of Tartu - Estonia)
“Guard cells in climate action” - *Guard cells sense changes inside the plant as well as in the surrounding environment to adjust stomatal aperture and by that plant gas exchange. To breed water-saving crops for a future world with elevated CO_2 and more frequent drought episodes we need to know molecular switches in response to VPD/drought and CO_2. I will present our results in studying mechanisms of stomatal movements in response to changes in the environment and ways to use knowledge gained in model plants for improving crops water management.*

Anna Matuszyńska (Institute for Computational Life Science, RWTH Aachen University - Aachen, Germany)
“Computational modeling of photosynthetic acclimation: how to start?” - *For those aspiring to embark on their modeling journey yet feeling perplexed about where to begin, what tools to use, or even the overarching purpose, this talk underscores the enduring significance and value of classical modeling approaches. I will present our Simulation-Based Learning Platform to Study Photosynthesis and discuss the importance of classical modelling methods in integrative biology. Bring your laptops!*

Guillem Rigaill (Institute of Plant Sciences Paris-Saclay - Gif-sur-Yvette, France)
“Data integration: size matters” - *For the study of multi-stresses, it is widely agreed that the effects of combined stresses differ from the sum of individual stresses. This conclusion comes from comparing differential gene lists for individual and combined stresses. These lists, typically obtained with just a few replicates (3 for RNA-seq), identify only 20% of the differences, suggesting a less than 4% overlap between any two lists. This may partially explain the observed differences between single and multiple stress responses. We re-evaluated this issue with an experiment involving 20 replicates, focused on two stresses: CO_2 and heat.*

12 PM – 12:30 PM: Session « Plant resilience to climate change » - Discussions

12:30 PM – 2 PM: Lunch

2 PM – 4 PM: Workshop « Communication & outreach »

4 PM – 4:30 PM: Break

4:30 PM – 6 PM: Session « Plant resilience to climate change »

Axel de Zélicourt (Institute of Plant Sciences Paris-Saclay - Gif-sur-Yvette, France)
“Combined transcriptomic and metabolomic analyses of the *Enterobacter sp.* SA187 beneficial effect on *Arabidopsis thaliana* under elevated CO_2” - *Here we will discuss about the beneficial effect of Arabidopsis thaliana inoculation with the beneficial bacterium Enterobacter sp. SA187 that increases plant growth under elevated CO_2 (eCO_2). This effect is associated with changes in primary metabolism and ethylene signaling as revealed with combined transcriptomic and metabolomic analyses. Thus, the SA187-plant interaction appears to be a good strategy for improving plant growth in eCO_2 atmospheres.*

Marina Cotta (Max Planck Institute for Plant Breeding - Cologne, Germany)
“Impact of increasing CO_2 levels on Lotus japonicus and its root-associated microbiota” - *In nature, plants interact with microbes that can provide beneficial functions, such as nutrient mobilization, in exchange of organic carbon. Currently, it is not known how expected increases in atmospheric CO_2 levels will impact these interactions. Using a novel gnotobiotic system that allows dynamic control and monitoring of CO_2 levels, we observe a significant interaction between altered plant growth and microbiota composition.*

Richard Berthomé (Laboratoire des Interactions Plantes-Microbes-Environnement - Toulouse, France)
"Interaction of plants with biotic AND abiotic constraints: toward robust resistances under warmer climate" - *In the context of global warming, the scenarios predict an increase in the risk of epidemics associated with a higher frequency, duration and intensity of extreme climatic events. In the case of temperature elevation, one of the climatic parameters expected to fluctuate the most in the coming years, a majority of plant resistance mechanisms are described as being negatively impacted, whatever the species of plant or pathogen. Understanding the responses of plants and pathogens to multiple and combined stresses is therefore crucial and constitutes one of the strategies for identifying solutions for adapting crops to climate change. Various projects designed to address these issues, focusing on the interaction between Arabidopsis and tomato - Ralstonia solanacearum - and changes in the abiotic environment (temperature rise under controlled conditions / change of season in the field) will be presented.*

6 PM – 8 PM: Pétanque tournament

8 PM: Dinner

Friday June 21

9 AM – 9:30 AM: Session « Plant resilience to climate change » - Discussions

9:30 AM – 10:30 AM: Session « Future research practices & opportunities »

Paul Leadley (Laboratoire Écologie Systématique & Évolution - Gif-sur-Yvette, France)
"The critical role of the agroecological transition in reinforcing synergies and reducing tradeoffs between agriculture, biodiversity and climate change" - *This talk will focus on how the agroecological transition can contribute to biodiversity goals, as well as climate change mitigation and adaptation objectives. After giving a broad overview of the interactions between agroecology, biodiversity and climate change, I will focus on the key role that diversification at field and landscape scales can play in simultaneously supporting agricultural production, enhancing cultivated and non-cultivated biodiversity, increasing resilience to climate change, and reducing greenhouse gas emissions, nitrogen pollution and pesticide pollution. I will then discuss how the agroecological transition and its benefits for biodiversity and climate are dependent on system-wide transformations of food systems. Finally, I will use examples from our local Living Lab, VivAgriLab, to illustrate how co-design between researchers and non-academic actors can result in concrete actions.*

10:30 AM – 11 AM: Break

11 AM – 12:30 PM: Session « Future research practices & opportunities »

Sophie Gendre (ARVALIS, Pôle Agronomie - Baziège, France)
"Climate change adaptation and mitigation, examples of technical support to help farmers in their transition" - *How to help farmers move towards a climate change sustainable agriculture? This presentation is going to focus on different projects on technical support for farmers' transition to climate change. First project is called Climate Farm Demo. It is a European project which aims to adapt agricultural production systems to climate change by adoption of Climate Smart Farming practices and solutions at Demo Events organised at Demo Farms across Europe. We will also speak about projects on crop rotation evolution with ASALEE tool. Then we will discuss about the low carbon label approach.*

Jean Colcombet (Institute of Plant Sciences Paris-Saclay - Gif-sur-Yvette, France)
"Scientists facing climate change: should we be neutral or not?" - *Modern scientific research relies on fossil fuel energy that has become abundant over the last two centuries and as a result, scientific research is associated with substantial greenhouse gas (GHG) emissions. With climate change threatening life on Earth, humanity is called upon to drastically reduce its GHG emissions in order to achieve neutrality (by 2050). Climate change and reduced energy availability will of course impact the organization of human society, including the way future scientific research will be carried out. The presentation will attempt to question the position of researchers in the face of this Anthropocene disorder.*

12:30 PM – 2 PM: Lunch

2 PM – 3 PM: Workshop « Communication & outreach » - Presentations

3 PM – 3:30 PM: Break

3:30 PM – 4:30 PM: Closing discussion - Round table

4:30 PM: End of the school

Serine as a hallmark of metabolic reprogramming to improve plant resilience under climate change conditions

Andrea Alcántara-Enguídanos[1,2], Sara Rosa-Téllez[1,2], Víctor Flors[3], Roc Ros[1,2]

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Global warming are triggering exacerbated biotic and abiotic stresses that compromise a several risk to crop yield. To face these threats plants possess a mechanism known as metabolic reprogramming. Recent findings shed light on serine as a metabolic signal in response to various stresses. Serine serves as the precursor for glucosinolates, secondary metabolites important for improving plant resilience against biotic stresses such as pathogens and insects. Nevertheless, rising atmospheric CO_2 concentrations constrain serine levels due to the reduced activity of the glycolate pathway of serine biosynthesis associated to photorespiration, compromising the plants' ability to cope with several stresses. Recent studies in our research group has demonstrated that, in such conditions, the genes of the Phosphorylates Pathway of Serine Biosynthesis (PPSB) are induced to avoid serine limitations. Therefore, this study aims to elucidate the specific role of PPSB in plant response to biotic stress. Particularly focusing on glucosinolates' production under climate change conditions by *in planta* transformation approaches, pathogen infection, gene expression and primary and secondary metabolomic analyses. From this work, we expect to generate frontier of knowledge in the understanding of molecular mechanisms governing the plant response to stresses, providing new tools for sustainable agriculture in the future climate conditions.

This work is part of the project Grant PID2019-107174GB-I00 funded by MCIN/AEI/10.13039/501100011033 and Grant AICO/2021/300 funded by the Generalitat Valenciana. It is also part of a Ph.D funded by the Universitat de València (Atracció de Talent 2020, UV-INV_PREDOC- 1337025).

High-throughput phenotyping of the core-European Heritage Barley Collection (ExHIBiT) under waterlogging

Villő Bernád[1], Emilie Jacob[2], Jason Walsh[1], Patrick Langan[1], Nadia Al-Tamimi[1], Kelly Houston[3], Luke Ramsay[3], Joanne Russel[3], Robbie Waugh[3], Paul Ruel[2], Hervé Demailly[2], Eleni Mangina[1], Laurent Gutierrez[2], Tancredi Caruso[1], Mortaza Khodaeiaminjan[1], Sónia Negrão[1]

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Barley, a globally significant crop for animal fodder and the malting industry, is increasingly vulnerable to climate change-induced extreme rainfall, leading to heightened occurrences of waterlogging. To improve barley waterlogging tolerance, we need to capitalise on existing genetic diversity and develop varieties for a sustainable agricultural production. Our project addresses the limitations of traditional phenotyping by employing advanced high-throughput techniques for non-destructive, continuous, and quantitative data collection. In this initiative, we established the European Heritage Barley collection (ExHIBiT), consisting of 365 lines of 2-row spring barley sourced from northern Europe. The ExHIBiT collection is a diverse blend of landraces (~14%), old cultivars (~18%), and elite lines (~67%), genotyped with a 50K SNP array, and agronomically characterised. From this, a 230-lines core collection was derived, and its utility in association mapping was demonstrated. This core collection underwent phenotyping in both field and controlled conditions using a high-throughput imaging platform, employing RGB, Fluorescent, and Hyperspectral cameras. The core collection was subjected to 14 days of waterlogging stress followed by a 7-day recovery and several traits ranging from growth to spectral indices were examined. We conducted a genome-wide association study (GWAS) to identify genetic regions contributing to waterlogging tolerance. Furthermore, the core collection was planted in field conditions for two consecutive years in both control and waterlogging for four days. Several agronomic l traits such as flowering time, yield and height were assessed, and GWAS was conducted. Eight accessions exhibiting particular resilience and susceptibility to waterlogging were selected for a small-scale field trial to investigate previously unexplored traits, including the microbiome diversity and malting characteristics.

Optimizing Nitrogen Fertigation for Enhanced Root Growth and Increased Productivity

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Root system plays a crucial role in exploring soil resources critical for plant growth. Excessive nitrogen (N) fertilizer application, aimed at boosting crop productivity, poses environmental challenges due to nitrate (NO_3^-) leaching. Developing optimal N fertigation is key and challenging due to the need for sufficient root system information. Therefore, the study focuses on the effect of different N regimes on root growth using in-situ Mini-Rhizotron (MR) root phenotyping and comparison to the destructive method. In a greenhouse experiment on bell peppers, we evaluated various N treatments including 50% reduction of N after fruit set (N50), 75% reduction of N after fruit set (N25), and farmers' fertigation (N100). Reduced N led to significant increases in root traits such as; root length, root length density (RLD), and surface area. Root distribution in the upper soil layer was higher under reduced N, with fine roots (<2 mm) exhibiting higher root length. Yield and shoot biomass were significantly higher under higher N contrary to root biomass, which was higher under low N. While enhanced root growth under N25 did not significantly improve yield, N50 achieved yields similar to N100, indicating potential for reduced N application. This research emphasizes the importance of optimizing N application for enhanced root growth, contributing to both increased productivity and environmental sustainability.

Effects of High Ambient Temperature on Plant Growth and Reproductive Development in Barley

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The increase in the average ambient temperatures due to climate change threatens crop production globally. Barley (*Hordeum vulgare*) is an important cereal crop and model plant to elucidate the genetic control of high-temperature adaptation in cereals. In the model plant *Arabidopsis thaliana*, phytochromes and the circadian clock genes control the growth and development in response to high ambient temperatures. In barley, *PHOTOPERIOD RESPONSE 1* (*PPD-H1*) and *EARLY FLOWERING 3* (*ELF3*) have been implicated in the control of development under high ambient temperatures. However, the genetic control of flowering time and reproductive development in response to high ambient temperatures in barley remains unclear. Natural variation at *PHYTOCHROME C* (*HvPHYC*) has been shown to interact with *PPD-H1* to accelerate flowering under different photoperiods. Nevertheless, little is known about their interaction with high ambient temperatures. Therefore, we tested the effects of *HvPHYC* and its interactions with *PPD H1* on development under high ambient night and day temperatures. For this purpose, we analysed the genetic, hormone and metabolite networks in the leaves and shoot apical meristem (SAM), which control flowering time, spike development and floret fertility downstream of *PHYC* and *PPD-H1* and in response to high ambient temperatures.

Deciphering novel plant responses and plant-microbiome interactions under heat stress and nutrition scarcity

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Climate change acts as a negative factor that will reduce productivity, by strengthening the detrimental effect of many abiotic stresses, such as extreme temperatures, drought, salinity, or nutrient scarcity. The plant root system is essential for plant adaptation to environmental changes, specifically heat stress and nutrient acquisition. Preliminary data from our lab indicate that high temperatures reduce Pi assimilation and alter microbiota community composition, factors that limit plant productivity. In nature, during extreme heat, the temperature of the soil-root environment is buffered by the soil thermal-geodynamics properties. However, in experiments in vitro or in the greenhouse, the root growth zone is heated to a similar temperature than the shoot. To solve this experimental limitation, a new engineered device (TGRooZ, Temperature Gradient Root Zone), which generates a soil-temperature gradient like the conditions found in the natural soil, was developed previously in the lab.
In this project, using the TG-RooZ, we want to study the effect of combined heat stresses and Pi deficiency on plant growth, nutrition, and yield. We will identify new fungi involved in the response to heat and Pi starvation. To address these objectives, we generated a novel collection of endophytic and root-associated fungi of tomato plants under heat stress. We will screen a selection of isolates looking for growth promotion effects in Arabidopsis under heat stress using the TGRooz device at 32º. With this system, the shoot stays at 32º while a colder temperature gradient is generated in the root system. These results will give us knowledge of new positive interactions between fungi and plants under heat stress, novel clues in plant thermotolerance and novel technologies for a sustainable agriculture.

Global analysis of regulatory networks modulating the stress response at the multilevel scale in plants

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Climate change and environmental stress pose critical challenges to agricultural production, disrupting plant cellular homeostasis with factors such as drought, soil salinity and pathogens. In the face of these adversities, plants reprogram their molecular processes to adapt, involving genetic regulation at multiple levels. In Spain, melon cultivation faces significant climatic challenges, although the country is the main exporter of this fruit in Europe. The Melonomics project has been key in providing the complete genomic sequence of melon in 2012, stimulating research into its biological mechanisms.
The aim of the project is to identify and validate in vivo the regulatory networks that manage the stress response in melon, in order to improve crop protection strategies. A specific validation of miRNAs miR398 and miR408 in response to environmental changes has been carried out, showing an increase in their expression in transgenic plants and positive effects on phenotypic characteristics. In addition, viroid-induced gene silencing has been explored as a novel approach to understand plant-environment interactions, revealing the activation of resistance mechanisms mediated by miRNAs in response to water stress.
These findings offer a deeper understanding of how melon plants cope with environmental stress, providing valuable insights to strengthen crop protection in a context of climate change and phytosanitary challenges.

Keywords: Climate change, environmental stress, agricultural production, drought, soil salinity, pathogens

Beneficial effect of *Enterobacter* sp. SA187 on growth and development of *Arabidopsis thaliana* under limited nitrogen conditions

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Nitrogen (N) is an essential but often scarce plant nutrient. Limited N availability adversely affects plant growth and crop yield, thus necessitating the use of N-fertilizers in agriculture to enhance or maintain productivity. However, widespread N-fertilizer application is a significant threat to agricultural sustainability and contributes to global climate change. We are studying how a plant growth-promoting bacterium, *Enterobacter* sp. SA187 (SA187), affects *Arabidopsis thaliana* growth under varying N concentrations and sources. SA187 consistently enhanced plant biomass, root length, and lateral root density under all low N conditions tested, regardless of the N source. Interestingly, the beneficial effect of SA187 increased with decreasing N concentration. The possible involvement of the ethylene signaling pathway and nitrate transporters in SA187-mediated growth promotion was tested. Ethylene-insensitive (*ein2-1*) and high affinity nitrate transporter (*nrt2.1* and *nrt2.5 x nrt2.6*) mutants indicated that ethylene signaling and nitrate transport may play a role in this beneficial effect. These preliminary findings suggest that establishing an SA187-plant interaction could be a promising strategy to enhance plant growth and development under limited N conditions and thus reduce N-fertilizer use. Our ongoing research employs dual (plant and bacterial) transcriptomics, metabolomics, elemental analyses, enzymatic activities, and assessments of plant nitrate and ammonium levels. By unraveling the physiological and molecular mechanisms of this interaction, we aim to provide novel insights into the role of non-N fixing bacteria in plant nutrition and productivity under low N conditions. Ultimately, these insights may contribute to sustainable agricultural practices.

Quantifying the impact of farmer-led regenerative management practices on soil health and cropping system outcomes

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Farming systems in the US High Plains are shifting towards regenerative management strategies aimed at improving soil health. Regenerative principles that increase soil health—such as living roots, crop diversity, minimal disturbance and animal integration—are often achieved through multiple management practices implemented concurrently; however, the majority of studies focus on single practices and are often investigated in controlled settings. Here, we aim to address the knowledge gap in how the implementation of multiple on-farm practices impact soil health, particularly in semi-arid agroecosystems. We collaborated with the Colorado Conservation Tillage Association, the lead of the FARMS (Farmers Advancing Regenerative Management Systems) Project, to support farmers innovating in regenerative agriculture through a comprehensive approach integrating peer network building, economic analyses and soil health testing. We collected and analyzed soil samples in 2020 and 2023 from 30 farms practicing a range of management approaches, from conventional to 10+ years of regenerative practices. Using farmer-reported management data of current and historical practices, we are developing a standardized indicator value to quantify the intensity of regenerative principles applied in each farming system and are examining causal relationships between management and biological, physical and chemical soil health metrics and crop outcomes. Preliminary analyses indicate that continuous living roots are the most significant management predictor of soil health indicators. Further lab analyses will elucidate possible mechanisms. This collaborative on-farm research provides a rich dataset that we hope will inform farmer decision-making and policies for agroecosystem management for climate resilience.

PRC2 involvement in plant response to cold stress: phenotypic and transcriptomic analysis in response to chilling and freezing temperatures

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Plants face changing and adverse environmental conditions, among which cold is of primary importance in the context of climate change. Indeed, frost is emerging as a key factor of change in cold climate plants in response to climate warming. The most characterized cold stress response is Cold Acclimation (CA), an adaptive process which allows plants to develop tolerance to cold. This involves a deep reprogramming of gene expression, which is based on epigenetic control through post-translational histone modifications.

PRC2 has been recently shown to be involved in plant response to environmental stress, through transcriptional regulation of plant stress-responsive genes. Nevertheless, the dynamics of H3K27me3 and PRC2 function during CA has not yet been studied in depth, particularly at genome-wide level.

To study PRC2 role in plant response to cold, we performed phenotypic and molecular experiments on wild type and *clf* plants, which lack one PRC2 catalytic subunit. Furthermore, since the *clf* mutation does not completely eliminate PRC2 activity, we used a PRC2 inhibitor, RDS3434, to analyze how the absence of PRC2 affects cold acclimation. We also performed a transcriptomic analysis under CA and NA (No Acclimation) conditions, in wild type, *clf* or RDS3434 treated plants.

Our results showed that at least two plant-specific families of transcription factors, namely WRKYs and NACs, participate to regulatory modules under the control of PRC2. Indeed, the absence of the PRC2 catalytic subunit leads to an upregulation of different components of these families, peculiar either to the early cold induction or to the acclimation establishment.

Integrating spatial constraints with metabolic models predicts C_3, C_4 and intermediate photosynthesis

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Improving photosynthesis holds great promise for increased crop productivity. While most plants perform C_3 photosynthesis, its efficiency is hindered by Rubisco's oxygenase activity and subsequent photorespiration. In plants under high photorespiration, photorespiratory glycine started being shuttled from the mesophyll and decarboxylated in the bundle sheath. This glycine shuttle concentrated photorespiratory CO_2 around the bundle sheath's rubisco, giving rise to C_3-C_4 photosynthesis. Eventually, a full carbon-concentrating mechanism emerged, with CO_2 initially fixed in the mesophyll and concentrated around and fixed by the bundle sheath's rubisco, resulting in C_4 plants. These metabolic changes minimise photorespiration resulting in improved growth and carbon fixation, and are associated with anatomical and physiological changes on the leaf tissue and cellular level. We are interested in understanding how these changes affect metabolic flux modes in the two cell types. To this end, we developed a mathematical model of mesophyll and bundle sheath metabolism, accounting for differences in tissue volume and photosynthetic capacity. Through flux balance analysis, we explore metabolic shifts necessary for efficient photosynthesis under various scenarios. In our findings, transitioning from C_3 to C_4 metabolic states correlates with increased bundle sheath tissue volume. Additionally, we investigate the effect of inactivating photosystem II in determining photosynthetic types. Moreover, alterations in spatial constraints affect energy metabolism, inducing shifts in electron transport rates. The gained knowledge shall guide metabolic engineering strategies for improved crop plant productivity and quality.

A kinetic model for temperature effect on non-photochemical quenching process

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Crop plants experience dynamic environmental conditions throughout their life cycle. Accurate prediction of crop photosynthetic performance thus needs to consider various environmental factors, e.g. fluctuations in light and temperature. Combined effect of changes in multiple stimuli can be better analyzed with the use of mathematical models. Here, we present a coarse-grained temperature-dependent photosynthesis kinetic model that focuses on photosystem II and the high energy-dependent quenching (qE) component of non-photochemical quenching (NPQ). To extend an existing NPQ model (Matuszyńska *et al.*, 2016) to account for enzymatic activity variation at different temperatures we implemented the Arrhenius equation. The required activation energies have been parametrized to the available literature. The model simulation results were compared with the chlorophyll fluorescence data collected using the MultispeQ device from *Solanum lycopersicum* grown in semi-controlled field conditions. In the first iteration, the model accurately simulated NPQ under low light and ambient temperature conditions but lacked accuracy in predicting values under high light and high temperature conditions. In the second iteration, we improved the simulation accuracy by incorporating measured pigment composition into the model. This adjusted model can already accurately predict plant photosynthetic performance under fluctuating conditions and sets the ground for further work on quantifying the combined effect of changes in light and temperature on photosynthesis.

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Characterization of molecular components required for switch in cell division orientation during the early lateral root development

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The root system of dicotyledonous plants consists of primary roots that branch to generate lateral roots (LR). LRs develop postembryonically and allow plants to expand their root system in response to environmental changes, thereby enhancing their ability to absorb essential resources. LRs arise from a small group of founder cells located deep within the primary root, founder cells first divide perpendicularly to the main root resulting in the formation of Stage I primordium. The cells then switch the division plane to form a two-layered Stage II primordium. Gradually more cell layers are added until a fully functional LR emerges. PLETHORA 3,5,7 (PLT3,5,7) transcription factors are essential for the switch in the division plane. Plants lacking PLT3,5,7 fail to develop LRs, yet the molecular mechanisms downstream of PLT3,5,7 remain elusive. I studied the transcriptomes of plt3,5,7 and the rescue line, and detected several putative PLT3,5,7 targets. Among the detected targets, genes coding for proteins implicated in the rearrangement of the cytoskeleton and organ shape are of special interest, and their functional role in LR development is being investigated with the aim of better understanding how organ shape is determined on the molecular level. Ultimately, a knowledge of the genetic mechanisms underlying LR development may be used to improve root systems of crop plants, so that they could better cope with changing environmental conditions.

Photosynthetic and morphological responses to cycles of drought and flooding in wheat and barley

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Climate change is increasing the frequency and intensity of stress events including drought and flooding and it is usually hard to deduce combined effects of multiple environmental stresses by known effects of single stress. With expanding global populations, ensuring food security is increasingly difficult, especially with unpredictable weather patterns.

This research program aims to compare the physiological responses of wheat and barley to cycles of contrasting environmental stress-drought and flooding. In the present investigation, two-week-old wheat and barley plants were subjected to control (80% soil moisture content [SMC]), drought (30% SMC) or flooding treatments for 15 days. Following that, previously stress treated plants were exposed to a further stress – drought followed by flooding (D-F) or flooding followed by drought (F-D) for a further 15 days. For recovery treatments, plants returned to normal irrigation for 15 days. Plants were measured at the end of the first stress treatment (Day 15), following further stress or recovery (Day 30) or following recover from double stress treatments (Day 45). By studying chlorophyll fluorescence, gas exchange and growth responses in both species, it can be shown primarily both individual and double stresses have less impact on barley than wheat. Post flooding responses suggest studying more on flooding followed by drought (F-D) treatments.

Synthetic redesign of plant photorespiration: photorespiratory bypasses towards more efficient carbon fixation

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Ribulose-1,5-bisphosphate carboxylase/oxygenase (RubisCO) is responsible for the conversion of carbon dioxide into biomass in the majority of plant species, yet is still prone to errors. The oxygenation reaction of RubisCO leads to the formation of 2-phosphoglycolate (2-PG), a harmful metabolite which is neutralized through the process of photorespiration. The photorespiratory pathway is an energetically expensive reaction that ultimately leads to the loss of 25% of the previously fixed carbon, decreasing the photosynthetic efficiency of C3 crops by 30%. Using a synthetic biology approach, our work aims to assemble, implement, and test both natural and synthetic photorespiratory bypasses in plants. To that end, we established the recently discovered β-hydroxyaspartate cycle (BHAC) and the new-to-nature tartronyl-CoA (TaCo) pathway in *Arabidopsis thaliana* chloroplasts, to redirect the carbon flux towards a carbon-neutral or even carbon-positive photorespiration. Analysing the implementation of heterologous metabolic pathways will enable a rational redesign of the pathways, iterating through the engineering cycle. Overall, we aim to contribute to the challenging goal of increasing photosynthetic efficiency, intertwining natural and synthetic metabolic networks, and shed light on the role of photorespiration in balancing plant metabolism.

Linking of an agroforestry system model and a plant hydraulic failure model

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This study explores the potential of agroforestry systems (AFS) as a measure against cavitation and embolism in crops under water deficit conditions. Prolonged water stress can disrupt the water transport system in plants, leading to cavitation or embolism, and impact on crop health (Tyree and Sperry 1989; Corso *et al*. 2020; Harrison Day and Brodribb 2023). Studying cavitation in agroforestry systems (AFS) poses challenges, necessitating a novel approach through modeling and numerical simulation. The proposed method integrates (i) the Hi-sAFe model (Dupraz *et al*. 2019), predicting AFS growth, and (ii) the SUREAU model (Cochard *et al.* 2021), focusing on plant hydraulic architecture. The objective is to bridge AFS modeling at the plot scale with plant hydraulic modeling at the individual scale. The HisAFe model predicts plot-scale processes, while the SUREAU model determines cavitation presence and severity in crops using Hi-sAFe outputs as inputs.

Anticipated outcomes include improved predictions of crop mortality due to drought events in AFS, which is crucial for understanding vulnerability in the context of climate change. The study establishes a correction mechanism in the Hi-sAFe model to quantify the impact of cavitation and embolism on the AFS plot, enhancing predictions related to plant water status. This approach contributes to more accurate crop health and resilience assessments within agroforestry systems.

This research proposes an innovative integration of AFS and plant hydraulic models, paving the way for precise predictions and proactive management strategies to safeguard crops amid evolving environmental challenges. The study's significance lies in its potential to address the impact of climate change and extreme weather events on agriculture, providing valuable insights for sustainable crop management.

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Guard cell interactomics

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Stomata are small pores surrounded by two guard cells on the plant leaf surface that enable gas exchange, a process that involves the uptake of carbon dioxide, release of oxygen, and transpiration of water vapor. Upon sensing of environmental and endogenous stimuli, guard cells respond by regulating stomatal aperture. Signal perception in the guard cell membrane and cytoplasm leads to the activation of signalling cascades involving kinases, phosphatases, and the intracellular messengers $Ca2^+$ and ROS. As a result, ion channels located in the plasma membrane are targeted by these messengers, regulating the turgor of guard cells. Many families of transporters and channel proteins have been described to date, but the complexity and redundancy of function amongst them poses a challenge to individually decipher the identity and function of some of the channels involved in gas exchange regulation.

The plasma membrane protein GUARD CELL HYDROGEN PEROXIDE-RESISTANT1 (GHR1) is a leucine-rich repeat receptor-like pseudokinase that regulates stomatal movements. We are using GHR1 as a tool to identify novel players in guard cell signalling through an interactomics approach. This doctoral project focuses on characterization of some of the identified interactors that are novel channel proteins that show guard-cell enriched expression and localization to the plasma membrane. The aim is to 1) uncover the function and specificity of the channels and the putative role of GHR1 in their regulation, 2) understand how these components integrate in guard cell signalling pathways, and 3) demonstrate their relevance for stomatal function, gas exchange and plant physiology.

Structure of the Plant Plastid-Encoded RNA Polymerase

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Plastids are a diverse family of organelles that possess their own genome and gene expression machinery. Chloroplasts are the plastids in plants and green algae where photosynthesis takes place. A key element of the plastid gene expression machinery is the plastid-encoded RNA polymerase (PEP), which transcribes plastid genes encoding central components of photosynthesis. PEP is a 1 MDa multisubunit complex with an enzymatic core similar to bacterial RNA polymerase and at least 12 associated proteins (PAPs)(1). PAPs are not homologous to transcription factors found in bacterial RNA polymerases, but they have been shown to be essential for expression of plastid photosynthetic genes and chloroplast maturation. However, we do not yet know the exact role of PAPs in regulating transcription by PEP.

We purified PEP from chloroplasts of white mustard (Sinapis alba). We present the structural models of native PEP and a PEP transcription elongation complex obtained by cryogenic electron microscopy (cryo-EM)(2). These models show that PAPs encase the core polymerase, likely promoting complex assembly and stability, and that PEP can interact with DNA and the nascent mRNA. It also provides insight into the molecular details of enzymatic activities found in several PAPs: superoxide dismutase, lysine methyltransferase, thioredoxin and amino acid ligase. This work lays the foundation for a more sophisticated understanding of the regulation of plastid gene expression and its role in plant development and adaptation.

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Exploiting seed priming as a mean to address drought tolerance in maize

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Climate change poses serious implications for the agri-food sector. Specifically, drought, characterized by prolonged periods of water scarcity, has strong detrimental effects on crop productivity. To mitigate the effects of drought, sustainable agricultural practices are highly required. Drought stress is well-studied mostly during the vegetative and reproductive stages, while its effects on germination are largely overlooked. Therefore, this work proposes to investigate the effects of drought at the germination stage in a vast collection of local maize varieties. The objectives of the work include: (1) identification of maize varieties susceptible or tolerant to drought, and (2) development of sustainable protocols to enhance seed germination under drought. This is proposed by using plant-derived biostimulants (PBs), natural substances that can promote plant growth and stress resilience while reducing the input of synthetic fertilizers. PBs are employed for seed priming, a technology designed to improve germination performance. PBs from red chicory and cauliflower waste products are obtained and applied as seed priming agents to investigate drought resilience at the germination stage in maize. The germination efficiency is monitored for 14 days under soil drought stress under greenhouse conditions. Multiple germination parameters (percentage, speed, synchrony, uniformity, seedling growth) are monitored to evaluate the effects of priming treatments and drought levels. Preliminary results evidence that PBs improve seed germinability under mild drought. This work is part of the project NODES which has received funding from the MUR – M4C2 1.5 of PNRR funded by the European Union - NextGenerationEU (Grant agreement no. ECS00000036).

Keywords: Climate change, drought, biostimulants, sustainable, bio-economy, seed priming, maize.

Metabolomic profiling of heat-stressed grape berries

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The projected rise in mean air temperatures together with the frequency, intensity, and length of heat waves in many wine-growing regions worldwide will profoundly impact grape berry development and quality. Several studies have been conducted, and a large set of molecular data was produced to understand understand better the impact of high temperatures on grape berry development and metabolism [1]. According to these data, it is highly likely that the metabolomic dynamics could be strongly modulated by heat stress (HS). Hence, the objective of the present study is to investigate the metabolome profiling on grape berries, exposed or not, to high temperatures. We applied HS directly on clusters from *V. vinifera* L. Cabernet Sauvignon (heat-sensitive genotype) and *V. vinifera* L. Merlot (heat-tolerant genotype) at different developmental stages. HS was applied continuously from 8:00 am to 16:00 pm for up to 10 days in the greenhouse. The temperature difference between the HS-treated and control bunches was 10°C. Berry samples were collected after both short-term and long-term HS treatment, and metabolomic analyses were conducted using the untargeted LC-MS approach technique. Data processing was performed by MS-DIAL 4.94 and MetaboAnalyst 6.0. Our first set of results highlights metabolites and distinct biochemical pathways impacted by HS, according to the thermotolerance ability of the evaluated cultivars. Our data also underline the temporal dynamics of metabolic responses triggered by HS, highlighting the importance of characterizing these metabolic changes at different time scales.

Keywords: grapevine, berry quality, metabolomics, high temperature, climate change

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Linking stomatal dynamics and hydraulics with leaf anatomy and photosynthetic pathway in *Alloteropsis semialata*

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Anatomical structure and photosynthetic pathway influence stomatal dynamics and water relations, and further impact the balance between carbon fixation and water loss in plants. However, little is known about how the evolution of C_4 photosynthesis interacts with anatomical structure and environmental factors to change stomatal dynamics and hydraulic traits. In this study, *Alloteropsis semialata* was used as a model system to show that C_4 individuals had a slower stomatal opening speed than C_3 species for a given guard cell length. Among C_4 diploids, stomatal opening was faster when plants migrated into wetter habitats. However, polyploid formation in some C_4 lineages resulted in larger guard cells, which further slowed stomatal opening. In addition, the enlargement of bundle sheath tissue in C_4 compared with non-C_4 plants was associated with greater leaf capacitance. There was a positive relationship between minor vein density and leaf hydraulic conductance across both C_3 and C_4 lineages, with the high vein density of Kranz anatomy linked to greater conductance. However, these traits only showed a weak relationship among C_4 plants. The anatomical changes accompanying the transition to C_4 photosynthesis were also associated with higher leaf capacitance and greater hydraulic conductance, but a less negative turgor loss point. However, subsequent diversification of opening speed and hydraulic traits have been caused by secondary adaptations to climate and polyploid formation.

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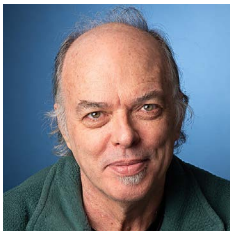

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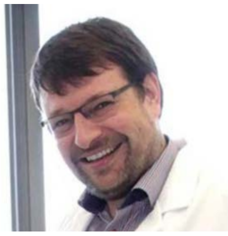

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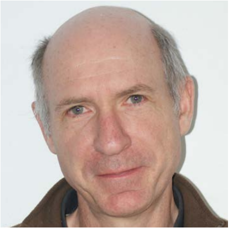

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