

Welcome to the 14th International Conference of the French Society of Plant Biology



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INTRODUCTION

The Organizing Committee, the Scientific Committee, the Federation of the European Societies of Plant Biology, the French Society of Plant Biology and the Biosciences and Biotechnology Institute of Aix-Marseille welcome you to Plant Biology Europe.

This international meeting covers a wide range of Plant Science topics across multiple disciplines and at different scales.

Among the many different themes that are being addressed during the meeting, a particular emphasis is placed on plants and climate changes, algal biology and bioenergy.

SCIENTIFIC COMMITTEE

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CRAG, Barcelona

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IRD, Montpellier

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GENERAL INFORMATION

Registration desk

There are no registration desks.

Name badges

Participants are requested to wear name badges at all times during the conference hours.

Bank, shops and services

You will find all facilities in the city center of Marseille (cash dispensers, currency exchange service, pharmacy, dozens of bars, restaurants and shops).

Tourist information

The tourist information office (<https://www.marseille-tourisme.com/>) is located on La Canebière, not far from the Vieux Port.

Police and Emergency

A police station is located on Avenue de la Corse or La Canebière, nearby the tourist information office. Medical emergency: Hôpital de la Conception, 147 boulevard Baille, 13005 Marseille. Subway M1: stop Baille. The general emergency phone number for all Europe is: 112. In France, you can also use: Medical emergency: 15. Police (or Gendarmerie): 17. Fire emergency: 18.

VENUE

PALAIS DU PHARO

58 boulevard Charles Livon, 13007 Marseille

From the City Center:

- Buses 82 and 82S at a 4 minutes walking distance, bus stop Le Pharo
- Buses 54, 83 at a 9 minutes walking distance, bus stop Place du 4 Septembre

From the Train Station Marseille – St Charles:

- Bus 82S – direct, commute of 28 minutes
- Subway M1 – 2 stops to the Old Port and then Buses 82 or 82S, commute of 30 minutes

From the Airport of Marseille:

- Shuttle bus L091 from the airport to the train station and then the public transportation as mentioned above

By Car – Parking:

- Q-Park Pharo at a 5 minutes walking distance
- Parking Indigo Marseille Vieux Port La Criée at a 10 minutes walking distance
- 120 Blvd de la Corderie Parking at a 17 minutes walking distance

In view of the heavy traffic in the city of Marseille, we strongly recommend that you use public transportation.

Information on public transport website of Marseille:

<https://www.rtm.fr/>

DETAILED PROGRAM

MONDAY 3 JULY

- 09:00 – 09:30 Opening Ceremony – Amphitheater 900
- 09:30 – 10:15 Plenary – Amphitheater 900
Malcom Bennett, University of Nottingham, United Kingdom
Uncovering the hidden half of plants: discovering novel ways roots sense and adapt to heterogeneous environments.
- 10:15 – 11:00 Plenary – Amphitheater 900
Raffaella Balestrini, National Research Council of Italy (CNR-IPSP), Italy
A central role of root symbionts: the plant response to environmental stresses
- 11:00 – 11:30 Coffee Break
- 11:30 – 13:00 Session 1: Plant and algal development and evolution Plenary Amphitheater 900
Chair: **Yoan Coudert**, CNRS/Ecole Normale Sup. de Lyon, France
- 11:30 – 11:50 **Air channels create a directional light signal to regulate hypocotyl phototropism**
Chrisitan FANKHAUSER
- 11:50 – 12:10 **Understanding how flowering plants build communication devices on their petals**
Lucie RIGLET
- 12:10 – 12:30 **A new framework for root gravitropic response kinetics**
Marta DEL BIANCO
- 12:30 – 12:50 **Developmental patterning of head-like inflorescences in Asteraceae**
Paula Elomaa
- 12:50 – 13:00 **Yoan Coudert**
Q&A



Session 2: Interfaces with plant and soil microbiota

Room 120

Chair: **Raffaella Balestrini**, National Research Council of Italy (CNR-IPSP), Italy

- 11:30 – 11:50 **Impact of double root symbiosis (arbuscular mycorrhiza and nodulation) on nutrient distribution in cereal crop-legume interaction**
Pierre-Emmanuel COURTY
- 11:50 – 12:10 **Evolution of microbial community dynamics during field retting of hemp “*Canabis Sativa L.*”**
Eliane BOU ORM
- 12:10 – 12:30 **Psychrotolerant plant-associated bacteria can enhance cold tolerance in crop plants**
Michelle PERAZZOLLI
- 12:30 – 12:50 **Role of zaxinone a novel growth-promoting apocarotenoid metabolite, in shaping rice rhizomicrobiota**
Teresa MAZZARELLA
- 12:50 – 13:00 **Raffaella Balestrini**
Q&A

Session 3: The genetic architecture of quantitative traits in plants

Room 76

Chair: **Martin Lascoux**, Sweden

- 11:30 – 11:50 **Fusing genome simulation and crop models for computer-aided breeding in future environments**
Arnaud DESBIEZ-PIAT
- 11:50 – 12:10 **Regulation of sulfur content in *Arabidopsis thaliana* natural variants**
Daniela RISTOVA
- 12:10 – 12:30 **Pervasive Under-Dominance in Gene Expression Underlying Emergent Growth Trajectories in *Arabidopsis thaliana* Hybrids**
Wei YUAN

- 12:30 – 12:50 **Reconsidering photoperiod-sensitivity for maize adaption to climate change**
Justine DROUAULT
- 12:50 – 13:00 **Martin Lascoux**
Q&A
- 13:00 – 14:00 Lunch
- 14:00 – 14:45 Plenary – Amphitheater 900
Marie Barberon, University of Geneva, Switzerland
Plasticity of root permeability for nutrient acquisition
- 14:45 – 15:30 Plenary – Amphitheater 900
Juliette de Meaux, University of Cologne, Germany
*Polygenic selection and the evolution of gene expression in *Arabidopsis lyrata**
- 15:30 – 16:00 Coffee Break
- 16:00 – 17:30 Session 4: Macro- and micro- nutrients in plants Amphitheater 900
Chair: **Jérémy Lothier**, University of Angers, France
- 16:00 – 16:20 **The ability of Sorghum bicolor to cope with ammonium nutrition depends on root PEPC activity**
Marin Pena AGUSTIN JAVIER
- 16:20 – 16:40 **Effect of N And Fe deficiencies in poplar roots and root exudates metabolites**
María Teresa CIESCHI VILLALBA
- 16:40 – 17:00 **Regulation of CRFs in plant nitrogen (N) sensing and signalling**
Marina BORGES OSORIO
- 17:00 – 17:20 **To be or not to be: a glimpse of micronutrients role in the prediction of plant tissue fate in soybean embryo axis**
Joao Paulo RODRIGUES MARQUES

17:20 – 17:40 **Unravelling the spatiotemporal component of carrier-mediated nutrient transport in Arabidopsis thalian roots**
Kevin ROBE

17:40 – 17:50 **Jérémy Lothier**
Q&A

Session 5: Domestication in retrospect and the future of breeding
Room 120

Chair: **Maud Tenailon**, CNRS, Paris-Saclay, France

16:00 – 16:20 **Changes in competitive ability over the course of durum wheat domestication are mediated by plant functional traits**
Taina LEMOINE

16:20 – 16:40 **Genetic and phenotypic diversity in timothy and a closely related species**
Yousef RAHIMI

16:40 – 17:00 **Genome-wide association studies on DNA pools identifies promising maize landraces and genomic regions to develop next generation varieties**
Stéphane NICOLAS

17:00 – 17:20 **Soil, climate and host genotype shape the seed transmissible microbiome structure in the fonio cereal**
Heribert HIRT

17:20 – 17:30 **Maud Tenailon**
Q&A

17:30 – 17:50 **FESPB Award for Best Young Scientist**
Adaptation and mitigation strategies for grapevine response to climate change based on its physiology
Nazareth Torres



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Session 6: Chromosomes and chromatin dynamics

Room 76

Chair: **Mathilde Grelon**, IJPB, Versailles, France

16:00 – 16:20 **Chromatin dynamics during fertilization of a liverwort, *Marchantia polymorpha***

Tetsuya HISANAGA

16:20 – 16:40 **Identification of the first synaptonemal complex central element proteins in plants**

Marion PEUCH

16:40 – 17:00 **Horizontal gene transfer in *Hordeum* species**

Marek SZECOWKA

17:00 – 17:10 **Mathilde Grelon**

Q&A

17:10 – 17:30 **FESPB Award for Best Young Scientist**

Exploring the Genetic Variability of Bean Germplasm for Nutritional Benefits

Carla Sofia Santos

TUESDAY 4 JULY

- 09:00 – 09:45 Plenary – Amphitheater 900
Kirsten Bomblies, ETH Zürich, Switzerland
Getting organised – the (re)evolution of fertility after genome duplication
- 09:45 – 10:30 Plenary – Amphitheater 900
Karel Riha, CEITEC MU, Brno, Czech Republic
P-bodies and post-transcriptional gene regulation in plant reproduction and stress response
- 10:30 – 11:00 Coffee Break

11:00 – 12:30

Session 7: Plant responses to abiotic stresses (Session 1)
Amphitheater 900

Chairs: **Laurent Laplaze**, IRD, Montpellier, France

Abdelazziz Smouni, Université Mohamed V, Rabat, Maroc

11:00 – 11:20 **Improving tomato plant growth under salt and heat stress – rhizosphere-based solutions**

Bruno SOUSA

11:20 – 11:40 **Coupling chloroplast activity to environmental constraints: TOR set the brake on photosynthesis**

Stefano D'ALESSANDRO

11:40 – 12:00 **RabA-mediated plasma membrane trafficking increases plant tolerance to drought and heat**

Yehoram LSHEM

12:00 – 12:20 **New insights on magnesium deficiency-induced molecular alterations in Arabidopsis thaliana**

Armand D. ANOMAN

12:20 – 12:30 **Laurent Laplaze & Abdelazziz Smouni**
Q&A

Session 8: Plant reproduction: mechanisms and evolution
Room 120

Chair: **Susana Coelho**, MPI, Germany

11:00 – 11:20 **The F-box protein UFO controls flower development by redirecting the master transcription factor LEAFY to new cis-elements**

François PARCY

11:20 – 11:40 **Timely endosperm elimination in Arabidopsis requires a programmed cell death pathway regulated by NAC transcription factors**

Nicolas M. DOLL

11:40 – 12:00 **MAP Kinase signaling in cell polarity – a lesson from the plant tolerance to drought and heat**

Martin BAYER



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12:00 – 12:20 **Evolutionary interplay between polyploidy and self-incompatibility in plants: case studies from allo- and autotetraploid Brassicaceae lineages**
Xavier VEKEMANS

12:20 – 12:30 **Susana Coelho**
Q&A

Session 9: Genome editing and its use for plant breeding
Room 76

Chair: **Josep Casacuberta & Ivan Reyna-Llorens**, Spain

11:00 – 11:20 **Controlling transcription from within transcribed regions in plants**
Yoav VOICHEK

11:20 – 11:40 **An iterative gene editing strategy broadens eIF4E1 genetic diversity in Solanum Lycopersicum, triggering resistance to multiple potyvirus isolates**
Kyoka KUROIWA

11:40 – 12:00 **Predictable gene editing through Prime Editing in model plants and potential for crop breeding**
Fabien NOGUE

12:00 – 12:20 **CRISPR-based tool development to engineer plant genomes at the megabase scale**
Julia ARRAIZA RIBERA

12:20 – 12:30 **Josep Casacuberta & Ivan Reyna-Llorens**
Q&A

12:30 – 12:45 **Publishing with Molecular Plant and Plant Communications**
Symposium by Molecular Plant

12:30 – 13:30 Lunch



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- 13:30 – 14:15 Plenary – Amphitheater 900
Mark Aarts, University of Wageningen - WUR, Wageningen, Netherlands
Arabidopsis thaliana natural variation for photosynthesis: a model to guide improving crop photosynthesis?
- 14:15 – 15:00 Plenary – Amphitheater 900
Daide Bulgarelli, University of Dundee – JHI, United Kingdoms
Structure, function and host control of the rhizosphere microbiota
- 15:00 – 15:30 Coffee Break
- 15:30 – 17:00 Session 10: Plant responses to abiotic stresses (Session 2)
Amphitheater 900
Chairs: **Laurent Laplaze**, IRD, Montpellier, France
Abdelazziz Smouni, Université Mohamed V, Rabat, Maroc
- 15:30 – 15:50 **Physiological and molecular responses of the Greek Mustard (*Hirschfeldia incana* L.) to Pb stress**
Said EL HASNAOUI
- 15:50 – 16:10 **Characterization of a uranium-tolerant green microalga with high potential for the remediation of metal-polluted waters**
Camille BEAULIER
- 16:10 – 16:30 **Physiological drought responses of plane trees in an urban context and impact on isoprene emissions**
Juliette LEYMARIE
- 16:30 – 16:50 **Restricted O₂ consumption in pea roots induced by hexanoic acid is linked to depletion of Krebs cycle substrates**
Sara GARGIULO
- 16:50 – 17:00 **Laurent Laplaze & Abdelazziz Smouni**
Q&A

Session 11: Organellar biology

Room 120

Chair: **Ben Field**, BIAM, Marseille, France

- 15:30 – 15:50 **CRY1-to-GUN1 anterograde pathway promotes early PSII biogenesis**
Chaojun CUI
- 15:50 – 16:10 **Genetic inactivation of mitochondrial complexes I and IV in Physcomitrium patens: deciphering the role of respiration in plant bioenergetics and primary metabolism**
Antoni Mateu VERA VIVES
- 16:10 – 16:30 **Role of mitochondrial activities in the under-ground early development of Arabidopsis seedlings**
Livia MERENDINO-ISENI
- 16:30 – 16:50 **Cytonuclear interactions in auto- and allopolyploids of Festuca-Lolium complex**
Jana SZECOWKA
- 16:50 – 17:00 **Ben Field**
Q&A

Session 12: Comparative genomics

Room 76

Chair: **Bruno Contreras-Moreira**, CSIC Zaragoza, Spain

- 15:30 – 15:50 **The first pan-genome of a non-vascular plant broadens the understanding of land plants adaptation to their environment**
Chloé BEAULIEU
- 15:50 – 16:10 **Adapting CRISPR from Physcomitrium patens to sexually dimorphic moss, Ceratodon purpureus**
Emilie-Katherine TAVERNIER
- 16:10 – 16:30 **The evolution of Arabidopsis centromeres**
Fernando RABANAL

- 16:30 – 16:50 **Divide and conquer: Evolutionary adaptations of the plant cytoskeleton during cell division**
Katharina BÜRSTENBINDER
- 16:50 – 17:00 **Bruno Contreras-Moreira**
Q&A
- 17:00 – 18:00 Poster Session A

WEDNESDAY 5 JULY

- 09:00 – 09:45 Plenary – Amphitheater 900
Aline Muyle, CEFE – CNRS Montpellier, FRANCE
Gene DNA methylation in plants: selective pressures and sex chromosome evolution
- 09:45 – 10:30 Plenary – Amphitheater 900
Bruno Contreras-Moreira, CSIC, Zaragoza, Spain
*Learning to build and interrogate the pangenome of *Brachypodium distachyon**
- 10:30 – 11:00 Coffee Break
- 11:00 – 12:30 Session 13: Plant adaptation to climate change
Amphitheater 900
Chairs: **Laura de Gara**, Italy
- 11:00 – 11:20 **Partial root drying of maize grown in a split-root system leads to local and systemic metabolic adjustments and hydraulic redistribution**
Monika WIMMER
- 11:20 – 11:40 **Two examples of genome-wide evolutionary responses of European forest trees to past climate changes**
Martin LASCOUX
- 11:40 – 12:00 **Exploring phenotypic space for mining genotypes and alleles in maize**
Jonas RODRIGUEZ



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12:00 – 12:20 **Impact of development-induced structural changes on drought responses of winter oilseed rape leaf – NMR relaxometry, water relations and multi-omics investigations**
Pierre-Nicolas BOULC'H

12:20 – 12:30 **Laura de Gara**
Q&A

Session 14: Epigenetic mechanisms and responses in plants
Room 120

Chair: **Leandro Quadrana**, France

11:00 – 11:20 **Uncovering the gene expression regulatory mechanisms underlying self-incompatibility dominance networks in Arabidopsis**
Rita A. BATISTA

11:20 – 11:40 **Global increase of the nuclear transcriptional regime during Arabidopsis photomorphogenesis: effects on gene expression**
Clara RICHET-BOURBOUSSE

11:40 – 12:00 **Deciphering the epigenetic and molecular logic of WOX5 function in the columella stem cell niche of Arabidopsis thaliana**
Ning ZHANG

12:00 – 12:20 **Mechanism of E3 ubiquitin ligase SIXERICO1/3 regulating high temperature resistance in tomato plants**
Kaixin WANG

12:20 – 12:30 **Leandro Quadrana**
Q&A

Session 15: Mechanics and stress responses
Room 76

Chair: **Benoit Landrein**, France

11:00 – 11:20 **Limited water stress modulates expression of circadian clock genes in Brachypodium distachyon**

roots and induces differential response of proline-metabolism related genes

Janos GYORGYEY

11:20 – 11:40 **Dynamics of the calcium signal elicited by mechanical stimulation of Arabidopsis root**

Sébastien THOMINE

11:40 – 12:00 **Multiscale modelling of cell adhesion and separation in plants**

Rawen BEN MALEK

12:00 – 12:20 **It's just a phase: Structural characterization of LLPS and its role in temperature sensing in plants**

Chloe ZUBIETA

12:20 – 12:30 **Benoit Landrein**

Q&A

12:30 – 13:30

Lunch

13:30 – 14:30

Poster Session B

14:30 – 15:30

Poster Session C

15:30 – 16:00

Coffee Break

16:00 – 17:30

Round table Plant Act

THURSDAY 6 JULY

09:00 – 09:45

Plenary – Amphitheater 900

Rosa Lozano-Duran, University of Tübingen – ZMBP, Tübingen, Germany

How to conquer a plant using just eight genes: learning from geminiviruses

09:45 – 10:30

Plenary – Amphitheater 900

Gwyneth Ingram, CNRS Lyon, FRANCE

Controlling communication during reproductive development: The genesis and roles of apoplastic barriers

10:30 – 11:00

Coffee Break



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11:00 – 12:30

Session 16: Plant Immunity

Amphitheater 900

Chair: **Rosa Loranzo-Duran**, Germany

11:00 – 11:20 **Investigating antiviral defenses protecting plant stem cells and germline**

Marco INCARBONE

11:20 – 11:40 **Gradual immune system maturation in the root affects plant microbe interaction**

Elhanan TZIPILEVICH

11:40 – 12:00 **Role of the plasma membrane signalling during plant virus propagation**

Sébastien MONGRAND

12:00 – 12:20 **Engineering danger sensing and signaling in plant immunity: use of oligosaccharins to enhance durum wheat resistance to fusariosis**

Valentina BIGINI

12:20 – 12:30 **Rosa Loranzo-Duran**

Q&A

Session 17: Photosynthesis: understanding and progress in its manipulation

Room 120

Chair: **Xenie Johnson**, CEA CNRS AMU, France

11:00 – 11:20 **From Algae to Sea Slugs: Functioning of Stolen Chloroplasts in Animal Cells**

Luca MORELLI

11:20 – 11:40 **Two vacuolar channels from the ALMT family regulate C4-organic acids metabolism**

Roxane DOIREAU

11:40 – 12:00 **From oxidative stress to antenna quenching: regulation of qH-energy dissipation in plants**

Aurélie CREPING



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12:00 – 12:20 **Chloroplast redox status modulates leaf development via changes in proteasomal activity and endoreduplication index**
Arce ROCIO CECILIA

12:20 – 12:30 **Xenie Johnson**
Q&A

Session 18: The genetics of natural variation of plant- plant interactions
Room 76

Chair: **Fabrice Roux**, Montpellier, France, Christophe Robaglia, BIAM, Marseille, France

11:00 – 11:20 **Evolution of cooperation in post-green revolution durum wheat cultivars**
Michel COLOMBO

11:20 – 11:40 **Chromatin regulation of and by gene islands in plants**
Louis-Valentin METEIGNIER

11:40 – 12:00 **Identification of genes and metabolites controlling plant-plant interaction**
Sophie JASINKSI

12:00 – 12:20 **Molecular bases of plant-plant interactions: identification of the molecular pathways depending on ESC-1, a RLK involved in the competitive response in Arabidopsis thaliana**
Marie INVERNIZZI

12:20 – 12:30 **Fabrice Roux**
Q&A

12:30 – 13:00 Closing Plenary



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ORAL PRESENTATIONS

PLENARY KEYNOTES

Uncovering the hidden half of plants: discovering novel ways roots sense and adapt to heterogeneous environments.

Malcom Bennett¹

¹University of Nottingham, Nottingham NG7 2RD, United Kingdoms

Plants exhibit a remarkable ability to modify their growth and development in response to environmental signals. This ability is particularly striking during root development where plants have to forage in highly heterogeneous environments. I will describe how plant hormones enable roots to sense and/or respond to environmental signals. Examples include discovering how plants sense availability of moisture in soil by linking intercellular water fluxes with movement of hormones like auxin and ABA, triggering changes in root branching designed to maximise capture of soil resources (Mehra et al, 2022, Science). Plant roots also employ volatile signals like ethylene to sense changes in soil physical properties like compaction stress using a novel gas diffusion based mechanism (Pandey et al, 2021, Science). I will conclude by describing how mechanistic insights about hormone-regulated root plasticity is helping in the design of stress tolerant crops.

Session sponsored by



A central role of root symbionts: the plant response to environmental stresses

Raffaella Balestrini¹

¹National Research Council of Italy (CNR-IPSP), Italy

Soil bacterial and fungal communities serve as the first protection for plants. Rhizosphere and root-associated microorganisms improve plant growth and wellness, and the plant ability to interact and cooperate with them should be considered as a fundamental trait for achieving more stress-tolerant and climate-flexible crops. Environmental stressors can seriously reduce the growth and reproduction of plants, affecting the plant physiology and metabolism. Beneficial microorganisms activate specific stress-protective pathways that assist plant hosts to mitigate the negative effects of stresses, promoting multiple mechanisms of protection that counteract detrimental effects. Furthermore, environmental stresses can also compromise the association of plants with beneficial microbes, thereby significantly limiting the plant fitness. The molecular bases that underlie the improved plant tolerance mediated

by soil microorganisms, as well as the decisions made by plants to engage with the appropriate microorganisms, are an area of intense research. Gleaned knowledge on this subject could in fact enable the development of crops that benefit more from the associated microbiota. Among root symbionts, the arbuscular mycorrhizal fungi undoubtedly play a relevant role in plant stress resilience processes, which will be here discussed in depth.

Plasticity of root permeability for nutrient acquisition

Marie Barberon¹

¹University of Geneva, Geneva, Switzerland

Plant roots forage the soil to acquire water and nutrients for growth and development. This function is closely linked to their anatomy: water and nutrients move radially through the concentric layers of epidermis, cortex, and endodermis before entering the vasculature. This arrangement allows for three uptake scenarios: the “symplastic pathway”, where the outer cells actively take up nutrients, which are then transported from cell to cell through plasmodesmata; the “apoplastic pathway”, where nutrients are transported in the apoplast and blocked by the endodermal apoplastic barrier (Casparian strips); and the “coupled trans-cellular pathway”, where nutrients are transported sequentially from one cell to another by polarized influx and efflux carriers and are barred by the endodermal diffusion barrier (suberin lamellae). My group aims to functionally characterize these pathways for nutrient acquisition by a combination of physiology, cell biology and developmental approaches. We are particularly interested in suberin lamellae and plasmodesmata function and regulations for nutrient acquisition.

Polygenic selection and the evolution of gene expression in *Arabidopsis lyrata*

Juliette de Meaux¹

¹University of Cologne, Cologne, Germany

Gene expression is presumably the first manifestation of gene function. Its variation is thus evidently shaped by natural selection. Patterns of gene expression variation, unlike other complex phenotypes, have the advantage that they can inform us on the molecular basis of physiological and morphological adaptation. I will review what the analysis of gene expression taught us about adaptation in the outcrossing plant species *Arabidopsis lyrata*, which evolved to withstand drought better than its relatives while also adapting to local conditions. We will discuss the role of gene expression in the polygenic adaptation of natural populations.

Getting organised – the (re)evolution of fertility after genome duplication

Kirsten Bomblies¹

¹ETH Zürich, Zürich, Switzerland

Polyploids, which arise from whole genome duplication, have contributed to genome complexity in all eukaryotic lineages. Polyploids are also common among our most important crops, and the ability to generate new polyploids is a promising agricultural tool as it confers immediate and often lasting resistance to a range of abiotic stresses, particularly drought. But neopolyploids often have extremely low fertility, making it hard to understand how they could survive as novel lineages, and limiting their utility in agriculture. Understanding how evolved polyploids overcome the initial challenges neopolyploids face is thus of both fundamental and applied interest. A previous genome scan we did a decade ago in *Arabidopsis arenosa* revealed numerous genes under selection in the tetraploids that likely relate to the re-establishment of full fertility. One of the major groups of genes that came out of this encode proteins essential for meiosis, which is a well-known challenge facing polyploids. We use *Arabidopsis arenosa*, which occurs naturally as an autotetraploid and a diploid, and from which we can make neopolyploids by doubling the diploids. This three-way comparison gives powerful insights into what the initial problems are that polyploidy causes, and how selection can generate solutions to these issues. I will discuss what we have learned about the problems polyploids initially face, how the established polyploids evolved solutions to those problems, and the genes that we found are important. I will also discuss an additional fertility challenge we have identified, as well as two genes that solve that issue. These studies give insights into polyploid evolution, as well as information that can be used to improve the fertility of neopolyploids for breeding novel agriculturally useful plants.

P-bodies and post-transcriptional gene regulation in plant reproduction and stress response

Karel Riha¹

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Gene expression is a multilayer process that can be regulated at the level of RNA production, processing, transport, translation and RNA stability. Many of these processes are associated with membraneless organelles, dynamic structures formed by multivalent interactions of proteins and nucleic acids that may exhibit properties of liquid-liquid phase condensates. In my presentation I will explore the role of P-bodies, cytoplasmic biocondensates sequestering translationally repressed mRNA and RNA decay proteins, in plant germline differentiation and stress response. I will show how dynamic behavior of P-bodies contributes to the regulation of meiosis and discuss a broader function of these structures in other plant physiological processes.

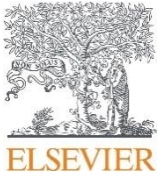
Arabidopsis thaliana natural variation for photosynthesis: a model to guide improving crop photosynthesis?

Mark Aarts¹

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Photosynthesis is the main driver of plant biomass production. While crop yields have been increased impressively through breeding the past century, there never has been a strong selection on high photosynthesis efficiency. With the growing demand for biobased materials, we are likely to soon need more high yielding crops. Can such be achieved by crop breeding for more efficient photosynthesis? We explore the opportunities to characterize the genetic variation for photosynthesis efficiency in the model species *Arabidopsis thaliana*. One of the challenges in investigating such genetic variation is the ability to adequately phenotype photosynthesis parameters. For this purpose, we use phenotyping platforms designed for high-throughput imaging of light use efficiency of photosystem II electron transport (Φ_{PSII} or F_q'/F_m') and related photosynthetic parameters through chlorophyll fluorescence measurements. It demonstrated to be very efficient and reliable in phenotyping several, large, genetically segregating *Arabidopsis* populations and diversity panels, under different growth conditions. The observed genotypic variation was used to identify nuclear encoded quantitative trait loci (QTL) for photosynthesis parameters, as well as variation residing on the chloroplast genome.

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Structure, function and host control of the rhizosphere microbiota

Davide Bulgarelli¹

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The microbiota populating the rhizosphere, the thin layer of soil surrounding plant roots, represents an untapped resource for sustainable crop production. The host genome drives, at least partially, the taxonomic and functional composition of these plant-microbial assemblages. Our lab uses barley, the world's fourth most cultivated cereal, as a model to gain novel insights in the genetic relationships between a plant genome and its associated microbiota. We previously demonstrated that wild and domesticated barley genotypes host contrasting microbiotas in the rhizosphere, and that this differential microbial recruitment is mediated by the barley genome. We built on these discoveries to implement an innovative approach where we used microbiota data as an external quantitative trait and high-resolution genomic information to identify regions of the barley genome shaping rhizosphere communities. In parallel, we capitalised on metagenomics sequencing and synthetic communities to define the probiotic potential of the microbiota of plants exposed to stress

conditions, including growth-limiting nitrogen supplies and pathogens. Here I will describe the experimental approaches that led us to these discoveries and the anticipated avenues for translational applications.

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**Molecular
Plant**

Gene DNA methylation in plants: selective pressures and sex chromosome evolution

Aline Muyle¹

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A longstanding question is whether epigenetics can play a role in adaptation. We know that, in plants, some epigenetic marks can be transmitted over many generations and accumulate epimutations over time. If these heritable epigenetic marks can affect the fitness of individuals, they could potentially be the target of selection and allow species adaptation like genetic alleles. However, it is difficult to assess the effect of epigenetic marks on fitness due to linked genetic variation. We used a population epigenomics approach relying on the Site Frequency Spectrum (SFS) to infer the intensity of selection acting on DNA methylation in the 1001 methylome dataset of *Arabidopsis thaliana*. Our work suggests that some genes methylated in the CG context are under selection to remain CG methylated. This selection could be due to an effect of CG gene body methylation on gene expression level. Over the past years, the role of epigenetics in driving sex chromosome evolution has been revealed, mostly in animals. During the second part of my talk, I will present recent results illustrating the importance of DNA methylation in Y chromosome degeneration and sex chromosome evolution in the plant *Silene latifolia*.

Learning to build and interrogate the pangenome of *Brachypodium distachyon*

Bruno Contreras-Moreira¹

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Pangenomes are the union of all genomic sequences known for a group individuals. These can be from different wild populations or diverse cultivars of a crop. Moreover, they often include non-domesticated related species that might provide alleles lost during breeding. Pangenomes are always unfinished, as new data can always be added. In this talk I will review how our community sampled *Brachypodium distachyon* plants around the Mediterranean, produced whole genome sequences for them and finally learnt, by trial and error, how to extract evolutionary and adaptation information from the resulting pangenome.

How to conquer a plant using just eight genes: learning from geminiviruses

Rosa Lozano-Durán¹

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Viruses, as intracellular parasites, need to subvert the host cell in order to enable viral replication and spread. Due to strict coding limitations, viruses commonly produce a reduced number of proteins; this is the case of geminiviruses, plant DNA viruses that are believed to contain only 4-8 translated open reading frames in their circular single-stranded genome. Strikingly, despite their limited armoury, geminiviruses are able to successfully infect host plants while dramatically altering plant development and physiology, ultimately causing devastating losses to crops worldwide. In our group, we aim to understand how geminiviruses manipulate the plant cell and lead to disease, for which we use a combination of approaches, including molecular biology, cell biology, and genetics. By studying individual viral proteins, our results have shed light onto the molecular mechanisms underlying the replication of viral DNA, plant anti-viral defence and geminiviral counter-defence, and symptom development; in addition, we are interested in the identification of novel virulence strategies potentially employed by geminiviruses to maximize their coding capacity and their impact on the host cell.

Controlling communication during reproductive development: The genesis and roles of apoplastic barriers

Gwyneth Ingram¹

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Angiosperm reproductive structures (anthers and ovules/seeds) are complex assemblies containing highly specialized, metabolically diverse, and in some cases genetically distinct compartments. Their successful development depends both on strict inter-tissue coordination, and upon selectively gated inter-tissue communication, particularly at the metabolic level. For these two requirements to be met, dynamic, extensive, and precise remodelling of tissue interfaces, affecting both symplastic (direct cytoplasm-cytoplasm) and apoplastic (involving diffusion through the extracellular matrix) connectivity, is a prerequisite. I will concentrate on apoplastic modifications occurring between key compartments in the developing seeds and anthers of *Arabidopsis thaliana*, and aim to illustrate how the timely deposition of intact apoplastic filters (barriers) is achieved in these contexts.

ORAL COMMUNICATION

SESSION 1: PLANT AND ALGAL DEVELOPMENT AND EVOLUTION

AIR CHANNELS CREATE A DIRECTIONAL LIGHT SIGNAL TO REGULATE HYPOCOTYL PHOTOTROPISM

Christian FANKHAUSER*

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Phototropism reorients aerial organs towards the light to improve photosynthesis. This response is initiated by blue light receptors called phototropins. A gradient of phototropin activation is believed to trigger asymmetric growth leading to growth re-orientation. However, how a light gradient is established across the stem to initiate phototropism is unclear. Here we show that intercellular air channels are required for an efficient phototropic response. Air channels enhance light scattering in Arabidopsis hypocotyls thereby steepening the light gradient across this photosensitive organ. We identify an embryonically expressed ABC transporter, which shapes the properties of cell walls surrounding air channels. Air channels contribute to efficient gas exchange with the atmosphere, but details about their development are scarce. We identify a key factor in the development of intercellular air channels and establishes the functional importance of these structures in phototropism.

UNDERSTANDING HOW FLOWERING PLANTS BUILD COMMUNICATION DEVICES ON THEIR PETALS

Lucie RIGLET^{1*}; Alice FAIRNIE ¹; May YEO ¹; Argyris ZARDILIS ¹; Edwige POYROUD ¹

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Colourful patterns on the petal epidermis are key signals to attract pollinators. Hibiscus trionum flowers display a striking bullseye pattern, made of a basal purple spot (flat, elongated, striated cells) and a white distal region (conical, smooth cells) separated by a boundary positioned at 1/3rd from the petal base. How is this boundary specified is unknown. We developed a quantitative imaging pipeline to decipher the mechanisms specifying the distinct regions of the bullseye in developing petals. We captured early cellular behaviour in petal epidermis and showed that growth and division are not uniform, following a pre-pattern long before the bullseye become visible. To probe the mechanisms accounting for a change in bullseye dimensions, we characterised natural variants/transgenic lines that differ in bullseye size and tested whether bumblebees can distinguish and prefer specific proportions. We are now building a computational model to simulate petal growth/patterning mechanisms.

A NEW FRAMEWORK FOR ROOT GRAVITROPIC RESPONSE KINETICS

Marta DEL BIANCO^{1*}; Sujit NATH ²; Robert THOMAS ²; Katelyn SAGEMAN-FURNAS ³; Suruchi ROYCHOUDHRY ²; Matyas FENDRYCH ⁴; Jiri FRIML ⁵; Netta COHEN ²; Stefan KEPINSKI ²

¹ Italian Space Agency; ² University of Leeds; ³ Duke University; ⁴ IEB; ⁵ ISTA
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A conserved trait in plants is the ability to adapt to environmental cues, including the gravity vector. In this context, angle dependence is necessary for the establishment of plant architecture, a fundamental trait for crop improvement. The debate regarding the nature of angle dependence is ongoing. We developed a high-throughput imaging system for the analysis of Arabidopsis primary root reorientation kinetics. Using this new tool, we were able to detect a previously undescribed complexity of the gravitropic response. In spite of this complexity, we show that angle, magnitude of the gravitropic response and auxin asymmetry are highly correlated across the entire response. By means of computational modelling, we suggest that the response can be described by a new angle-dependent viscoelastic model, with time-dependent behavioural regimes. Combined, our work provides a novel coherent framework for understanding the biophysical and molecular basis of gravitropism.

DEVELOPMENTAL PATTERNING OF HEAD-LIKE INFLORESCENCES IN ASTERACEAE

Paula EMOLAA^{1*}; Zhang TENG¹; Cieslak MIKOLAJ²; Owens ANDREW²; Gu PHILMO²; Hart JEREMY²; Wang FENG¹; Prusinkiewicz PRZEMYSŁAW²

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The inflorescences in the sunflower family (Asteraceae), flower heads or capitula, are iconic examples of the geometric beauty found in nature. They may consist of hundreds of florets arranged in regular left- and right-curving spirals whose numbers follow the mathematical Fibonacci series. We have recently resolved the growth dynamics of flower heads in the model plant *Gerbera hybrida* and shown with DR5 reporter lines how high spiral numbers emerge in the expanding meristem. The molecular data was integrated into a computational model to explain phyllotactic patterning in Asteraceae heads. We have extended our studies to explore how head vasculature is associated with organ phyllotaxis. By applying synchrotron-based micro-CT imaging, we have explored the vascular networks in heads in diverse Asteraceae species. Despite the large differences, the observed vascular patterns can be generated by a common computational model suggesting a conserved underlying mechanism.

SESSION 2: INTERFACES WITH PLANT AND SOIL MICROBIOTA

IMPACT OF DOUBLE ROOT SYMBIOSIS (ARBUSCULAR MYCORRHIZA AND NODULATION) ON NUTRIENT DISTRIBUTION IN CEREAL CROP-LEGUME INTERACTION.

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Intercropping cereal crops with legumes offers an agroecological solution to improve sustainability and environmental impacts. Roots of cereal crops and legumes could be connected by a network formed by the mycelium of arbuscular mycorrhizal fungi (AMF). Legumes also form nodules with rhizobial bacteria. In these mutualistic symbioses, nutrients are exchanged between plants and root microorganisms. We addressed following questions: How is the legume and the cereal crop nutrition modulated when one or two root symbioses are formed? How plant physiology and AMF species modulate the functioning of mycorrhizal roots and nodules? Gene regulation of plant and symbionts was studied in roots and nodules through transcriptomic analysis. The 3D repartition of AMF in the root system was assessed after root transpiration. Nutrient exchanges were studied through stable isotope tracing. Our results give new insights in the functioning and physiology of plant/microbe and plant-plant interaction.

EVOLUTION OF MICROBIAL COMMUNITY DYNAMICS DURING FIELD RETTING OF HEMP "CANNABIS SATIVA L."

Eliane BOU ORM^{1*}; Anne BERGERET ²; Suvajit MUKHERJEE ³; Sébastien GREC ³; Sandrine BAYLE ¹; Jean-Charles BENEZET ²; Luc MALHAUTIER ¹

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Hemp field retting is a bioprocess in which the stem cell wall polysaccharide network is degraded by a complex microbial consortium to facilitate further extraction of fibres. This process is carried out by farmers in an empirical way and depends on pedoclimatic conditions, which makes it difficult to control. This work aims to unravel the biodiversity-ecosystem function relationship. Retting is examined by exploring the temporal dynamics of the microbial communities considering 4 ecological indicators (density, diversity, structure, and activity). DNA metabarcoding approach and enzymatic activity are performed. The stem and extracted fiber color, the fiber biochemical composition, and the stem microstructure are evaluated. Results show that the first 2 weeks of retting are characterized by intense microbial



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colonization and significant biochemical changes in the composition of the fiber cell wall. This study provides the first thorough description of the hemp field retting microbiome.

PSYCHROTOLERANT PLANT-ASSOCIATED BACTERIA CAN ENHANCE COLD TOLERANCE IN CROP PLANTS

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Climate change is causing warmer winter and spring periods with increased frequency of chilling and frost damage on crop plants. Psychrotolerant plant-associated bacteria could improve plant tolerance to cold stress. This work aims to identify psychrotolerant bacteria associated with cold-adapted plants and to understand mechanisms responsible for cold tolerance in crops. The bacterial community structure associated with alpine and Antarctic plants was characterized by metataxonomic analyses and taxa associated with cold tolerance were highlighted. Psychrotolerant bacterial endophytes collected from cold-adapted plants improved the shoot growth of tomato seedlings under chilling stress and limited frost damage on apple and strawberry leaves. Bacterium-inoculated plants showed enhanced metabolic changes in response to chilling exposure and recovery, suggesting intimate interactions between psychrotolerant bacteria and the plant host.

ROLE OF ZAXINONE, A NOVEL GROWTH-PROMOTING APOCAROTENOID METABOLITE, IN SHAPING RICE RHIZOMICROBIOTA.

Teresa MAZZARELLA^{*}; Matteo CHIALVA; Jian You WANG; Cristina VOTTA; Patrizia VACCINO; Salim AL-BABILI; Luisa LANFRANCO ¹; Valentina FIORILLI

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Zaxinone is an apocarotenoid, produced by Zaxinone Synthase (ZAS) which belongs to the carotenoid cleavage dioxygenases gene family. Zaxinone plays a role in plant growth and arbuscular mycorrhiza (AM) establishment. A rice loss-of-function zas mutant shows a retarded root and shoot growth and higher levels of strigolactones (SLs). The impact on plant fitness and on SLs biosynthesis suggests that zaxinone could also influence the recruitment of root microbial communities. We used meta-barcoding analysis to study bacteria and fungi in bulk soil, rhizosphere, and root endosphere in rice wild-type (wt) plants and zas mutant lines across a time point experiment. Our data showed that the microbial communities changed in the different compartments and during plant development; furthermore, zas mutants showed a different relative abundance of AM fungi compared to wt. Overall, these findings highlight that ZAS knock-out influences the assemblage of rice root microbiota.



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SESSION 3: THE GENETIC ARCHITECTURE OF QUANTITATIVE TRAITS IN PLANTS

FUSING GENOME SIMULATION AND CROP MODELS FOR COMPUTER-AIDED BREEDING IN FUTURE ENVIRONMENTS

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A new frontier for plant breeding is to predict the behavior of unobserved crop varieties in unobserved environments. We present a virtual system that couples genomic prediction (GP), genome simulation, and crop growth models (CGMs). Trained from existing populations, the genetic architecture of input parameters for a CGM are embedded into a genome simulator. In turn, a CGM which is used to model the behavior of simulated offspring in different environments. Modeling flowering time in maize as proof-of-concept, we are testing how interactions between recombination, genetic architecture, and parental sampling determine the genotypic space of input trait parameters. We also test how this influences genotype-to-phenotype relations modeled by the CGM. We aim to develop a framework to guide breeding of new crop varieties under climate change and test for new breeding strategies.

REGULATION OF SULFUR CONTENT IN ARABIDOPSIS THALIANA NATURAL VARIANTS

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Sulfur (S) is an essential nutrient for all organisms. Apart from the importance of S for primary metabolism, S plays important role in the synthesis of secondary metabolites that are crucial for biotic interactions. Moreover, plant secondary metabolites can act as regulators of development, growth and defense, and can be reallocated to primary metabolism.

Natural variation of S leaf content was observed in numerous plant species, in *A. thaliana* accessions it can vary up to 6-fold, suggesting that such variations may be signs of differing adaptive strategies being employed by plants facing different biotic or abiotic pressures. Here, we use quantitative genetics combined with systems biology and physiology, to identify the importance of this variation. We found significant associations of S content with sulfate uptake, accumulation of other macronutrients, expression of genes involved in secondary metabolism, and concentrations of various metabolites.



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PERVASIVE UNDER-DOMINANCE IN GENE EXPRESSION UNDERLYING EMERGENT GROWTH TRAJECTORIES IN ARABIDOPSIS THALIANA HYBRIDS

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We are only beginning to incorporate non-additive effects into our understanding of complex traits such as growth. F1 hybrids provide a facile means for comparing between additivity and non-additivity by creating many novel allele combinations and interactions. We studied the transcriptome of 141 random crosses of *Arabidopsis thaliana*, and found additivity to be rare, consistently observed for only about 300 genes enriched for roles in stress response. Rare-allele burden affects the expression level of these genes but not F1 growth. Non-additive gene expression, especially at below parental average level, is in comparison much more common. Rare-allele burden in this set, unlike in the additive ones, is strongly correlated with F1 growth. This underscores under-dominance as the predominant driver of emergent behavior of rosette growth in *A. thaliana* F1 hybrids, laying the foundation for understanding molecular mechanisms and evolutionary forces that lead to dominance complementation.

RECONSIDERING PHOTOPERIOD-SENSITIVITY FOR MAIZE ADAPTION TO CLIMATE CHANGE

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Flowering time, which is fundamental to local adaptation and productivity of crops, is controlled by integrated networks of external and internal signals. Maize, initially short-day dependent, spread from tropical to temperate environments, which has shifted the control of flowering regulation toward temperature and away from photoperiod sensitivity (PS). As temperatures rise, the shift from photoperiod pathway to autonomous pathway (temperature driven) will affect maize production. We hypothesize that genetic diversity for PS contained in tropical material could be reintroduced into temperate varieties to facilitate their adaptation to climate change. A series of PS haplotypes introgressed into temperate genetic backgrounds and evaluated across a daylength gradient was tested for effects on flowering time and yield, and used to parametrize models for predicting photoperiodic effects. This will provide insights for maize adaptation to climate change by manipulating flowering time.



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SESSION 4: MACRO- AND MICRO-NUTRIENT IN PLANTS

THE ABILITY OF SORGHUM BICOLOR TO COPE WITH AMMONIUM NUTRITION DEPENDS ON ROOT PEPC ACTIVITY

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Ammonium (NH₄⁺) is the preferred N source for most plant species. However, when NH₄⁺ is the sole source of N most crops develop stress symptoms. The causes of ammonium stress are multifactorial and include pH alteration, excessive energy consumption, and other nutrients imbalance. Adequate C supply can enhance ammonium stress tolerance, and the cytosolic enzyme phosphoenolpyruvate carboxylase (PEPC) plays a vital role in the replenishment of C skeleton in the tricarboxylic acid cycle (TCA). Sorghum has six PEPC isoforms encoded by SbPPC1-6 genes. SbPPC3 encodes the non-photosynthetic PEPC3 isoform, which is the predominant form in roots and is induced by different stresses, including ammonium stress. We observed the growth of sorghum knocked down plants for SbPPC3 was compromised under ammonium nutrition. Moreover, they displayed alterations in the C and N metabolic pathways, evidencing that root PEPC activity is key for sorghum to cope with ammonium nutrition.

EFFECT OF N AND FE DEFICIENCIES IN POPLAR ROOTS AND ROOT EXUDATES METABOLITES

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Poplar is a fast-growing tree that combines rapid maturation and wide geographic distribution with economic relevance for wood and biomass production. Poplar is an important model to study wood formation. In contrast, poplar responses to environmental stresses and especially nutrient deficiencies have been scarcely studied. Thus, the aim of this work is to determine how metabolomics profiles of poplar roots and root exudates are affected by N and Fe deficiency. This is expected to highlight metabolic strategies acquired by the plant to cope with nutritional deficiencies. Plants presented deficiency symptoms as iron chlorosis, decrease in biomass weight and water uptake. Poplar roots, root exudation in pure water as well as in nutrient solution were collected and analyzed by LC MS/MS. As preliminary results, poplar roots accumulated specific flavonoids, salicylates, stilbenes and coumarins. Future studies will aim at investigating the effect of combined N limitation and Fe deficiencies.

REGULATION OF CRFS IN PLANT NITROGEN (N) SENSING AND SIGNALLING

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Nitrogen in soil is a key factor limiting plant yield. Plant success relies on rapid sensing of intrinsic N status and activation of molecular responses to adjust N use. Plants take up N mainly as NO₃⁻ and NH₄⁺. NO₃⁻ is often the preferred N source, while excessive NH₄⁺ uptake may be toxic. NO₃⁻ signalling affects many cellular processes, in tight link with auxin and CK signalling: through complex crosstalk, they orchestrate a communication network driving plant growth. My focus is on Cytokinin Response Factors (CRFs). CRFs intersect auxin and CK signalling with stress responses. Recent reports link CRFs to NO₃⁻-induced transcriptional reprogramming, and to a role in integrating N sensing in roots via CK to auxin-guided shoot growth. Yet, how CRFs are regulated remains unclear. Combining cell biology, genetics, proteomics, and physiology of Arabidopsis, I dissect the molecular layers of CRF regulation and their role in modulating adaptive growth in response to different N sources.

TO BE OR NOT TO BE: A GLIMPSE OF MICRONUTRIENTS ROLE IN THE PREDICTION OF PLANT TISSUE FATE IN SOYBEAN EMBRYO AXIS

Joao Paulo RODRIGUES MARQUES^{1*}; Gabriel SGARBIERO MONTANHA ²; Hudson WALLACE PEREIRA DE CARVALHO ²

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Soybean is an important commodity for the Brazilian GDP. The 2022/2023 season is estimated to reach ca. 152,7 million tons. Coupling synchrotron-based techniques, such as high-resolution X-ray fluorescence spectroscopy with plant anatomy favor the understanding fate of tissue-specific nutrients. We focused in a ontogenetic study of the soybean hypocotyl-radicle axis (SHRA) understanding elemental-tissue markers in pristine seed tissues and their role in the differentiation of SHRA. The hypocotyl presents a circle pattern of manganese (Mn) surrounding the vascular cylinder and iron (Fe) wedges in specific regions between the hypocotyl vascular bundles. At the radicle, Mn and calcium (Ca) are related to the meristem and surrounded by Fe. At 48 hai, the Mn circle in the hypocotyl predicts the differentiation of endodermis/pericycle, whereas the Fe wedge is linked to protoxylem and metaxylem differentiation regions. At the root apex, the elemental tissue-specific patterns are kept.



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UNRAVELLING THE SPATIOTEMPORAL COMPONENT OF CARRIER-MEDIATED NUTRIENT TRANSPORT IN ARABIDOPSIS THALIANA ROOTS.

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Within the roots, nutrients and water are transported from the epidermis to the vasculature through a combination of three pathways. A common feature of these pathways is the need of plasma membrane located carriers for ions to enter the symplast. The identification of the main nutrient carriers started several decades ago, however, due to the lack of information on in planta carriers' localization, these pathways are still poorly characterized and the path of nutrients within the root remain elusive. To tackle this issue, we are generating a developmental map of the main nutrient carriers in roots. For this purpose, we assess expression and carriers' localization in root. Also, as we are still ignorant regarding the relations between suberin deposition in the root endodermis and nutrient carrier localization and function, we are investigating its impact on nutrient carriers. The data obtained in this project will help redefine our models of nutrient transport in roots.



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SESSION 5: DOMESTICATION IN RETROSPECT AND THE FUTURE OF BREEDING

CHANGES IN COMPETITIVE ABILITY OVER THE COURSE OF DURUM WHEAT DOMESTICATION ARE MEDIATED BY PLANT FUNCTIONAL TRAITS

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Domestication and plant breeding have shifted phenotypic values of crops, leading to phenotypic convergence between species, the so-called domestication syndrome. Since the Green Revolution, such syndrome has been supposedly related to a decrease in crop competitive ability, since breeding has targeted reduced intraspecific competition in order to maximize group yield. Yet, such hypothesis remains poorly experimentally tested. Here we measured above and belowground traits of 40 genotypes representative of key stages in durum wheat domestication and assessed their competitive ability when grown with the same competitor. We found non-linear changes in trait values between the four compartments, which reflected changes in competitive ability, highlighting that the direction of conscious or unconscious selection varied during the course of domestication. Interestingly, we found that elite lines were more tolerant to competition than wild genotypes but less tolerant than landraces.

GENETIC AND PHENOTYPIC DIVERSITY IN TIMOTHY AND A CLOSELY RELATED SPECIES

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The development and growth in domesticated and wild accessions of timothy (*Phleum pratense*) and its closely related species *P. nodosum* from the Nordic countries were evaluated in the field and in a greenhouse. Domestication seems not to have had a strong effect on the biomass production since there was no significant difference in this trait between timothy cultivars and wild accessions, or between cultivars and wild accessions of *P. nodosum*. However, most cultivars flowered earlier than the wild accessions in both species. We found some of the wild accessions producing higher proportion of vegetative tillers and to be important genetic resources for improved forage quality. Based on whole-genome resequencing, different LD decay patterns was found among different types of accessions, as



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well as significantly different nucleotide diversity and genomic differentiation was found and used to identify regions under selection through Extended Haplotype Homozygosity (EHH).

GENOME-WIDE ASSOCIATION STUDIES ON DNA POOLS IDENTIFIES PROMISING MAIZE LANDRACES AND GENOMIC REGIONS TO DEVELOP NEXT GENERATION VARIETIES

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Landraces have a large diversity that could help to cope with climatic change and low input agriculture. To identify promising maize landraces and genomic regions to enlarge the genetic diversity of modern varieties, the DNA pools of 156 American and European landraces as well as 264 French landraces were genotyped with a SNP array. French landraces were evaluated for different agronomic traits. They were compared to elite cultivars produced across 20th century, represented by 327 inbred lines. We identified several genomic regions involved in agronomic traits, environmental adaptation, tolerance to abiotic stresses by detecting selective footprints and studying association with both environmental variables and agronomic traits. Promising landraces were identified by estimating their genomic contribution to inbred lines and by genomic selection. Most landraces do not have closely related lines while 10 landraces have a lot and cumulated half of the total contribution to inbred lines.

SOIL, CLIMATE AND HOST GENOTYPE SHAPE THE SEED TRANSMISSIBLE MICROBIOME STRUCTURE IN THE FONIO CEREAL

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Domestication of crops resulted in the selection of valuable traits for modern agriculture but also the loss of beneficial alleles. Since plants evolve in close interaction with microbial partners, we analyzed the contribution and vertical transmission of the seed microbiome in the semi-domesticated cereal fonio millet, a crop that can grow in dry and hot conditions. We found that each of the seven genetic distinct fonio groups harbors a highly diverse endophytic bacterial taxon. In addition to a shared and heritable core microbiome of 191 strains, the fonio seed microbiome was shaped by soil composition, host genotype, and geo-climatic factors. Using genome-wide association studies (GWAS), embryo development and



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stress/defense response loci were found to contribute to microbiome diversity in fonio. Our study expands our understanding of the role of the seed-associated microbiome in plant fitness, establishing seed-microbiome engineering as a potential new technology in crop breeding.

SESSION 6: CHROMOSOME DYNAMICS

CHROMATIN DYNAMICS DURING FERTILIZATION OF A LIVERWORT, *MARCHANTIA POLYMORPHA*

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In most eukaryotes, sperm chromatin is distinct because nucleosomes are replaced by non-histone proteins such as protamines. Upon fertilization protamines must be removed from the paternal chromatin to restore histones-based chromatin. In animals, this essential process is achieved via de novo nucleosome assembly by the HIRA complex. Surprisingly, hira mutants are fertile in flowering plants and little is known about de novo nucleosome assembly at fertilization in plants that evolved sperm with protamine. To study this process, we established the zygote of the liverwort *Marchantia polymorpha* as a model. In vitro fertilization enabled us to describe chromatin dynamics of the male pronucleus. Further, we isolated a mutant defective in nucleosome assembly on the male pronucleus, suggesting that the causal gene is involved in de novo nucleosome assembly on the paternal genome. Further analyses will identify molecular mechanisms regulating chromatin dynamics during fertilization in plants.

IDENTIFICATION OF THE FIRST SYNAPTONEMAL COMPLEX CENTRAL ELEMENT PROTEINS IN PLANTS

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During meiosis prophase, the synaptonemal complex is formed between homologous chromosomes. This proteinaceous complex has a highly conserved ultrastructure across species and is involved in the formation and/or regulation of crossing overs, which are essential for the first meiotic division. It is composed of three elements: the lateral elements, the transverse filaments, and the central elements. In several model species, central element proteins have been characterized, but, as of today, no central elements have been described in plants.

Through cytological work we report the identification of the first plant central element proteins, SCEP1 and SCEP2, identified at meiotic stages in *Arabidopsis thaliana*. Interactions between these proteins and known synaptonemal complex proteins were identified by multimer structure predictions using AlphaFold2 and yeast two hybrid assays. A phylogenetic study shows that SCEP1 and SCEP2 homologs can be found in all major Angiosperm clades.

HORIZONTAL GENE TRANSFER IN HORDEUM SPECIES

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Horizontal gene transfer (HGT) can offer an evolutionary advantage but its stability and transmission to future generations are not well understood in plants. *Hordeum* is a suitable model to study these processes. Species of sect. *Stenostachys* obtained foreign DNA, including protein-coding genes, from diverse panicoid grasses via at least nine independent HGTs. Segments of over 440 kb and 219 kb containing five stress-related protein-coding genes and transposable elements (TEs) were found in *Hordeum bogdanii* and *Hordeum pubiflorum* respectively.

Screening of genomes of several *Hordeum* species for foreign DNA using assemblies of Panicoideae family grasses identified further putative foreign DNA regions. We are identifying TEs and protein-coding genes in these regions. We aim to explore the diversity of TEs in *Hordeum* genomes, test their possible association with foreign protein-coding genes, their activity, and their potential association with transfers from multiple panicoid donors.

SESSION 7: PLANT RESPONSES TO ABIOTIC STRESSES (1)

IMPROVING TOMATO PLANT GROWTH UNDER SALT AND HEAT STRESS – RHIZOSPHERE-BASED SOLUTIONS

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Mediterranean tomato production is facing major challenges under the current climatic scenario. Following our previous studies on the impacts of combined salt and heat stress on tomato plants, this work focused on the role of arbuscular mycorrhizal fungi (AMF), in conjunction with biochar, in improving tomato performance under these stress conditions. Upon 21 days of stress exposure, mycorrhizal plants possessed higher tolerance to salt, heat, and combined stress, showing enhanced growth and increased flowering rate. In general, these plants also presented better photosynthetic performance and despite no major signs of oxidative stress being found among groups, they were able to modulate their antioxidant system, investing in non-enzymatic metabolites, mostly in roots. Thus, this efficient defensive crosstalk, possibly coupled with other mechanisms, shows that AMF- and biochar-based solutions represent a high-potential strategy to improve crop tolerance to climate change.

COUPLING CHLOROPLAST ACTIVITY TO ENVIRONMENTAL CONSTRAINTS: TOR SET THE BRAKE ON PHOTOSYNTHESIS

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Chloroplasts are the powerhouse of the plant cell, yet they are resource-intensive and may cause oxidative damage if their activity overshoots the demands of the cell. Therefore, the activity of chloroplast needs to be regulated to match the environmental conditions especially under stress. I will present our results on a novel post-translational mechanism linking the conserved TOR kinase that promotes growth and the ancient guanosine tetraphosphate



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(ppGpp) signaling pathway that regulates chloroplast activity. I will show that RelA SpoT Homologue 3 (RSH3), a nuclear-encoded chloroplastic enzyme responsible for ppGpp biosynthesis, interacts directly with the TOR complex via a plant-specific N-terminal region (NTR) which is hyper-phosphorylated in a TOR-dependent manner. Altogether we demonstrated that the TOR-RSH3 pathway provides a direct post-translational mechanism to adjust chloroplast activity with plant growth, a new precedent for the regulation of organellar function by TOR

RABA-MEDIATED PLASMA MEMBRANE TRAFFICKING INCREASES PLANT TOLERANCE TO DROUGHT AND HEAT.

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High temperatures and prolonged droughts are increasingly damaging to crops with continued climate change. Yet, processes of plasma membrane (PM) repair and trafficking in plant tolerance of heat and drought are poorly understood. Rab proteins are small GTPases important in vesicle trafficking regulation. Little is known about the role of RabA in plant response to abiotic stress. Recently we showed that RabA2b transcription was upregulated in Arabidopsis during abiotic stress response. Analysis of the RabA2b native promoter during stress showed strong activity in plant vasculature and required abscisic acid. Overexpressing RabA2b in Arabidopsis strikingly improved drought resistance and enhanced thermal tolerance. RabA2b localized to the PM. PM proteomic analysis showed enrichment of stress coping proteins and cuticle modifiers. Finally, the cuticle permeability of transgenic leaves was greatly reduced. Overall, we provide new insights into RabA2b modes of action in stress tolerance.

NEW INSIGHTS ON MAGNESIUM DEFICIENCY-INDUCED MOLECULAR ALTERATIONS IN ARABIDOPSIS THALIANA

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Magnesium (Mg²⁺) is involved in more than 600 biological processes in plants, including but not limited to photosynthesis, carbon assimilation, translation, synthesis of nucleic acids and energy production. Mg²⁺ deficiency (Mg-D) is characterized amongst others by starch and soluble sugars accumulation, chlorosis and growth reduction. Recently, it was shown that Mg-D also impairs the circadian clock function. To gain more insights into those processes affected by Mg-D, and especially the interconnections between Mg-D, carbohydrates and the circadian clock, we further characterized Arabidopsis thaliana plants under Mg-D, utilizing a



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metabolomic and transcriptomic approach, and also mutants affected in their starch content. Our results show that the impact of Mg-D on the circadian clock is not mediated by starch. Through a coexpression network we built from our transcriptomic data, we also unveil new possible targets of Mg-D.

SESSION 8: PLANT REPRODUCTION: MECHANISMS AND EVOLUTION

THE F-BOX PROTEIN UFO CONTROLS FLOWER DEVELOPMENT BY REDIRECTING THE MASTER TRANSCRIPTION FACTOR LEAFY TO NEW CIS-ELEMENTS

Francois PARCY*¹; Philippe RIEU¹; Laura TURCHI¹; Emmanuel THEVENON¹; Eleftherios ZARKADAS²; Max NANAQ³; Hicham CHAHTANE¹; Gabrielle TICHITSKY¹; Jeremy LUCAS¹; Romain BLANC-MATHIEU¹; Chloe ZUBIETA¹; Guy SCHOEHN²

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In angiosperms, flower development requires the combined action of the transcription factor LEAFY (LFY) and the ubiquitin ligase adaptor F-box protein, UNUSUAL FLORAL ORGANS (UFO), but the molecular mechanism underlying this synergy has remained unknown. On the basis of biochemical and genome-wide studies, we establish that UFO instead acts by forming an active transcriptional complex with LFY at newly discovered regulatory elements. Structural characterization of the LFY-UFO-DNA complex by cryo-electron microscopy further demonstrates that UFO performs this function by directly interacting with both LFY and DNA. Finally, we propose that this complex might have a deep evolutionary origin, largely predating flowering plants. This work reveals a unique mechanism of an F-box protein directly modulating the DNA binding specificity of a master transcription factor.

TIMELY ENDOSPERM ELIMINATION IN ARABIDOPSIS REQUIRES A PROGRAMMED CELL DEATH PATHWAY REGULATED BY NAC TRANSCRIPTION FACTORS.

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Due to its nutritive value, the endosperm in plant seeds is vital for humankind. Endosperm size is modulated by the degree of its elimination during embryo invasion. In Arabidopsis, cell wall weakening mediated by the bHLH-type transcription factor ZHOUPH promotes embryo invasion. However, whether a programmed cell death (PCD) process is involved in endosperm elimination has been subject to debate. Here we show that PCD promoted by multiple NAC transcription factors in the embryo-adjacent endosperm is the cause of gradual endosperm elimination. We show that accelerating PCD in the zhouphi mutant rescues its embryo growth defects, and that zhouphi nac multiple mutant endosperm persists until seed desiccation. These data suggest that a combination of cell wall weakening and PCD facilitate endosperm elimination and embryo invasion

MAP KINASE SIGNALING IN CELL POLARITY – A LESSON FROM THE PLANT EMBRYO

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Breaking symmetry by asymmetric cell divisions is essential for establishing different cell identities in multi-cellular development. Cell-cell signaling by receptor kinase/MAP kinase signaling pathways seems to be a reoccurring mechanism in polarizing cells and establishing different cell identities in land plants.

We are using the early Arabidopsis embryo as system to study initial events in cell polarization by the ERECTA-YODA signaling pathway – a prototype receptor kinase/MAP kinase signaling pathway. By comparing the function of this pathway in the embryo with its role in planar patterning of the leaf epidermis, we identified principal functions as well as context-specific modifications.

We present new data on the impact of polar YODA activation on early embryogenesis and shed light on the mechanism and evolution of distinct modes of YDA activation in the zygote on a molecular and structural level.

EVOLUTIONARY INTERPLAY BETWEEN POLYPLOIDY AND SELF-INCOMPATIBILITY IN PLANTS: CASE STUDIES FROM ALLO- AND AUTOTETRAPLOID BRASSICACEAE LINEAGES

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Polyploidy and mating system transitions are major processes of plant evolution. Theory predicts a positive association between polyploidy and autogamy, but empirical surveys have produced mixed results. We studied two polyploid Brassicaceae lineages: natural autotetraploid populations of *Arabidopsis arenosa*; synthetic allotetraploid individuals between *Capsella grandiflora* and *C. orientalis* mimicking evolution of *C. bursa-pastoris*. Using a recently developed pipeline to genotype the self-incompatibility (SI) locus from short reads data, we show that *A. arenosa* polyploids have similar S-allele diversity as diploids, suggesting the absence of strong bottleneck associated with polyploidy and functional SI. We also show that synthetic *Capsella* allopolyploids' mating system can be inferred from dominance relationships between S-alleles inherited from the parents. Hence the interplay between polyploidy and SI is complex but can be predicted from their functional and evolutionary properties.



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SESSION 9: GENOME EDITING AND ITS USE FOR PLANT BREEDING

CONTROLLING TRANSCRIPTION FROM WITHIN TRANSCRIBED REGIONS IN PLANTS

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Transcriptional regulatory sequences control when and where genes are transcribed. Despite separate evolution of cell type-specific gene expression mechanisms, plant transcription regulation understanding is often extrapolated from animal systems. We investigated how transcription regulatory sequences are organized in *A. thaliana*. We found that transcription factor binding and expression quantitative trait loci are enriched downstream of the transcription start site (TSS). Using a massively parallel reporter assay we show sequences downstream of the TSS control transcription, losing this ability when positioned upstream of the TSS. This position-dependent effect is unique to plants, unlike animal enhancers that are position independent. We also identified a sequence motif within transcribed regions that controls gene expression of thousands of genes during development. These observations likely describe only the tip of the iceberg of differences between plant and animal transcription.

AN ITERATIVE GENE EDITING STRATEGY BROADENS EIF4E1 GENETIC DIVERSITY IN SOLANUM LYCOPERSICUM, TRIGGERING RESISTANCE TO MULTIPLE POTYVIRUS ISOLATES

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Resistance to potyviruses have been largely provided by the selection of natural variant alleles of eukaryotic translation initiation factors (eIF) 4E in many crops. However, the sources of such variability are limited for certain species. Different methods of mutagenesis have been applied on the eIF4E genes to generate virus resistance, but with limited success due to their physiological importance and redundancy. Here, we sequentially edited in cherry tomato the genomic sequences coding for two regions of eIF4E1, known to be important for susceptibility to potyviruses. We show that editing of one region is not sufficient but combining amino acid mutations in both regions result in resistance to multiple potyviruses without impairing translation initiation. Our work demonstrates that precision editing allows to design plant factors based on the evolutionarily selected alleles and enlarge the gene pool to potentially provide advantageous phenotypes such as pathogen resistance.

PREDICTABLE GENE EDITING THROUGH PRIME EDITING IN MODEL PLANTS AND POTENTIAL FOR CROP BREEDING

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CRISPR-Cas9 technology has transformed plant research and precision crop breeding since its discovery. However, the system is mostly inefficient for predicted editing. Recently, Prime Editing technology has been developed to allow for simultaneous generation of nucleotide transitions and transversions and short defined indels. We report here an improved methodology for routine Prime Editing in two model plants *P. patens* and *Arabidopsis* and evidences that prime editing is possible in the crop plant potato. Modifications of the 3' extension of the pegRNA, and the addition of synonymous mutations in the RT-template sequence of the pegRNA improve the editing rate without affecting the quality of the edits. In addition, we demonstrate the possibility of performing Prime Editing with two independently coded peptides, facilitating future improvements of the Prime Editor strategy in plants. Finally, potential and limitations of Prime Editing in plants will be discussed.

CRISPR-BASED TOOL DEVELOPMENT TO ENGINEER PLANT GENOMES AT THE MEGABASE SCALE

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CRISPR/Cas has revolutionized genome engineering due to its straightforward and inexpensive design. Despite being widely adopted in plant genetics research, CRISPR-based tools are still mostly limited to single base-pair modifications. Here, we present the first efforts in the development of a platform to delete, edit and write plant genomes at the megabase scale in *Physcomitrium patens*. We aim to establish a pipeline for systematic plant transformation and multiplex editing at a high-throughput level. We have optimized Cas9 multiplexing efficiency, increasing the frequency of single mutants to the regular recovery of 5-plex mutants. In parallel, we have used dual targeting to delete large genomic regions (up to 20Kb) and have achieved efficient multiplex oligonucleotide insertion using homology arms of 20nt. Taken together, these results show the potential of our platform to perform genome-wide genetic screens, precise chromosomal restructuring, and minimizations in a plant context

SESSION 10: PLANT RESPONSES TO ABIOTIC STRESSES (2)

PHYSIOLOGICAL, AND MOLECULAR RESPONSES OF THE GREEK MUSTARD (*HIRSCHFELDIA INCANA* L.) TO Pb STRESS

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Lead (Pb) contamination is a widespread environmental problem due to its toxicity to living organisms. We identified *H. incana*, collected from the mine in the Eastern region of Morocco, as a Pb-tolerant and accumulator plant. *H. incana* plants cultivated in hydroponic conditions at 100 µM of Pb showed high tolerance and high Pb accumulation capacity in roots and aboveground parts. We then carried out RNA deep transcriptome sequencing of *H. incana* under two conditions, control, and treatment with 100 µM of Pb(NO₃)₂. A total of 577 and 270 differentially expressed genes were identified in roots and aboveground parts respectively in response to Pb stress. Several genes related to the jasmonic acid biosynthesis pathway were upregulated, suggesting jasmonate to be involved in *H. incana* L responses to Pb stress. In this study, we provide data for further genomic analyses of the molecular mechanisms leading to Pb tolerance and accumulation in plants.

CHARACTERIZATION OF A URANIUM-TOLERANT MICROALGA OF THE GENUS *COELASTRELLA* WITH HIGH POTENTIAL FOR THE REMEDIATION OF METAL-POLLUTED WATERS

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Uranium (U) pollution of terrestrial and aquatic ecosystems poses a significant threat to the environment and human health because this radionuclide is chemotoxic. Here, we isolated a unicellular green microalga of the genus *Coelastrella* that is much more tolerant to U than *Chlamydomonas reinhardtii* and *Chlorella vulgaris*. *Coelastrella* is able to accumulate U very rapidly and, then, progressively release it into the medium, behaving as an excluder to limit the toxic effects of U. The ability of *Coelastrella* to capture U is remarkably high, with up to 600 mg U sorbed per g dry biomass. *Coelastrella* is able to grow and capture 25-55% of U from natural metal-contaminated waters from a reclaimed U mine. The isolated *Coelastrella* sp. is a very promising microalga for the remediation of polluted waters with valorization of algal biomass that accumulates neutral lipids. In addition, *Coelastrella* is a very promising model to identify response and adaptation mechanisms to U stress.

PHYSIOLOGICAL DROUGHT RESPONSES OF PLANE TREES IN AN URBAN CONTEXT AND IMPACT ON ISOPRENE EMISSIONS

Juliette LEYMARIE^{1*}; Alice CLAUDE ¹; Ludvine BRAJON ²; Luis LEITAO ¹; Christophe BOISSAERD ³; Séverine PLANCHAIS ²; Anne REPELLIN ¹; Paul NADAM ¹; Valentin LAMETH ¹; Carmen KALALIAN ³; Valérie GROS ³; Jean-François CASTELL ⁴; Ruben PUGA FREITAS ¹

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Trees emit a wide range of Biogenic Volatile Organic Compounds (BVOC) that can lead to secondary pollutants formation. As BVOC emissions are regulated by environmental factors, their abundance could be modified by the stressful environment of cities. Young *Platanus x hispanica* trees, known as strong isoprene emitters, were grown in a suburb of Paris, France, and subjected to controlled water deficit. We complemented the ecophysiological characterization of tree response to drought with the quantitation of isoprene emissions at the leaf scale, using an original device. This provided insightful information about isoprene emissions in relation to water use efficiency and photosynthesis. Early response to drought induced stomatal limitation of carbon assimilation, with insignificant impact on isoprene emissions. As stress progressed, leaf shedding occurred and the trees showed lower isoprene emissions, most likely a result of the disruption of photosynthetic energy conversion process.

RESTRICTED O₂ CONSUMPTION IN PEA ROOTS INDUCED BY HEXANOIC ACID IS LINKED TO DEPLETION OF KREBS CYCLE SUBSTRATES

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Hexanoic acid (HA) produced by microorganisms in waterlogged soils causes a decline in plant root O₂ consumption, but it is unknown if lack of respiration is due to mitochondrial dysfunction or substrate starvation. We treated *Pisum sativum* L. roots with 20 mM HA acid at pH 5 and 6 for 1 h and measured leakage of electrolytes, malate, citrate and non-structural carbohydrates (NSC). Afterwards, mitochondria were isolated to assess their functionality, evaluated as electrical potential formation and O₂ consumption. HA treatment resulted in root tissue extrusion of K⁺, malate, citrate and NSC, but the leakage of the organic acids and NSC was increased at pH 5 with the inhibition of O₂ consumption and a slight alteration of mitochondrial activity. In conclusion, we propose that undissociated form of HA enters the root cells inducing the efflux of organic acids and NSC and the starvation of mitochondrial respiratory substrates of Krebs cycle with a subsequent decline in O₂ consumption.



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SESSION 11: ORGANELLAR BIOLOGY

CRY1-TO-GUN1 ANTEROGRADE PATHWAY PROMOTES EARLY PSII BIOGENESIS

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Genomes Uncoupled 1 (GUN1), a nuclear-encoded chloroplast pentatricopeptide repeat (PPR) protein, mediates chloroplast-to-nucleus retrograde signaling as a master integrator of diverse retrograde signals. Although PPR proteins primarily function in organelle RNA metabolism, a target RNA of GUN1 remained unknown. This study reveals GUN1 as a bonafide PPR protein with the C-terminal small MutS-related (SMR) domain, which recognizes and processes a psbD transcript derived from a blue light-responsive promoter (BLRP), a transcript referred to as psbD BLRP. Loss of GUN1 decelerated early chloroplast biogenesis with a significantly compromised synthesis of psbD BLRP-encoded D2 protein. A subsequent reverse genetics approach unraveled GUN1 as a downstream effector of the blue light receptor CRY1, revealing an anterograde signaling pathway from CRY1 to GUN1, required to promote psbD BLRP processing, D2 synthesis, and PSII biogenesis.

GENETIC INACTIVATION OF MITOCHONDRIAL COMPLEXES I AND IV IN PHYSCOMITRIUM PATENS: DECIPHERING THE ROLE OF RESPIRATION IN PLANT BIOENERGETICS AND PRIMARY METABOLISM

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In photosynthetic organisms, respiration is needed to support metabolism during the night and in non-photosynthetic tissues. Respiration is also active under illumination, although the molecular pathways connecting photosynthetic and respiratory metabolisms are far from clear. We used the moss *Physcomitrium patens* as a model. We monitored cytosolic ATP levels during dark-to-light transitions and observed a light-driven increase of ATP that involves both chloroplast and mitochondria. We also isolated lines lacking a functional respiratory complex I or IV, that show impaired growth and unbalanced carbon and nitrogen metabolism. Even though the photosynthetic apparatus is not different in composition, the respiratory mutants are photosynthetically less efficient, with reduced rates of both net CO₂ fixation and net O₂ evolution. Our results contribute to a better understanding of the interplay between photosynthesis and respiration in plants.



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ROLE OF MITOCHONDRIAL ACTIVITIES IN THE UNDER-GROUND EARLY DEVELOPMENT OF ARABIDOPSIS SEEDLINGS

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Under the soil, seedling development follows a dark-specific program (skoto-morphogenesis) consisting of small, non-green cotyledons, a long hypocotyl, and an apical hook to protect meristematic cells during emergence. In agriculture, farm machinery causes soil compaction that affects seedling emergence and O₂ diffusion (hypoxia), especially when soil is water-saturated after heavy rainfalls. We recently identified the role of mitochondrial COX-dependent respiration and AOX1A enzyme in reprogramming skoto-morphogenesis in response to mitochondrial stress in Arabidopsis.

In hypoxic conditions induced by soil compaction, mitochondrial respiration is impacted, and the resulting mitochondrial stress can promote the apical hook over-bending required for seedling emergence through the compact soil. We hypothesize that the functional state of the bio-energetic organelles, mitochondria, is used by seedlings as an environmental sensor to control developmental adaptation to the soil settings.

CYTONUCLEAR INTERACTIONS IN AUTO- AND ALLOPOLYPLOIDS OF FESTUCA-LOLIUM COMPLEX

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Key metabolic processes catalyzed by multi-subunit enzyme complexes which comprise nuclear- and organelle-encoded proteins are dependent on maintaining the stoichiometric ratios among the subunits. As polyploidization increases the number of nuclear genes without directly altering the dosage of the cytosolic genomes, cytonuclear interactions may be disrupted. We analyze mechanisms of restoration of the stoichiometry in auto- and allopolyploids of Festuca-Lolium complex. So far, our data suggest that increase in the chloroplast number and plastid genome copies only partially contribute to the restoration of the balance and we estimate the role of changes in gene expression.

Another challenge for allopolyploids is the coordination of biparentally inherited nuclear genome and genome of plastids inherited uniparentally. Therefore we study homoeologue specific expression of the nuclear-encoded genes involved in cytonuclear interactions to determine the contribution of each parental allele.

SESSION 12: COMPARATIVE GENOMICS

THE FIRST PAN-GENOME OF A NON-VASCULAR PLANT BROADENS THE UNDERSTANDING OF LAND PLANTS ADAPTATION TO THEIR ENVIRONMENT

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In plants, intraspecific comparative genomic studies have exclusively targeted angiosperms, due to the lack of genomic data in other lineages. To broaden our knowledge, we investigated the first genetic diversity dataset in a non-vascular plant. 134 accessions of *Marchantia polymorpha* were sequenced and combined with existing reference genomes to generate a pangenome.

We extracted the *M. polymorpha* core and accessory genomes. We compared them with angiosperms, revealing commonalities and clade-specific innovations.

We conducted GWAS of 5M SNPs with biotic and environmental variables to discover the basis of adaptation in this species. Among the candidate loci, we identified bryophyte-specific genes involved in secondary metabolites biosynthesis and originating from horizontal gene transfer.

These analyses demonstrate that studying intraspecific diversity beyond the angiosperms offers an unexplored context to discover innovations that allowed land plants to thrive.

ADAPTING CRISPR FROM *PHYSCOMITRIUM PATENS* TO SEXUALLY DIMORPHIC MOSS, *CERATODON PURPUREUS*.

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Here we demonstrate successful CRISPR-Cas9 genome editing in the dioecious moss species, *Ceratodon purpureus*. Using an existing selection system from the hermaphroditic moss, *Physcomitrium patens*, we demonstrated genetic knock-outs of the APT gene through CRISPR targeted mutagenesis. In addition, thanks to the shared innate, unique ability of these two mosses to efficiently undergo homology-directed repair (HDR), we showed targeted knock-ins of two reporter genes in *C. purpureus* via CRISPR mediated HDR. Our results suggest that the molecular tools available in *P. patens* can be extended to other mosses, making mosses powerful hubs for evolutionary studies. In particular, the conserved UV sex chromosome system in *C. purpureus* offers a valuable model for studying sex-specific regulatory networks.



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These findings pave the way for cross-species studies using phylogenetic and functional genomic analyses.

THE EVOLUTION OF ARABIDOPSIS CENTROMERES

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Despite their conserved function, centromeres show diverse sizes and structures between species, termed the centromere paradox. However, it is unknown whether centromere diversity reflects ancient trans-species variation, or instead, rapid post-speciation divergence. Furthermore, the mechanisms that generate centromere diversity have remained obscure. To address these questions, we assembled the centromeres from 66 *Arabidopsis thaliana* and two *A. lyrata* accessions with PacBio HiFi long-reads, revealing extreme intra- and inter-species diversity. We show that centrophilic ATHILA transposons have recently invaded the satellite arrays. To counter ATHILA invasion, chromosome-specific bursts of satellite homogenization generate higher-order repeats and purge transposons, consistent with cycles of repeat evolution, which ultimately contribute to speciation.

DIVIDE AND CONQUER: EVOLUTIONARY ADAPTATIONS OF THE PLANT CYTOSKELETON DURING CELL DIVISION

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The colonization of terrestrial habitats by ancestral streptophyte algae, followed by the rise of land plants was accompanied by a switch in the mode of cell division from a cleavage-like to an inside-out mechanisms, in which new cell walls are inserted at the cell center and expand centrifugally to fuse with the maternal cell wall at a predetermined cortical region. The switch in cell division coincides with the evolution of two plant-specific mitotic cytoskeleton arrays, the preprophase band and phragmoplast. The molecular mechanisms underlying these adaptations, however, are still enigmatic. Using a combination of phylogenetic, molecular, and cell biological analyses, we provide first evidence for emergence of plant-specific IQ67-Domain proteins in the streptophyte lineage and evolutionarily conserved functions in regulation of mitotic microtubule arrays, potentially by providing scaffolds that aided the rewiring and neo-functionalization of protein-protein-interaction networks.



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SESSION 13: PLANT ADAPTATION TO CLIMATE CHANGES

PARTIAL ROOT DRYING OF MAIZE GROWN IN A SPLIT-ROOT SYSTEM LEADS TO LOCAL AND SYSTEMIC METABOLIC ADJUSTMENTS AND HYDRAULIC REDISTRIBUTION

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In the field, plants are often exposed to non-uniform water supply, but little is known about physiological responses to partial root drying under limited water supply. Here we assessed whether compensatory water uptake and/or alteration of root architecture occurred under these conditions.

Maize was grown for 20 d in a split-root system, before applying 'local drought' or 'full drought' for 10 d. Shoot length and gas exchange were measured daily, root exudates were collected, biomass, relative water content (RWC), osmolality and proline content were determined at the final harvest.

Local drought resulted in reduced biomass, RWC and increased osmolality. A surprisingly well-maintained root growth in the dry root compartment was systemically achieved by hydraulic redistribution rather than by altering root architecture. Local and systemic osmolyte adjustments contributed to this hydraulic redistribution and enhanced water availability, and in consequence plant water relations

TWO EXAMPLES OF GENOME-WIDE EVOLUTIONARY RESPONSE OF EUROPEAN FOREST TREES TO PAST CLIMATE CHANGES

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While species response to climate change remains hard to forecast, past responses can be informative. In sessile oak (*Quercus petraea*), we monitored genomic changes since the Little Ice Age (LIA, 1450 to 1850). Allelic frequency changes were estimated for four age-structured cohorts dating back to 1680, in each of three different oak forests. We found imprints of genome-wide linked selection in the three forests during the late LIA, and a shift of selection during more recent time periods of the Anthropocene. In Norway spruce (*Picea abies*), we leveraged large genomic data to test for the presence of natural selection during recolonization and establishment of a contact zone in Scandinavia after the Last Glacial Maximum. We used different approaches to show that natural selection contributed to its rapid establishment and maintenance. Many of the loci under selection were related to phenology. Altogether, these two examples suggest that trees responded rapidly to past climatic cycles.



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EXPLORING PHENOTYPIC SPACE FOR MINING GENOTYPES AND ALLELES IN MAIZE

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Crop species rely on genetic and phenotypic diversity to adapt to various environments. Genotypes respond differently, resulting in genotype-by-environment interactions (GxE). Recent advances in phenomics and modeling allow for the prediction of GxE for traits related to sustainability and productivity. However, a phenotype-centered framework that effectively navigates the interplay between genetics, physiology, and the environment is needed. Here we present maize data from phenotyping platforms and field experiments and explore strategies to integrate concepts and techniques from ecophysiology, ecology, and math to: (i) define and describe phenotypic space across spatial, temporal, and biological scales; (ii) identify unique phenotypic combinations and constraints; and (iii) identify territories of the phenotypic space representing favorable adaptations for crop improvement. Our findings demonstrate the value of phenotype-focused perspectives for adapting crops to climate change.

IMPACT OF DEVELOPMENT-INDUCED STRUCTURAL CHANGES ON DROUGHT RESPONSES OF WINTER OILSEED RAPE LEAF - NMR RELAXOMETRY, WATER RELATIONS AND MULTI-OMICS INVESTIGATIONS

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Global warming is leading to an increase in the occurrence of drought periods, which negatively impacts crops. Using nuclear magnetic resonance (NMR) relaxometry combined with water status measurements and omics approaches (metabolomics, ionomics, transcriptomics), we investigated the drought responses in young and mature winter oilseed rape leaves from plants subjected to progressive soil drought followed by a rewatering phase. In an original way, low-field NMR revealed the impact of the development-induced structural changes in mesophyll tissues on the leaf hydraulics response to water stress. Mature leaves showed progressive cell dehydration, whereas young leaves exhibited strong osmotic adjustment and putative variations in cell wall elasticity as part of an adaptive strategy promoting water-stress avoidance and post-drought recovery.

SESSION 14: EPIGENETIC MECHANISMS AND RESPONSES IN PLANTS

UNCOVERING THE GENE EXPRESSION REGULATORY MECHANISMS UNDERLYING SELF-INCOMPATIBILITY DOMINANCE NETWORKS IN ARABIDOPSIS

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In this study we investigate how gene expression mechanisms have evolved to establish a dominance hierarchy in a complex multiallelic locus – the self-incompatibility system of Arabidopsis. In this system, dozens of alleles co-exist in a dominance continuum and the reproductive success of an individual depends on the ability of a dominant allele to repress the activity of numerous recessive alleles. This complex gene regulatory network relies on the activity of miRNA-like elements that are believed to function through DNA methylation. Here, we explore the characteristics of these elements and their potential participation in pre- and post-transcriptional gene silencing pathways. Our results show that these miRNA-like elements have unusual molecular properties, and function independently of RdDM, but are nevertheless robust in controlling transcript levels of targeted alleles, challenging our current understanding of canonical gene regulatory pathways and their evolution.

GLOBAL INCREASE OF THE NUCLEAR TRANSCRIPTIONAL REGIME DURING ARABIDOPSIS PHOTOMORPHOGENESIS: EFFECTS ON GENE EXPRESSION

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In previous studies, we reported that the massive change in gene expression triggered by light during Arabidopsis photomorphogenesis involves an average ~2-fold increase of RNA Pol II activity in cotyledon nuclei and a genome-wide increase in chromatin hallmarks of transcription elongation, complementarily showing that light induces a switch from a relatively quiescent to a more active transcriptional status. Yet, because of data normalization, the transcriptomic consequences of global shifts in transcription are not revealed with classical RNA-seq analyses. We therefore developed a new methodological setup using exogenous RNA as a spike-in for absolute quantification of RNA-seq. This approach enabled us to assess to which extent, and for which genes, a global intensification of RNA Pol II activity affects transcript level during photomorphogenesis. This study provides a new standpoint on how light signaling and chromatin machineries modulate genome expression during cell transitions.



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DECIPHERING THE EPIGENETIC AND MOLECULAR LOGIC OF WOX5 FUNCTION IN THE COLUMELLA STEM CELL NICHE OF ARABIDOPSIS THALIANA

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In the root apical meristem, the Quiescent Center (QC) maintains columella stem cells (CSCs) undifferentiated through the activation of the transcription factor WOX5. Although QC cells thus superficially resemble niche cells of animal stem cell niches, recent studies suggest that they can also replace primary CSCs. WOX5 activity controls QC specification, QC cell division, and in a non-cell-autonomous manner, CSCs pluripotency. Furthermore, ectopic expression of WOX5 can reverse differentiation into stem cell tumors. How WOX5 regulates these different processes is largely unknown. In this study, we address the epigenetic and molecular logic of WOX5 function in pluripotency regulation by a comprehensive analysis of the genomic function of WOX5. Our data shows that WOX5 acts as a bifunctional transcriptional factor that modifies the epigenetic landscape of QC cells. We identify effector pathways that link stem cell regulation to previously known and unexpected cellular functions.

MECHANISM OF E3 UBIQUITIN LIGASE SLXERICO1/3 REGULATING HIGH TEMPERATURE RESISTANCE IN TOMATO PLANTS

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E3 ubiquitin ligases are widely involved in regulating plant growth and development in response to stress. We identified two E3 ubiquitin ligases, SLXERICO1/3, that can regulate high temperature resistance in tomato, and subsequently discovered a heat shock transcription factor SLHsfB3b using yeast two-hybrid screening library technology, and further confirmed their interactions by bimolecular fluorescence complementation and co-immunoprecipitation. The ubiquitination assay showed that SLXERICO1/3 could ubiquitously degrade SLHsfB3b, and SLHsfB3b negatively regulated tomato heat resistance. Specifically, SLHsfB3b could interact with SLHsfA6a, which exerts its positive regulation of high temperature resistance. Overall, we elucidated the molecular pattern of SLXERICO1/3 could improve high temperature resistance in tomato by regulating the SLHsfB3b-SLHsfA6a molecular module. The study is expected to provide scientific knowledge for the creation of high temperature resistant germplasm.

SESSION 15: MECHANICS AND STRESS RESPONSES

LIMITED WATER STRESS MODULATES EXPRESSION OF CIRCADIAN CLOCK GENES IN BRACHYPODIUM DISTACHYON ROOTS AND INDUCES DIFFERENTIAL RESPONSE OF PROLINE-METABOLISM RELATED GENES

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We report a comprehensive study on core circadian clock genes in the model monocot *Brachypodium distachyon* under mild drought stress in roots and green plant parts. Based on these, the expression of key genes of proline metabolism was followed revealing that proline accumulation in shoots is regulated in a circadian manner via the removal of it. Comparative monitoring of core clock gene expression in roots and green plant parts has shown that both phase and amplitude of expression in the roots of *Brachypodium* plants differ markedly from those in the green plant parts, even under well-watered conditions. Moreover, circadian clock genes responded to water depletion differently in root and shoot. Besides we study LOB-domain TF-family in *Brachypodium*, in relation to thermo-morphogenesis. These plant-specific proteins are involved in diverse developmental processes from floral development to the emergence of lateral roots therefore important regulators of plant architecture.

DYNAMICS OF THE CALCIUM SIGNAL ELICITED BY MECHANICAL STIMULATION OF ARABIDOPSIS ROOT

Sébastien THOMINE^{*}; Vassanti AUDEMAR ¹; Yannick GUERRINGUE ¹; Joni FREDERICK ²; Isaty MELOGNO ¹; Pauline VINET ¹; Avin BABATAHERI ²; Jean-Marie FRACHISSE ¹

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During their progression in the soil, roots sense the forces exerted by the soil and physical obstacles and transduce them into cytosolic Ca²⁺ concentration increases. The duration, amplitude, frequency and spatial distribution of the calcium elevation determine the signature allowing specific responses to diverse cues. To investigate the relationship between root deformation and calcium signaling, we imaged plants expressing R-GECO1-mTurquoise Ca²⁺ nanosensor growing on a microfluidic device allowing application of a controlled mechanical pressure on the root. Our experiments revealed that (i) transient calcium signals are elicited both at onset and release of a pulse of pressure, indicating that strain rather than stress triggers signaling, (ii) signals are localized to the tissue under pressure and do not propagate, (iii) signals exhibit a strong attenuation upon repetitive stimulations. The system opens perspectives to investigate other responses to mechanical stimulation.



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MULTISCALE MODELLING OF CELL ADHESION AND SEPARATION IN PLANTS

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Cell adhesion plays an essential role in the development of plants. In tomato, type VI glandular trichomes store metabolites in an intercellular cavity localized between four secretory cells. The dynamic changes in the material properties of the cell wall are a key element that lead to the fracture of the middle lamella leading to cell separation and the formation of the cavity. We used two approaches to show how these mechanical aspects relate to biochemical changes in the cell wall. I) we investigated the nature and properties of the trichome cell wall during the course of cavity formation. Ii) we made use of the homogenization theory and continuum damage mechanics to reconstitute a multiscale model of the development of the cavity. A modular architecture was used to implement the model and tune the level of its complexity. It led to a useful generic tool and provides fundamental insights into the maintenance and regulation of cell adhesion in plants.

IT'S JUST A PHASE: STRUCTURAL CHARACTERIZATION OF LLPS AND ITS ROLE IN TEMPERATURE SENSING IN PLANTS

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The increased average temperatures due to global warming have already altered plant phenology for wild and domesticated species, presenting a critical challenge for food security in the coming decades. Plants are able to perceive even small changes in temperature and subsequently reprogram their growth and development for reproduction and survival. However, the molecular mechanisms for this are still largely unknown. We have recently determined that EARLY FLOWERING 3, a core component of the circadian clock, acts as a direct thermosensor via liquid-liquid phase separation (LLPS). Using a combination of biophysical and structural techniques, we determined the dynamics and molecular mechanisms underlying the transition from the dilute to condensed phases in vitro. Based on these data, we explore how altering LLPS correlates with changes at the phenotypic level (hypocotyl length, plant morphology, flowering time) for Arabidopsis plants grown at different temperatures.

SESSION 16: PLANT IMMUNITY

INVESTIGATING ANTIVIRAL DEFENSES PROTECTING PLANT STEM CELLS AND GERMLINE

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Stem cells are essential for the development of multicellular organisms, so their infection by pathogenic viruses must be prevented. In plants, a small group of stem cells harbored within the shoot apical meristem (SAM) generates all postembryonic above-ground tissues, including the germline cells. Many viruses do not proliferate in these cells, yet the molecular bases of this exclusion remain only partially understood. We show that a plant-encoded RNA-dependent RNA polymerase, after activation by the plant hormone salicylic acid, amplifies antiviral RNAi in infected tissues, providing stem cells with RNA-based virus sequence information and preventing virus proliferation. We find RNAi to be necessary for exclusion of several RNA viruses. We developed cutting-edge live imaging techniques to track virus movement through meristems and flowers in 3D and over time. Finally, we developed biological tools to investigate the factors protecting plant germlines from virus infection.

GRADUAL IMMUNE SYSTEM MATURATION IN THE ROOT AFFECTS PLANT MICROBE INTERACTION

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Stem cells are essential for the development of multicellular organisms, so their infection by pathogenic viruses must be prevented. In plants, a small group of stem cells harbored within the shoot apical meristem (SAM) generates all postembryonic above-ground tissues, including the germline cells. Many viruses do not proliferate in these cells, yet the molecular bases of this exclusion remain only partially understood. We show that a plant-encoded RNA-dependent RNA polymerase, after activation by the plant hormone salicylic acid, amplifies antiviral RNAi in infected tissues, providing stem cells with RNA-based virus sequence information and preventing virus proliferation. We find RNAi to be necessary for exclusion of several RNA viruses. We developed cutting-edge live imaging techniques to track virus movement through meristems and flowers in 3D and over time. Finally, we developed biological tools to investigate the factors protecting plant germlines from virus infection.



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ROLE OF THE PLASMA MEMBRANE SIGNALLING DURING PLANT VIRUS PROPAGATION

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The plant plasma membrane (PM) is a dynamic and organised structure that acts as a platform for signalling. Data is published regarding the role of PM in response to bacterial or fungal infection. However, little is known about how the PM is implied in virus signalling. In plants, viruses enter the first cell, hijack their machinery to replicate and propagate via plasmodesmata.

In this presentation, we aimed at understanding how plants sense and slow down viruses through the description of the organisation of PM-bound proteins. Super resolution microscopy was used to study the fine organisation of PM-proteins during signalling. We showed that Ca²⁺-dependent kinase was able to hamper propagation of potexvirus, through the phosphorylation of the nanodomain-located protein REMORIN, which leads to a modification of its interactome and callose accumulation at plasmodesmata. REMORIN interact with ACTIN DEPOLYMERIZATION FACTOR making a link between PM and the actin cytoskeleton.

ENGINEERING DANGER SENSING AND SIGNALING IN PLANT IMMUNITY: USE OF OLIGOSACCHARINS TO ENHANCE DURUM WHEAT RESISTANCE TO FUSARIOSIS

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Plant diseases cause substantial crop losses worldwide compromising food safety because of the presence of toxins derived from infections. Thus, sustainable yield increase, diminishing usage of chemicals, enhancing crop resilience to biotic stress represent the main, concomitant, targets to be pursued in agriculture in a short period. Numerous studies indicate that local application of plant cell wall-derived elicitors, such as oligogalacturonides (OGs), derived from partial degradation of pectin, induce systemic resistance against pathogens in different plant species. The aim of this study was to establish the efficacy of OGs in protecting durum wheat, characterized by an extreme susceptibility to fusariosis caused by *Fusarium graminearum*. Furthermore, the study of durum wheat plants with potentially altered endogenous OG levels, i.e. OG-Machine lines, is facilitating the elucidation of molecular mechanisms regulating plant defense activation upon sensing danger signals in cereals.

SESSION 17: PHOTOSYNTHESIS: UNDERSTANDING AND PROGRESS IN ITS MANIPULATION

FROM ALGAE TO SEA SLUGS: FUNCTIONING OF STOLEN CHLOROPLASTS IN ANIMAL CELLS.

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Photosynthesis is a process used by phototrophs to obtain energy from light. Excessive exposure, however, is deleterious and is tackled with photoprotective strategies by plants and algae. One of them is the xanthophyll cycle: violaxanthin is converted into zeaxanthin under high light to dissipate excessive energy. Some sacoglossan sea slugs feed on macroalgae and acquire functional chloroplasts through a process called kleptoplasty. In some species, the stolen kleptoplasts function for several weeks to a few months even without algal nuclear genes necessary to encode most plastid proteins. In this study, we investigated the photophysiology sea slugs and their algal food to determine the conserved photoprotective mechanisms. Kleptoplast robustness depends on the algae/animal combinations, and not all mechanisms associated with a certain chloroplast can be acquired by all sea slug species simply through feeding. In conclusion, photosynthetic sea slugs are what they eat... but not quite!

TWO VACUOLAR CHANNELS FROM THE ALMT FAMILY REGULATE C4-ORGANIC ACIDS METABOLISM.

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In plants organic acids (malate, fumarate) constitute a significant part of the C fixed by photosynthesis. These organic acids are part of primary metabolic pathways. In Arabidopsis, the vacuole is an important transient store of malate and fumarate, allowing to keep constant the cytosolic pools. Notably, the role of the vacuole as a stock of organic acids is still to be understood. Opening the question if and how vacuolar transport of organic acids regulates photosynthetic metabolism? My studies focus on two members of the ALMT ion channel family that are present only in plants. These two ALMTs are localised in the tonoplast of mesophyll cells where they mediate the uptake of malate and fumarate in the vacuole. Notably, the KO mutants for those two channels display a modified composition of the fixed C stocks in the mesophyll, leading to an early leaf senescence. Our studies identify key molecular actors at the tonoplast able to influence the photosynthetic fixation of C in plants.



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FROM OXIDATIVE STRESS TO ANTENNA QUENCHING: REGULATION OF QH-ENERGY DISSIPATION IN PLANTS

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The sustained quenching mechanism qH, involved in the long-term protection of the photosynthetic apparatus, is independent of previously known regulatory proteins and triggers of energy dissipation. Its activation requires the plastid lipocalin (LCNP). Suppressor of quenching1 (SOQ1) inhibits LCNP and prevents quenching; and a short-chain dehydrogenase reductase is involved in the relaxation of qH (ROQH1). The main target of qH is the light harvesting complex (LHCII) trimers, the major antenna of photosystem II.

We recently found that LCNP is activated through monomerization caused by oxidation of its methionines (Met-O). The monomer is then free to bind MGDG in the thylakoid membrane, possibly at the level of the Lhcb6 antenna that promotes qH induction. SOQ1 would prevent qH by reduction of Met-O in LCNP.

We are now investigating the changes responsible for the strong and stable dissipative state of qH-quenched LHCII, and the mechanism underlying ROQH1-dependent relaxation.

CHLOROPLAST REDOX STATUS MODULATES LEAF DEVELOPMENT VIA CHANGES IN PROTEASOMAL ACTIVITY AND ENDOREDPLICATION INDEX

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Leaf development is accompanied by an early accumulation of reactive oxygen species (ROS) originating at the photosynthetic electron transport chain (PETC). The introduction of the alternative PETC acceptor flavodoxin in tobacco chloroplasts reduces leaf size associated with lower cell expansion and endoreduplication. Proteomic analysis revealed that components of the light-harvesting systems accumulated before electron transport proteins, providing a plausible mechanism for the early oxidative burst. Flavodoxin expression did not affect the biogenesis of the PETC but prevented ROS build-up. The proteasome, a key negative modulator of organ size, was significantly induced in the proteome profiling of the transgenic lines. The results provide novel insights on leaf growth regulation by plastid-generated redox signals and highlight the potential of investigating the link(s) between chloroplast oxidoreductive biochemistry and plant development.

SESSION 18: THE GENETICS OF NATURAL VARIATION OF PLANT- PLANT INTERACTIONS

EVOLUTION OF COOPERATION IN POST-GREEN REVOLUTION DURUM WHEAT CULTIVARS

Michel COLOMBO^{1*}

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In agriculture, intraspecific competition is undesirable, since it drives the evolution of traits toward phenotypic values lowering group performance. Kin selection (KS) theory provides a relevant framework to model these issues. The KS theory aims at understanding the evolution of traits, for which the phenotype of an individual affects both the performance of that individual and the performance of other individuals in interaction. It predicts that a phenotype that decreases individual's performance can be favored by KS if the performance of some other related individuals in interaction is increased by the interaction. The KS theory has been used to explain the evolution of cooperative phenotypes with beneficial effect on group performance. Interestingly, the KS theory has been poorly mobilized in agriculture. In this talk, using the framework of the KS and durum wheat as a model species, we will ask whether post-green revolution breeding has produced more cooperative phenotypes.

CHROMATIN REGULATION OF AND BY GENE ISLANDS IN PLANTS

Louis-Valentin METEIGNIER*

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In *Arabidopsis thaliana*, small euchromatin islands that contain expressed genes are interspersed within repressive heterochromatin. Until recently, how the expression of euchromatin islands occurred in such a repressive environment remained unknown. We have demonstrated a role for the Topoisomerase VI protein complex in safeguarding the expression of euchromatin island genes by regulating H3K9me2 homeostasis. In *Arabidopsis* and many other plants, island genes can belong to functionally-related pathways such as those involved in the biosynthesis of specialized metabolites. Surprisingly, some plant specialized metabolites share structural similarities with well-known chromatin chemical modifiers, and I will show preliminary results that might involve specialized metabolites in the chromatin-level control of plant immunity and plant-plant interactions.

IDENTIFICATION OF GENES AND METABOLITES CONTROLLING PLANT-PLANT INTERACTION (ALLELOPATHY)

Sophie JASINKI^{1*}; Oumayma MHALDI ¹; Zeyun XUE ¹; Justine DEL BIANCO ¹; Jean-Christophe TOTOZAFY ¹; Fabrice ROUX ²; François PERREAU ¹; Catherine RAMEAU ¹; Alexandre DE SAINT GERMAIN ¹

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Today, our agriculture is facing many challenges, including the necessity to progressively reduce the use of herbicides for weed management. Innovative strategies could come from new knowledge on the natural mechanisms of plant-plant interactions, such as allelopathy, a process by which plants can modify the growth of neighboring plants through the release of chemical compounds. Therefore, a precise description of the molecular mechanisms involved is necessary for a better control of these interactions. Using a large collection of genotypes of the model plant *Arabidopsis thaliana* and an innovative phenotyping device for allelopathic properties (Plant-Soil feedback), our team was able to identify, through association genomics studies (GWAS), many candidate regions/genes potentially involved in the biosynthesis of allelopathic signals. We are currently validating candidate genes involved in glucosinolate and coumarin metabolism using functional genomics.

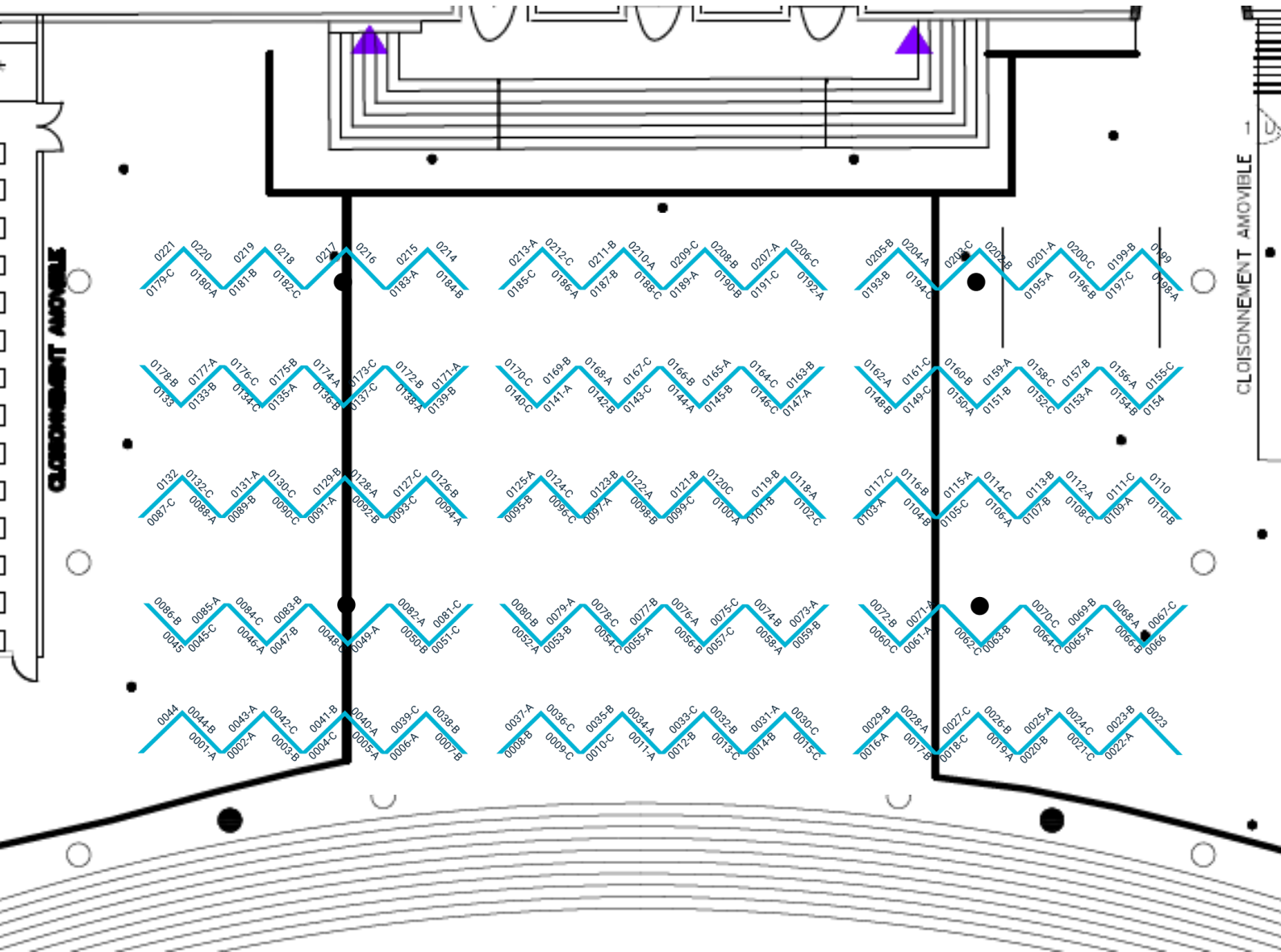
MOLECULAR BASES OF PLANT-PLANT INTERACTIONS: IDENTIFICATION OF THE MOLECULAR PATHWAYS DEPENDING ON ESC-1, A RLK INVOLVED IN THE COMPETITIVE RESPONSE IN ARABIDOPSIS THALIANA.

Marie INVERNIZZI^{*}; Cyril LIBOUREL; Mathieu HANEMIAN; Fabrice ROUX; Dominique ROBY

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Understanding the genetic and molecular mechanisms underlying plant-plant interactions (PPI) is essential to understand the functioning of natural plant communities to optimize crop species mixtures. However, there is still little information about these molecular mechanisms, and only a few genes associated with natural variation of PPI have been cloned. Based on a GWAS, the gene ESCAPE-1 (ESC-1) was identified and functionally validated as mediating the competitive response of *Arabidopsis thaliana* to the presence of the annual grass *Poa annua*, by establishing an escaping strategy. The identification of this member of the Proline-rich extensin-like receptor-like kinase family is unexpected because PPI was so far mostly assumed to result from passive interactions. Combining a transcriptomic approach with the identification of protein interactors of ESC-1 allowed to decipher the regulatory networks and to identify key genes involved in the ESC-1-dependent response to *P. annua*.

POSTERS PRESENTATIONS FLOOR PLAN



POSTER SESSIONS A

Tuesday 4th of July | 17:00 to 18:00

Biomechanics	0001-A
Chromosome dynamics	0002-A
Comparative genomics	0005-A, 0006-A
Domestication in retrospect and the future of breeding	0011-A
Epigenetic mechanisms and responses in plants	0016-A
Genome editing and its use for plant breeding	0019-A, 0022-A
Interfaces with plant and soil microbiota	0025-A, 0028-A, 0031-A, 0034-A
Macro and micro nutrients in plants	0037-A, 0040-A, 0043-A, 0046-A, 0049-A
Organellar biology	0052-A, 0055-A, 0058-A, 0061-A
Photosynthesis: understanding and progress in its manipulation	0065-A, 0068-A, 0071-A, 0073-A
Plant adaptation to climate change	0076-A, 0079-A, 0082-A
Plant and algal development and evolution	0085-A, 0088-A, 0091-A, 0094-A, 0097-A, 0100-A
Plant Immunity	0103-A, 0106-A, 0109-A, 0112-A, 0115-A, 0118-A
Plant reproduction: mechanisms and evolution	0122-A, 0125-A, 0128-A, 0131-A
Plant responses to abiotic stress	0135-A, 0138-A, 0141-A, 0144-A, 0147-A, 0150-A, 0153-A, 0154, 0156-A, 0159-A, 0162-A, 0165-A, 0168-A, 0171-A, 0174-A, 0177-A, 0180-A, 0183-A, 0186-A, 0189-A, 0192-A, 0195-A, 0198-A
Synthetic biology	0201-A
The genetic architecture of quantitative traits in plants	0204-A, 0207-A
The genetics of natural variation of plant-plant interactions	0210-A, 0213-A

POSTER SESSIONS B

Wednesday 5th of July | 13:30 to 14:30

Chromosome dynamics	0003-B
Comparative genomics	0007-B, 0008-B
Domestication in retrospect and the future of breeding	0012-B, 0014-B
Epigenetic mechanisms and responses in plants	0017-B
Genome editing and its use for plant breeding	0020-B, 0023-B
Interfaces with plant and soil microbiota	0026-B, 0029-B, 0032-B, 0035-B
Macro and micro nutrients in plants	0038-B, 0041-B, 0044-B, 0047-B, 0050-B
Organellar biology	0053-B, 0056-B, 0059-B, 0063-B
Photosynthesis: understanding and progress in its manipulation	0066-B, 0069-B, 0072-B, 0074-B
Plant adaptation to climate change	0077-B, 0080-B, 0083-B
Plant and algal development and evolution	0086-B, 0089-B, 0092-B, 0095-B, 0098-B, 0101-B
Plant Immunity	0104-B, 0107-B, 0110-B, 0113-B, 0116-B, 0119-B, 0121-B
Plant reproduction: mechanisms and evolution	0123-B, 0126-B, 0129-B, 0133-B
Plant responses to abiotic stress	0136-B, 0139-B, 0142-B, 0145-B, 0148-B, 0151-B, 0154-B, 0157-B, 0160-B, 0163-B, 0166-B, 0169-B, 0172-B, 0175-B, 0178-B, 0181-B, 0184-B, 0187-B, 0190-B, 0193-B, 0196-B, 0199-B
Synthetic biology	0202-B
The genetic architecture of quantitative traits in plants	0205-B, 0208-B
The genetics of natural variation of plant-plant interactions	0211-B

POSTER SESSIONS C

Wednesday 5th of July | 14:30 to 15:30

Chromosome dynamics	0004-C
Comparative genomics	0009-C, 0010-C
Domestication in retrospect and the future of breeding	0013-C, 0015-C
Epigenetic mechanisms and responses in plants	0018-C
Genome editing and its use for plant breeding	0021-C
Interfaces with plant and soil microbiota	0024-C, 0027-C, 0030-C, 0033-C, 0036-C
Macro and micro nutrients in plants	0039-C, 0042-C, 0045-C, 0048-C, 0051-C
Organellar biology	0054-C, 0057-C, 0060-C, 0062-C, 0064-C
Photosynthesis: understanding and progress in its manipulation	0067-C, 0070-C, 0075-C
Plant adaptation to climate change	0078-C, 0081-C, 0084-C
Plant and algal development and evolution	0087-C, 0090-C, 0093-C, 0096-C, 0099-C, 0102-C
Plant Immunity	0105-C, 0108-C, 0111-C, 0114-C, 0117-C, 0120-C
Plant reproduction: mechanisms and evolution	0124-C, 0127C, 0130C, 0132-C, 0134-C
Plant responses to abiotic stress	0137-C, 0140-C, 0143-C, 0146-C, 0149-C, 0152-C, 0155-C, 0158-C, 0161-C, 0164-C, 0167-C, 0170-C, 0173-C, 0176-C, 0179-C, 0182-C, 0185-C, 0188-C, 0191-C, 0194-C, 0197-C, 0200-C
Synthetic biology	0203-C
The genetic architecture of quantitative traits in plants	0206-C, 0209-C
The genetics of natural variation of plant-plant interactions	0212-C

BIOMECHANICS

0001-A MECHANICAL CONTRIBUTION OF THE SEED OUTERINTEGUMENT TO SEED MORPHOGENESIS THROUGH THE STUDY OF AP2 MUTANTS

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Like in many plant organs, seed morphogenesis relies on mechanical interactions between tissues and is tuned by biochemical and mechanical cues. Accordingly, we recently developed a model where seed growth is restricted by the cell walls of a mechanosensitive layer of the seed coat in response to the tension induced by endosperm expansion. To further study the properties of the mechanosensitive layer, I use *apetala2* (*ap2*) seeds as the cells of the seed coat outer-integument have lost their identity in this mutant. I showed that *ap2* seeds have defects in testa mechanical properties and response to forces that can explain its growth phenotype: an initial reduction of growth rate and anisotropy but a subsequent lengthening of the growth phase that lead to the production of large and round seeds. Finally, I also used *ap2* seeds to identify the genetic determinant of seed mechanical properties and response to forces through a transcriptomic approach.

CHROMOSOME DYNAMICS

0002-A

PREDICTING GENE REGULATION THROUGH CO-OCCURRENCE AND EVOLUTIONARY CONSERVATION OF TRANSCRIPTION FACTOR BINDING SITES

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Transcription factors (TFs) regulate gene expression through the binding of specific DNA sequences called transcription factor binding sites (TFBS) [1]. However, the intrinsic binding affinity of a TF for its TFBS does not always translate into in vivo binding and to a transcriptional effect. Thus, models based on motif recognition can be poor predictors of functional TFBS (i.e. TFBS that are bound and regulatory in vivo). LEAFY (LFY), a plant-specific TF playing a crucial role in floral development, is highly conserved in sequence and binding specificity [5]. Since functionally important TFBS tend to be more evolutionarily conserved [2], and multiple TFs can bind to the same regulatory region to fine-tune gene expression [3], we aimed to characterize and build a machine-learning model to predict LFY-dependent gene regulation in *Arabidopsis thaliana* by leveraging information about (a) evolutionary conservation and (b) co-occurrence at LFY sites on LFY-regulated genes.

0003-B

HOW LIGHT REPROGRAMS PLANT CELLS: IMPACT ON THE 3D ORGANISATION OF TRANSCRIPTION

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Light is a source of energy, used in photosynthesis, and an essential information for plants to adapt their physiology and development to a daily and seasonally changing environment. Soon after germination, light induces rapid transcriptional changes in the dark adapted seedling and large-scale chromatin changes. Using a customized image analysis workflow to resolve the spatial distribution of RNA Pol II clusters in isolated nuclei, we found a light-specific pattern of transcriptional activation engaging prominently clusters at the nuclear periphery of cotyledons cells. This suggests a non-random, functional distribution of the transcriptional compartment responding to light. Furthermore, a similar response is found in the

underground, root tissue. Future investigation will determine whether this involves local or distal light perception and whether specific photoreceptors are involved in this nuclear reorganization process.

0004-C
THE PAIRING AND (NON)SYNOPSIS OF LARGE NON-RECOMBINING REGION IN YOUNG SEX CHROMOSOME SYSTEM - GENUS SILENE

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Meiosis is a key process of heredity, assuring genetic variation and accurate transmission of the genetic material among generations. During the first meiotic division prophase I, the homologous chromosomes are brought together by synaptonemal complex (SC) that extends along the entire length of meiotic bivalents, ensuring precise chromosome synapsis and recombination. The synapsis is mostly applicable for all the autosomes, but the sex chromosomes escape this rule. While in animals XY pairing (and SC substructure) differs between the sexes, in plants it still remains enigmatic. To explore the unusual sex chromosome dynamics, we used high resolution microscopy to analyse heteromorphic sex chromosomes in a model plant, *Silene latifolia*, and the XY pairing in polyploid relatives. We show the difference between single bivalent and tetravalent structures in the context of the same genetic background and discuss possible implications on the evolution of the non-recombining region.

COMPARATIVE GENOMICS

0005-A

CENTROMERES IN COMMON BEAN (PHASEOLUS VULGARIS): LESSONS LEARNED FROM CHROMOSOME SCALE GENOME ASSEMBLIES

Gianluca TEANO^{1*}; Juan C. ALVAREZ-DIAZ ¹; Christophe KLOPP ²; Marion VERDNAUD ¹; Stéphanie PFLIEGER ¹; Ariane FRATIAS ¹; Andrea PEDROSA-HARAND ²; Valérie GEFFROY ¹

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Common bean (*Phaseolus vulgaris*) is the most important grain legume for human consumption. We generated two highly contiguous chromosome-scale genome assemblies of genotypes BAT93 and JaloEEP558 using PacBio HiFi sequencing and chromosome conformation capture data (Hi-C). In common bean, centromeres are defined by two unrelated satellite repeats, CentPv1 and CentPv2, which associate with the centromere-specific histone H3 (CENH3). CentPv1 is present in 8 chromosomes, while CentPv2 is present on the other 3. Published results proposed these two repeats as mutually exclusive. Surprisingly, in 5 chromosomes of BAT93 and JaloEEP558 HiFi assemblies, both CentPv1 and CentPv2 repeats co-localized. To confirm this specific feature of chromosomes harboring both CentPv1 and CentPv2, we performed Chromatin Immune precipitation of CENH3. Mapping these data on the HiFi genomes, in combination with methylation data will shed light on the evolutionary history of centromeric repeats in common bean.

0006-A

INTERPRETING THE CHEMODIVERSITY IN A PHYLOGENETIC CONTEXT: A CASE STUDY OF THE GENUS NEPETA

Tijana BANJANAC^{*}; Branislav SILER ¹; Tamara LUKIC ¹; Uros GASIC ¹; Luka PETROVIC ¹; Dragana MATEKALO ¹; Skoric MARIJANA ¹; Jasmina NESTOROVIC ŽIVKOVIĆ ¹; Slavica DMITROVIC ¹; Milica MILUTINOVIC ¹; Neda ANICIC ¹; Jelena BOZUNOVIC ¹; Biljana FILIPOVIC ¹; Milos TODOROVIC ¹; Danijela MISIC ¹

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Nepeta L. is the largest genus of the Lamiaceae family. The species of this genus are famous for their biopesticidal potential and medicinal properties. Within the genus, we found considerable variability in the qualitative and quantitative content of iridoid and phenolic compounds. Using state-of-the-art metabolomics techniques (UHPLC/LTQ-Orbitrap MS, GC/MS, UHPLC/DAD/(+/-)HESI-MS2), we comprehensively assessed the overall diversity of



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iridoids and phenolics in the selected chemodiverse *Nepeta* taxa at the intra-species level. To reconstruct phylogenetic relations among the selected chemodiverse taxa from across the *Nepeta* genus, genomic ITS molecular marker and two maternally inherited plastid DNA regions (trnL-trnF and rbcL) were analyzed. A consensus phylogenetic tree was constructed to interpret the distribution of the most abundant iridoid and phenolic compounds. It was not possible to uncover clear regularities between phylogenetic relationship and chemotype affiliation.

0007-B
CHROMOSOME REARRANGEMENT AND GENOME COMPLEXITY IN HEXAPLOID HIBISCUS SYRIACUS (GANGNEUNG AND BAEKDANSIM): INSIGHTS FROM PSEUDOCHROMOSOME ASSEMBLY AND COMPARATIVE ANALYSIS

Hyunjin KOO^{1*}; Sangjin GO ¹; Minah JUNG ¹; Seongmin HONG ¹; Ah-Young SHIN ¹; Yong-Min KIM ¹

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Rose of sharon (*Hibiscus syriacus*) is one of the most widespread garden shrubs globally and has a complex genome structure resulting from multiple rounds of polyploidization events. We constructed two reference genome assemblies for hexaploid *H. syriacus* accessions with long read sequencing and Hi-C scaffolding. Both varieties had 12 typical groups of chromosomes shown in hexaploid genomes containing three syntenic chromosomes, and two extraordinary groups with four and two syntenic chromosomes. Comparison of genome structures suggested that extensive chromosomal rearrangements occurred in both genomes during consecutive diploidization processes. Further analysis revealed a substantial expansion in Chr9 of Baekdansim, primarily influenced by a repeat burst after the variety divergence event. Population analysis using 94 re-sequencing datasets of worldwide collection of *H. syriacus* indicated the high genomic complexity. Further evolution of *H. syriacus* will be presented in the poster.

0008-B
MOLECULAR MARKERS IN THE DETECTION OF INTERSPECIES HYBRIDIZATION – A MODEL STUDY ON THE GENUS CENTAURIUM HILL

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The species of the genus *Centaurea* Hill are characterized by a pronounced phenotypic plasticity, while interspecific hybridization readily occurs. Previous studies reported

hybridization events between *C. erythraea* and *C. tenuiflorum* in the Mediterranean region, but the status of a potentially hybrid taxon (termed "*Centaurium x tenuiflorum*") remains unclear. Therefore, molecular markers (EST-SSR, ITS, and chloroplast DNA markers) were combined and their usefulness in estimating overall genetic variability and in identifying phylogenetic relations between *Centaurium* taxa was scrutinized. Both EST-SSR and ITS markers proved to be well suited to distinguish the parental taxa *C. erythraea* and *C. tenuiflorum*, and a putative hybridogenic taxon "*C. x tenuiflorum*", the last one being more related to *C. erythraea*. Conversely, maternally inherited chloroplast markers (*trnL-F*, *rbcl* and *psbA-trnH*) nominated *C. tenuiflorum* as a donor of plastid.

0009-C

PLANT-TFCLASS: A STRUCTURAL CLASSIFICATION FOR PLANT TRANSCRIPTION FACTORS

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Transcription factors (TFs) bind DNA at specific sequences to regulate gene expression. This universal process is achieved thanks to their DNA-binding domain (DBD). In mammals, the vast diversity of DBD structural conformations and the way they contact DNA has been used to organize TFs in the TFClass hierarchical classification. Such classification was missing from plants that possess many DBD types absent from mammals. We reviewed DBD 3D-structures and models available for plant TFs to classify most of the 56 recognized plant TF types within the TFClass framework. This extended classification adds six new classes and 35 new families corresponding to DBD structures absent in mammals. Plant-TFClass provides a unique resource for TF comparison across families and organisms.

0010-C

COMPARATIVE ANALYSIS OF CHLOROPLAST GENOMES OF TWO ADENOPHORA SPECIES

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Adenophora verticillata and *Adenophora stricta*, which belong to the family campanulaceae, were well-known as medicinal plants. However, it is very similar shape, especially roots, and has been used as herbal medicine and/or biomaterials regardless of classification. Therefore, in this study, we performed chloroplast genome sequencing to identify a genetic marker that can distinguish these two species. The total reads of *A. verticillata* and *A. stricta* were 247,553,132 and 229,873,920 reads, respectively. As a result of mapping the analytical sequence with *Adenophora triphylla* chloroplast genome as reference, the total number of SNPs in *A. verticillata* and *A. stricta* was 48 and 1,153, of which homozygous SNPs were 44 and 1,107, respectively. These results suggest that the homozygous SNPs between the two



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species can be utilized in the development of genetic markers that distinguish the two species.

DOMESTICATION IN RETROSPECT AND THE FUTURE OF BREEDING

0011-A THE PROTEOMES THAT FEED THE WORLD

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Plants form the nutritional basis of effectively all life on earth; increasing demands for protein-rich plant-based alternatives must be met to sustain the growing population. Despite the gradual elucidation of crop genomes, less remains known concerning crop proteomes. Thus, an international assembly of partners and the doctoral program “The Proteomes that Feed the World” was formed. The program aims to map proteomes of the 100 most critical crop plants for human nutrition using a high throughput proteomic workflow. We used a universal protein extraction method with automated sample preparation and offline peptide separation protocols, and an optimized micro-LC-MS/MS protocol. This method successfully defined with high efficiency, reproducibility, and coverage of the proteome of several crops like *Chenopodium quinoa*, *Sorghum bicolor*, *Solanum tuberosum*, and *Solanum lycopersicum*. Raw MS data, protein identification, and quantification results will be available on PRIDE and ProteomicsDB.

0012-B GENOMIC PREDICTION AND LANDSCAPE GENOMICS IN A LARGE MAIZE LANDRACES COLLECTION USING HIGH-THROUGHPUT POOL GENOTYPING IDENTIFIES PROMISING SOURCES OF DIVERSITY FOR PREBREEDING

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Maize landraces are a valuable source of genetic diversity for facing climate change due to their local adaptation. High-throughput pool genotyping (HPG) is a cost-effective approach to genotype maize landraces and identify promising sources of alleles for tolerance to abiotic stress. We applied this approach on a large world-wide collection of maize landraces to i) characterize its genetic structuration; ii) identify genomic regions involved in adaptation through environmental association studies; iii) perform genomic prediction (GP) of both adaptive and agronomic traits. Landraces were structured according to their history and environmental conditions. GP yielded high accuracy, allowing to identify promising landraces. We identified genomic regions associated with bioclimatic variables that could be putatively involved in adaptation to abiotic stress. Combining eco-genetic and genomic prediction opens an avenue for using these genetic resources for prebreeding.

0013-C

SOCIO-ANTHROPOLOGICAL STUDY OF THE USES AND PERCEPTIONS OF ANTIBIOTICS IN HUMAN AND ANIMAL IN THE DEPARTMENT OF VÉLINGARA/SENEGAL

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Context: As part of the implementation of the Thiellal ("health" in Pulaar) project in the town of Velingara (Kolda region) and in four of its departmental communes (Ouassadou, Pakour, Velingara and Pakour), the a socio-anthropological study was carried out to identify the social factors that influence the use of chemical products and to report on the practices and The objective of this paper is therefore to identify the social factors that influence the use of chemicals and to report on the practices and perceptions that users have with regard to these products. The objective of this paper is therefore to discuss the types of antibiotics used in the area, the types of distribution channels (formal/informal), the modes of disposal after use and the meaning given to their use.

Method: For the realization of this study in January 2022, we used a qualitative approach with: - 19 semi-structured interviews with health workers (community relays), livestock keepers, and livestock service agents; - 8 focus groups (08 villages) with men and women of varying ages living in the villages The villages chosen for the study - Observations were carried out with the populations (11 villages) targeted by the project, as well as with but also with the livestock services (03) and health posts (6).

Results : The analysis of the data allowed us to identify the different types of antibiotics that are used, to identify the circuits and modes of supply of the products, their uses and the perceptions that the population and health workers have of antibiotics. The results show that farmers make little use of Veterinarians and livestock agents. They mostly selfmedicate their animals by going to buy products at weekly markets or from street markets. Self-medication is also widely practised by humans. They often use paracetamol. The Villagers cannot generally distinguish different antibiotics. Finally, there is a lack of veterinary staff in the studied area.

0014-B

META-ANALYSIS OF WILD AND DOMESTICATED CROP PHENOTYPIC SPACES

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Plant domestication has led to divergences between domesticated and wild forms, manifesting at both phenotypic and genomic levels. Although the phenotypic domestication syndrome is well-documented in many species, there is currently a lack of a comparative framework to examine these divergences across species. While there has been significant research on genomic spaces, demonstrating that cultivated genetic diversity represents a subset of wild diversity, there has been little investigation into the disjunction of phenotypic spaces between wild and domesticated plants. To address these gaps we have undertaken to identify the traits of the domestication syndrome for 14 wild-domesticated pairs, to study their phenotypic divergence and the evolution of correlations between traits. Here we present our approach and preliminary results on a few species, showing that the overlap between phenotypic spaces varies greatly. Future work involves establishing a phenotypic index of domestication.

0015-C

THE EFFECT OF TAEXPA6 AND TAGW2 GENE EXPRESSION ON GRAIN WEIGHT AND THE TRADE-OFF WITH GRAIN NUMBER IN WHEAT

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Many efforts were made to improve yield by increasing grain weight (GW) in wheat. But, a trade-off with grain number (GN) has been a bottleneck. The ectopic expression of an expansin (TaExpA6, Line ExpA6) in wheat grains increased GW and yield avoiding the trade-off. The objective was to disentangle this trade-off. Four wheat genotypes were tried: the successful Line ExpA6, its wild type (WT), a triple mutant silencing TaGW2 (Line GW2), showing trade-off between GW and GN, and its WT. The experiment consisted of a Completely Randomized Block Design with four replicates at field conditions. Both lines increased GW over the WT, with or without the trade-off (Lines GW2 and ExpA6, respectively). Line GW2 reached higher ovary size at anthesis than its WT, while similar values were found between Line ExpA6 and its WT. Grain weight dynamics were different between Lines GW2 and ExpA6, which were accordingly associated with transcriptomic of TaExpA6 and TaTGW2 in growing grains.

EPIGENETIC MECHANISMS AND RESPONSES IN PLANTS

0016-A

SHORT-TIME AND INTER-ANNUAL EPIGENETIC MEMORIES IN RESPONSE TO DROUGHT IN TREES.

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Climate change is followed by droughts and forests decline. Trees that are sessile organisms must adapt to survive through two biological processes: phenotypic plasticity and adaptation. Recent studies suggest that both mechanisms involve an epigenetic component. Little is known about trees ability to memorize a drought/rewatering cycle after the recovery that could allow a priming effect. An experimental setup was designed to evaluate the tree's recovery after a drought/rewatering cycle. The response was evaluated 1 week or 1 year after the recovery phase of *P. nigra* natural populations. The short-time memory was also evaluated on epivariants affected for the DNA methylation machinery. Phenotypic evaluation for each genotype as well as omics analyses in their cambium were done. Differentially expressed and methylated genes were identified and spliced variants in natural populations and epivariants in relation to short-time or inter-annual memories suggesting an epigenetic control.

0017-B

ROLE OF CHROMATIN IN THE CONTROL OF TRANSCRIPTIONAL VARIABILITY BETWEEN PLANTS

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Proper gene expression is needed for plants development and environmental response. However, an observation is still not understood: multiple phenotypes can derive from one genome in one environment. This unexpected variability has been overlooked for a long time. Phenotypic and transcriptional variability are not the same as plasticity or genetic variation as it is observed without environmental and genetic differences. There are evidences this variability could be at least partly genetically controlled and biologically relevant. However, we still lack information about the mechanisms regulating plant-to-plant variability.



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Genes with a high transcriptional variability are characterised by a compact chromatin environment. We found that mutants affecting H2A.Z deposition in the chromatin cause a reduction in transcriptional variability. We will show our results in analysing the role of chromatin in the regulation of gene expression variability, and its phenotypic consequences.

0018-C

WATER-FRESH PLANTS FLOATING ON PLASTIC-WATERS: FIRST INSIGHTS ON THE EPIGENETIC EFFECTS OF PET NANOPLASTICS ON SPIRODELA POLYRHIZA (L.) SCHLEID

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A vast amount of literature about the impact of nanoplastics (NPs) on animals is available, whereas information about their potential threat on other organisms is limited. The aim of this work was therefore to test if NPs of polyethylene terephthalate (PET), with a size of around 220 nm, can impact the growth and the physiology of *Spirodela polyrhiza*, with a novel focus on possible particle-induced epigenetic effects (i.e. alteration of DNA methylation patterns). The presence of NPs at environmentally realistic concentrations did not significantly affect the growth of *S. polyrhiza*, while some changes occurred in plant ionome and redox status: treated plants showed a higher concentration of hydrogen peroxide and glutathione. Moreover, Methylation Sensitive Amplified Polymorphism (MSAP) analysis demonstrated that PET NPs induced an increment in DNA methylation levels, pointing out for the first time an adaptation to the presence of this hazardous material through epigenetic processes.

GENOME EDITING AND ITS USE FOR PLANT BREEDING

0019-A

DEVELOPMENT OF GENOME-EDITED TOMATOES WITH HIGH ASCORBATE CONTENT

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Ascorbate, an essential antioxidant substance, must be obtained from food sources because human lack of ascorbate biosynthetic enzyme. Tomato is one of the most widely consumed fruits, thus elevation of ascorbate content in tomato fruits will improve their nutritional value. In tomatoes, ascorbate contents were accumulated during the yellow stage of the fruit and decreased during the late ripening stage. Among the *Solanum lycopersicum* ASCORBATE PEROXIDASE (SLAPX) genes responsible for degradation of ascorbate, SLAPX4 has been characterized as a gene specifically induced during fruit ripening. Mutation of SLAPX4 by the CRISPR/Cas9 system increased ascorbate content in ripened fruits. In contrast, there were no significant differences in the ascorbate content of the leaves and the plant growth phenotype. Collectively, we suggest that mutations in SLAPX4 can be used for the development of genome-edited tomatoes with high ascorbate content in fruit.

0020-B

FUNCTIONAL ANALYSIS OF UORFS IN TOMATO LYCOPENE SYNTHESIS GENES

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Lycopene is a pigment in tomato fruits with strong antioxidant activity, and increasing the lycopene content in tomatoes is a major goal for crop development. The amount of lycopene in tomatoes can be increased by editing the upstream open reading frame (uORF) of the lycopene biosynthetic genes. uORF is a small ORF located in the 5'-untranslated region of mRNA that either inhibits or stimulates the translation of the primary ORF (pORF). We found potential uORFs of LR1 (Lycopene-related gene) and LR2 in tomato (*Solanum lycopersicum*). Dual luciferase reporter assay was used to evaluate the uORF function of these genes, and it was confirmed that the mutated uORF enhanced translation. To enhance the translation of LR1 and LR2, we generated transgenic tomato plants with mutated uORFs using the CRISPR/Cas9 system. We proposed that translational activation of the target gene(s) by mutation of the uORF would be a useful strategy to obtain transgene-free plants with improved lycopene content.



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0021-C

HAIRY ROOTS AS A POWERFUL TOOL FOR INVESTIGATING THE DEVELOPMENTAL FUNCTION OF THE BNATAA1 GENE FAMILY IN BRASSICA NAPUS

Helene ROBERT BOISIVON^{1*}; Veronika JEDLICKOVA ¹; Marie STEFKOVA ¹; Jan BUTULA ¹; Katerina MACOVA ¹; Jana STAVENIKOVA ¹; Marek SEDLACEK ¹

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Auxin is an essential phytohormone for plant morphogenesis. TRYPTOPHAN AMINOTRANSFERASE OF ARABIDOPSIS (TAA1) and flavin monooxygenase YUCCA enzymes produce auxin from tryptophan. Reducing auxin production in Arabidopsis *taa1* and *yucca* mutants impacts plant development, fertility, and stress responses. A functional analysis identified two pairs of *BnaTAA1* homoeologs and 5 *BnaTAA1*-related loci in *B. napus*. We developed a hairy root transformation system for promoter analysis and genome editing. We generated mutants in *BnaTAA1* loci by CRISPR-based mutagenesis. The transgene-free regenerated plants carried a combination of mutations in *BnaA02.TAA1/BnaC02.TAA1* genes. Mutant plants were monitored for phenotypes. Furthermore, hairy roots expressing *pBnaTAA1:GUS* served as a fast and straightforward system to analyze the promoter activity of *BnaA02.TAA1* and *BnaC02.TAA1* genes. In conclusion, using hairy root cultures, we initiated a study of the auxin biosynthesis pathway in oilseed rape.

0022-A

FUNCTIONAL CHARACTERIZATION OF RNA-BINDING PROTEINS, SLRBP6 AND SLRBP11, IN TOMATO

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RNA-binding proteins (RBPs) are known to be involved in various responses in plants, such as regulation of flowering time, seed maturation, and response to environmental stresses. To determine the function of RBPs in tomato, the *SLRBP6* and *SLRBP11* genes containing RNA recognition motif (RRM) were isolated from tomato. *SLRBP6* is highly expressed in red ripening fruit while *SLRBP11* expression is high in flower. In addition, expression of both *SLRBP6* and *SLRBP11* decreased by salt treatment. Subcellular localization analysis showed that *SLRBP6* and *SLRBP11* are localized in nucleolus. In order to investigate the function of *SLRBP6* and *SLRBP11*, we generated transgenic tomato plants overexpressing *SLRBP6* and *SLRBP11*, as well as *slrbp6* and *slrbp11* mutant plants using the CRISPR/Cas9 system. Phenotypic analysis of the transgenic plants revealed that *SLRBP6* and *SLRBP11* are related to seed setting and maturation in tomato plants.

0023-B

EFFECT OF ABA 8'-HYDROXYLASE GENES ON TOMATO POLLEN DEVELOPMENT

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Abscisic acid (ABA) is a phytohormone that plays an important role in plant development and stress response. ABA content depends on degradation and biosynthetic pathways regulated by cytochrome P450 707A (CYP707A) and 9-cis-epoxycarotenoid dioxygenase (NCED), respectively. In this study, we isolated four CYP707A genes (SLCYP707A1 to SLCYP707A4) from tomato and investigated their effects on tomato flowers. Among the four genes, SLCYP707A1 was highly expressed in various tomato tissues and stages of flower development. To investigate the role of SLCYP707A1, we generated knockout (slcyp707a1) plants using the CRISPR/Cas9 system and overexpression (35S::SLCYP707A1) plants using the 35S promoter. The slcyp707a1 plants showed significant reduced pollen viability compared to the non-transgenic plants. The 35S::SLCYP707A1 plants not only had reduced viability but also reduced pollen counts. These results suggest that SLCYP707A1 may affect in pollen development and viability by regulating ABA.

INTERFACES WITH PLANT AND SOIL MICROBIOTA

0024-C

UNRAVELING DIFFERENTIAL EFFECTS OF ARBUSCULAR MYCORRHIZAL FUNGI SPECIES ON THE PERFORMANCE OF TOMATO PLANTS INFECTED WITH THE PLANT PARASITIC NEMATODE MELOIDOGYNE INCOGNITA

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The aim of this study was to evaluate the effect of different strains of arbuscular mycorrhizal fungi (AMF) as biocontrol agents against the parasitic root knot nematode *Meloidogyne incognita* on tomato plants. In greenhouse, the experimental design had two factors: 1) AMF (4 treatments with different AMF isolates + non-AMF control), and 2) Nematodes (simultaneous inoculation with AMF [T1], inoculation 2 weeks after AMF [T2], and non-nematode control). After 60 days, nematodes in T1 reduced the biomass of non-AMF plants, while inoculation with any of the AMF isolates counterbalanced this deleterious effect. In T1, two out of the four AMF isolates increased the number of nematode galls, while one AMF isolate increased the nematode reproduction in T2. These results showed that AMF did not reduce nematode development but counteracted their damage on plants growth in T1. Gene expression analyses of plant hormones will be conducted to elucidate the complex plant-AMF-nematode interaction.

0025-A

MOLECULAR INTERPLAY BETWEEN RAPESEED SEEDLINGS AND AN ENDOSYMBIOTIC MICROBE IN THE EARLY RESPONSE TO SALINITY STRESS

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Here, we demonstrate that the endophytic fungi *Acremonium alternatum* promotes the vitality and growth of the economically important crop oilseed rape. Our results showed that inoculated plants under salinity stress increased the fresh and dry weight by approximately 13% and 12%, respectively. We used omics approaches to analyse proteome and metabolome composition. *A. alternatum* induced changes in several amino acids, phenolic compounds or pantothenic acid. The proteomic analyses further reveal an increase in the total amount of antioxidant proteins which correlates with the observed decrease of hydrogen peroxide and superoxide radicals. We also observed that inoculation increased the accumulation of the whole complex of vacuolar ATPase, which can increase the ability to compartmentalise salt



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into the vacuoles and maintain ion homeostasis inside the cell. Our study provides unique insight into the molecular processes of plant-microbe interaction under salinity stress.

0026-B

THE STRINGENT RESPONSE IS INVOLVED IN THE INTERACTIONS BETWEEN PLANT GROWTH-PROMOTING FUNGUS TRICHODERMA VIRIDE AND CANOLA (BRASSICA NAPUS L.)

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Decreasing plant productivity is currently one of the urgent issues, with robust population growth and rapid progression of climate change. The use of growth-promoting microorganisms, including fungi from Trichoderma genus, is gaining much interest to develop sustainable agriculture. Research should focus on the identification of molecular pathways underneath plant-microbe interactions to fully exploit their potential. Stringent response has been identified in bacteria, plants, animals, and fungi. In plants, RSH proteins (RelA/SpoT homologs) regulate cell metabolism and plant productivity. We analysed promoter regions of Brassica napus RSH genes and showed the presence of many cis-regulatory elements responsive to biotic factors. Gene expression analysis of B. napus RSH1-RSH3 and CRSH showed differential mRNA levels in response to Trichoderma viride DAR5. Our results indicate the involvement of plant and fungal RSH proteins in the colonization of B. napus root by the fungal symbiont.

0027-C

INFLUENCE OF THE FANLEAF VIRUS ON THE GRAPEVINE HOLOBIONT: A STUDY FROM THE SOIL TO THE LEAVES

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The grapevine FanLeaf virus (GFLV) is a plant pathogenic virus associated with an infectious disease, leading to a progressive degeneration of grapevine plants until death. At present, about 60% of the French vineyard would be affected. It is specifically transmitted from plant to plant by a soil-borne ectoparasitic nematode, Xiphinema index. In a vineyard plot located in Champaign (France), rhizospheric soil and fine roots were sampled on many symptomatic and asymptomatic grapevine plants. Meta-genomics and -transcriptomics approaches were developed to follow (i) the species distribution, (ii) the genes and (iii) the expressed genes of fungi, bacteria and virus (microbiota) in both compartments. Our data revealed different microbial communities, and plant and microbial gene expression among plant tissues and

between symptomatic and asymptomatic plants. For the first time, our results bring some information about the influence of the microbiota in a grapevine holobiont disease.

0028-A

MINING THE SEAGRASS MICROBIOTA: THE ENDOPHYTE COMMUNITY OF POSIDONIA OCEANICA SEEDS

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Several species of endophytic bacteria, fungi and actinomycetes colonize the inner plant tissues, where they establish mutualistic interactions with beneficial effects for their hosts. Most of the information available is referred to terrestrial plants, while less is known for marine plants. Adult *Posidonia oceanica* hosts a complex endophytic microbial community, but we do not know which endophytes are already present in seeds. This work investigated the composition of *P. oceanica* seed microbiota by employing a double strategy: compiling the whole inventory by metagenomic analysis of the bacterial and fungal community, and isolating their culturable fraction. A total of 42 bacterial strains were isolated and identified, including 18 species of halophilic or salt-tolerating species. Some species are known for their putative beneficial effects for the host plant and could be exploited in conservation/restoration programs to improve the seed storage and seedling development.

0029-B

SYSTEMIC EFFECTS OF THE GRAPEVINE ROOT MICROBIOTA AND ITS RELATIONSHIP WITH WINE METABOLITES

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Enhancing plant productivity by using the plant growth-promoting microbes (PGPM) could provide a sustainable solution in wine production, as they can improve plant growth, water and nutrient uptake, and protection from stresses. We monitored the impact of a commercial bioinoculant containing PGPM on grapevine root and grape berries microbiota and on wine metabolites. We considered two vineyards with different ages and for each one we analysed plants treated with PGPM and control ones. A metabarcoding analysis targeting bacteria and fungi was applied to describe the microbiota of soil, root compartments and skin of grape berries in all the thesis considered. The impact of PGPM was investigated in wine and must metabolites composition by using Nuclear Magnetic Resonance, this highlighted a higher amino acid content (malic and citric acid) in treated wines. This provides new insights into the systemics effects of PGPM on the grapevine microbiota and at different plant age.



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0030-C

ISOLATION AND IDENTIFICATION OF PATHOGEN-INHIBITING SUBSTANCES FROM WILD PLANTS

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Wild plants play an important role in the ecosystem but are also utilized due to their bioactive compounds. In this study, we have investigated seven wild plant species for which antimicrobial properties and phytosanitary effects were observed, but not yet been studied in detail. Ethanolic plant extracts have been screened in vitro in bioassays for their antimicrobial activity against soilborne and leaf pathogenic microorganisms. The highest antimicrobial properties were found for *Daucus carota*, *Pimpinella saxifraga*, *Oenothera biennis* and *Peucedanum oreoselinum*.

In order to identify the respective bioactive compounds, the extracts were fractionated via solid phase extraction (SPE) and again tested. With a growth inhibition of up to 66%, the fraction eluted by SPE with 50% ethanol solution of the seeds of *P. saxifraga* was the most inhibitory fraction. Further subfractionation of extracts and its testing will lead to the identification of the inhibiting pure substance.

0031-A

MOLECULAR AND PHENOTYPIC CHARACTERIZATION OF THE MICROSymbionTS NODULATING THE ENDEMIC RETAMA DASycARPA IN THE HIGH ATLAS MOUNTAINS OF MOROCCO.

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Bacterial populations nodulating the shrubby legume *Retama dasycarpa* grown in the High Atlas Mountains of Morocco was examined. The analysis of the *rrs* gene sequences of 40 representative strains selected after REP-PCR fingerprinting showed that all the strains belong to *Bradyrhizobium* genus.

Following the result of the *rrs*, twelve representative strains were retained for further analysis. The multi-locus sequence analysis (MLSA) using six housekeeping genes divided the selected strains into four distinct groups within the genus *Bradyrhizobium*. Whereas a *nodC*, *nodA* and *nifH* phylogeny confirmed that they were affiliated to symbiovars *retamae* and *Genistearum*. Furthermore, phenotypic characteristics, plant growth promoting (PGP) activities and legume host range inoculation were performed. This work provides new



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scientific information, for the first time, on the microsymbionts associated with the endemic legume *R. dasycarpa*.

Keywords *Retama dasycarpa*, Bradyrhizobium, MLSA, PGP.

0032-B

TRANSGENERATIONAL EFFECTS OF MYCORRHIZA IN CLONAL AND SEXUAL OFFSPRING

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We investigated the role of transgenerational effects of mycorrhiza on the growth and mycorrhizal colonization of clonal and sexual offspring of *Fragaria vesca*. We hypothesised that the ecological and evolutionary significance of transgenerational effects (TGE) would be stronger in clonally derived offspring due to differences in TGE mechanisms between sexual and clonal reproduction. We found that transgenerational effects on plant growth due to mycorrhiza were consistently stronger in sexual than clonal offspring. This suggests that TGE triggered by mycorrhiza have a significant impact on the plant's relationship with the fungal symbiont, and that they can be adaptive particularly for sexually reproducing individuals. Overall, we provide evidence that the type of reproductive strategy significantly influences the plant's response to mycorrhiza in both intra- and trans-generational contexts, and that TGE can have important ecological and evolutionary implications for clonal plants.

0033-C

INSIGHT INTO PLANT-PATHOGEN PROTECTION BY ARBUSCULAR MYCORRHIZAL FUNGI THROUGH HIGH-THROUGHPUT PHENOTYPING AND ROOT METABOLOMICS

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Most land plants form a mutualistic symbiosis with Arbuscular Mycorrhizal (AM) fungi. This interaction has been shown to enhance plant defence responses to biotic stress, called Mycorrhiza Induced Resistance (MIR). AM fungal species differ in their abilities to enhance plant defences and underlying biochemical mechanisms are still poorly understood. Phenotyping observations and root metabolomic profiling of tomato plants colonised with different AM fungal single species and mixtures revealed varying abilities to enhance growth and defence responses, and identified MIR effective and non-effective species, which when combined in mixtures, resulted in mostly non-additive effects. Biochemical MIR-related patterns specific to effective AM fungal species and an increase in repressed metabolic features highlight AM fungal-specific abilities to improve growth and/or disease resistance in



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plants, and enabled insight into the biochemical MIR-related functional specialization of AM fungi.

0034-A
UNDERSTANDING PLANTS' INFLUENCE ON PLANT-MICROBE INTERACTIONS

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The communication between plants and microbes can result in beneficial, pathogenic, or neutral interactions. We aim at understanding how plants shape their microbial community by examining a set of phylogenetically diverse plant species for their exudation profiles (nutrients or chemical signals) to understand which metabolites result in association with different microbes. Preliminary results have shown that root exudate profiles are dynamic within and across species and are influenced by their environment (hydroponic and soil systems). Bacteria grown in media with root exudates show an increase in growth. With the knowledge of the metabolites and microbes, we plan to complete microbe-metabolite assays to see which species and metabolites play key roles in the plant-microbe interaction interface. This research can help inform us of the structure and function specific plant and microbe interactions, improve plant health, and yield for more sustainable agricultural practices.

0035-B
P2CS 2023: UPDATE OF THE PREDICTED TWO-COMPONENT SYSTEMS DATABASE

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The aim of P2CS is to stimulate the discovery of new functional families involved in transcriptional pathways, specifically Two Component Systems (TCS), through an in-silico approach and provide the community with the first international knowledge database. With this update, we provide a large-scale computational solution by taking advantage of annotation/data accumulated in our database in combination with genome-mining and text-mining approaches and extend our classification by integrating around 240.000 bacteria and more than 2.000 plant and fungal genomes.. From in silico prediction, classes of unknown TCS functions are identified as key players in environmental microbiomes, and their sensor/output signal categories are predicted by innovative deep-learning methods. Many of the organisms studied in our institute are ubiquitous in soils and aquatic environments. Our database will thus be an invaluable reservoir for biostimulation, bioremediation or biocontrol studies.

0036-C

PLANT MICROBIOMES IN SUSTAINABLE VITICULTURE

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The intensification of agriculture has mostly been supported by the increasing use of water resources at the expense of environmental water balance and hydrological cycle. Moreover, in recent decades climate change and the consequent expansion of drought has further compromised the availability of water, making current agricultural systems even more fragile both from ecological and economical point of view. Therefore, it is urgent to improve the resilience of agro-systems by promoting a more rational use of biological and natural resources. Microbiomes have emerged as main influencers in the physiology of many multicellular organisms. The present work aim to investigate the natural biodiversity of the grapevine endophytic microbiota arisen in Mediterranean areas with arid climate (Algeria and Sicily) to define microbe consortia to be used in sustainable viticultural practices in adverse environmental conditions.

MACRO- AND MICRO-NUTRIENT IN PLANTS

0037-A

EVALUATION OF YEARLY DIFFERENCES IN THE L-CITRULLINE CONTENT OF WATERMELON (CITRULLUS LANATUS) GERMPLASM

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This study was conducted to evaluate any yearly changes in the citrulline content of 102 watermelon germplasms using HPLC analysis during two years - 2019 and 2022. Results indicated significant differences in citrulline content among the accessions each year and also between the two years. Compared to 2019, in 2022 the citrulline content in watermelon showed a varied difference from as little as 0.3 times increase to as much as 7.2 times for individual accessions, and the average value was 1.6 times higher. Considering the influence of environmental factors, comparison of the weather conditions during the cultivation period in 2022 with 2019 indicated no significant difference, with an average difference in temperature of 1°C and an average precipitation of 10mm. However, the average humidity was found to decrease significantly from 78% to 69%, which was consistent with the reported research results that a dry climate increases the citrulline content of watermelon.

0038-B

MOLECULAR CLONING AND ANALYSIS OF A GENE ENCODING A MONOSACCHARIDE UPTAKE TRANSPORTER IN CRYPTOMERIA JAPONICA

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Sugars are essential nutrients for plants, in which they play a diverse range of roles. The transport of sugars across plant cell membranes is mediated by membrane proteins classified as transporters, and elucidating the mechanisms underlying sugar membrane transport is important for a better understanding of tree growth and physiology. In this study, we isolated a gene (cDNA), CjSTP4, encoding a monosaccharide transporter from sugi (*Cryptomeria japonica*). To investigate the monosaccharide uptake function of CjSTP4, we conducted complementation tests using a yeast strain deficient in hexose uptake. Transformation of the yeast strain with CjSTP4 complemented this deficiency, indicating that CjSTP4 plays a role in hexose uptake. Expression analysis revealed that CjSTP4 is expressed in all parts of the sugi trees examined in this study, including male strobili, inner bark, and roots. It would appear that CjSTP4 functions in the membrane transport of monosaccharides throughout sugi trees.

0039-C

MORPHOLOGICAL, CHEMICAL, GENETIC DIVERSITY AND NUTRITIONAL CHARACTERISTICS OF MOROCCAN MENTHA SPECIES

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The genus *Mentha* L. is one of the most important taxa of the Lamiaceae family, it has been valued since ancient times by means of its aromatic and therapeutic properties. *Mentha* is used for its antioxidant, tonic, digestive, antiseptic and refreshing properties. The systematics of the *Mentha* genus is very complicated and still ambiguous, mainly due to the variation in basic chromosome number, frequent interspecific hybridization and their high polymorphism. Combining morphological, chemical, and genetic studies will enable us to identify the *mentha* species and eliminate any remaining ambiguity while presenting a genetic empress for each species. Most medicinal plants provide practically almost all of the organic and mineral components recognized as necessary for human nutrition. The use of mint is still restricted to its essential oils or even by infusing its leaves and stems, It would be advantageous to know its nutritional content so that we can get more benefit from it.

0040-A

HOW DO GROWTH RESPONSES TO ELEVATED TEMPERATURES AFFECT NITRATE UPTAKE, TRANSPORT AND ASSIMILATION IN ARABIDOPSIS THALIANA?

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In response to mild warm temperatures, *Arabidopsis thaliana* young seedlings adjust their development by elongating vegetative organs like hypocotyls. These growth responses are called thermomorphogenesis and are mostly allowed by modifications in hormones biosynthesis and/or signalling. But thermomorphogenesis effects on nutrients homeostasis, and especially on nitrogen nutrition are unknown. Our main hypothesis is that higher temperatures could affect nitrate-related actors and/or homeostasis in order to promote cell elongation. Firstly, actors from nitrate homeostasis necessary for thermomorphogenic responses will be identified via mutant phenotyping and transcript levels analyses. Secondly, some steps of nitrate homeostasis will be analysed in response to temperature. This works will set the basis for a better understanding of nitrate utilisation in seedlings subjected to high ambient temperature.



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0041-B

TRANSCRIPTOMIC AND METABOLOMIC CHANGES IN TRITICUM AESTIVUM TRIGGERED BY THE COMBINED TREATMENT OF MICROPLASTICS AND TRACE ELEMENTS

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Triticum aestivum can serve as a natural indicator for determining the ecological impact of microplastics. There is lots of concern about how plants absorb and accumulate microplastic. The co-effect of microplastic and trace elements are still vague. This work investigated the relationship between 6 trace elements (TE) and polystyrene microplastics (PSs) and discuss how it can affect the development of wheat. The results showed that combined treatment of PS with 3 TEs (Mo oxide, Se Acid and Sodium Mo dihydrate) increased the growth and secondary metabolites. The optimal concentration of selected TEs proves more beneficial in stimulating the secondary metabolites. The metabolic analysis revealed 67% of metabolites up-regulated and 14% down-regulated. The most significant up-regulated metabolites were glutathione, diosmin, schaftoside, and so on. And, the transcriptomic analysis revealed that secondary and amino acid metabolisms related genes were up-regulated.

0042-C

MODULATORY ROLE OF NITRATE IN GLYCOLYSIS AND PHOTOSYNTHETIC CARBON METABOLISM UNDER AMMONIUM NUTRITION

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The activation of the flux of carbon compounds into the GS-GOGAT cycle under ammonium nutrition has traditionally been attributed to the increased demand of carbon skeletons for an immediate and rapid assimilation of the ammonium ion, thus preventing its accumulation and toxicity in the cell. However, the increased flux of carbon compounds is accompanied by an increased synthesis of methylglyoxal (MG), a highly toxic metabolite derived from the accumulation of triose phosphates (TPs) in the Calvin-Benson cycle (CBC) and glycolysis. Here, we present the main regulatory effects of the μ M nitrate in ammonium-fed spinach plants on their carbon metabolism: photosynthesis and glycolysis. These results may shed light on some important principles that have traditionally been considered as a putative key factor in explaining the origin of ammonium toxicity.

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0043-A

MACRONUTRIENT CHLORIDE NUTRITION MODULATES PSII BIOCHEMISTRY OF PLANTS

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Although defined as an essential micronutrient, we have shown that adult plants accumulate chloride (Cl⁻) to typical macronutrient levels to optimize cell elongation and the plant-use efficiency of water, nitrogen and CO₂/energy (Colmenero-Flores et al., 2019; Cakmak et al., 2023). Maximal Cl⁻ demand occurs during early vegetative growth, when Cl⁻ limitation determines a strong biomass reduction, a deficiency that could not be compensated by additional NO₃⁻ supply. This phenotype was associated with changes in PSII biochemistry, including a reduction of the Electron Transport Rate (ETR).

This work aims to determine how Cl⁻ affects chloroplast anatomy and photosynthetic parameters such as ETR, thylakoid proton gradient and non-photochemical quenching (NPQ) during early and late plant growth.

Key words: Chloride nutrition, photosynthesis, ETR, NPQ

0044-B

THE INFLUENCE OF HUMIC SUBSTANCES AND AMINO-ACIDS ON GROWTH AND NITROGEN NUTRITION OF PLANTS (ARABIDOPSIS, WHEAT)

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N is an essential macro-element for plants and, for most of them, is taken up as inorganic N source from the soil (nitrate or ammonium). There is thus an urgent need for strategies allowing a better N use efficiency in crops. For this goal, the use of molecules such as humic substances or amino-acids, which could stimulate and optimize N use is a promising strategy. However, the links between humic substances, growth and N metabolism are not well documented in plants.

We have studied the influence of humic substances and amino-acids on growth, N uptake and metabolism of the model plant Arabidopsis thaliana and of wheat plants either in controlled in vitro conditions or in hydroponic cultures. Addition of both humic substances



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and amino-acids results in effects on growth and development in a dose-dependent manner. We have also explored the effects of these molecules in response to variations in N nutrition.

0045-C

IRON PULSING: A NOVEL SEED INVIGORATION TECHNIQUE TO BOOST THE GROWTH AND YIELD OF RICE

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Rice is synonymous with life for the people of Asian countries like India. The unprecedented growth of population and continuous shrinkage of arable lands make it obligatory to find out sustainable ways to increase the yield of the existing rice crops to attain the global goal of food security. Iron pulsing is a novel technique that uses iron salts to treat rice seeds during germination. This brief treatment enhances the growth and vigor of rice plants through better nitrogen and carbon assimilation. Besides, the efficacy of the treatment persists till the maturity of the plants. Iron pulsing improved the agro-morphological traits and yield of the rice plants along with making the grains nutritionally enriched and rich in iron. However, we are yet to unravel the underlying molecular mechanism pertaining to this treatment. Altogether, iron pulsing is a propitious approach that can be an innovative agricultural tool to promote the growth, yield, and quality of rice grains.

0046-A

REGULATION OF INTRACELLULAR FREE ZINC CONCENTRATION IN ARABIDOPSIS THALIANA ROOTS

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Zinc (Zn) is an essential micronutrient for all living organisms. Zn malnutrition affects one third of the global human population and plants are the main entry point for Zn into the food chain (Assunção et al., 2022, 10.1093/jxb/erac014). Enhancing Zn accumulation in crops is required to improve plant nutritional value and growth in nutrient-deficient soils. Zn uptake in plant root is regulated by F-bZIP transcription factors that directly perceive intracellular Zn concentrations ([Zn]_i; Lilay et al., 2021, 10.1038/s41477-021-00856-7). Here, we use eCALWY, a genetically encoded fluorescent Zn sensor, expressed in the cytosol of Arabidopsis cells to investigate the regulation of [Zn]_i in root cells (Lanquar et al. 2014, 10.1111/nph.12652). [Zn]_i lies in the 100 pM range and increases transiently upon Zn elevation in the medium. We investigate [Zn]_i in mutants lacking Zn transporters. This research will highlight the mechanisms leading to Zn deficiency responses or toxicity.

0047-B

ENHANCED PRIMARY ROOT GROWTH IN TOMATO THROUGH CHLORIDE NUTRITION: INSIGHTS FROM TRANSCRIPTOMIC ANALYSIS

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We have recently defined chloride (Cl⁻) as a beneficial macronutrient for plants, with new functions in the use of water, nitrogen and carbon. While its effects on leaf anatomy have been studied, little is known about the impact of Cl⁻ nutrition on root development. Here we determined primary root (PR) growth and development (using imaging and microscopy, respectively) in tomato plants treated with 0 and 5 mM Cl⁻ salts in hydroponics. Results showed that Cl⁻ promotes PR growth by enhancing cell division and elongation in the proliferation domain. Furthermore, we employed RNA-seq to examine molecular mechanisms underlying Cl⁻ functions in tomato PRs. Strikingly, we identified 47 differentially downregulated genes but no upregulated genes. The putative role of some candidate genes involved in Cl⁻-dependent PR responses are discussed. This study is the first to transcriptomically characterize the Cl⁻ effects as a macronutrient, providing insights into its role on root development.

0048-C

NITROGEN RESPONSIVE GENES AND NITROGEN USE EFFICIENCY IN RICE AFFECTED BY WATER SUPPLY AND NITROGEN FERTILIZATION

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Nitrogen is an essential element for plant growth and development. Two major nitrogen forms that plants can be available are ammonium and nitrate. Ammonium is directly assimilated in plants, on the other hand, nitrate should be ammonified in order to be an incorporation into organic compounds. Three types ((NH₄)₂SO₄, KNO₃ and NH₄NO₃) of nitrogen fertilizer have been applied for rice production. Rice responding genes contribute to evaluate nitrogen use efficiency (NUE). The phenotypic difference in rice plants were not significant, and KNO₃-fed rice root showed shorter than others. The level of soluble carbohydrates was greatly affected by nitrogen sources rather than water supply. NUE and NUE_g showed an opposite pattern with soluble carbohydrates. The expression of ammonium (OsAMT1.1 and OsAMT1.2) and nitrate (OsNRT2.3a) transport-involved genes decreased at KNO₃ condition. Accordingly, it is suggested that further study is required to understand nitrogen metabolism genes-affected NUE.

0049-A

IMPACT OF THE ENVIRONMENTAL INFLUENCE ON THE TRANSCRIPTIONAL VARIABILITY OF GENES INVOLVED IN NITROGEN NUTRITION

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Nitrogen, which is one of the most determining factors in the growth, survival and reproduction of plants is unfortunately also one of the most fluctuating elements spatially and temporally in the soil. A tight regulation of the expression for the genes involved in its uptake and transport is therefore decisive. However, some genes involved in nitrogen nutrition present a high level of transcriptional variability between plants even in absence of genetic and environmental differences.

In this context, we are analysing the role of the high expression variability for the high-affinity nitrate transporter, namely NRT2.1, in the response to fluctuation in nitrate in *Arabidopsis thaliana*. We will also show our results of the impact of certain fluctuating nitrate conditions on this inter-individual variability.

0050-B

THE ARABIDOPSIS PLASTIDIAL/MITOCHONDRIAL BOLA PROTEINS ARE ESSENTIAL FACTORS FOR OPTIMAL PLANT DEVELOPMENT AND NUTRIENT PARTITIONING

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The universal Iron-sulfur (Fe-S) clusters embedded in proteins support numerous fundamental biological processes including photosynthesis and respiration. The assembly and delivery of Fe-S centres takes place within specialised machineries involving numerous proteins and cofactors, some of which are still poorly characterised in plants. This is the case of BOLA proteins, described in several model organisms but whose importance and role in plants have not yet been evaluated. We found that two members of this family in *Arabidopsis thaliana*, BOLA1 and BOLA4, are present in most tissues, with a dual targeting to the mitochondrion and the plastid. Contrary to *bola* single mutants that are asymptomatic, double *bola1bola4* mutants show early primary root growth arrest and dwarf phenotype, with altered iron and sulfur content and partitioning. Overall, our results show that BOLA1 and BOLA4 are essential for optimal growth and development, and are new important actors in iron homeostasis.

0051-C

GROWTH AND QUALITY ASPECTS OF NITROGEN NUTRITION IN GRAIN AND GRAPEVINE PRODUCTION

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Crops such as wheat and grapevine need nitrogen for growth biomass development and formation of harvest such as grain or wine berries. The amount of nitrogen applied is mainly responsible for the harvested amount and the quality of the product. Growth is altered by timing, rating and form of the nitrogen applied. For instance, the timing of nitrogen application in wheat alters quantity and quality of grain storage proteins such as gliadin or glutenin and their subfractions. Moreover, the type of nitrogen applied as nitrate, urea or amino acids may also alter uptake and the resulting quality. In terms of grapevine an analysis of the effect of rating and type of nitrogen sources alters Nitrate Uptake Efficiency (NUE), differently triggers key enzymes and their transcripts and changes sensory quality of the wine. In terms of nitrogen nutrition of wheat, a reduction in fertilization can be achieved without a loss of yield or quality and with beneficial effects on the environment.

ORGANELLAR BIOLOGY

0052-A

ROLE OF CHLOROPLAST NUCLEOIDS IN C4 PHOTOSYNTHETIC DIFFERENTIATION IN ZEA MAYS.

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In C4-plants, the separation of photosynthetic functions between specialized mesophyll (M) and bundle sheath (BS) chloroplasts allows a CO₂-concentrating mechanism leading to a more efficient carbon fixation than C3-plants. The regulatory network behind the C4 differentiation remains undiscovered in particularly at the level of plastid gene expression (PGE). Presuming that the regulation of PGE occurs in the nucleoids (plastid protein-DNA-RNA complexes), differentially expressed regulatory proteins between M and BS nucleoids are responsible for the C4 differentiation. We have developed a purification protocol of chloroplasts and nucleoids from maize M and BS cells. Analyzing nucleoid complexes extracted from M or BS chloroplasts is based on a combination of high-accuracy quantitative mass spectrometry and transcriptome analysis in order to reveal regulatory proteins and post-transcriptional target mRNAs maturation implicated in C4-differentiation. Here, we present preliminary data.

0053-B

INFLUENCE OF PLASTIDIAL ACTIVITIES ON NUCLEAR ORGANIZATION

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Photomorphogenesis launches a global increase in gene expression, chloroplast biogenesis and photosynthesis establishment. In Arabidopsis, these morphological, metabolic and molecular changes induced by light are accompanied by a reorganization of nucleus architecture in cotyledon cells with the compaction of heterochromatin domains into conspicuous foci named chromocenters. Here we report that affecting plastid biogenesis, using lincomycin or plastid polymerase loss-of-function, impacts heterochromatin organization differently in the absence or presence of light. Plastid inhibition leads to the



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formation of numerous fuzzy pseudo-chromocenters in photomorphogenic cotyledons while it promotes heterochromatin aggregation in etiolated cotyledons. We now aim to characterize the signaling events and mechanisms underlying plastid capacity to modulate nucleus and epigenome dynamics and their relevance for adaptive responses to developmental and environmental signals.

0054-C

MTDNA REPAIR MACHINERY IS CENTRAL IN SALT STRESS RESPONSE

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The importance of organelles as central coordinators of plant responses to internal/external stimuli has become increasingly important. Mitochondria play a role as stress sensors of environmental stimuli, being a component of a complex communication network involving organelles and the nucleus. WHY2 among the proteins involved in mtDNA repair is the most abundant, evidences suggest an important role of WHY2 in mitochondrial genome replication and that permit a complete mtDNA activity. Recent results on WHY2 show a link between mtDNA stability and proper mitochondrial morphology, kinetics and functionality, indicating a fundamental role in mitochondrial activity during stress responses. Failure in maintaining the mitochondrial genome stability results in the accumulation of mutations and genomic rearrangements that can become deleterious. In the present work data will be reported showing the connection between mtDNA maintenance, high levels of WHY2 and the response to abiotic stress.

0055-A

IS RIP1, AN RSH1 INTERACTING PROTEIN, INVOLVED IN PPGPP SIGNALING AND STRESS ACCLIMATION IN PLANTS?

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The unusual hyperphosphorylated nucleotide guanosine tetraphosphate (ppGpp) is a secondary messenger that plays an important role in the regulation of chloroplast function and photosynthesis in plants. Abiotic stress and hormone treatment induce ppGpp accumulation in the chloroplast. However, it is not known how ppGpp biosynthesis is



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activated under these conditions. In order to understand how, we searched for target proteins that interact with the RelA/SpoT Homolog (RSH) enzymes which are responsible for synthesizing/hydrolyzing ppGpp in the chloroplast. Using a Yeast Two-Hybrid screen we identified RSH1 Interacting Protein 1 (RIP1) that specifically interacts with the ppGpp hydrolase RSH1 in Arabidopsis. The interaction was confirmed *in vivo*. We then investigate the physiological functions of plant RIP1, and the physiological relevance of the RIP1/RSH1 interaction. Our findings open new perspectives for the intra-chloroplastic regulation of ppGpp signalling in plants.

0056-B

INTERATOME PLATFORM: CHLOROPLAST PROTEIN-PROTEIN INTERACTION NETWORK PROJECT

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Protein-protein interactions are critical elements of biological systems and their analysis can provide valuable insights into the functions of proteins. The InterATOME Platform fully automated and improved the Y2H protocol which was previously used for the Arabidopsis Interactome Mapping - AIM project (Science 2011). The platform has been involved in the construction of the largest pathogen effector interactors database and in several plant biology international collaborations. Furthermore, we recently synthesize the whole Arabidopsis chloroplast ORFeome. In order to create the first chloroplast protein-protein interaction network, we are currently screening the chloroplast gene encoded proteins against the whole AIM library (12K Arabidopsis proteins). Preliminary results underline strong connections between chloroplast and endoplasmic reticulum (ER) proteins involved in biotic and abiotic stresses response and retrograde signalling pathways.

0057-C

ROLE OF THE PLASTIDIAL FUNCTIONAL STATES ON SKOTO-MORPHOGENESIS IN ARABIDOPSIS THALIANA

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When seeds are under the soil, seedlings show a longer hypocotyl, an apical hook, and a non-green cotyledon. This developmental program is known as skotomorphogenesis. Recently, we discovered that apical hook is over bended in response to mitochondrial deficiency during early development.

Due to the ability of etioplasts to generate ATP through etio-respiration and the similarities and interactions between mitochondria and plastids, we explored the role of plastids in

skoto-morphogenesis. We found that etiolated seedlings showed an apical twist with an increased capacity of mitochondrial AOX enzymes when exposed to the plastid transcription and translation inhibitors. The metabolomics indicated an accumulation of mitochondrial metabolic intermediaries in the plastid transcription-limited seedlings, which implies the involvement of mitochondria in the developmental response and points out that communication from plastids to the nucleus could occur directly or via the mitochondria.

0058-A

RIBONUCLEASES AND RNA QUALITY CONTROL IN THE CHLOROPLAST

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The chloroplast is the plant compartment in which light energy is captured and transformed into chemical energy, ultimately making life on Earth possible. They are descendants of free-living photosynthetic bacteria and maintain a small but essential genome. Pervasive transcription coupled to inefficient termination leads to a highly complex primary transcriptome including sense RNA (sRNAs) and antisense RNA (asRNAs). Therefore, the transcriptome is heavily processed by a combination of RNA-binding proteins and ribonucleases to produce the functional RNA population. One poorly understood aspect of chloroplast gene expression and regulation is the function(s) of asRNAs and more globally double-stranded RNA (dsRNA) related processes. Our work suggests that chloroplast ribonucleases degrade asRNAs avoiding the formation of dsRNAs with their corresponding sRNAs. We aim to produce the first global analysis of the prevalence of dsRNA in the chloroplast.

0059-B

APOCAROTENOIDS: B-CYCLOCITRAL AND ITS DERIVATIVE B-CYCLOCITRIC ACID INDUCE A COMPLEX MULTI-BRANCHED SIGNALING PATHWAY IN ARABIDOPSIS THALIANA

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β -Cyclocitral (β CC) is a volatile compound derived from the oxidation of β -carotene in the chloroplasts. β CC elicits a retrograde signaling pathway modulating the expression of nuclear genes and enhancing tolerance to photo-oxidative stress. β CC converted to the water-soluble β -cyclocitric acid (β CCA). Both β CC and β CCA confer stress tolerance but the molecular mechanisms of tolerance are still elusive. A comparative transcriptomic analysis of β CC- and β CCA-treated plants identified a network of genes involved in xenobiotic detoxification, hypoxia, and stress defense. Compared to β CCA, β CC showed a significant three fold upregulation of genes. In total 119 genes were differentially regulated by the two compounds and among them 46 genes were uniquely upregulated by β CC. This indicates that β CC and

β CCA pathways do not fully overlap, with β CCA possibly mediating only a branch of the β CC-signaling pathway.

0060-C

THE ARABIDOPSIS NPK1-RELATED PROTEIN KINASES REGULATE RESPONSES TRIGGERED BY THE ENDOPLASMIC RETICULUM STRESS

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The Arabidopsis NPK1-related Protein kinases ANP1-3 belong to the MAPKKK superfamily and were previously described to be crucial for cytokinesis, elicitor-induced immunity, and development. Lack of ANPs also induce a typical cell wall damage syndrome similar to that observed in plants treated with the endoplasmic reticulum (ER) stress inducer tunicamycin (Tm). Here, we investigated the possible involvement of ANPs in signaling events mediating the ER stress, characterized by the accumulation of unfolded/misfolded proteins in the ER and the activation of the unfolded protein response (UPR). We uncover a role of ANPs in the regulation of UPR activation and show that plants overexpressing ANPs display higher resistance to prolonged ER stress. The aim of this study is to generate knowledge on signaling mechanisms mediating the ER stress response and cell wall deposition and how they contribute to sense and adapt to adverse environmental clues.

0061-A

THE CORRELATIVE CRYO-WORKFLOW TO IDENTIFY ULTRASTRUCTURE OF NATIVE GUARD CELLS

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Plant anatomy offers a visualized way to understand structural characteristics of plant cells, which closely combines with a cascade of physiological, metabolic, or biochemical processes. However, how precisely and deeply the cellular structures can be decoded relies heavily on perceived electron microscope techniques. Sample fixation and embedding are of vital importance to influence image quality. Traditional chemical fixations and high water content in biological specimen usually cause serious artefacts to change cell surface topography or even damage membrane integrity. For this, keeping native plant cells without any pretreatments directly in a vitreous state would be a smart strategy, since the rapid cooling process by cryo-fixation technique could avoid the ice contamination. Here, we developed cryo-Focused Ion Beam-Scanning Electron Microscope (cryo-FIB-SEM) as a powerful tool to decode the ultrastructural characteristics of guard cells in a near-to-native state.

0062-C

UNVEILING THE MITOCHONDRIAL UNFOLDED PROTEIN RESPONSE (UPRMT) IN ARABIDOPSIS THALIANA

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Mitochondria are key organelle involved in many different cellular processes, from the production of energy to stress sensing and response. However, to preserve proper organelle function, is necessary to maintain mitochondrial protein homeostasis. This is usually assured by the action of the mitochondrial protein quality control (mtPQC), a complex network of chaperones and proteases. However, when there is an accumulation of misfolded/unfolded proteins that goes beyond its capability the cell mounts the mitochondrial unfolded protein response (UPRmt). UPRmt is a mitochondrial stress response by which mitochondria promote the expression of nuclear-encoded genes to restore organelle function.

In this work we investigate proteotoxic stress and UPRmt in Arabidopsis thaliana. Mutant plant lines showing a constitutively active UPRmt have been identified and characterized. Mitochondrial morphology and dynamics, Ca²⁺ signaling and stress marker gene expression profile were determined.

0063-B

THE LENGTH OF PRENYL CHAINS SYNTHESIZED BY CIS-PRENYLTRANSFERASE DEPENDS ON THE SUBCELLULAR LOCALIZATION OF THE ENZYME

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Cis-prenyltransferases (CPTs) are enzymes responsible for adding a specific number of isoprene units (i.u.) to extending polyisoprenoid chains. Arabidopsis roots accumulate a mixture of long-chain polyisoprenoids (18-23 i.u.) synthesized by CPT1, and a single short polyprenol Pren-7 synthesized by CPT6. Both enzymes are localized in the endoplasmic reticulum (ER). Arabidopsis leaves accumulate a mixture of medium chain polyprenols (9-11 i.u.), synthesized by the chloroplast CPT7. In this work, we show that the subcellular location of CPTs effects on the length of the synthesized polyisoprenoid chains. Hybrid CPTs consisting of the catalytic domain of either CPT1 or CPT6 and of the chloroplast-targeting peptide from CPT7, expressed in Arabidopsis, synthesize in chloroplasts polyprenols with different length than native CPT1 and CPT6 in the ER. The lipid products of HYB7-1 are shorter than those synthesized by CPT1 while the products of HYB7-6 are longer than those of CPT6. This research was supported by grant funded by the National Science Centre of Poland 2019/35/B/NZ1/03794.

0064-C

DYNAMICS OF GLOBAL TRANSLATION LEVEL IN ARABIDOPSIS THALIANA

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In plants external changes are anticipated and coordinated with various biochemical processes by endogenous timing systems, circadian clocks. Here we apply polysome analysis to investigate dynamics in global translation level over the (light/dark) diel and (light/light) circadian cycles in 14-d-old *Arabidopsis thaliana* seedlings. We detected gradual changes in the global translational level over the diel cycle. Polysome loading was higher during the day and was lower during the night. Furthermore, our data also revealed gradual changes in the global translation level over the circadian cycle. We found that polysome loading increased and decreased in the 'subjective' light and night phases, respectively. Thus, our data suggests that the global translation level might be under control of the circadian clock. To shed more light on the translational regulation by circadian clock we next plan to directly monitor protein synthesis rate by puromycin labeling.

PHOTOSYNTHESIS: UNDERSTANDING AND PROGRESS IN ITS MANIPULATION

0065-A

UNCOVERING NOVEL MOLECULAR PLAYERS INVOLVED IN SUSTAINED PHOTOPROTECTION DURING PROLONGED EXCESS OF LIGHT EXPOSURE

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Slowly relaxing non photochemical quenching (NPQ) components are essential to protect plants exposed to persistent excess light and prevent irreversible photodamage of their photosynthetic apparatus, allowing repair and acclimation processes that take place at longer time scales. However, once they are activated, it takes significant time to relax, even when the stimulus that triggered their activation is removed, limiting photosynthetic performances and biomass production. In this work we performed chemical mutagenesis and genetic screenings in Arabidopsis mutants lacking sustained NPQ components qH (lcnp-1) and qZ (npq1-2lut2-1) to identify suppressors and enhancers and uncover novel molecular players involved in the slowly relaxing mechanisms already known and new components that are still unknown. We isolated several mutants using chlorophyll fluorescence imaging and will determine the causative mutations through a whole genome sequencing approach of putative allelic mutants.

0066-B

PLANT (APO)CAROTENOIDS AND PHOTOSYNTHESIS IN FAR RED-ENRICHED LIGHT SIMULATING PROXIMITY SHADE

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Proximity shade induced by neighbor vegetation is characterized by a decrease in the red (R) to far-red (FR) ratio of the incident light which induces various physiological changes allowing plants to acclimate to this environmental constraint. We grew Arabidopsis thaliana (Col-0), a shade-avoider species, in a growth chamber equipped with FR LEDs to simulate proximity shade conditions, with the R/FR ratio dropping from 1.4 (in white light, W conditions) to 0.2 (in far red-enriched light, W+FR conditions). In W+FR, Col-0 displayed the typical shade avoidance syndrome with hypocotyl elongation 5-times greater than in W. W+FR treatment also induced a marked reduction of the carotenoid levels which was correlated with a down-regulation of several genes involved in carotenoid biosynthesis. However, this loss of



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photosynthetic pigments was associated with a noticeable increase in plant biomass. The effects of W+FR conditions on the plant photosynthetic characteristics will be presented.

0067-C

COMPARATIVE ANALYSIS OF FOLIAR SPRAY OF COPPER OXIDE AND ZINC OXIDE NANOPARTICLES ON PHOTOSYNTHESIS AND PHYSIOLOGY OF RAPHANUS SATIVUS L. UNDER SALINITY STRESS

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The study aims to compare the effects of foliar spray of copper oxide (CuO NPs) and zinc oxide nanoparticles (ZnO NPs) on photosynthetic efficiency and physiology of *Raphanus sativus* L. subjected to different concentrations of NaCl. Two weeks old radish seedlings treated with 150 mM and 300 mM NaCl alone and in supplementation with metal oxide nanoparticles (MO NPs) (100 ppm) for 10 and 17 days. Under salinity stress the growth and photosynthetic parameters of crop reduces, and it accumulated considerable amount of phenolics and proline to tolerate stress environment. Foliar application of MO NPs improved the growth of stressed plants by enhancing leaf area, chlorophyll fluorescence, improving phenolic contents and plant pigments, lowering oxidative damage (H₂O₂) and stress indicator (proline). The interactive study concluded that influence of CuO NPs in overcoming the effects of NaCl is more than ZnO NPs at both concentrations and time intervals.

0069-B

PROTON COUPLED ION TRANSPORT AT THE CHLOROPLAST ENVELOPE

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Photosynthesis depends critically on pH in chloroplasts. An alkaline stroma is required for carbon fixation, but it is not known how alkaline stromal pH is formed and regulated. By measuring stromal pH with the fluorescent probe BCECF we demonstrated that envelope K⁺/H⁺ antiporters KEA1 and KEA2 are involved in stromal pH adjustment upon light to dark transitions. Now we evaluated H⁺ coupled ion transport at the envelope membrane for different ions and show that external K⁺ causes a strong but transitory alkalinization whereas external Na⁺ causes a slow irreversible alkalinization of the stroma, especially in light when a membrane potential is present. External NO₃⁻ caused a strong slowly recovering stromal acidification. Strongest but transitory acidification was observed with NO₂⁻, possibly due to transport of protonated HNO₂. We will try to identify the molecular nature of the NO₃⁻ transport system.

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0070-C

DISRUPTION OF CHLOROPLAST ENVELOPE K⁺/H⁺ ANTIPORTERS KEA1 AND KEA2 AFFECTS CYTOSOL PH AND PM MEMBRANE POTENTIAL.

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KEA1 and KEA2 are chloroplast envelope K⁺/H⁺ antiporters. We have shown before that stromal pH is higher in Arabidopsis kea1kea2 mutant chloroplasts. As 50% of mesophyll cell volume is made up of chloroplasts, this could affect cytosol pH. Using pH sensitive microelectrodes we find that the cytosol in mesophyll cells is more acidic in the mutants. Membrane potential was however also reduced, pointing to reduced Plasma Membrane H⁺-ATPase activity causing the acidic cytosol. PM H⁺-ATPase phosphorylation and hydrolytic activity were similar comparing wild type and mutants. However, ATP dependent vesicle acidification in reconstituted membrane vesicles isolated from kea1kea2 mutants was much reduced compared to wild type, indicating that the ATPase could not sustain a pH gradient despite normal ATP hydrolytic activity. This could be caused by increased membrane permeability, or reduced H⁺/ATP coupling ratio of the ATPase.

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0071-A

PRECISE ESTIMATION OF CHLOROPHYLL A, B AND CAROTENOID CONTENT BY DECONVOLUTION OF THE ABSORPTION SPECTRUM AND NEW SIMULTANEOUS EQUATIONS FOR CHL DETERMINATION.

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The precise determination of photosynthetic pigment content in green organisms, chlorophylls (Chls) and carotenoids (Cars), is important to investigate many photosynthetic processes. The most used methods for Chl content determination by spectrophotometry are based on simultaneous equations. The advantage over chromatography is the easiness and speed, but issues in sample preparation or measurement are not detectable.

We propose a new method to measure Chl a, Chl b and total Cars based on the fit of the absorption spectrum of pigment extracted in acetone using spectra of purified pigments as references. The method allows a more precise and accurate pigment estimation as compared to classical equations, even in incorrectly prepared acetone solutions. The method also allows

the discovery of artifacts in sample preparation or measurement drastically reducing mistakes.

We also propose new simultaneous equations that provide more reliable results in comparison with currently used equations.

0072-B

SLOW TYPE ANION CHANNELS COULD TAKE PART IN THE MOBILIZATION OF THE INORGANIC CARBON FROM ROOT TO SHOOTS IN ARABIDOPSIS THALIANA.

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Some studies show that the roots can also participate in the inorganic carbon uptake of land plants. The process might have a positive impact on the photosynthetic efficiency and on the plant productivity under different stresses like drought.

After a review of the literature, transcriptomic analysis of *Arabidopsis thaliana* under sodium bicarbonate treatment, gene expression and physiological analysis of mutant plants grown in hydroponics cultures and sodium bicarbonate treatments, we believe that inward rectifying anion channels in the root cortex and epidermis (e.g. NRT2.1; SULTR1.2) could take up carbon from the environment while outward channels in endodermis like slow type anion channels SLAH1 and SLAH3 might have an important role in the mobilization of inorganic carbon from the roots to the shoots. We also found that decrease in root suberization might be also relevant for the uptake.

The project is supported by the grant NKFI FK 134874.

0073-A

STUDY OF PHOTOSYNTHETIC ELECTRON FLOW UNDER MN DEFICIENCY IN MARCHANTIA POLYMORPHA

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Photosynthesis is the only biochemical process that converts sunlight energy into chemical energy in the form of ATP and NADPH. Under stress conditions or when ATP/NADPH demand is altered, plants switch to Cyclic Electron Flow (CEF). CEF reinjects electrons from PSI via Ferredoxin into the plastoquinone pool leading to ATP formation without NADPH production. We study the effect of Manganese deficiency on CEF in liverwort *Marchantia polymorpha*. In this condition, the ratio of PSII/PSI is lower. We hypothesize that under Manganese deficiency, CEF is enhanced, thus protecting Photosystem II. In this context, light-induced P700 and Plastocyanin (Pc) absorbance changes were measured via DUAL KLAS_NIR. Slow oxidation of P700, faster re-reduction of P700+ and significant decrease in Pc/P700 ratio under Mn deficiency points to the fact that pool size of electrons that can be donated to P700+ is higher, thus indicating higher CEF and possibility of super complex formation around PSI.

0074-B

PLASTID TERMINAL OXIDASE (PTOX) PROTECTS PHOTOSYSTEM I AND NOT PHOTOSYSTEM II AGAINST PHOTOINHIBITION IN ARABIDOPSIS THALIANA AND MARCHANTIA POLYMORPHA

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The plastid terminal oxidase PTOX controls the oxidation level of the plastoquinone pool in the thylakoid membrane and acts as a safety valve upon abiotic stress, but detailed characterization of its role in protecting the photosynthetic apparatus is limited. Here we used PTOX mutants in two model plants *Arabidopsis thaliana* and *Marchantia polymorpha*. We created a green *Arabidopsis* PTOX mutant expressing the bacterial carotenoid desaturase CRTI and a double mutant in *Marchantia* lacking the plant-type and the alga-type PTOX enzymes. In both species, lack of PTOX affected the redox state of the plastoquinone pool. Exposure of plants to high light intensity showed higher susceptibility of photosystem I to light-induced damage in the absence of PTOX while photosystem II was more stable demonstrating that PTOX plays both, a pro-oxidant and an anti-oxidant role in vivo. Our results shine new light on the function of PTOX in protection of photosystem I and II.

0075-C

OPTIMIZING TRANSIT PEPTIDE-MEMBRANE PROTEIN LEADER PAIR FOR ACCURATE INSTALLATION OF BICARBONATE TRANSPORTERS INTO THE INNER ENVELOPE MEMBRANE OF C3 PLANT CHLOROPLASTS

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In C3 plants, the oxygenase activity of RubisCO leading to photorespiration and productivity loss can be curbed by introducing cyanobacterial carbon concentrating mechanisms (CCMs). The strategy's first phase envisages the introduction of the bicarbonate transporters (SbtA and BicA) to the chloroplast inner envelope membrane (IEM) to turbo charge RubisCOs CO₂ supply. Targeting BicA and SbtA to the chloroplast IEM needs suitable IEM targeting signals, which are poorly characterized at present. Multiple transmembrane domain (TMD) proteins require a non-cleavable targeting signal in addition to the transit peptide (TP). We have generated constructs with the SbtA/BicA gene fused to the TP and MPL of *Arabidopsis* IEM proteins to test this. We find that targeting foreign multiple TMD proteins to the chloroplast requires the TP and the MPL. The context formed by the TP, MPL, and TMDs determines the sub-cellular localization of the protein.



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PLANT ADAPTATION TO CLIMATE CHANGES

0076-A

THE ROLE OF TREHALOSE IN ENSIFER ARIDI LMR001T, A NEW SPECIES ISOLATED FROM DESERT IN MOROCCO, ON HYPER-OSMOADAPTATION AND SYMBIOSIS DEVELOPMENT WITH VACELLIA SP.

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Ensifer arid LMR001, a new species nitrogen-fixing bacterium isolated from desert of Merzouga in Morocco, has multiple survival capacities. It adapts to particularly difficult environmental stress. Hence, this new species represents an interesting model to study mechanisms of adaptation related to these types of environments. A transcriptomic study by using the RNAseq technique have revealed genes involved in several metabolisms including trehalose. These genes were differentially expressed in response to salt and water stress. To explore the roles of these metabolisms and function in stress adaptation, in this study mutants were generated, with an analysis of their transcriptions and a comparative characterization of their phenotypic responses. We found that the mutation of genes involved in the transport of trehalose *thuR* and in the biosynthesis of trehalose *otsB*, improved the symbiosis interaction with *Vaccellia* sp and the growth in a hyper-osmotic medium of the two mutants.

0077-B

OLD BUT GOLD: EXPLOITING THE UNDERUTILIZED OILSEED CROP CAMELINA SATIVA TO UNCOVER AND PROMOTE TOLERANCE TO ABIOTIC STRESS FOR IMPROVING CLIMATE RESILIENCE

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The old European oilseed camelina (gold-of-pleasure) is receiving attention because of its inherent tolerance to abiotic stress and capacity for genetic improvement. To uncover its stress adaptation strategies, the UNTWIST project (H2020; GA 862524) uses a systems approach to dissect camelina's responses to heat and drought by evaluating 54 genetically diverse camelina lines in field trials and controlled stress environments. Genomics and metabolomics enabled the selection of four contrasting lines for characterisation in additional field trials and controlled large-scale stress experiments. A drought experiment in an automated phenotyping setup will be presented, which revealed the differential responses of the lines under control and stress conditions at multiple levels. Integration of the results with complementary omics data (e.g., metabolome, transcriptome) is supporting the development of mechanistic models and identification of markers for the improvement of climate-smart crops.

0078-C

THE RETINOBLASTOMA-RELATED (RBR) CONTROLS THERMOMORPHOGENESIS BY REGULATING CELL PROLIFERATION AND CELL ENLARGEMENT IN A TEMPERATURE-DEPENDENT MANNER"

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It is widely accepted that Arabidopsis RBR-E2F transcriptional regulatory pathway controls cell proliferation but how this mechanism regulates growth and development when the temperature is raised by a few degrees is less elaborated. Here we show Arabidopsis seedlings growing at 28C versus 22C develop longer roots consisting of more cells in the root meristem. To confirm that temperature induces cell division, we manipulate proliferation activity by changing the level of the cell cycle repressor RETINOBLASTOMA-RELATED (RBR) either in an ectopic RBR expressing line or in an RBR mutant (rbr1-2). Here we show data that RBR could influence thermomorphogenic response both in the hypocotyl and in the root but through different mechanisms. Contrary to the cell cycle genes, key thermomorphogenic genes involved in thermo and auxin signaling eg. PIFs, ELF3, TIR1, and YUCCA8 were stimulated by ectopic RBR at 28C, suggesting a direct regulatory role for RBR in temperature-induced elongation growth.

0079-A

TRAINING GRAPEVINES GENERATES A METABOLOMIC SIGNATURE OF WINE

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Training systems are an option to handle the pronounced apical dominance of grapevines and to influence diverse traits of the corresponding wine. This provides a way to respond to changing climatic conditions. With training systems, sun exposure of berries or the water consumption of the vine can be influenced. However, it is still unclear if different training systems generate signatures in the metabolome of the wine. By an untargeted metabolomics approach using (SPME) GC-MS wine (volatiles) and leaves were evaluated. Different training directions such as vertical shoot positioning systems, hanging shoot systems, and minimal pruning systems were distinguishable in wine. It was shown, that different training systems generate a metabolomic signature in the wine which was more pronounced than in leaves. Moreover, the sensory analysis showed changes in the aroma of the different vines. Thus, the influence of the training system ranges from the leaf metabolome to the wine metabolome.

0080-B

HIGH ENDOGENOUS LEVEL OF SALICYLIC ACID CORRELATES WITH ROSETTE, BUT NOT ROOT PHENOTYPES IN ARABIDOPSIS

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Phytohormone salicylic acid (SA) has a crucial role in plant physiology. Its role is best described in the context of plant response to pathogen attack, however, some genetic/metabolic variations can also result in SA overaccumulation in plants. Such plants often show enhanced resistance, but also various signs of growth retardation. We performed an extensive phenotyping of a collection of Arabidopsis thaliana mutants accumulating different SA levels, focusing on plant development, transcriptome and phytohormonal profile, callose deposition in apoplast and in plasmodesmata, cell-to-cell connectivity and SA level/signalling under various growth conditions in soil and in vitro. We observed a strong correlation between SA content and rosette-related phenotypes, while root behaviour was largely SA independent. Our data provide new insights into SA mode of action in distinct plant tissues, and present a novel approach to study mechanisms underlying growth-defence trade-off.

0081-C

APPLICATION OF MELATONIN-FUNCTIONALIZED BIOPOLYMERS AT SEED STAGE TO MITIGATE DROUGHT STRESS IN TOMATO PLANTS (SOLANUM LYCOPERSICUM CV. 'HONDROKATSARI')

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Improving plant tolerance against abiotic stress factors is important for sustaining global food security. Plants show prolonged, increased tolerance when exposed to sub-optimal environmental conditions when treated at seed stage with certain chemical agents of natural or synthetic origin, resulting in higher crop yields. Polymers such as chitosan (CTS) and naturally-derived hydrogels (HYDR) provide a smart delivery system for phytohormones. The protective effect of melatonin (Mel) applied directly or as functionalized polymer coatings (CTS-Mel, HYDR-Mel) were studied in 'Hondrokatsari' tomato cultivar against drought stress. An array of agronomic, physiological, biochemical and molecular parameters were evaluated, following material characterization. Current findings suggest that CTS-Mel and HYDR-Mel formulations are a promising 'green' approach to mitigate abiotic stress effects in plants, although further research is needed to decipher their *modus operandi*.

0082-A

PLANT NATURAL GENETIC VARIATION IN RESPONSE TO ELEVATED CO₂

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The rise in atmospheric CO₂ concentration is one of the major drivers of climate change. By the end of the century, atmospheric CO₂ content could reach 1000 ppm, more than twice as much as at the beginning of the century (IPCC, 2021). In the vast majority of plants, large-scale studies have shown that elevated CO₂ (eCO₂) has a negative impact on mineral content. The decline in the mineral status of plants is still largely unexplained, but has serious consequences for food safety. Several elements suggest that solutions exist to mitigate or even eliminate the negative effect of eCO₂ on the mineral status of plants. One of the main avenues lies in the exploration of the natural genetic variability of plants. We recently performed a GWAS that identified several genes associated with the alteration of mineral status under eCO₂. I will present here the first results of the functional characterization of two of these genes, involved in N and Fe homeostasis under eCO₂.

0083-B

NPR1 RELOCATION BETWEEN CHLOROPLAST AND NUCLEUS IS REGULATED BY CIRCADIAN RHYTHM AND LIGHT/DARK EXPOSURE.

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We found that the nuclear nonexpressor of pathogenesis-related genes 1 (NPR1) is an endogenous oscillator in pNPR1::NPR1GFP at a 16L/8D cycle. The amount of nuclear NPR1 started to increase late at night and reached the highest level in the morning. Since cTP-NPR1-GFP, which targets the chloroplast, showed a pattern similar to that of NPR1-GFP, the

translocation of NPR1GFP to the nucleus is thought to be a retrograde signal transmitted via the chloroplast. Nuclear NPR1 showed a pattern similar to that of the evening-phased TOC1 and opposite to that of the morning-phased CCA1. NPR1 was observed in the nucleus under constant darkness but was not detected in the nucleus under constant light. When NPR1 was absent from the nucleus, treatment with ethylene, salicylic acid (SA), or an oxidative stress inducer caused NPR1 to relocate to the nucleus. We also aim to investigate genes regulated by nuclear NPR1 to identify the intrinsic regulator of NPR1 relocation and its physiological role.

0084-C

GAS EXCHANGE AND CHLOROPHYLL FLUORESCENCE VARIABILITY RESPONSES OF FOUR POTATO GENOTYPES FACING ENVIRONMENTAL STRESSES.

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Potato crop regularly faces drought and heat stresses. These stresses induce changes in the photosynthesis efficiency due, for instance, to stomatal closure or photosystem degradation. It is known that a higher net CO₂ assimilation rate is not necessarily correlated to higher yield. It is therefore worth to characterise the various types of responses to drought and heat stress, to identify which varieties can be grown in different stressfull environments. The photosystem efficiency has been measured by the monitoring of the gas exchanges (i.e. stomatal conductance or net CO₂ assimilation rate) and chlorophyll fluorecence (i.e. electron transport rate) on four potato varieties during two period of water shortage interspersed by a week of rehydration combined to high temperature (+30°C in the afternoon). We observed that different mechanisms are involved according to varieties which could be adapted to either a short period of repeated stress or a long period of single stress.



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PLANT AND ALGAL DEVELOPMENT AND EVOLUTION

0085-A

COMPARISON OF THE EFFECT OF TWO CATEGORIES OF ARTHROSPIRA PLATENSIS POLYSACCHARIDES (EXO AND ENDOPOLYSACCHARIDES) ON TOMATO GROWTH: EFFECT ON MORPHOLOGICAL, HISTOLOGICAL AND BIOCHEMICAL PLANT GROWTH TRAITS

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Microalgal polysaccharides have gained popularity in last years as biostimulants. Thus, *Arthrospira platensis* was chosen to study the effect of polysaccharides on tomato plants growth. Exocellular (EPS) and bound polysaccharides (BPS) were applied at different plant growth stages and their effects studied. While, no effect was shown on germination, all treatments enhanced growth and modified chemical composition of treated plants depending on polysaccharides kind and their application method. BPS used by fertigation stimulated roots growth and protein content. Leaves number and size and pigments content were increased with all treatments. Similarly, all treatments increased the leaves carbohydrates and phosphorus content with a maximum obtained after BPS by soil application. The histological study showed a modification of xylem formation in roots and ground parenchyma cells in leaves. Thus, *A. platensis* endo and exopolysaccharides could act as an interesting plant growth promoter.

0086-B

COMPARISON OF LEAF MORPHO-ANATOMICAL CHARACTERS IN AMARANTHUS SPP.: PHENOTYPING AS AN INVESTIGATIVE TOOL FOR ENVIRONMENTAL AND AGRICULTURAL SCIENCES

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Plant phenotyping is an important tool that can provide insight into the interaction between plants and the environment, often as supporting information for genotype studies. The



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resulting knowledge can be useful in eco-physiological research, to understand how species adapt to their growing conditions and to biotic competition. In recent years, phenotyping techniques for the study of plant morpho-anatomical traits have developed in the field of the imaging analysis, starting from microscope images up to high-scale acquisitions through remote sensing. In this work, we focused on the detailed study of single-leaf morphometric traits through the processing of photographic and confocal microscope acquisitions. Four species of *Amaranthus* were used, being plants of interest due to their high invasiveness into fields. Their morphological traits could become a useful tool to describe their adaptative responses and to define strategies for the sustainable management of the agro-ecosystem.

0087-C

GENETIC DIVERSITY OF LETTUCE (*LACTUCA SATIVA* L.) GERMPLASM RESOURCES BASED ON PHENOTYPIC TRAITS AND DNA PROFILES

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Lettuce (*Lactuca sativa* L.) is one of the most important leafy vegetables cultivated worldwide and consumed throughout the year. Genetic diversity in the lettuce germplasm resources is important for the development of improved varieties by providing novel traits and beneficial alleles. In this study, we investigated morphological trait and GBS-derived SNP genotypes of lettuce genetic resources in National Agrobiodiversity Center (NAC). Although the portion of leaf lettuce was rather high, it consisted of main four types of differing phenotypically cultivars (butterhead, crisphead, leaf, and romaine). GBS was used for the analysis of genetic diversity in this sample of 2,002 cultivars. A total of 7,321 SNP loci were obtained and a cluster analysis revealed four main groups. The results obtained from this research will be useful for database construction and cultivar identification for breeding of lettuce.

0088-A

PUCHI REGULATES VERY LONG CHAIN FATTY ACID METABOLISM AND TISSUE FUNCTIONAL PATTERNING IN DEVELOPING LATERAL ROOTS

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The architecture of the root system is an important trait for the plants to explore the soil in research of nutrients. Root branching relies on the post-embryonic formation of a new root organ, named lateral root primordium, from selected cells within the primary root.



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In *Arabidopsis*, the AP2/ERF transcription factor PUCHI is required for lateral root primordia (LRP) initiation and morphogenesis. Previous studies have shown that loss of PUCHI function alters the LRP developmental program and functional patterning. Furthermore, PUCHI induces the very long chain fatty acid (VLCFA) biosynthetic pathway in branching roots. Our recent results suggest that PUCHI also regulates the VLCFA incorporation pathway, especially for cutin formation. Based on these results, the precise control of the PUCHI-dependent network over VLCFA production and incorporation, and its influence on the mechanisms of LRP functional patterning is under investigation.

0089-B

A SUPPRESSOR SCREEN TO IDENTIFY YAK1 TARGETS INVOLVED IN PLANT GROWTH REGULATION.

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YAK1 (Yet Another Kinase) is a conserved DYRK kinase that has recently been identified in plants as a negative regulator of proliferation and as a differentiation activator. YAK1 activity is controlled via phosphorylation by TOR, a highly conserved kinase that is the major growth regulator in eukaryotes. However, the regulatory cascade of the TOR-YAK1 signalling axis remains poorly known. In order to identify YAK1 targets, we performed a screen of suppressors of a YAK1 over-expressor. We will present the suppressor mutants isolated classified according to their phenotypes and discuss how they could help us decipher the different roles of the TOR-YAK1 signalling axis.

0090-C

CHARACTERIZATION OF MYB AND MADS-BOX TRANSCRIPTION FACTORS INVOLVED IN TRICHOME DEVELOPMENT IN NICOTIANA TABACUM.

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Glandular trichomes are multicellular epidermal hair-like structures secreting or storing secondary metabolites. A better understanding of their development, which is under tight genetic control and different from that of *Arabidopsis* single-celled trichomes, is of great biotechnological interest.

With *Nicotiana tabacum* as a model for capitate trichome development in Solanaceae, we have identified several transcription factors involved in different steps of their development including a R2-R3 MYB and an AGAMOUS-like isoform.

Using reverse genetics, we found that the R2-R3 MYB is involved in the initiation of trichome development while the AGAMOUS-like protein is involved in later steps controlling glandular head development. In order to unravel the regulatory network involving these transcription factors we are using a combination of -omics approaches: genomics, transcriptomics and proteomic assays to respectively identify their transcriptional targets and protein interactors.



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0091-A

SYNERGISTIC AND ANTAGONISTIC HORMONAL INTERACTIONS CONTROL ADVENTITIOUS ROOT REGENERATION AND DEVELOPMENT.

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Plants display an unparalleled regenerative capacity that is widely exploited in modern agriculture for asexual propagation of elite genotypes. A critical point for this successful propagation entails the regeneration of adventitious roots (ARs), which is governed by a multitude of endogenous and environmental cues. Phytohormones interact to integrate and translate these cues into precise molecular signatures to provide a coherent developmental output. We have shown that auxin signaling controls the early events of AR initiation in *Arabidopsis* hypocotyl by modulating the homeostasis of jasmonate (JA) which cooperatively acts with cytokinins (CK) to repress AR development. By comparing AR development in hybrid poplar and hybrid aspen respectively easy-to-root and difficult-to-root genotypes we showed that differential response to JA likely explains the different phenotypes. We showed that JA and CK likely cooperate to repress AR development in Norway spruce de-rooted seedlings.

0092-B

ESTABLISHING THE HOMOSPOROUS FERN CERATOPTERIS RICHARDII AS A GENETIC MODEL ORGANISM

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The homosporous fern *Ceratopteris richardii* (C-fern) belongs to the pteridophytes, the sister lineage to seed plants, making it an interesting organism for evolutionary studies. While important genetic resources, like a reference genome and a stable transformation protocol using the gene gun are already established, we aim to increase this genetic repertoire to establish C-Fern as a novel genetically tractable model organism.

We will present our progress on (1) generating a transcriptome atlas including sporophytic and gametophytic tissues essential to track transcriptional activity during C-Fern development, (2) Establishment of a CRISPR/Cas12a system in C-Fern for multiplex gene editing. Further, we (3) provide recent developments for stable genetic transformation, by systematically testing transformation methods established in other species.

0093-C

THE SNRK2.4 AND SNRK2.10 KINASES REDUNDANTLY REGULATE DEVELOPMENTAL LEAF SENESCENCE

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Leaf senescence is the last stage of development which leads to controlled death of the cell, tissue and finally whole organ. Leaf senescence is one of the most important processes conditioning plant fitness and survival as an organism and as a species; it is critical for seeds, fruits and storage organs quality.

In plants, SNF1-Related protein Kinases type 2 (SnRK2s) are key players in response to osmotic stress and salinity, e.g. SnRK2.4 and SnRK2.10 kinases, members of ABA non-activated SnRK2s, are rapidly activated and maintain leaf resistance to salinity. Here we present for the first time their role in the regulation of leaf development in non-stress conditions. Performed by us series of physiological, biochemical and molecular tests revealed that SnRK2.4 and SnRK2.10 kinases work redundantly to promote leaf senescence in accordance with leaf age and stage of plant development. We also present some evidence explaining the molecular mechanism of both kinases' action.

0094-A

THE INTERPHASIC REGULATION OF CORTICAL MICROTUBULES FOR THE ESTABLISHMENT OF PLANT CELL DIVISION PLANE

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Cell division plane is crucial for tissue organization and morphogenesis in plants. Important regulators are microtubules (MT), that organize into two cortical arrays in interphase, then two mitotic arrays. The preprophase band (PPB) is a pre-mitotic MT array that accurately predicts the cell division site. The PPB-deficient trm678 mutant was mostly able to maintain cell division orientation, indicating that division plane positioning might depend on earlier interphasic MT arrays.

To elucidate the integrative role of interphasic cortical MT arrays in this process, we propose to produce a spatiotemporal reference framework of plant cell division, by the analysis of MT arrays relative to parameters such as cell cycle, morphology and position of the nucleus, cell size, shape and neighbors, in cells expressing 3 subcellular markers. Our approach involves high-resolution 3D confocal imaging and analysis of mutant lines of components of the TTP complex, an important regulator of MT arrays.

0095-B

A GENETIC STRATEGY TO EVALUATE THE SPECIFIC EFFECTS OF KINASES INHIBITORS IN PLANTS: THE CASE OF TOR.

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Target of Rapamycin (TOR) kinase is the central component of the TOR signaling pathway which regulates cell growth and metabolism in response to environmental cues in eukaryotes. Our long-term goal is to understand how this conserved central regulator of eukaryotic growth has integrated new functions through evolution of photosynthetic organisms. Since the last ten years, new ATP-competitive inhibitors have greatly helped the study of the TOR signaling pathway in plants. Here we will show how a genetic approach can help to evaluate the specific effects of such inhibitors, a crucial aspect to accurately characterize the TOR signaling pathway. We will also discuss how this strategy can be transferred to other kinases.

0096-C

MECHANISM OF THE CONTROL OF CELL ADHESION

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Cell adhesion in plants is mediated by the cell wall. During the development of the plant, the cell wall is subjected to remodeling events, which affect HomoGalacturonans (HGs) structure and generate Oligagalacturonides (OG). However, the mechanism by which the plant controls and maintains cell adhesion in response to these cell wall changes is not yet understood. Our results confirm that a transduction pathway impact the transcription of remodeling enzymes potentially via signaling OGs. Thus, in order to better understand the impact of these OGs, we i) determined how altered expression pattern of remodeling enzyme impacts the structure of HGs ii) identified signaling OGs iii) explored how the perception of signaling OGs helps to maintain and control cell adhesion. Our multidisciplinary approach leads to the identification of pectin derived compounds able to restore the cell adhesion in our mutant and to the identification of new actors involved in the control of cell adhesion in plants.



Supported by:



0097-A

E2FS REGULATE G1/S AND G2/M TRANSITIONS THROUGH MODULATING FBL17 AND MYB3R4 EXPRESSIONS

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It is widely accepted that in plants RBR-E2F transcriptional regulatory pathway defines cell division timing and duration that determines final plant organ size at a cellular level. In Arabidopsis those parameters depend on the activity of two groups of CYCLIN-DEPENDENT KINASE INHIBITORS (CKIs): KRPs and SMRs. KRPs (KIP-RELATED PROTEINS) control the G1-S phase transition via regulating CDKA;1 activity, while SMRs (SIAMESE and SIAMESE-RELATED) inhibit CDKBs at G2-M transition. The CDKA;1-KRPs-FBL17-RBR-E2F pathway builds a general module controlling G1/S-phase transition while a recently reported MYB3R-SCL28-SMOS1-SMR pathway sets the balance between cell number and size without affecting organ size by defining cell cycle progression and cell doubling time uniquely in G2/M phase. Here we present that E2Fs, the primary effectors of RBR co-repress FBL17 and MYB3R4 genes thereby adjusting cell proliferation frequency and set the final cell size by fine tuning the level of KRPs and SMRs.

0098-B

GENETIC REGULATION OF BROWN ALGAL LIFE CYCLES: DEVELOPMENT AND EVOLUTIONARY TRANSCRIPTOMIC SURVEYS

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Phaeophyceae is a clade of eukaryotic multicellular photosynthetic organisms phylogenetically very distant from the well-studied green lineage. Most brown algal species alternate a diploid sporophytic and a haploid gametophytic phase during their life cycle. However, generation identity is independent of ploidy as haploid sporophytes can develop through parthenogenesis. Previous studies, in Ectocarpus, identified genes that control the developmental program of the sporophyte generation. In two nearly isomorphic species Ectocarpus sp. 7 and Dictyota dichotoma, we used transcriptomic data along the development to analyse gene co-expression during the life cycle. Furthermore, the relative importance and

complexity of these generations varies across the brown algal phylogenetic tree. To determine whether generation-biased genes are conserved among brown algae, we analysed RNAseq data from adult stages of ten phylogenetically diverse brown algal species with a high diversity of life cycles.

0099-C

SOSEKI PROTEINS CONNECT CELL POLARITY TO DEVELOPMENT IN THE MOSS PHYSCOMITRIUM PATENS

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The morphogenesis of living organisms necessitates the interpretation of directional information by cells. These spatial landmarks are considered to emerge from cell polarity but the underlying mechanisms by which they instruct cells and tune morphogenesis remain enigmatic in plants. We tackle this problem by exploring the development of the moss *Physcomitrium patens* and the polar SOSEKI (SOK) proteins. SOK are broadly conserved in plants but their developmental roles are unknown. Using gain- and loss-of-function approaches, we observe that the phenotype of various SOK overexpression and mutant lines is disrupted and that this coincides with defaults in developmental transitions induced by the plant hormone auxin. The polar organization of overexpressed SOK proteins at cell interfaces in filaments let us hypothesize a role in the regulation of intercellular exchanges, hence connecting axial polarity and the regulation of plant development.

0100-A

STUDY OF THE MECHANISMS AND CONDITIONS LEADING TO THE EVOLUTION OF PHOTO-ENDOSYMBIOSIS

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About 1.8 Ga ago, cyanobacteria were phagocytosed by eukaryotes, leading to primary endosymbiosis and giving rise to chloroplast. Since then, other eukaryotes have included photosynthetic eukaryotes (secondary/tertiary endosymbiosis), which appear to have evolved many times independently. Despite the ubiquity of photo-endosymbiosis in the environment, these early mechanisms remain widely unknown.

The aim is to study the first steps leading to the maintenance of a photosynthetic organism within a eukaryote. To this end, we are using unicellular models, the host ciliate *Tetrahymena thermophila* and the photosynthetic alga *Chlorella variabilis* and the cyanobacterium



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Synechococcus elongatus. These models allowed us to study the selective advantage that phagocytosis of a photosynthetic organism can bring to its host under unfavorable conditions. The results show the importance of O₂ for a better survival of *T. thermophila* having phagocytosed photosynthetic organisms in anaerobic conditions.

0101-B THE EVOLUTION OF PLASMODESMATA

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Intercellular communication via plasmodesmata (PD) likely was a prerequisite for the emergence of land plants. In seed plants, PD numbers at cell interfaces are precisely adjusted during development by postcytokinetic secondary PD formation, either de-novo or by fission of a matrix PD.

Bryophytes are thought to lack the ability to form secondary PD, but our electron microscopical PD counts provide evidence for PD fission in all three bryophyte taxa. Distinct PD modifications found in mature walls of bryophytes support the modern moss phylogeny. In contrast to bryophyte gametophyte meristems with only a single initial, the multicellular meristem of the *Anthoceros agrestis* sporophyte forms secondary PD like other multiplex meristems. Thus, also in bryophytes, it strictly depends on the meristem type whether secondary PD formation is required.

We also looked at the development of PD networks in ferns and lycophytes and investigated the occurrence of 'true' PD in streptophyte algae.

102-C A SUPPRESSOR SCREEN REVEALS SUPPRESSOR OF NOG1A AS A NOVEL REGULATOR OF THE 2D TO 3D GROWTH TRANSITION IN PHYSCOMITRIUM PATENS

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3-dimensional (3D) growth is a unifying feature of all land plants, but we know little about how it is regulated. The model moss *Physcomitrium patens* has been developed as a model system in which to dissect the genetic basis of 3D growth. We previously demonstrated that 3D growth is dependent on NO GAMETOPHORES 1 (NOG1), which encodes a protein with a ubiquitin-associated (UBA) domain. *nog1* mutants exhibit cell division orientation defects and cannot establish 3D growth. We recently performed a *nog1* suppressor screen to generate mutations that alleviate the *nog1* mutant phenotype and discovered three suppressor of *nog1* (*snog1*) mutants (*snog1a*, *snog1b* and *snog1c*), which have restored capacity for 3D growth. The causative mutation in the *snog1a* mutant was mapped to a gene that encodes a protein with



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a UBA domain, similar to NOG1. Thus, we propose that NOG1 and SNOG1A play a role in destabilizing proteins required to respectively repress or promote 3D growth.

PLANT IMMUNITY

0103-A

PRIMING OF SPECIAL METABOLISM IN ARABIDOPSIS THALIANA MEDIATES ELICITOR-INDUCED RESISTANCE TO FUNGAL INFECTION

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Biotic elicitors trigger in plants a robust but transient expression of defense-related genes, followed by a reduced susceptibility to pathogen infection. To investigate the molecular basis of elicitor-induced resistance, we analyzed the transcriptome of Arabidopsis leaves treated with the bacterial elicitor flg22 and inoculated, after 24 h, with the fungal pathogen Botrytis cinerea. In the absence of infection, defense-related genes were not significantly up-regulated 24 h after elicitation, though a transient repression of growth-related genes could be observed. In contrast, flg22-treated plants showed, upon infection, increased expression of genes involved in special metabolism. Genetic analysis confirmed that indolic compounds and aliphatic glucosinolates contribute to flg22-induced resistance. Moreover, elicitation did not affect seed production, suggesting that priming of special metabolism allows increased resistance to pathogens with minimal impact on fitness.

0104-B

RESISTANCE TO VIRUSES BASED ON EIF4E: FROM NATURAL VARIATION TO EDITED GENES

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eIF4E translation initiation factors have emerged as major susceptibility factors for RNA viruses. Natural eIF4E-based resistance alleles are found in many species and are mostly variants that maintain the translation function of the protein. eIF4E genes represent therefore targets for engineering viral resistance, and gene-editing technologies can be used to make up for the lack of natural resistance alleles in some crops. However, redundancy among eIF4E genes can restrict the efficient use of knockout alleles in breeding. Using Arabidopsis and Tomato, we show how gene-editing technologies can be used to design de novo functional alleles, using knowledge about the natural evolution of eIF4E genes in different species, to drive resistance to viruses without affecting plant physiology. We will show that there is a trade-off to find between resistance and functionality, and discuss these results in the light of resistance durability.



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0105-C

DOES COPPER STRESS MODIFY THE OFFENSIVE STRATEGY OF PHYTOPHTHORA INFESTANS TOWARDS POTATO?

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Copper (Cu) is classified as an essential heavy metal and a component of the most common fungicides. Therefore, the main goal of our study was to determine the effect of Cu (5 and 10 mg/L) on (patho)biology of economically significant pathogen *Phytophthora infestans* (Mont.) de Bary - the causative agent of potato late blight. To gain insight into the effect of Cu on *vr/avr P. infestans*, a selected aspects of nitro-oxidative status were analyzed. We noted Cu-dependent reactive oxygen and nitrogen species (RNS) generation in the pathogen structures. For example, in *avr* isolate Cu 5 mg/L provoked ca. 2-fold and 4-fold increase of superoxide anion and hydrogen peroxide, respectively, accompanied by RNS changes. Moreover, it was examined whether and to what extent the observed Cu-dependent nitro-oxidative changes affected *P. infestans* ability to cause disease symptoms on potato (*Solanum tuberosum* L.). This research was funded by National Science Centre – project no UMO-2021/41/N/NZ9/01525.

0106-A

NITRIC OXIDE AND VOLATILE ORGANIC COMPOUNDS IN THE DEFENSE RESPONSES AND RESISTANCE OF TOMATO PLANTS AGAINST BOTRYTIS CINEREA INDUCED BY TRICHODERMA VIRENS TRS 106

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Trichoderma virens TRS 106 decreases grey mould disease caused by *Botrytis cinerea* in tomato plants (*S. lycopersicum* L.) by enhancing their defense responses. The histochemical analyses revealed that *B. cinerea* infection causes nitric oxide (NO) accumulation in chloroplasts, undetectable in plants treated with TRS 106, while treatment of plants with TRS 106 caused systemic spreading of H₂O₂ and NO accumulation in apoplast and nuclei. SPME-GCxGC TOF-MS analysis revealed 24 volatile organic compounds (VOC) released by tomato plants treated with TRS 106, including hexanol derivatives, e.g., 4-ethyl-2-hexynal and 1,5-hexadien-3-ol, and salicylic acid derivatives, e.g., 4-hepten-2-yl and isoamyl salicylates, considered in the protection of tomato plants against *B. cinerea* for the first time. The results are valuable for further studies of the location and function of NO in plants treated with *Trichoderma* and check the contribution of detected VOC in plant protection against *B. cinerea*.



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107-B

HEAT SHOCK AND ANTIOXIDANT TREATMENTS COMPROMISE SYMPTOMLESS NON-HOST RESISTANCE OF BARLEY TO TOBACCO MOSAIC VIRUS CAUSING HYPERSENSITIVE CELL DEATH

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Our aim was to elucidate how a combined heat shock & antioxidant treatment influences symptomless non-host resistance of barley to Tobacco mosaic virus (TMV)? Heat shock (49 °C, 20 sec) 2 hours before TMV inoculation was followed by leaf infiltration of antioxidants (superoxide dismutase + catalase) or control infiltration. At 2 and 5 DAI both antioxidant and heat shock treatments alone resulted in 50-100% higher TMV levels. Combining heat shock & SOD+CAT resulted in even higher TMV levels and often the appearance of visible necrotic lesions (HR). Even when heat shock & SOD+CAT did not result in visible HR, death of mesophyll cells was detected coupled to high TMV levels. Combined heat shock & antioxidant treatments result in compromised non-host resistance of barley to TMV and appearance of HR, pointing to the role of ROS in symptomless non-host resistance to virus infections.

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0108-C

EFFECTS OF SALICYLIC ACID ON PLANT CUTICLE COMPOSITION AND DYNAMICS

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Salicylic acid (SA) is a phytohormone mainly connected with plant immune responses. High SA concentration also strongly inhibits plant growth. The general explanation of growth inhibition is that induced immunity redirects plant nutrient flow. We hypothesise that such modification in nutrient flow would also affect cuticle composition and dynamics. The cuticle is the first physical barrier between the plant and the outer environment. Its composition and dynamics are highly regulated because the biosynthesis of the cuticle is highly energy-consuming. In this work, we focus on the effect of SA on cuticle dynamics and composition. We monitor the cuticle wax properties using GC-MS in Arabidopsis thaliana mutants with modulated SA concentration. Within the analysis of cuticular wax dynamics, plants are labelled in an atmosphere with higher content of ¹³CO₂. The obtained data contribute to the detailed understanding of how SA inhibits plant growth.

0109-A

ELF18-INDUCED LONG NONCODING RNA 11 NEGATIVELY REGULATES THE EXPRESSION OF PATHOGENESIS-RELATED LIPASE 5 IN ARABIDOPSIS INNATE IMMUNE RESPONSE

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Long noncoding RNAs (lncRNAs) function as key players in diverse biological processes, including plant innate immunity. Here, we analyzed a dataset of custom lncRNA arrays generated from Arabidopsis treated with elf18 and isolated ten lncRNAs named ELF18-INDUCED LONG-NONCODING RNA (ELENA). ELENA11 showed a different expression pattern in tissue- and PAMP-specific manners. ELENA11 is located between At5g24170 and PATHOGENESIS-RELATED LIPASE 5 (PRLIP5). ELENA11-overexpressing plants showed reduced PRLIP5 expression and callose deposition compared to the wild-type under PAMP treatments, whereas ELENA11 knock-out plants showed enhanced PRLIP5 expression and callose deposition, indicating that ELENA11 acts as a negative regulator of PRLIP5 expression. Also, ELENA11-overexpressing plants were susceptible to Pto.DC3000 compared to the wild-type, but ELENA11 knock-out plants were resistant. These results demonstrate that ELENA11 plays an important role in PAMP-triggered innate immune response.

0110-B

PHYTOHORMONES PRODUCED BY FUNGAL PLANT PATHOGEN AS MEANS OF COMMUNICATION

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Phytohormones are small molecules essential for plant life processes regulation including plant-microbe communication. Plant pathogens are developing strategies to overcome plant defence and one such strategy is manipulation of plant phytohormone pathways. Some pathogens synthesize phytohormones themselves. Pathogenic fungus *Leptosphaeria maculans* can synthesize a variety of phytohormones including auxins and salicylic acid (SA). The production of auxins can be stimulated by biosynthetic precursors and it is connected with induced transcription of biosynthetic genes LmTAM1 and LmIPDC2. Application of auxin modulated necrotic lesion area caused by the pathogen on the host plant. The presence of SA has been documented by LC-MS in the *L. maculans* mycelium and orthologues of plant biosynthetic gene AtICS1 were identified. While the production of auxins has been documented in various fungi, to our best knowledge this is the first direct evidence of SA biosynthesis in a pathogenic fungus.

0111-C

PHYTOPHTHORA INFESTANS WITHSTANDS A HOST-DEPENDENT NITROSATIVE CHALLENGE BY MODIFYING THE PROTEIN ACETYLATION STATUS

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The potential contribution of reactive nitrogen species (RNS) to epigenetic mechanisms has yet to be recognized in phytopathogens, including the unique oomycetes. The study aimed to gain insight into the histone acetylation status in the *Phytophthora infestans* structures in the face of nitrosative challenge and indicate how NO₂⁻ governs the epigenetic control of gene expression. To mimic nitrosative stress to which the pathogen is exposed, especially during in planta growth, avr/vr *P. infestans* isolates in reference to the potato (*Solanum tuberosum* L.) cv. Sarpo Mira were treated with specific RNS donors. Nitrosative conditions affect the expression of genes encoding nuclear HDACs and HATs and contribute to the opposite regulation of HDACs and HATs activity. Moreover, PifHDAC3 protein accumulation under in planta phase suggests an essential role of HDAC during the pathogen's offensive strategy. This research was funded by National Science Centre – project no. UMO-2018/31/B/NZ9/00355.

0112-A

ULVA LACTUCA ARABINOGALACTAN-PROTEINS ACTIVATE IMMUNE RESPONSES IN PLANTS VIA ELICITOR ACTIVITY

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Arabinogalactan-proteins (AGPs) are ubiquitous in the plant kingdom and possess multiple physiological functions. Recently, AGP-like glycoproteins were identified in the green alga *Ulva lactuca*, and found to activate induced resistance (IR) in oilseed rape (*Brassica napus*) against *Leptosphaeria maculans* (the causal agent of stem canker). Interestingly, ulvans from *U. lactuca* are also known for their ability to activate IR. We found that AGP-like glycoproteins induced a higher IR response than ulvans. This study questioned how plants respond to stimulation by more than one elicitor at the same time. Using the model plant *Arabidopsis thaliana*, we investigated how the application of a combination of elicitors affects IR. Our analysis revealed different patterns of immune responses depending on the elicitor tested. Notably, combined elicitor treatments led to a unique set of immune responses; although no significant increase in IR was observed, compared to individual elicitor treatments.

0113-B

LOCALIZATION OF BACTERIAL SPOT INFECTION IN PEPPER PLANTS. THE INVOLVEMENT OF OXIDATIVE STRESS

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The interaction between the bacterium *Xanthomonas euvesicatoria* strain 269p and pepper plants (*Capsicum annuum* L.) was investigated. The infectious process was studied using several different modes of in vivo inoculation under controlled conditions. The spread of the pathogen in different parts of the plants was monitored by qDNA detection (qPCR) as well as by re-isolation of viable bacterial cells. Several parameters of oxidative stress were analyzed and compared in symptomatic and asymptomatic regions of the same leaf. The infection with *X. euvesicatoria* was found to be strictly local. Bacterial colonization was limited at entry points and spread in the healthy plant tissue was blocked. Oxidative burst and changes in antioxidant defense were detected in the infectious lesions. ROS overproduction mimics the hypersensitive response, but it is rather, similar to lesions simulating disease.

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0114-C

CHARACTERIZATION OF THE Rpv2 LOCUS, CONFERRING TOTAL RESISTANCE AGAINST DOWNY MILDEW IN GRAPEVINE.

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Downy mildew is one of the more damageable diseases on grapevine. To avoid the use of phytochemicals, an alternative is the breeding of resistant varieties carrying resistance factors. The American species *Vitis rotundifolia* is totally resistant to downy mildew. Genetic mapping of resistance loci in *V. rotundifolia* cv. Trayshed identified a locus for total resistance to downy mildew, named Rpv2, which is localized on chromosome 18 in a region containing a cluster of TIR-NBS-LRR genes. Gene annotation associated with their putative function and their expression analysis during infectious cycle, allowed identification of two candidate genes for Rpv2 resistance. Functional validation to determine which gene confers the resistance associated to Rpv2 is in progress. Knowledge of Rpv2 resistance mechanism and of its potential breakdown will permit us to evaluate whether this gene would be suitable for integrating future breeding programs for new resistant grapevine varieties.



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0115-A

DECIPHERING PLANT RESILIENCE MECHANISMS TO FACE THE MULTIPLE DISEASE CHALLENGE IN FRUIT TREES

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As perennial plants, fruit trees must cope, individually, with the fluctuating threat of multiple pathogens over the years. In this long-lasting battle for plant immunity, disease resilience is emerging as a key mechanism for tree survival and fitness. More fundamental research is required to improve our understanding of disease resilience mechanisms, which in turn could be particularly relevant for a more sustainable fruit production. As this approach is novel for that field, we propose i) a clear definition of resilience for fruit producing trees, ii) a methodology for studying its phenotypic components which requires repeated measures of “resilience biomarkers”, iii) to decipher the genetic architecture of resilience components, and iv) an innovative strategy based on high-throughput phenotyping and genomics for identifying resilient genotypes. All in all, disease resilience appears as a meaningful breeding perspective in a context of unprecedented plant protection restrictions.

0116-B

IN VIVO APPLICATION OF XANTHOMONAS EUVESICATORIA-SPECIFIC BACTERIOPHAGE BSXEU269P/3 REDUCES THE SPREAD OF BACTERIAL SPOT DISEASE IN PEPPER PLANTS

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Bacterial spot caused by *Xanthomonas euvesicatoria* is one of the most economically important pepper diseases worldwide. The present study was focused on the pathosystem pepper plants (*Capsicum annuum* L.) - *X. euvesicatoria* (wild strain 269p) - bacteriophage BsXeu269p/3 and the possibility of bacteriophage-mediated biocontrol of the disease. Two new model systems were developed for the monitoring of the effect of phage treatment on the infectious process in vivo. Application of BsXeu269p/3 to *X. euvesicatoria* 269p-treated pepper plants reduced the amount of the bacterium at the inoculation points. We showed that the pathogen develops on the leaf surface (epiphytic stage) and spreads to neighboring plants by rain-induced aerosol. Treatment of plants with BsXeu269p/3 reduced the intensity of pathogen transfer to/from new hosts/plants.

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0117-C

DECIPHERING THE MECHANISMS UNDERLYING BROWN ALGAE-VIRUS INTERACTIONS

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The interaction between the filamentous brown alga *Ectocarpus* and the *Ectocarpus siliculosus* Virus-1 (EsV-1) represents a model for DNA viral infection in brown algae. *Ectocarpus* gametes are susceptible to EsV-1 infection but the alga vegetative tissues remain disease-free until the development of reproductive structures. The onset of fertility triggers viral replication in a subset of gametangia enabling the synchronous release of viruses and gametes to the environment and infection of healthy algae.

The molecular mechanisms underlying viral synchronization with the algae life-cycle remain unknown. Using cell biology and transcriptomics we are dissecting the molecular mechanisms underlying viral silencing in vegetative tissue and the further activation in reproductive structures. Our results are consistent with a EsV-1-derived genomic insertion playing a key role in algae-virus interactions. In addition, we have identified candidate genes likely to participate in anti-viral defence.

0118-A

ARABIDOPSIS EIF4E1 PROTECTS THE TRANSLATIONAL MACHINERY TO RESTRICT VIRUS ACCUMULATION DURING TuMV INFECTION

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Successful subversion of translation initiation factors eIF4E determines the infection success of potyviruses, a major group of viruses affecting plants.

Here, we explore whether the inactivation of eIF4E is a good strategy to engineer potyvirus resistances. We study the role of the Arabidopsis eIF4E1 whose inactivation was previously reported as conferring resistance to the potyvirus clover yellow vein virus (CLYVV) at the expense of hypersusceptibility to another potyvirus called turnip mosaic virus (TuMV). We show that during TuMV infection, eIF4E1 is required to maintain the global plant translation activity and to restrict virus accumulation by preventing the degradation of the translation initiation protein eIFiso4G1.

These findings bring mechanistic insights to the subversion of the plant translation apparatus during potyvirus infection and highlight the importance of preserving the functionality of translation initiation factors when implementing potyvirus resistances.

0119-B

IS EXPOSURE TO CHRONIC IONIZING RADIATION SYNERGISTIC OR ANTAGONISTIC TO THE IMMUNITY OF AQUATIC PLANTS?

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Ionizing radiation compromises plants' growth and development. Along with cellular responses, it challenges plants' immunity. This study is focused on discovering biochemical mechanisms responsible for compromised immunity in *Phragmites australis* after exposure to ionizing radiation. Experimental materials were collected in Chernobyl Zone. We quantified 1340 proteins using UHPLC-MS. Among them, 174 proteins were differentially accumulated. We revealed a higher impact of sampling variability than radionuclide contamination on proteome and the antioxidant system. Nevertheless, the leaf-sheath assay indicated higher fungal infection on leaves from contaminated sites. Further milestones include the evaluation of pest infestation and probing site-specific protein carbonylation. Our findings may fill the gap between the fundamental radiobiology and relevant management practices for contaminated lakes.

Acknowledgement: This study was supported by the projects: APVV-20-0545 & VEGA 2/0106/22.

0120-C

TISSUE-SPECIFIC GLUCOSINOLATE PROFILE AND ACTIVITY OF MYROSINASE AND SPECIFIER PROTEINS AFFECT THE OUTCOME OF GLUCOSINOLATE HYDROLYSIS IN KOHLRABI

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Glucosinolates (GLS) are phytochemicals predominantly found in Brassica vegetables. Upon tissue damage, GLS hydrolysis by myrosinase often causes the release of isothiocyanates (ITC), which are involved in plant defense. However, when specifier proteins such as epithiospecifier protein (ESP) or nitrile-specifier protein (NSP) are present, alternative GLS breakdown products are formed. The role of specifier proteins is still unclear. To better understand the function of specifier proteins, we determined the protein abundance patterns of BoNSP1 and BoNSP2, BoESP1-3, BoESM1-like protein and myrosinase in nine mature kohlrabi organs (leaf midvein, leaf lamina, leaf margin, leaf stalk, bulb core, bulb middle part, bulb peel, stem and root) based on LC-MS proteome analysis and correlated them with GLS



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hydrolysis product formation. Further, ESP and myrosinase activity were studied. The specifier protein and myrosinase activity were consistent with glucosinolate hydrolysis product formation.

0121-B

CAN FUNGAL INFECTION MODIFY INSECT PREFERENCE TO OILSEED RAPE LEAVES?

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Little is known about how plants cope with multiple stresses in the natural environment. This study focuses on the combined interaction of fungal infection by *Leptosphaeria maculans* and arthropod infestation by *Plutella xylostella* in oilseed rape. The aim was to unravel whether *L. maculans* infection could alter oilseed rape attraction and palatability to *P. xylostella*. Feeding preference tests were complemented by defense signaling, glucosinolate (GLS) and volatile (VOC) levels in *L. maculans*-infected leaves. Infected leaves were preferred by caterpillars 3 days post inoculation (dpi) but not at 7 dpi. Genes involved in the salicylic acid and ethylene signaling were upregulated in infected leaves at 3 and 7 dpi; *L. maculans* increased the level of total aliphatic GLSs, specifically glucobrassicinapin at 3 dpi; and altered the content of specific VOCs. We suggest that *P. xylostella* preference is affected by *L. maculans*-induced changes in the plant metabolic composition.

PLANT REPRODUCTION: MECHANISMS AND EVOLUTION

0122-A

DECIPHERING THE MOLECULAR MECHANISMS OF GIBBERELLIN-MEDIATED FLOWERING CONTROL IN APPLE

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Alternate bearing consists in an irregular flowering and fruit load over consecutive years that produce important crop losses. In many fruit trees such as apple, alternate bearing is related to the floral induction and it is believed to be controlled by the phytohormone gibberellin (GA). GA acts as a potent promoter of floral induction in Arabidopsis by negatively regulating DELLA proteins, which in turn, inhibit the activity of floral promoter regulatory proteins. In perennial woody plant species, GA suppresses floral induction/initiation and DELLAs may act as co-activators of unknown floral promoter proteins. We are using a yeast-two-hybrid approach to identify DELLA-interacting partners in apple and the glucocorticoid receptor system to define DELLA-transcription factor complexes target genes. By using these approaches, we expect to obtain a protein-protein interaction network around DELLA and shed light into its function in the control of the apple GA-mediated floral induction.

0123-B

DISTRIBUTION OF AUXIN DURING THE DEVELOPMENT OF THE REPRODUCTIVE STRUCTURES IN GINKGO BILOBA (L.)

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Unraveling the genetic and molecular basis of plant reproductive development is of key importance from both the scientific and economic perspective. Thanks to three decades of research many master regulators of flower, fruit and seed development have been identified, downstream pathways have been discovered and the role of hormones have been investigated. Most of these studies have been performed on model angiosperms, thus there is the need to expand the view on the diversity of the reproductive strategies that have evolved across seed plants. We have focused on Ginkgo biloba reproduction. Key stages of both female and male reproductive structures have been identified, and the role of hormones during their development has been investigated. The immunolocalization of auxin during the development of Ginkgo reproductive organs, and in situ hybridization studies of auxin-related



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genes provide new interesting insights on the hormonal regulation of *Ginkgo biloba* reproductive development.

0124-C

POLLEN-OVULE INTERACTIONS IN GINKGO BILOBA (L.): NEW INSIGHTS FROM MOLECULAR STUDIES

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Most studies on spermatophyte reproduction were conducted on angiosperms model species. However, of the five main lineages of seed plants, four belong to gymnosperms. The study of *Ginkgo biloba* becomes even more interesting because of its isolated phylogenetic position and remarkable evolutionary history. Pollination represents a central event in the complex process of *Ginkgo* ovule development, as confirmed by the observation that unpollinated ovules abort and by omics analysis. It is likely that the female tissues specifically recognize a pollen determinant, which might be: (1) present on the highly decorated exine surface, (2) exposed on intine after pollen hydration and de-coating or (3) synthesized de novo upon germination. Likely, more levels of communications are necessary. As for its biochemical nature, it could be a peptide, ncRNA, or the sugary moiety of AGPs. Finally, the mechanical component could have a role given that *Ginkgo* pollen undergoes dramatic changes upon hydration.

0125-A

THE ROLE OF SILENE LATIFOLIA HANABA TARANU (SLHAN) GENE IN FLORAL DEVELOPMENT

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Silene latifolia is a dioecious plant model for studying sex chromosomes evolution and other aspects of dioecy. Despite the long-term effort, the molecular mechanisms underlying sex determination in *S. latifolia* and the role of sex-linked genes remain unresolved. Our group recently induced formation of the gynoeceum in male flowers through DNA demethylation in floral buds, which disrupted the suppression of the carpel development pathway. Using RNA-seq, we have screened for candidate genes that show differential expression patterns in males, females, and hermaphrodites. We identified a sex-linked homolog of the GATA transcription factor HANABA TARANU (HAN), which is known to be involved in floral patterning. In female transgenic lines with silenced SLHAN, an increased number of axillary bud meristems were observed, which is a phenotype characteristic of male individuals. This study shows the role of the SLHAN in the context of sexual dimorphism and flower development in *S. latifolia*.



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0126-B

QUANTITATIVE EFFECTS ASSOCIATED WITH MALE FERTILITY RESTORATION BY THE Rf1 GENE IN SUGAR BEET

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In sugar beet plants the presence of the S-cytoplasm impairs pollen production. This effect can be suppressed by the Rf1 gene – its fertility restoring allele shows quadruplication of a sequence coding for an OMA1-like protein. The purpose of this study was to check if fertility restoration by the Rf1 gene is associated with accumulation of mRNAs encoding this OMA1-like protein. Two populations were included in the analysis – they segregated into male-sterile and male-fertile (restored) plants. Accumulation of Rf1/rf1 transcripts was analyzed with both RT-PCR and real-time RT-PCR. The latter analysis showed that in one of these populations male-fertile plants had approx. 10 times more Rf1/rf1 mRNA than male-sterile plants. In the second population sterile and fertile plants were comparable with respect to accumulation of the analyzed mRNA. Electrophoretic analysis of RT-PCR products showed that in both populations male-fertile plants exhibited a specific isoform of their Rf1 mRNA.

0127-C

ENGINEERED ARABIDOPSIS POLLEN: NEW FRONTIERS IN UNDERSTANDING PAPAVER SELF-INCOMPATIBILITY

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The self-incompatibility (SI) system in poppy (*Papaver rhoeas*) is mediated by the interaction of two S-determinants: a pollen-expressed plasma membrane-localised protein (PrpS) and a stigma-expressed secreted protein (PrsS). Interaction of cognate PrpS–PrsS triggers a signalling network, causing rapid growth arrest and PCD of incompatible pollen. We previously demonstrated that challenging transgenic Arabidopsis pollen expressing PrpS with cognate recombinant Papaver PrsS proteins triggers remarkably similar cellular events to those observed in incompatible Papaver pollen, including alterations to the actin cytoskeleton, cytosolic acidification, increased ROS and PCD. This engineered Arabidopsis system provides genetic tools that were previously unavailable to study Papaver SI. Here we present data on the intracellular sites of SI-induced ROS production in incompatible pollen tubes and show that that cellular ATP levels and cytosolic pH play a pivotal role in mediating Papaver SI.

0128-A

THE ROLE OF CELL LAYERS IN COMPLEX FLORAL MORPHOLOGY

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During flower development, homeotic genes from the ABC model specify floral organ identities, but how they determine the multiple and complex characteristics of a floral organ across tissues and layers is unknown. Here, we use the model petunia, whose petals are fused into an elongated cylinder (the tube) topped by a flat and pigmented surface (the limb). We isolated cell layer-specific mutants for the B-class gene PhDEF: when PhDEF is mutated in the epidermis, it strongly affects limb development but the tube develops normally. Conversely, when PhDEF is mutated in the mesophyll, the limb develops normally but the tube is extremely reduced. This indicates that the petunia petal development is highly modular, and that the action of PhDEF is not the same in the different cell layers of the petal and contributes to this modularity. We use these mutants to explore the cell layer-specific gene regulatory networks controlled by PhDEF, by a combination of single-cell RNA-Seq and ChIP-Seq.

0129-B

ANALYSIS OF A GENE REGULATORY NETWORK UNDERLYING FLORAL TRANSITION IN APPLE

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Floral induction is a key developmental stage for fruit trees, particularly for horticultural crops such as the apple (*Malus domestica* Borkh.), because it determines the success of commercial orchards by its influence on fruit quantity and quality, as well as stability of production from year to year. Therefore, understanding the control of flowering is crucial to ensure fruit security and improve fruit production.

In this study, we aim at deciphering a gene regulatory network (GRN) that controls floral transition in apple. To this end, we are making use of massive micro RNAs (miRNAs) sequencing to identify differentially accumulated miRNAs in apple apical meristems during floral induction and initiation. The temporal and spatial expression pattern of these miRNAs and their potential target genes will be studied using RNA in situ hybridization. These data in combination with genome-wide studies (e.g. DAP-seq) will allow us to build a GRN involved in the floral transition of apple.



Supported by:



0130-C

EVOLUTION AND DEVELOPMENT OF LIGNIN POLARITY IN CARDAMINE EXPLOSIVE FRUIT

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Fruit of Cardamine species employ an explosive mechanism to disperse their seeds, which differs from the non-explosive fruit found in *Arabidopsis thaliana*. This trait is strictly associated with an asymmetric pattern of lignin deposition in endocarp b cells of the fruit valve, a feature necessary for explosive seed dispersal. Our study sets out to determine the genetic basis for polar lignin deposition. To this end, we are developing *Cardamine chenopodifolia* as an experimental system for comparative analysis. *C. chenopodifolia* bears aerial explosive fruit with polar lignin deposition, and subterranean non-explosive fruit with apolar lignification. Surprisingly, we found that light was sufficient to make subterranean fruit explosive. We leverage this result to identify differentially expressed transcripts between fruit types in *C. chenopodifolia*. Specifically, we compare the role of different laccases and peroxidases in the formation of polar vs non-polar lignin deposition.

0131-A

THE INTERACTION BETWEEN PHOTOPERIOD, AGE, AND GIBBERELLIN PATHWAYS AFFECT FLOWERING TIME IN DAY-NEUTRAL TOMATO.

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Photoperiod is an important environmental factor that interacts with distinct endogenous pathways to regulate flowering. In *Arabidopsis*, these pathways, and the interaction between them, have been widely explored, but in crops such as tomato, they are scarcely known. In this work, we explore how photoperiod, gibberellin and age flowering pathways interact and regulate flowering in tomato. We have generated double mutants/transgenics in genes related to these pathways and evaluated flowering time under different photoperiodic conditions. Additionally, we characterized the interaction of these pathways with the flowering-associated phloem-mobile SINGLE FLOWER TRUSS (SFT, the tomato FLOWERIG LOCUS T) to look for independent pathways of this universal inductor. We are currently identifying common targets of the photoperiodic, age, and GA-associated flowering pathways by RNAseq. Understanding the interactions of these flowering pathways can help breeding programs for tomato and other crops.



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0132-C

SYSTEMATIC PARENT-SPECIFIC EXPRESSION PERTURBATIONS IN HYBRID ENDOSPERMS MAY EXPLAIN HOW EFFECTIVE PLOIDY DIFFERENCES CAUSE HYBRID SEED FAILURE

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Hybrid seed inviability (HSI) is a common post-zygotic reproductive barrier in angiosperms caused by endosperm mis-development. Recent studies suggest that effective ploidy divergence driven by parental conflict may be responsible for HSI, yet these phenomena remain poorly characterized at the molecular level. We analyzed endosperm transcriptomes in 12 reciprocal crosses within and among three diploid wild tomato lineages and tested 5,015 endosperm-expressed informative genes common to all hybrid crosses for Differential Parental Expression (DPE between hybrid and their corresponding intraspecific endosperms). Strikingly, allelic expression is systematically more perturbed in the parent with lower effective ploidy. We illustrate and discuss the complex interplay between parental expression proportions, total and parent-specific expression in abortive endosperms. Overall, our analyses yield candidate genes and pathways that may underpin the unknown epigenomic imbalances underlying HSI.

0133-B

STRANDED POSIDONIA OCEANICA SEEDS ENCLOSED IN FRUITS RETAIN THEIR REPRODUCTION POTENTIAL AND ARE EVENTUALLY RETRIEVED BY THE SEA

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Posidonia oceanica meadows are the most productive coastal ecosystem in the Mediterranean, yet they are currently receding in many regions. P. oceanica slowly spreads vegetatively by clonal propagation, but it can also reproduce sexually by releasing large quantities of seeds, enclosed in fleshy buoyant fruits that allow seed dispersal. Fruits stranded on beaches are usually regarded as lost in terms of reproduction potential. Considering the size and large amount of energy storage contained in each seed, the cost of such loss for the plant may be remarkable. Here, we measured the potential of fruit return to water by incoming tides, by tagging fruits and seeds. Furthermore, we quantified the effect of air, sun and heat exposure on the viability and fitness of stranded fruits and naked seeds. Results show that on average more than half of fruits and seeds return to the sea after stranding events, and that fruits confer significant protection from desiccation and viability loss.



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**0134-C
STAMEN GALORE — OCCURRENCE AND REGULATION OF STAMEN-PRODUCING RING MERISTEMS**

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Floral meristems are dynamic stem cell systems that generate floral organ primordia and often terminate while the gynoecium forms. However, many species develop additional ring meristems during floral morphogenesis, that generate stamen primordia continuously while the floral meristem has already ceased activity. This results in ‘polystemous’ flowers (include more than twice the number of stamens than petals or sepals), and decouples the timing of stamen initiation from carpel initiation. Polystemy has originated several times independently, but so far nothing is known so far about the differential regulation of these two types of stem cells in very close vicinity. We use *Eschscholzia californica* (California poppy) a member of the Ranunculales, the sister lineage to the core eudicots, as model system to understand the molecular mechanism regulating polystemy. Here, we provide a systematic overview of the occurrence of polystemy in dicots and summarize our results from the LCM-RNAseq.

PLANT RESPONSES TO ABIOTIC STRESSES

0135-A

THE INOCULATION WITH ENSIFER MELILOTI SV. RIGIDULOIDES IMPROVES CONSIDERABLY THE GROWTH OF ROBINIA PSEUDOACACIA UNDER LEAD-STRESS

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With the aim to use black locust for phytostabilization of the Zaida abandoned mine tailings in Eastern Morocco, we isolated and characterized its indigenous microsymbionts. Thus, out of 27 bacteria isolated, four strains were selected for the analyses of symbiotic, molecular, phenotypic, as well as plant growth properties under increasing lead-acetate concentrations. The Phylogenies of rrs, the MLSA, and symbiotic genes analyses showed the affiliation of the strains with *Ensifer meliloti* sv. *rigiduloides* and *E. kummerowiae* sv. *meliloti*.

Inoculation experiments under metal stress showed that both strains improved plant growth and chlorophyll content. The plant proline content increased as a response mechanism to increasing concentrations of lead.

Our results show that *E. meliloti* sv. *rigiduloides* strain RPZ12 improves plant growth under lead stress conditions more than *E. kummerowiae* sv. *meliloti* strain RPZ17. This is the first description of symbiovar *meliloti* in *E. kummerowiae*.

0136-B

EFFECT OF SILICON SUPPLY ON ROOT SULPHUR UPTAKE IN S-FED AND S-DEPRIVED BRASSICA NAPUS L.

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Sulphur (S) deficiencies can have a direct impact on the growth of the crop. Silicon (Si) is known to improve plant resistance to nutritional stresses. This study aimed to evaluate whether a Si supply could mitigate the negative effects of S deficiency in *B. napus* and assess its impact on root sulphate uptake capacity and S accumulation. Plants were grown with or without S and fed or not with Si. The effects of Si supply on growth, S content, expression of root sulphate transporter genes were monitored. Si had no effect on growth and S uptake capacity. In S-deprived plants, a strong induction of the expression of genes encoding two transporters involved in the uptake of sulphate was observed. In comparison to -S-Si plants,



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Si supply led to a lower induction of BnaSultr1.1 gene expression in -S+Si plants. In conclusion, silicon supply does not lead to changes in S status, a significant effect on the expression of genes encoding sulphate transporters has been observed.

0137-C

ARABIDOPSIS GLUTATHIONE PEROXIDASE-LIKE ENZYMES: NON-HEME ROS-SCAVENGERS IN THE SIGNAL TRANSDUCTION NETWORK CONNECT REDOX REGULATION TO PLANT DEVELOPMENT

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Plants contain glutathione peroxidase-like (GPXL) proteins, which catalyse the reduction of H₂O₂ or hydroperoxides to water or alcohols using glutathione or thioredoxin as electron donors. They can fine-tune ROS level and redox homeostasis or modify activity of interacting regulatory proteins. Arabidopsis thaliana possesses 8 AtGPXL genes. Mutation in one of them may affect the ROS levels, vitality, glutathione redox potentials, the growth and stress responses of plants. We have performed detailed characterization of Atgpxl2, -3, -4 and -5 mutants and plants overexpressing AtGPXL4 or -5 under different conditions and developmental stages. Relationships with ethylene signalling and polyamine metabolism were also discovered. It was shown that these non-heme ROS-scarvengers are part of the diverse signalling networks and connect redox processes to development of plants. This work was supported by the Hungarian National Research, Development and Innovation Office (Grant Number: K 138589).

0138-A

THE LSD1 AND CRK5 DIFFERENTIALLY AFFECT FOLIAR TEMPERATURE IN ARABIDOPSIS

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The LSD1 is a small zinc finger protein, while CRK5 acts as a receptor kinase. Both of them play roles as negative regulators of cell death. However, their cell death-related phenotype is different. The lsd1 mutant accumulates salicylic acid, which induces stomatal closure and inhibits catalase activity, while the crk5 shows increased stomatal opening and enhanced photorespiration. Our gas exchange and fluorescence data revealed increased NPQ and decreased transpiration in lsd1, while the crk5 plants showed the opposite phenotype. This

differential regulation was supported by foliar temperature changes. In our study, the *crk5* plants showed lower temperature gradient under the excess light compared to the wild-type, while the *lsd1* plants showed the opposite effect. Lanolin application to the abaxial part of the leaf, which blocked gas exchange, bridged the temperature differences between genotypes, indicating that it results from deregulated stomatal conductance in analysed plants.

0139-B

MULTIPLE REGULATORY LEVELS SHAPES SULFUR METABOLISM IN RICE UNDER SALINITY

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The comprehension of stress-induced metabolic alterations in rice is crucial for ensuring rice production and preserve rice biodiversity in salt-affected soils.

In this study, glutathione was identified as the redox metabolite mainly involved in the tolerance against salt stress. As glutathione functions as a major sulfur repository, we investigate on the crosstalk between sulfur and glutathione metabolism in rice under salinity. We observed that the tolerant varieties up-regulate glutathione level in response to salt and show lower levels of inorganic sulfur compared to sensitive varieties. The increase of glutathione levels also correlates with the accumulation of mRNAs of genes related to sulfur metabolism, as *SULTR2.1* and *APR*. These results suggest a differential sulfur assimilation efficiency in relation to salinity tolerance. The involvement of miRNAs-dependent gene expression regulation and epigenetic modifications occurring on differentially expressed genes were analyzed.

0140-C

COMPARATIVE PROTEOMIC ANALYSIS OF TOMATO (SOLANUM LYCOPERSICUM L.) IN RESPONSE TO HYPOXIA STRESS

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Tomato (*Solanum lycopersicum* L.) is a vegetable frequently exposed to the hypoxia stress induced by submergence, flooding or oxygen limitation in hydroponic cultivation systems. Proteomic techniques were used to study the molecular mechanisms involved in the response of tomato to waterlogging stress. Three-week plants of waterlogging-tolerant and waterlogging-sensitive accessions were exposed to waterlogging for 7 days, then plants recovered for 14 days and another 7 days of the hypoxia treatment was applied. Root samples



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were used for 2D-DIGE with MALDI TOF/TOF and the expression analyses of gene and protein encoded alcohol dehydrogenase 2 (ADH2) and immunolabelling of ADH was conducted. Proteins detected in abundance were proposed as crucial factors for hypoxia stress priming. Both tomatoes revealed high amount of ADH2, which indicates intensive alcohol fermentation. Immunohistochemical analysis confirmed the presence of ADH in parenchyma cells of cortex and vascular tissue.

0141-A

LEAD TOLERANCE AND ACCUMULATION IN HIRSCHFELDIA INCANA: METABOLOMIC AND BIOCHEMICAL APPROACH

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Hirschfeldia incana, a brassicaceae that grows naturally in Pb contaminated sites and exhibits significant biomass and strong Pb tolerance and accumulation capacity. This plant is described as a good model for studying plant response to Pb. The metabolomic profile of *H. incana* treated with Pb after 3 and 15 days in hydroponic conditions was assayed by GC-MS. Results showed an increase of organic acids from the beginning of treatment and a decrease of lipids and steroids, revealing signs of toxicity. However, The concentration of lipids and steroids increased after 15 days of treatment. A comparison of biochemical parameters between treated and untreated plants showed an increase in peroxidase activity in leaves and roots and a decrease in catalase activity in roots after 3 and 15 days of treatment with Pb. The content of sugars and phenols increased in the leaves and roots after 3 and 15 days of treatment. These findings will allow to understand more the response of *H. incana* to Pb.

0142-B

MOLECULAR AND FUNCTIONAL CHARACTERIZATION OF ARABIDOPSIS THALIANA ARM GENE INVOLVED IN PLANT STRESS RESPONSE

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The Arabidopsis ARM protein has recently been shown to interact with the telomerase AtTERT. The complex network ARM/AtTERT can modulate gene expression, possibly through interactions with nuclear, cytoplasmic, and plasma membrane proteins involved in transcriptional regulation, photomorphogenesis, rhythmic processes, and stress response. In this study, we aimed in characterizing the ARM gene from Arabidopsis thaliana and its role in

the plant, development using a combination of biochemical, molecular-biological, genomic, and bioinformatic approaches, we also investigate whether there are any additional biochemical or functional similarities between these putative Arabidopsis and human homologs.

This work was supported by Czech Science Foundation (21–28265S).

0143-C

GUN1 INVOLVEMENT IN THE REDOX CHANGES OCCURRING DURING CHLOROPLAST DEVELOPMENT AND HEAT STRESS RESPONSE

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Plant development and response to environmental changes require a mutual communication between plastids and the nucleus. By retrograde signals, plastids transmit information about their functional and developmental state to adjust nuclear gene expression. GENOMES UNCOUPLED 1 (GUN1), a chloroplast-localized protein, acts as one of the main players of retrograde signaling. Redox changes greatly influence plant response to endogenous and environmental stimuli. We focused on the interplay between GUN1 and redox regulation during plastid biogenesis and heat stress response (HSR). Arabidopsis wild type (wt) and gun1 seedlings, were grown for six days in presence or absence of lincomycin, which perturbs chloroplast development. To study HSR, 15-day-old wt and gun1 plantlets grown at 22°C were exposed to 3 hours of heat stress (HS) at 45°C. Results indicate that in response to both lincomycin and HS, GUN1 is required for the redox-dependent plastid-to nucleus communication.

0144-A

DNA CONTENT AND CELL CYCLE ON MAIZE PLANT (ZEA MAYS L.) UNDER HEAVY METALS STRESS

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Heavy metals affect organisms at the molecular level, showing various abnormalities. The purpose of this study is to determine the effects of heavy metals on DNA content and cell cycle phases (G1, S, G2M), in the leaves of the maize plant. Maize plants were treated with a certain concentration of metals: Ni and Cr (50ppm, 100ppm, 200ppm, 400ppm), and Pb (20ppm, 50ppm, 100ppm, 200 ppm), separately. The analysis of the samples was carried out by flow cytometry method. Our results indicate small changes of the DNA content caused by



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the increasing concentration of the metals compared to the control group, as well as in the cell cycle phases, depending on the variations of the metals and concentration levels with a decrease in the distribution of the cells in the G1 phase and an increase in G2M. Our study shows that the maize plant can be used as a model to evaluate the effect of Ni, Cr and Pb, depending on their concentration in relation to the DNA content and cell cycle phases.

0145-B

ALTERATIONS IN SPECIALIZED METABOLITES' PROFILE OF DAUCUS CAROTA L. CALLI INDUCED BY LOW-TEMPERATURE PLASMA TREATMENT

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Non-thermal plasma (NTP) technology offers a promising future in plant metabolic engineering, being energy efficient and Eco-friendly alternative to the conventional treatments [1]. Plasma environment is enriched with reactive oxygen and nitrogen species (RONS) that participate in various signaling pathways in plants by regulating their metabolic and developmental processes. In the present study calli of different carrot (*Daucus carota* L.) varieties was treated by using plasma needle device designed for biomedical applications [2]. Metabolite profiling revealed that plasma treatment could induce severe qualitative and quantitative changes of the major phenolic compounds detected in carrot calli. Current metabolic alteration was followed by the significant shift in the antioxidant capacity of the treated calli. Obtained results outline the potential application of plasma treatment as a novel elicitor for the production of bio-active compounds in plant in vitro culture systems.

0146-C

COLD STRESS TOLERANCE IN FLAX (LINUM USITATISSIMUM L.): CHARACTERIZATION AT THE PHYSIOLOGICAL, METABOLIC, TRANSCRIPTOMIC AND GENETIC LEVELS.

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Flax (*Linum usitatissimum* L.) is an ancient versatile crop which is gaining renewed interest due to its potential contribution to climate change mitigation and its resilience to changing climatic conditions. To ensure optimal yields, winter flax and spring flax varieties are therefore cultivated. While contrasted differences in responses to cold stress have been described between these two types, the underlying metabolic, transcriptomic and genetic mechanisms remain unknown. Their deciphering may help breeding efforts in adaptation to climate changes. Preliminary work highlighted swertisin and swertiajaponin as putative biomarkers of flax cold tolerance. Multi-omics characterisation of a spring and a winter variety was carried out following different cold treatments. The phenotypic and genetic analyses of their progeny is currently ongoing. The results could help determine specific biomarkers and QTLs for cold stress tolerance and thus facilitate breeding strategies.

0147-A

MITIGATION OF CADMIUM TOXICITY IN MAIZE PROTOPLASTS BY GALACTOGLUCOMANNAN OLIGOSACCHARIDES

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Heavy metal accumulation, e.g. cadmium (Cd), in the environment is the stress factor that negatively affects plants' vitality and eventually leads to the reduced production and quality of crops, including maize (*Zea mays* L.). Galactoglucomannan oligosaccharides (GGMOs) are biologically active compounds released from cell wall polysaccharides. GGMOs have a positive effect on plant growth and development in non-stress as well as stress (Cd) conditions. This work aimed to answer the question: "Is the prevention of Cd entry into the protoplast and the rate of the cell wall biosynthesis related to the action of GGMOs?" Although the exact mechanism of GGMOs action in the Cd stress is still not fully known, we found that GGMOs decreased the Cd uptake by maize protoplasts, which was related to the increase of the cell wall regeneration rate and protoplast viability.

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0148-B

TEMPORAL GENETIC ANALYSIS OF WATER-DEFICIT RESPONSE IN MAIZE

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Drought is of increasing concern as a leading cause of crop losses worldwide. During a growing season, the timing, duration, and severity of drought is unpredictable, and mechanisms underlying the response to water deficit can be growth-stage specific. We are developing an

approach that capitalizes on advances in phenomics to investigate shifts in the genetic basis of plant response to water deficit. A large diversity panel of maize was imaged on a daily basis in the PHENOARCH phenotyping platform with precise control of water-deficit conditions. Using morphological and physiological traits extracted from image data, longitudinal genome-wide dissection reveals dynamic changes in genomic regions across time. We present this in the context of a new framework for testing hypotheses about temporal mechanisms for response to water deficit.

0149-C
RECENT ADVANCES IN THE LONG-DISTANCE TRANSPORT OF SUGARS BY THE PHLOEM AND CONSEQUENCES ON SOURCE-SINK RELATIONS

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The distribution of photoassimilates in the plant relies on the phloem functions from source to sink organs. Phloem sugar transport is regulated by SUC/SUT and SWEET sugar transporters. We observed that deregulation of SUT1 or SUT2 in Tomato lines had various consequences on plant growth, sugar phloem transport rate and phloem sap composition. Similar effects were observed in response to the deregulation of SUC2 in Arabidopsis mutants and impairs source-sink relations, with consequences on root development and leaf evapotranspiration. Meanwhile, we observed natural variations in the metabolite profiles of phloem exudates of Arabidopsis accessions grown in low or non-limiting N supply. Nutrient phloem transport thus also depends on downstream regulation of the central metabolism and water fluxes.

0150-A
NUCLEAR OSFKBP20-1B MAINTAINS SR34 STABILITY AND PROMOTES THE SPLICING OF RETAINED INTRONS UPON ABA EXPOSURE IN RICE

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Alternative splicing (AS) is a critical means by which plants respond to changes in the environment, but few splicing factors contributing to AS have been reported and functionally characterized in rice (*Oryza sativa* L.). Here, we explored the function and molecular mechanism of the spliceosome-associated protein OsFKBP20-1b during AS. We determined the AS landscape of wild-type and osfkbp20-1b plants upon abscisic acid (ABA) treatment by transcriptome sequencing. To capture the translating intron-containing mRNAs, we blocked transcription with cordycepin and performed polysome profiling. OsFKBP20-1b interacts with OsSR34 and regulates its stability, suggesting a role as a chaperone-like protein in the spliceosome, and facilitates the splicing of mRNAs with retained introns after ABA treatment.



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Our findings reveal that spliceosome-associated immunophilin functions in alternative RNA splicing in rice by positively regulating the splicing of retained introns to limit ABA response.

0151-B

UNRAVELING THE PROCESS OF THERMOREGULATION DURING THE SEED DEVELOPMENT IN BRASSICA NAPUS

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Studies on plant development under warm temperature conditions provide knowledge about the temperature's influence on crop yield. Brassica napus is the second most widely produced oilseed worldwide. Characterizing the thermomorphogenesis of B. napus grown in long-term heat stress conditions identified accelerated plant growth, reduced fertilization rate, and increased seed abortion rate. The accelerated and defective embryo development and pre-harvest seed sprouting in plants grown under heat stress suggest a possible reduction in seed dormancy. We identified a reduced expression of ABA biosynthetic genes and dormancy markers. However, the phenotypes were not reverted by external ABA applications. We hypothesized a link between high temperatures, accelerated embryo growth, and the mechano-sensing pathway during the early seed maturation phase under heat stress. Studies in this research area will pave the way toward producing thermotolerant varieties of B. napus with better crop yield.

0152-C

THE ROLE OF HOST SPECIES DIFFERENCES IN PHYLLOPLANE PH REGULATION IS SHAPING BACTERIAL COMMUNITIES.

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Plants can differ in their ability to regulate pH conditions on their leaf surfaces (phylloplane), ranging from acidic carnivorous plants to alkaline Malvaceae. These physiological differences also extend to their ability to buffer against external pH changes. In this study we took a metatranscriptomic approach to examine phylloplane bacteria on five plant species that differ

in phylloplane regulation. Young leaves were inoculated with a common microbial community sourced from a soil slurry. Leaves were also treated with one of two external pH treatments, pH 6.5 or pH 2. After exposure to the pH treatment, we collected phylloplane microbes and performed total RNA extractions and sequencing. Bacterial gene expression structure was not significantly impacted by pH but by plant host. Differential expression analysis revealed differentially expressed genes between pH 2 and pH 6.5. Indicator genes analysis revealed specific functional gene groups significantly associated with each plant species, underlining the importance of the active recruitment done by plant hosts in shaping their phylloplane microbiota.

0153-A

MODULATION OF C/N RESOURCES AND WATER UPTAKE ARE RELEVANT FOR THE ACCLIMATION OF RICE PLANTS TO COLD STRESS

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OsCPK17 mediates rice cold stress response via phosphorylation of C/N-related enzymes and the aquaporin PIP2;1/2;6, but the downstream effects of its action on primary metabolism were unknown. Since SnRK1, an energy-homeostasis effector, shares common phosphorylation targets with OsCPK17 (e.g.,SPSs, NRs), we next asked if there is cross-talk between the kinases, and uncovered by LC-MS/MS, the OsSnRK1-dependent phosphoproteome upon cold. Our results suggest that i. CPK17 manages resources upon stress by redirecting C/N stocks towards alanine synthesis, a putative stable pool of these resources; ii. impacts the accumulation of fructose 1-6 biphosphate, a substrate of key enzymes for the regulation of C assimilation/partitioning; iii. impacts the accumulation of chlorophylls. Curiously, phosphorylation of PIP2;1/2;6 is also SnRK1-dependent. This study further unravels the downstream effects of stress signaling into developmental decisions by the modulation of metabolism and water uptake.

0154-B

SHORT TIME EXOGENOUS FORMALDEHYDE APPLICATION MEDIATED CHANGES IN CHLOROPHYTUM COMOSUM L. (SPIDER PLANT) CELLULAR METABOLISM

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Chlorophytum comosum L. plants effectively absorb air pollutants, including formaldehyde (HCHO). In the present study, biochemical changes in C. comosum leaves induced by 48 h exposure to exogenous HCHO, applied as 20 mg m⁻³, were analyzed. HCHO application increased Chl a/b ratio, and decreased Chl b and carotenoid content. HCHO treatment affected sugar metabolism, towards the utilization of sucrose and synthesis or accumulation



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of glucose, and decreased activities of aspartate and alanine aminotransferases, suggesting that these enzymes do not play any pivotal role in amino acid transformations during HCHO assimilation. The obtained results suggest that HCHO affects nitrogen and carbohydrate metabolism, effectively influencing photosynthesis, shortly after plant exposure to this volatile compound. The presented results confirm for the first time the direct influence of short time HCHO exposure on the studied parameters in the *C. comosum* plant leaf tissues.

0154

CHANGES IN METABOLITES AFTER DIFFERENT SALICYLIC ACID TREATMENTS METHOD AND FORMS

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A comparative study of different forms and application methods of salicylic acid (SA) on young pea plants was carried out. The plants were treated with acid, salt and volatile forms of SA using different applications methods as pre-treatment before the toxic metal stress. We investigated whether acid or salt form of SA provide better protection against Cd stress and wanted to clarify their mode of action. Methyl salicylate (MeSA) is a volatile form of salicylic acid which has been identified in several plants. Lipid peroxidation rate and antioxidant enzymes activity was determined and a metabolomics measurements was performed using Pegasus 4D GCxGC TOFMS (LECO). It was found that the plants responded differently to different forms of SA. The lipid peroxidation rate changed and the elements of the TCA cycle and the biosynthesis of sugars was also affected by the different treatments.

The work was supported by PRÉMIUM2019-462, NKFIH K142899.

0155-C

REACTIVE OXYGEN SPECIES AFFECT CYTOSOLIC CALCIUM DYNAMICS TO ORCHESTRATE SALT RESPONSE IN RICE (ORYZA SATIVA, L.)

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The presence of a central Ca²⁺-ROS hub responsible for signal sorting between stimulus perception and specific response in plant cells is an intriguing hypothesis. Ca²⁺ signaling is known to be specific, exhibiting different signatures in response to different stimuli, but the specificity of ROS signaling has not yet been demonstrated. In rice, we recently reported different salt-induced cytosolic ROS signatures in different genetic backgrounds (i.e., salt-tolerant and sensitive plants). In this work we demonstrate that the Ca²⁺ transients induced by salt are also different in the two rice varieties. Furthermore, we report data showing that Ca²⁺ dynamics are influenced by ROS in the roots of salt-sensitive rice varieties, whereas this is not the case in salt-tolerant plants. Finally, we show data demonstrating the possibility



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of modulating the dynamics of salt-induced Ca²⁺ transients in the sensitive variety, thus inducing a partial tolerance to stress.

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0156-A

RNA SPLICING REGULATION OF CYP18-1 AND PHOSPHATASE IN ARABIDOPSIS UNDER HEAT STRESS

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Cyclophilin is also referred to as 'spliceophilin' because it functions in RNA splicing when located in the nucleus of animal cells. To identify the function of plant cyclophilin in RNA splicing under heat stress, a study was conducted on the cyclophilin18-1 (CYP18-1) in *Arabidopsis thaliana*. As a result, CYP18-1 mutant exhibited a sensitive phenotype under heat stress conditions, while overexpression of CYP18-1 conferred a heat stress-resistant phenotype in *Arabidopsis*. Further molecular biological studies revealed that CYP18-1 interacts with spliceosome proteins in the nuclear speckles and promotes the dephosphorylation of splicing factor PRP18a. In addition, PP2A B'eta, belonging to the PP2A type B56 phosphatase, promotes the dephosphorylation of PRP18a together with CYP18-1. Through the above studies, an intersection between CYP18-1 and the phosphatase PP2A B'eta in the RNA splicing regulatory mechanism under heat stress has been identified.

0157-B

UNRAVELLING THE ROLE OF POLYAMINE METABOLISM IN NI-INDUCED STRESS IN TOMATO CULTIVARS WITH CONTRASTING ANTIOXIDANT POTENTIAL

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Polyamines (PA) are often correlated with metal stress tolerance, for their antioxidant, signalling, and chelating properties. The response of two tomato varieties (Gold Nugget-GN; Purple Calabash-PC) to Ni stress was recently studied. Data showed that GN accumulated more Ni and activated more antioxidants than PC. Thus, the present work analysed Ni effects on PA metabolism in GN and PC. Levels of putrescine (Put) rose under Ni stress, while

spermidine (Spd) and spermine (Spm) did not change. Diamine oxidase (DAO) and polyamine oxidase (PAO) activities increased due to Ni, especially in GN plants. GN also showed higher levels of H₂O₂, lower Spm and higher Put under Ni stress than PC. The activation of PAO, coupled with Put rise, points to the stimulation of the back-conversion catabolism, in which Put is produced from Spd/Spm with the release of H₂O₂. Thus, Ni-exposed GN plants seem to activate signalling mechanisms mediated by Put and H₂O₂ more effectively than PC.

0158-C

BIOMONITORING OF OXIDATIVE STRESS RESPONSES IN MAIZE DUE TO SOIL CONTAMINATION IN THE VICINITY OF THE FERRONIKEL SMELTER IN DRENAS, KOSOVO

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Biomonitoring of heavy metals (Ni, Pb, Cr, Cd, Fe, Mn) pollution in the vicinity of the Ferronikel smelter in Drenas, Kosovo, through specific biomarkers for heavy metals and their accumulation in maize, was the main objective of this research. Results show that Ni and Cr concentrations in soil samples from some localities of Drenas (103-809 mg/kg) and their accumulation levels were significantly higher in comparison with the control group. There was an adverse negative correlation between Ni concentration and δ -aminolevulinic acid (ALA) dehydratase activity and total chlorophyll content, and a positive correlation with ALA content. The level of malondialdehyde and glutathione significantly increased in relation to the concentration of heavy metals in soil and plant. Our study clearly showed that heavy metal emissions from this industry generate oxidative stress in maize plants and the ALA-D enzyme can be used as a very sensitive biomarker for the evaluation of heavy metal pollution.

0159-A

HEAVY METAL-INDUCED EXPRESSION OF OAT (AVENA SATIVA L.) METALLOTHIONEIN GENES

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Metallothioneins (MTs) are cysteine-rich proteins involved in maintaining micronutrient homeostasis and detoxifying harmful metal ions. In plants, MTs are divided into four types based on their amino acid sequence. We investigated the response of oat to Zn, Cd, and Zn+Cd treatment at early stages of growth. The biomass of Zn-treated plants was almost two times higher than in control plants whereas the biomass of plants treated with Cd and Zn+Cd was two times smaller than in control. In shoots treated with Zn+Cd expression of all four MTs was elevated, but in roots only the amount of MT4 transcript was higher. Expression of



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MT1 and MT2 was also elevated in shoots of Cd-treated plants. Zn treatment caused an increase in expression of MT2 and MT3 in oat roots. Our results indicate that MTs play a role in the response of oat to heavy metal stress but each MT type functions differently depending on the type of metal and the plant organ.

Grants4NCUStudents 4101.00000026 by NCU for NC and MA.

0160-B

GENOME-WIDE EXPLORATION OF THE GENETICS OF TRANSPORTERS OF BIOGENIC POLYAMINES IN BARLEY FOR NITROGEN-REMOBILIZATION CROP IMPROVEMENT

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Since cells cannot store reduced N as NH₃ or NH₄⁺, polyamines (PAs) are important N storage compounds in plants. Therefore, manipulating them may improve N use efficiency. Homeostasis of PAs is maintained by multiple feedback mechanisms at the levels of biosynthesis, catabolism, efflux, and uptake. The molecular characterization of the PA uptake transporter (PUTs) in most crop plants remains largely unknown, and knowledge about polyamine exporters (BATs) in plants is lacking.

We conducted the first systematic study to comprehensively analyze the PA transporter gene families, PUTs, and BATs, in barley. Moreover, homology modeling allowed for the prediction of the 3D structures of the proteins of interest. Molecular docking provided insight into the PA binding pockets of HvPUTs and HvBATs, facilitating the understanding of the mechanisms and interactions involved in the HvPUT/HvBAT-mediated transport of Pas

This work was supported by NCN Poland (project number 2018/29/B/NZ9/00734).

0161-C

IDENTIFYING AND EXPLORING THE CO-EXPRESSION NETWORKS IN ARABIDOPSIS HALLERI TO SHED LIGHT ON POSSIBLE BIOLOGICAL PATHWAYS AND GENES INVOLVED IN METAL STRESS IN PLANTS

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Arabidopsis halleri is a hyperaccumulating pseudo-metallophyte that has been extensively studied for its metal tolerance and hyperaccumulation traits. This study used weighted gene co-expression network analysis (WGCNA) to identify scale-free organ-specific co-expression networks of 19,653 genes of root and 18,081 genes of shoot. "Photosynthesis" and "photosynthesis- antenna proteins" were identified as the most enriched and common pathway to both root and shoot, while "glucosinolate biosynthesis," "autophagy," and "SNARE



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interactions in vesicular transport" were specific to root and "circadian rhythm" was enriched only in shoot. Hub and bottleneck genes were screened to validate their possible involvement in heavy metal stress, and combining co-expression modules with protein-protein interactions identified potential biomarkers for plant stress responses. These findings provide insights into new avenues of research for abiotic stress tolerance in plants.

0162-A

EXPLORATION OF ORGAN SPECIFICITY REGARDING THE ACCUMULATION OF POLYCYCLIC AROMATIC HYDROCARBONS (PAHS) IN PLATANUS × ACERIFOLIA (AITON) WILLD.

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The PAHs accumulation capacity of the branches, leaves, and stem wood of *P. Acerifolia*) from urbanized area were analyzed using GCMS to define the species and organ-specific potential for PAHs remediation from cities. The results pertaining to 17 studied PAHs showed deviations among branches (1138.13 ng g⁻¹ DW), leaves (984.21 ng g⁻¹ DW), and wood (850.32 ng g⁻¹ DW). According to the yield of each PAH, deviations among analyzed organs were observed for 13 PAHs. The highest concentrations were noted for Phenanthrene (Phe; 197.46 ng g⁻¹ DW). Unique organ-specific accumulation potential in the *P. acerifolia* were not observed. In some cases, branches accumulated higher concentrations of certain PAHs, such as Phe, FL, Pyr, Benzo[a]anthracene, and Dibenzo[a,h]anthracene. Leaves accumulate more 4- and 5-ring PAHs (Crysene, Benzo[k]fluoranthene, Indeno[1,2,3-cd]pyrene, and Benzo[g,h,i]perylene), while in wood only Naphthalene and 2-methyl-naphthalene were detected at slightly higher levels.

0163-B

VOLATILE ORGANIC COMPOUNDS (VOCs) EMISSION FROM LEAVES OF THE HOMOIOCHLOROPHYLLOUS RESURRECTION PLANT HABERLEA RHODOPENSIS DURING DESICCATION AND REHYDRATION: AN UNSOLVED MYSTERY.

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Resurrection plants have the unique ability to withstand extreme dehydration and recover after rehydration. Despite extensive studies on their metabolic and physiological modifications, the emission of leaf volatile organic compounds (VOCs) has been poorly investigated during the dehydration and rehydration cycle. In the present study, the leaf emission of VOCs was assessed in the resurrection angiosperm *Haberlea rhodopensis* Friv. (Gesneriaceae) that belongs to the homoiochlorophyllous type. The temporal dynamic of VOC

emission during dehydration and rehydration was monitored continuously by applying proton transfer reaction – time of flight-mass spectrometry (PTR-MS) and gas chromatography-mass spectrometry. Our study on the VOC emission, together with parallel analysis of the photosynthetic activity and photoprotective mechanisms, provides new insights into the potential role of VOCs for the “drying without dying” ability.

0164-C
GENOME-WIDE ASSOCIATION STUDY OF SALT TOLERANCE IN TOMATO

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Salinity is a common abiotic stress in many tomato production areas due to the scarcity of fresh water in arid and coastal regions of the world. Thus, there is a need to understand the underlying mechanisms of genetic diversity for salt tolerance. In our study, we analyzed a panel of 150 genome-wide sequenced wild tomato. This panel was phenotyped during early growth and adult stages in both control and salt stress treatments. Characterization of salinity tolerance was performed on the basis of various traits, including mineral contents, metabolomics, root architecture and agronomic characteristics. We conducted a genome-wide association study on these traits and identified dozens of QTLs. Several candidate genes within these QTL have functions related to salt stress tolerance. Some of them are consistent with previously published QTLs. These results provide new insight into the genetic architecture of salt tolerance in tomato and provide new genes for functional validation.

0165-A
PHYSIOLOGICAL ANALYSIS OF CHLORIDE-INDUCED RESPONSES DURING NITROGEN DEFICIENCY IN TOMATO PLANTS

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Chloride (Cl⁻) has been traditionally considered a harmful ion for plants because of its high accumulation in organs and its antagonism with nitrate (NO₃⁻) under salinity conditions.^{1,2} However, we recently demonstrated the opposite when it gradually accumulated in leaves, defining Cl⁻ as a beneficial macronutrient for plants that improves growth and the efficiency in the use of water, carbon and nitrogen (N).^{3,4} A major problem for crops is the inefficient application of N fertilizers, causing N deficiency stress in plants and environmental and human health issues⁵. Therefore, in this work we analysed physiological traits in tomato

plants grown under different Cl⁻ and NO₃⁻ treatments. . Our results showed that the application of 5 mM Cl⁻ allowed to reduce NO₃⁻ supply, maintaining similar plant growth. Overall, Cl⁻ remains as a potential strategy to reduced N deficiency stress symptoms improving growth, turgor maintenance, photosynthesis and antioxidant response in tomato plants.

0166-B

AMINO ACID TRANSPORTERS OF ATAVT6 FAMILY IN ARABIDOPSIS THALIANA AS TARGET FOR CROP IMPROVEMENT

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Amino acid transporters (AATs) play a key in plant growth, development, and stress tolerance. In the present study, five AtAVT6 genes (AtAVT6A to AtAVT6E) were functionally characterized. Time-course experiments were performed using qRT-PCR. The expression analysis demonstrated that the AtAVT6A was significantly induced in response to cold treatment, while AtAVT6B and AtAVT6C were induced under salt conditions. Additionally, AtAVT6C and AtAVT6E were induced upon heat treatment, while AtAVT6D was induced distinctly under drought stress. These results suggest the significance of AtAVT6 genes in Arabidopsis thaliana in response to abiotic stresses and hormone treatments. Further using transporter assay in xenopus we demonstrated that AtAVT6D is involved in transport of aspartate and glutamate. Transgenic plants overexpressing AtAVT6D showed small silique size but increased grain weight. Data obtained will be presented in the meeting.

0167-C

EFFECTS OF SEVEN RARE EARTH ELEMENTS ON THE GROWTH, PHOTOSYNTHETIC PIGMENTS, ASCORBATE CONTENT, AND LIPID PEROXIDATION LEVEL OF LEMNA MINOR L.

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Rare Earth elements (REE) have become essential in strategic sectors. Their increased use over the last decade has led to anthropogenic REE releases detectable in the environment. This study investigated morphological and biochemical effects of Ce, Nd, Gd, Dy, Ho, Yb, and Lu on Lemna minor L. that was grown under standard procedures and exposed at 0.1 and 1 mM. After 3, 7, and 12 days of treatment, different stress indicators were measured. Results showed that Ho, Lu, and Dy exerted the most toxic effect on the growth rate, while Ce and Yb, at a lower concentration, did not show significant effects. At low concentrations, REEs

had no or slight effect on the chlorophyll and carotenoid contents, while at 1 mM they caused a significant decrease in the pigment content at longer exposure times. Changes in ascorbate and lipid peroxidation also occurred. Because *L. minor* can accumulate REEs, it is important to have further studies on its importance in the bioremediation of aquatic ecosystems.

0168-A

COMPARISON OF SALINITY STRESS TOLERANCE AMONG LEAF AND SEED CULTIVARS OF RED AMARANTH (*AMARANTHUS CRUENTUS* L.)

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The current expansion of soil salinity is compromising agricultural production. There is a need to rely on crops able to produce food on saline soils. Amaranths (*Amaranthus* spp., Amaranthaceae) are C4 plants of which several species are cultivated either for their protein-rich seeds as pseudocereals or for their nutritious leaves. *A. cruentus*, used for both leaf and seed production, shows promise as a nutritious and multi-stress tolerant crop. Six seed and two leaf accessions were tested for salinity tolerance (0, 50 and 100 mM NaCl) at the vegetative stage under hydroponic conditions. Growth rate, photosynthetic activity and biomass production were monitored. Biomarkers and metabolites involved in stress tolerance were quantified in leaves and roots. The distribution in plants of several minerals, in particular sodium and potassium, was investigated. Our results allowed us to discriminate genotypes tolerant to 50 mM NaCl.

0169-B

GERMINATION AND GROWTH IN THE PRESENCE OF IMIDAZOLIUM BASED IONIC LIQUIDS

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The environmental safety of solvents tailored for specific purposes is still being questioned and explored. In this regard, a series of experiments was set up using 6 different synthesized and 1 commercial imidazolium-based ionic liquids (ILs), in order to test their effect on germination and early growth of wheat, barley, and cucumber. Seeds were exposed to either 0 (control), 10, 100, or 1000 mg/l of selected ILs during germination; seedlings were then transferred to pots containing complete nutrient solution and grown under controlled conditions. Substantial differences between the effect of the selected ILs on wheat, barley,

and cucumber were found. The tuning of the lipophilicity of imidazolium cations by introduction of polar groups in the alkyl side chain reduces toxicity with respect to the unsubstituted [bmim][Cl].

0170-C
DROUGHT-DERIVED PHYSIOLOGICAL METABOLISM IN WILD RICE RELATIVES UNDER DIFFERENT WATER POTENTIALS

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Drought due to climate change is a big concern for rice production. The 24 *Oryza* species, which have different habitats, have been discovered throughout the world, and this implies that rice plants are capable of being greater adaptability to various environments. In this study, we tried to understand responses from wild rice relatives under different levels of water potential (drought) compared to previously known drought-sensitive and tolerant cultivated rices. Two cultivar rice (*O. sativa* L. cv Gayabyeo, drought-sensitive; *O. sativa* L. cv. Sangnambatbyeo, drought tolerance) and three wild rice (*O. meridionalis*, *O. nivara*, *O. punctata*) were used in this study. Taken together all results (physiological and gene expression), it is estimated that *O. nivara* was drought-sensitive and *O. meridionalis* and *O. punctata* was drought-tolerant species.

0171-A
UNRAVELING AGO10-MEDIATED PLASTICITY IN RESPONSE TO ENVIRONMENTAL STIMULI

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In plants, shape generation depends on oriented cell divisions integrated with growth, developmental patterning, and genetically encoded cell fate determination. In the *Arabidopsis* root vasculature, ARGONAUTE10 (AGO10) is required for the control of formative cell divisions in the centre of the stele, since its loss leads to ectopic xylem strands, increased procambial cell number, and enhanced root growth. Modulation its expression might be involved in developmental response to environmental cues. It was shown that AGO10 is involved in response to water stress and required for adaptation to different nutrient regimes. Performing wound-inducing we found that ago10 mutants display increased lateral root numbers compared to WT. Our preliminary data indicate that ago10 is hypersensitive to cytokinin and jasmonic acid and shows increased variability during stress conditions. This suggest that AGO10 buffers hormonal responses during development and required for plant phenotypic robustness.

0172-B

EXPRESSION PATTERN ANALYSIS OF R2R3-MYB TRANSCRIPTION FACTORS FOR THE ANTHOCYANIN PRODUCTION IN DIFFERENT VEGETATIVE STAGES OF ARABIDOPSIS AND TOMATO LEAVES

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Anthocyanin is a type of flavonoid that appears purple in plants. PAP1, PAP2, and MYB113 are the three major R2R3-MYB transcription factors that regulate flavonoid biosynthesis in *Arabidopsis thaliana*. In this study, we found that the three MYB genes regulate anthocyanin accumulation in different leaf stages. Under limited nutrient conditions, PAP1 and PAP2 genes were highly induced in juvenile leaves. Conversely, MYB113 was expressed mainly in adult leaves. In addition, we investigated the role of trans-acting siRNA4 (TAS4) in the post-transcriptional regulation of anthocyanin expression in *Arabidopsis* leaves. In plant growth, the inhibition of PAP1 and PAP2 gene expression by TAS4 was observed only in juvenile leaves, and MYB113 inhibition was observed in adult leaves. Similar to *Arabidopsis*, the tomato R2R3-MYB transcription factor could differentially regulate anthocyanin accumulation in young and adult leaves.

0173-C GROWTH AND ANTIOXIDANT RESPONSES OF BARLEY UNDER DROUGHT AND CU CO-EXPOSURE – A TRADE-OFF AFFAIR?

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Climate change and industrialization increase the frequency and severity of stress, which seriously impact crop production and food security. Drought, the most limiting factor for plant growth, often occurs in scenarios of soil contamination by metals, like Cu. Thus, this study aimed at evaluating the combined effects of drought and Cu on *Hordeum vulgare* L. (barley plant). Data showed that the co-exposure was highly detrimental to plant growth, severely impacting photosynthesis by changing sugars and ABA metabolism. Also, drought and Cu differently affected ROS production, with their combination leading to higher oxidative damage. Curiously, the combined stresses also led to an investment in the barley plant's antioxidant defenses, particularly in leaves. Altogether, the interaction between drought and Cu suggests a trade-off effect between plant growth and energy allocation to defensive pathways.



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0174-A

IDENTIFICATION AND CHARACTERIZATION OF DROUGHT-INDUCED LONG NONCODING RNAs (DRILs) IN RICE

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Long noncoding RNAs (lncRNAs) act as transcriptional regulators in plants and animals. To date, they have been reported to regulate various biological processes, such as phosphate homeostasis, grain yield in rice. However, the lncRNAs involved in abiotic stress responses remain poorly identified. In this study, we analyzed the expression profiles of lncRNAs using public transcriptome datasets derived from abiotic stress-treated rice. We found that thousands of lncRNAs was significantly altered in the shoot and root tissues under different abiotic stresses (drought, salinity, low temperature, and ABA). We selected novel drought-induced lncRNAs (DRILs). Real-time PCR analysis revealed the differential expression of these DRILs under various stress conditions. The expression of abiotic stress-responsive genes was upregulated by transiently overexpressed DRIL1 and 4. Therefore, DRILs may be involved in the transcriptional regulation of abiotic stress-responsive genes in rice.

0175-B

IDENTIFICATION OF OXIDOREDUCTASE INVOLVED IN EARLY STEP PHYTOECDYSTEROIDS BIOSYNTHESIS IN SPINACH

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Phytoecdysteroids (PEs) are plant-derived ecdysteroids that are well-known as an insect molting hormone. 20-Hydroxyecdysone (20E) is a major PE and plays a defensive role to prevent feeding by phytophagous insect. Unlike insects, however, little is known about the 20E biosynthesis genes in plants. Therefore, this study was performed to identify oxidoreductase genes involved in the 20E biosynthesis of spinach (*Spinacia oleracea*). First, seven oxidoreductase genes were isolated as candidates through comparative transcriptome analysis of spinach samples with different 20E contents. Afterwards, through a loss-of-function study using the VIGS (virus-induced gene silencing) system, four oxidoreductase genes that showed a high correlation with changes in 20E content were identified. Furthermore, the predictive proteins of these four genes were found to dock near the active site with 7-dehydrogen cholesterol (7DC), one of the precursors of PEs biosynthesis.

0176-C

A ROLE FOR BZIP1/BZIP53 AND BZIP63 IN ENERGY HOMEOSTASIS IN ARABIDOPSIS

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Plant obtains their energy through photosynthesis and to ensure survival and reproduction they designed mechanisms to efficiently manage their energy resources. Two conserved kinases, Target of Rapamycin (TOR) and Sucrose-Non-Fermenting-1-Related (SnRK1) are sensors of the energy status and have antagonist functions. TOR promotes while SnRK1 limits growth under favorable and limited energy conditions, respectively. Phosphorylation of the bZIP type Transcription Factor bZIP63 by SnRK1 results in transcriptional reprogramming favoring adjustment to energy shortage. We have shown that this bZIP63-dependent reprogramming partly involves a cross regulation between bZIP63 and the circadian clock component PRR7. The heterodimerization of bZIP63 with bZIP1 and bZIP53 further refines this regulatory scheme. How these three bZIPs interact to maintain a balanced use of energy is not yet fully understood. Further insight into this aspect were obtained based on genetic evidence obtained from an analysis of single, double and triple mutants for bZIP1, bZIP53 and bZIP63 grown un different photoperiods and will be presented.

0177-A

GENES INVOLVED IN NITROGEN REMOBILIZATION DURING DARK AND LIGHT CONDITIONS IN BARLEY LEAVES

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Leaf senescence is a highly controlled process aimed at the remobilization of resources, including nitrogen. To study the survival strategy behind leaf senescence dark-induced leaf senescence (DILS) model was applied. Using bioinformatics and functional genomics we identified and analyzed the expression profiles of nitrogen metabolism pathway genes in barley (HvNMPs), an important cereal crop, to better understand their roles in metabolic remobilization during senescence. We identified 14 NMPs (HvARGAH, HvOCT, HvNOS-like, HvALDH10-1 and 10-2, HvGABA-T1 and T2, HvGAD1, 2, 3, 4, HvNiR, HvNR1 and 2). In light, most NMPs were upregulated except for HvARGAH and HvNOS-like which were downregulated. During DILS the expression of the genes was decreased except for HvGABA-T1 which was upregulated. The results broaden our knowledge of stress acclimation in barley, focusing on remobilization process during leaf senescence.

Work was supported by the National Science Centre PL (2017/27/B/NZ9/02135)

0178-B

DROUGHT-INDUCED CHANGES IN MULTISPECTRAL TRAITS OF COMMON BEAN

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Due to rapid climate change, drought is becoming a major problem for food production. The aim of this study was to investigate the effect of drought on the multispectral traits of common bean. Twenty plants were grown in PVC tubes filled with washed and dried quartz sand. All plants were irrigated with 25 mL of Hoagland solution and 25 ml of water. Plants from water deficit treatment had no additional irrigation, whereas plants from control treatment were irrigated throughout the experiment. Multispectral imaging was carried out on the eighth day of the experiment using the CropReporter (PhenoVation B.V., Wageningen). Drought treatment significantly decreased reflectance in red (7.4%), green (20.1%), specific green (22.5%), far red (15.3%), saturation (28.3%), value (20.2%), near infra-red (4.2%), green leaf index (48.8%) and normalized differential vegetation index (15.6%), and increased reflection in blue (8.0%), hue (4.1%), anthocyanin index (40.8%) and chlorophyll index (19.1%).

0179-C

UNRAVELING THE ROLE OF PROLINE IN GLYPHOSATE-MEDIATED TOXICITY – TOLERANCE MECHANISM OR STRESS SIGNAL?

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The cumulative use of glyphosate (GLY) has been resulting in soil contamination scenarios. Once uptaken by non-target plants, GLY impairs growth and disrupts the redox homeostasis, paired with an overaccumulation of proline (Pro). This study aims at unravelling whether Pro accumulation in response to GLY is a tolerance mechanism or a stress symptom, using Arabidopsis T-DNA mutants of Pro pathway-related genes (p5cs1-1, p5cs1-4, and prodh). Upon 14 d of growth, a substantial decrease in fresh biomass, accompanied by an increase in H₂O₂ and lipid peroxidation, in both WT and mutants with high Pro levels (prodh) was found. In contrast, Pro deficient mutants (p5cs1-1 and p5cs1-4) evidenced a prompt activation of the antioxidant system (higher GSH and AsA contents, and antioxidant enzymes' activity), preventing oxidative damage and reducing GLY-induced growth inhibition. Overall, data suggest that Pro overaccumulation is being perceived as a stress signal rather than a defence mechanism.

0180-A

COMPARATIVE STUDY OF PHOTOSYNTHESIS PERFORMANCE OF HERBICIDE-TREATED YOUNG TRITICALE SEEDLINGS UNDER DROUGHT AND FLOODING STRESS

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We assessed the photosynthesis performance of young triticale plants pretreated with the herbicide Serrate® (Syngenta), and subjected to drought or flooding for 7 days and then for 4 days of recovery. The photosynthesis-related parameters in Serrate-treated plants did not show significant alterations except in leaf pigments during the recovery phase. Both drought and flooding caused a significant reduction in gas exchange parameters, Fv/Fm and Fv/F0 values and leaf pigments during the stress period, and the decrease was most pronounced due to drought. After restoring the normal irrigation, the photosynthesis and fluorescence parameters tended to increase which is indicating a recovery of plants. The comparative assessment of photosynthesis-related parameters demonstrated that triticale plants subjected to flooding are recovering better than plants subjected to drought stress
Acknowledgements: This work was supported by Grant KP-06-H36/3-30.09.2020, Bulgarian National Science Fund.

0181-B
TRANSCRIPTOME ANALYSIS OF ATDSS1 MUTANTS IN RESPONSE TO OXIDATIVE STRESS

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DSS1 (deletion of split hand/split foot 1) is a highly conserved, eukaryotic, and multifunctional protein. DSS1 as a small intrinsically disordered protein binds to multiple proteins when it gains a final conformation. There are two highly homologous genes, DSS1(I) and DSS1(V) in the Arabidopsis genome. Our aim is to examine Atdss1 mutants through oxidative stress. We obtained separate stable lines of Arabidopsis containing mutations in DSS1s using CRISPR/Cas9 technology. After H₂O₂ treatment, mutant seedlings showed increased sensitivity to oxidative stress in comparison to WT plants. Transcriptome analysis showed that dss1(I)del25 and dss1(V)ins18 mutations caused 2762 and 2335 differentially expressed genes compared to WT under oxidative stress, respectively. We found that upregulated expression was in genes involved in homologue recombination and RNA transport in both dss1 lines. The most downregulated genes are classified into flavonoid biosynthesis and MAPK signaling pathway.

0182-C
DYNAMICS OF THE MEMBRANE PROTEOME OF ARABIDOPSIS THALIANA ROOTS IN RESPONSE TO URANIUM STRESS

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Uranium (U) is a non-essential and toxic metal to living plants. Yet, plants are able to take up U naturally present in the soil and accumulate uranyl ions preferentially in the root cell wall

and the apoplast. However, molecular targets of U are still poorly identified, and proteomic analyses have only focused on the soluble proteome of plants. To gain a more complete picture of the plant proteome dynamics, here we studied effects of U (i.e. 5 μ M and 50 μ M) on root membrane proteins from *Arabidopsis thaliana* using a label free quantitative proteomic workflow based on a nanoLC-MS/MS approach. By this method, we identified 466 differentially regulated proteins after U exposure. Data interpretation revealed that U primarily interferes with membrane-bound enzymes and transporters associated with amino acid metabolism, water transport, intercellular junction assembly and endosome organization. These results provide new insights into the phytotoxic action of U.

0183-A

INVOLVEMENT OF ARABINOGLACTAN PROTEINS IN ARABIDOPSIS THALIANA ROOT RESPONSE TO OSMOTIC AND SALT STRESS

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Arabinogalactan proteins (AGPs) are plant cell wall hydroxyproline-rich glycoproteins that play a key role in diverse plant functions such as root interactions with microorganisms. At the root tip, border cells are released along with a thick mucilage forming the “Root Extracellular Trap” (RET) which contains various glyco-polymers including AGPs. AGPs in the RET were shown to modulate root biotic interactions within the rhizosphere. Meanwhile, their function in abiotic stress regulation is still unclear. The objective of the present study is to investigate the role of AGPs in *Arabidopsis thaliana* under osmotic and salt stresses. By using biochemical and cell imaging approaches, the response of different mutants affected in the biosynthesis of AGPs is studied. The effects of stress on seedling growth, root morphology and RET are investigated. The most affected mutants will be further studied to better understand the role of root AGPs in abiotic stress tolerance.

0184-B

LEAD AND ZINC TOLERANCE AND ACCUMULATION IN METALLICOLOUS AND NON-METALLICOLOUS POPULATIONS OF PEGANUM HARMALA L: POTENTIAL USE IN PHYTOSTABILIZATION

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The medicinal plant *Peganum harmala* L. grows in eastern Morocco including heavy metals (HM) contaminated soils. This work aims to compare the effect of lead and zinc (Pb, Zn) on growth, physiological, antioxidant enzyme activity and Pb/Zn accumulation capacity between non-metallicolous (NMP) and 3 metallicolous (MP) populations of *P. harmala*. Plants were hydroponically grown for 15 days with HM. Results showed that Pb and Zn reduced the aboveground biomass in all populations except Zaida-MP and roots biomass in NMP compared to MPs. Pb and Zn increased Proline content, CAT, SOD, and APX activity in NMP compared to MP. Pb increased anthocyanin content only in Zaida-MP. NMP accumulated Pb and Zn both in roots and shoots more than MPs, showing that NMP accumulates higher but tolerates less than MP. Zaida-MP accumulates less amount of Pb and Zn in their tissues and tolerates more than the other populations. This suggests Zaida-MP of *P. harmala* as the ideal population for phytostabilization.

0185-C

CLIMATE-TOLERANT, BIOFORTIFIED CARROTS: A SUSTAINABLE MICRONUTRIENT-RICH HIGH-VALUE CROP TO ENHANCE FOOD SECURITY

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Carrots (*Daucus carota* L.) are one of the most widely grown and enjoyed root vegetables in the world, and one of the richest sources of vitamin A. But like most crops, abiotic stress (especially drought) is one of the largest challenges limiting facing carrot growers and it significantly reduces crop productivity by 50% or more. Biofortification is a sustainable technique to curb malnutrition and diseases and alleviate micronutrient deficiencies. This project aims to identify drought-tolerant carrot genotypes and RNA sequencing to provide candidate genes responsible for drought tolerance in carrots. A comprehensive set of physiological experiments was carried out which identified 27 drought-tolerant carrot genotypes. RNA sequencing provided a significant number of differentially expressed transcripts in carrots in response to drought. This research will establish a foundation for a sustainable source of climate-tolerant, biofortified micronutrient-rich carrots to enhance food security.

0186-A

BIOCHEMICAL ALTERATIONS IN TRITICALE SEEDLINGS PRETREATED WITH SELECTIVE HERBICIDE AND SUBJECTED TO DROUGHT OR WATERLOGGING STRESS

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Triticale is a relatively tolerant crop to stress. Serrate® (Syngenta) is selective herbicide against annual grass and broadleaf weeds in triticale field. Young triticale plants grown as soil culture were sprayed with Serrate, then water stress was applied for 7 days, and finally the seedlings were left for 4 days of recovery. The selected biochemical parameters as content of stress markers and non-enzymatic antioxidants, and activities of antioxidant and herbicide-detoxifying enzymes were analyzed at 96h, 168h of stress, and at 96h of recovery. Serrate did not cause distinct alterations in the antioxidant defence, confirming that triticale is tolerant. Drought stress provoked more pronounced changes in the measured parameters. During the recovery, biochemical parameters tended to reach the control levels, and plants recovered better after waterlogging.

Acknowledgments. This study was supported financially by grant KP-06-N36/3 (30.09.2020) of Bulgarian National Science Fund.

0187-B

GENETIC ANALYSIS OF THE RICE JASMONATE RECEPTORS REVEALS SPECIALIZED FUNCTION FOR OSCO12

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Jasmonate (JA) regulates plant growth, development and stress responses. Coronatine insensitive 1 (COI1) protein is a receptor for jasmonoyl-L-isoleucine (JA-Ile), a biologically active form of JA. Monocots such as rice possess three COI genes, namely OsCO1a, OsCO1b and OsCO12 due to gene duplication. To assess the function of OsCO12 and its functional redundancy with the OsCO1 genes, we developed a series of rice mutants in the 3 JA receptors via CRISPR Cas9 and characterized their phenotype and their responses to jasmonate.

Characterization of OsCO12 revealed important roles in root growth, male sterility and leaf cell death. Collectively, these results indicate a specialized function of OsCO12 in the regulation of plant development in rice and indicate that subfunctionalization of JA receptors has occurred in the monocot phylum.

0188-C

IMPACT OF CADMIUM AND ZINC ON HEMP (CANNABIS SATIVA) HYPOCOTYLS: IMAGING AND TRANSCRIPTOMICS APPROACHES TO ASSESS THE ROLE OF SILICON

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Cannabis sativa produces bast fibres used in the construction sector, as well as for biocomposites and geotextiles. Bast fibre formation can be studied in the hemp hypocotyl, where elongation and radial thickening are temporally separated. Imaging and transcriptomics were here performed on hemp hypocotyls to understand the impact of cadmium and zinc on bast fibres and to assess the effect of silicon. Cadmium and zinc affected the morphology of bast fibres whose lumen was smaller and gelatinous cell walls thicker. With silicon, the lumen and cell walls of the fibres in the presence of cadmium and zinc were wider and thinner. Transmission electron microscopy confirmed the effects of silicon on bast fibres. RNA-Seq revealed the presence of specific transcriptomic signatures in control hypocotyls and those exposed to cadmium or zinc, in the absence and presence of silicon. The Principal Component Analysis showed 6 groups corresponding to each of the conditions studied.

0189-A

HERBICIDE PRE-TREATMENT PROVOKES DIFFERENTIAL ADAPTIVE RESPONSES TOWARDS DROUGHT AND FLOODING IN WHEAT AND TRITICALE

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The cross-adaptation of wheat and triticale exposed to drought and flooding was evaluated after treatment with a selective herbicide. The observed changes in the physiological status of the stressed plants revealed the ambivalent effects of herbicide priming in the two tested crops. Histochemical staining for ROS detection and transcript profiling of ROS scavenging enzymes were employed for the comparative analyses of stressed and recovered plants. Transcript accumulation exhibited crop-specific variations as a result of the combined treatments. The upregulation of L-Proline biosynthesis genes in drought-stressed individuals was more pronounced in wheat. The accumulated data suggest that commonly used weed-managing products could be beneficial for plant resilience under certain conditions but their use may also have negative consequences depending on the crop and stress type

Acknowledgments

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0190-B

ARABIDOPSIS CELL SUSPENSION CULTURE AND RNA SEQUENCING REVEAL REGULATORY NETWORKS UNDERLYING PLANT PROGRAMMED CELL DEATH.

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Programmed cell death (PCD) is an essential component of plant development and can also mediate responses to abiotic and biotic stress. However, studying the transcriptional regulation of PCD in plants is hindered by difficulties in sampling small groups of dying cells that are often buried within the bulk of living tissue. We addressed this challenge by using RNA sequencing of *A. thaliana* suspension cells, a system that allows precise monitoring of PCD activation and progression. The use of three PCD-inducing treatments in combination with three cell death inhibitors allowed isolation of 'core' and stimuli-specific PCD genes, inference of underlying gene regulatory networks and identification of putative transcriptional regulators. Further, phenotyping of *Arabidopsis* T-DNA insertion mutants in selected candidate genes confirmed a role for several in PCD and stress tolerance regulation, and validated the potential of these resources to identify novel genes involved in PCD pathways.

0191-C

DROUGHT RESPONSE OF GENE EDITED CAMELINA SATIVA MUTANTS MODIFIED FOR FLOWERING PRECOCITY AND ARCHITECTURE TRAITS

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Camelina sativa is an ancient native oilseed species that has broad environmental adaptability, low-input requirements, resistance to multiple stresses with diverse applications. Its potential use in agroecological transition with double cropping systems drive specific breeding strategy in particular by further shortening its life cycle. Multiplex edition by CRISPR/Cas9 of flowering time genes *SVP*, *TFL1*, *LHP1*, *EFL3* and *FLC* generated combinatory mutations leading to flowering precocity and shoot architecture changes. We characterised the phenotype of these mutants in response to drought and showed that their flowering time was not affected contrary to branching. Untargeted metabolomics was also carried out to investigate whether flowering mutations could modify specialized metabolite profiles upon drought. Understanding the interaction between flowering and stress response will be of importance to better design resilient crops adapted to agroecological transition and climate change.

0192-A

ALTERED GROWTH AND AUXIN METABOLISM IN HEAT-STRESSED ARABIDOPSIS WITH MODIFIED DMS3 EXPRESSION

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DMS3 protein is a component of RNA-directed DNA methylation that regulates genome integrity and gene expression. *Arabidopsis thaliana* wild type (wt), line overexpressing DMS3 protein (oeDMS3), and line with non-functional DMS3 protein (dms3 1) were exposed to 40 °C for 6 h at two developmental stages – two (2L) and eight-leaf stage (8L) or both (2L+8L). Projected leaf area (APT) was measured for 12 days, while auxin metabolite profile and biomass were determined 2 and 9 days after the last treatment, respectively. Compared with wt, oeDMS3 had lower APT and biomass at 2L, while heat-treated dms3 1 showed no significant changes but in general had lower APT and biomass. Auxin metabolism of oeDMS3 and dms3 1 was affected differently, with lower ANT (anthranilate) and higher oxIAA (2-oxoindole-3-acetic acid) in oeDMS3 at 2L+8L, and higher ANT and oxIAA in dms3-1 at 2L. Results suggest that DMS3 is involved in plant growth and auxin metabolism under both optimal and heat stress conditions.

0193-B

OPTIMIZATION OF TOBACCO RATTLE VIRUS-BASED VIRUS-INDUCED GENE SILENCING SYSTEM IN SPINACH

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Virus-induced gene silencing (VIGS) is an effective tool for studying gene function in spinach. To develop a more reliable VIGS system, we optimized agrobacterium strains and densities and inoculation methods based on the previously reported tobacco rattle virus (TRV)-based VIGS system in spinach. The agrobacterium strains such as GV2260, EHA105, and LBA4404 were evaluated, and among which GV2260 was the most effective, followed by EHA105 and LBA4404. The agrobacterium density was evaluated with OD600 of 0.5, 0.8, 1.0, and 1.5 using the GV2260, and all other densities except 1.5 (approximately 60% reduction) were found to reduce gene expression by more than 80%. The infection method was evaluated with agrobacterium GV2260 (OD600=1.0) for syringe infiltration, wound infiltration (sand paper), and agrodrench, among which syringe infiltration was the most effective, and the other two were found to be very inefficient compared to syringe infiltration.

0194-C

A MELATONIN-ENRICHED BIOSTIMULATOR EFFICIENTLY IMPROVES SOLANUM LYCOPERSICUM SEED GERMINATION VIA UPREGULATING ANTIOXIDANTS AND THE EXPRESSION OF GENES RELATED TO SALT STRESS TOLERANCE



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Bee-honey(BH), as a multi-biostimulator, has been involved in modulating plant development and adaptation to drought and salt stress, but is poor in melatonin(MT). However, there are no research works on the impact of MT-enriched BH(BH-MT) on germination of tomato seeds under salt stress(Sst). This study reported significant increases salt stress tolerance in germinated tomato seeds by treating the seeds with BH-MT. Sst considerably decreased seed germination, germination index, germination energy, radical length. Conversely, Sst noticeably increased starch content, Enzymatic activities, soluble protein, free proline, glutathione, and MT contents. Enzymatic activities, antioxidant contents, and gene expressions were elevated due to elevated levels of oxidative stress biomarkers. As a result, a significant reduction in H₂O₂, O₂^{•-}, MDA was evidently noticed. The above findings indicate the use of BH-MT, as a multi-biocatalyst, to improve salt stress tolerance in tomato seeds.

Keywords: tomato; biostimulants; seed germination; salt stress; antioxidant capacity; gene expression

0915-B

ENDOSPERM CELLULARIZATION FAILURE INDUCES A DEHYDRATION-STRESS RESPONSE LEADING TO EMBRYO ARREST

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In Arabidopsis, crosses between diploid maternal plants and tetraploid pollen donors give rise to triploid seeds containing embryos that arrest at the torpedo stage of seed development surrounded by a largely uncellularized endosperm. The resulting seeds collapse and fail to germinate, a phenomenon that has been termed the “triploid block”. In this study, we performed transcriptome analyses of triploid torpedo-stage Arabidopsis embryos isolated from seeds containing cellularized and uncellularized endosperm. We found that embryos surrounded by an uncellularized endosperm elicited an osmotic stress response that was connected with abscisic acid (ABA) synthesis and signaling pathway. Inhibited ABA synthesis and signaling aggravated the triploid block, while increasing endogenous ABA levels or the exogenous application of ABA-induced endosperm cellularization and suppressed the triploid block, revealing a role for ABA in endosperm-mediated embryo arrest.

0196-B

COMPARATIVE ANALYSIS RADIOSENSITIVITY IN RADIOTOLERANT A. THALIANA AND RADIOSENSITIVE NORWAY SPRUCE (PICEA ABIES) SHOWED DIFFERENTIAL MOBILIZATION OF MOLECULAR PATHWAYS ASSOCIATED WITH DEFENCE, PROTECTION AND STRESS RESPONSES IN GAMMA RADIATION EXPOSURE.



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Radiosensitivity is highly variable in plants. We aimed to explore the basis of differential radiosensitivity in *A. thaliana* and Norway spruce by comparing their physiological, cellular, and molecular responses to gamma radiation. Plant's exposure to 48 h of gamma resulted in growth inhibition only in Norway spruce at 290 mGyh⁻¹ and damaged organelles in Norway spruce at ≥ 1 mGy h⁻¹, but only slight mitochondrial damage in *A. thaliana* at ≥ 100 mGy h⁻¹. Persistent dose dependent DNA-damage was observed in both species, but significantly more in Norway spruce. Comparative RNA-seq revealed upregulation of DNA damage repair, antioxidants, hormones, and cell wall components at ≥ 1 mGy h⁻¹ in *A. thaliana*, but in Norway spruce, DNA damage repair, chromatin remodelers and antioxidants were upregulated at ≥ 40 mGy h⁻¹. To conclude, *A. thaliana*, efficiently activates crucial pathways at low doses of gamma and showed radiotolerance, while Norway spruce appeared less responsive and radiosensitive.

0197-C
ENHANCEMENT OF PARAQUAT AND DROUGHT TOLERANCE BY SMALL PARAQUAT RESISTANCE PROTEINS

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The Small Paraquat resistance protein (SPQ) of the halophytic plant *Lepidium crassifolium* was shown to confer paraquat resistance to overexpressing Arabidopsis plants. SPQ-type genes are present in all plant genomes but have barely been characterized. Overexpression of the Arabidopsis SPQ can also enhance resistance to paraquat, while the Arabidopsis insertion mutant is slightly hypersensitive. Overexpression of SPQs enhanced sensitivity to abscisic acid and could improve drought tolerance by reducing water loss, stabilizing photosynthetic electron transport, reducing oxidative damage and enhancing plant viability in a water-limited environment. Enhanced drought tolerance could be confirmed by characterizing parameters of growth, morphology and photosynthesis with a plant phenotyping platform using RGB and chlorophyll fluorescence imaging. Our results suggest that plant SPQs can connect ROS and ABA signalling and through that influence responses to environmental stresses.

0198-A

SNRK2.10 KINASE DIFFERENTIALLY MODULATES EXPRESSION OF HUB WRKY TRANSCRIPTION FACTORS GENES UNDER SALINITY AND OXIDATIVE STRESS IN ARABIDOPSIS THALIANA.

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In the plant cell, information about changes occurring in the surrounding is transmitted to the nucleus by multiple phosphorylation cascades, e.g., by SNF1-Related protein Kinases type 2 (SnRK2s) which are key players in response to water deprivation. The first wave of ROS produced under salinity is involved in triggering signaling required for the fast stress response. Here we established that salinity or plant treatment with H₂O₂ or methyl viologen induced the expression of several TFs from WRKY family. WRKY expression was affected by SnRK2.10 kinase in a stress-specific manner. Finally, we present a bioinformatics analysis of identified WRKY targets and visualization of the intracellular distribution of H₂O₂.

Our results indicate that the stress-related functioning of SnRK2.10 is fine-tuned by the source and intracellular distribution of ROS and the co-occurrence of other stress factors, thus SnRK2.10-dependent signaling displays high plasticity and variable specificity.

0199-B

MOLECULAR RESPONSE OF FRAGARIA VESCA TO DIFFERENT ENVIRONMENTAL CONDITIONS

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The scientific community has been warning about climate change for several years. The year 2022, when high temperatures accompanied by drought were recorded throughout Europe, became a stark warning for society. *Fragaria vesca* was chosen as a model and cultivated at different soil moisture levels and maximum daily temperatures of up to 35 °C. We used advanced molecular biology and mass spectrometry to analyse molecular processes (metabolome, hormone, lipidome and proteome). Our results showed that individual parts of the plant (leaves, petioles and roots) react differently to the ambient conditions. We observed the modulations of protein levels, hormones or ROS metabolism within the plant. Furthermore, we monitored the changes in the key metabolites (pipecolic acid, N-hydroxy pipecolic acid, alpha-, beta- and gamma-aminobutyric acid), which play important roles in plant defence against pathogens. These results show new crosstalk between responses to abiotic and biotic stress.

0200-C

INVOLVEMENT OF THE ARABIDOPSIS-SPECIFIC MIR5628 IN THE PYL6-TRANSCRIPT DEGRADATION IN RESPONSE TO ABA

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ABA signaling is modulated by a negative feedback regulatory scheme. We observed a strong and sustained repression of the ABA receptors, PYR/PYL/RCARs (positive regulators), along a time course of ABA treatment, thus, defining the regulation of ABA receptors genes as a step in resetting the ABA signaling pathway. PYL1/4/5/6 mRNAs are degraded in response to ABA (cordycepin assay), and decapping may play a role in the control of PYL4/5/6 transcripts decay. In addition, the Arabidopsis-specific microRNA, miR5628, is transiently induced by the ABA signaling and guides PYL6-mRNA cleavage in response to ABA. Then, the exoribonuclease XRN4 may degrade the resulting RISC 5'- and 3'-cleaved fragments of PYL6 mRNA. Thus, control of the stability of PYR/PYL/RCAR transcripts is a fundamental step in maintaining homeostasis of ABA signaling.

SYNTHETIC BIOLOGY

0201-A

AN ECO-FRIENDLY METHOD TO SYNTHESIZE GOLD NANOPARTICLES IN PLANTS

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Nanoparticles (NPs) are utilized for various applications in medicine and agriculture. Currently, NPs are made by chemical synthesis, which utilizes few reagents toxic to the environment. A green technology method using alfalfa cells can be a sustainable alternative. Even though they are proven safer in living systems, their release into the environment and their applications need to be ratified. Different shapes and sizes of gold nanoparticles (AuNPs) were synthesized using living plants. AuNPs have other surface properties. Thus, we anticipate that results would support their various applications. In this work, AuNPs are synthesized, having different functional groups over their surface. These functional groups are used to coat AuNPs with multiple chemicals. These inherent surface properties of plant-synthesized AuNPs may be used to transfer certain chemicals to cells. Thus, the results demonstrate that plant-synthesized AuNPs could be used as efficient and promising nanocarriers.

0202-B

CHARACTERIZATION OF NADPH-CYTOCHROME P450 REDUCTASE GENE DRIVEN FROM TOMATO.

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Cytochrome P450 reductase (CPR) reacts as a redox partner and is essential for P450 enzyme reactions. Analysis of the tomato genome revealed that there are two CPR genes in tomato (SLCPR1 and SLCPR2). For enzymatic analysis, the SLCPRs were heterologously expressed in *E. coli* and purified using ADP-agarose affinity column. SLCPR1 showed high activity with protein substrate such as cytochrome c, whereas SLCPR2 had higher activity when reacted with chemical substrates such as MTT, Ferricyanide. And SLCPR1 was more stable to pH and heat than SLCPR2. Both SLCPRs were showed redox reaction with several plant P450 enzymes which are involved in hormone and secondary metabolites biosynthesis or degradation pathways. Collectively, we suggest that SLCPRs can be used for studying biological functions of plants P450s, also for applications of P450 responses, such as xenobiotic or drug metabolism studies.



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0203-C

MU TAILPIECE FUSED PLANT-DERIVED ACE2 (ACE2 MK) ENHANCED BINDING ACTIVITY AND INHIBITION OF SARS-COV-2

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COVID-19 is caused by SARS-CoV-2 and currently ongoing worldwide since the first outbreak. The ACE2 is known as a crucial cell entry receptor for SARS-CoV-2 infection. Inhibition of the interaction between SARS-CoV-2 and ACE2 has been proposed as an important target for the prevention and treatment of COVID-19. In this study, we produced four different structures of ACE2 protein with or without IgM mu tailpiece (μ tp) and KDEL motif in *N. benthamiana* plant for the enhancement of ACE2 activity. The binding activities between each ACE2 and RBD of SARS-CoV-2 including variants, or SARS-CoV-2 virus were investigated, and ACE2 fused with μ tp showed better binding activity. Importantly, ACE2 μ K exhibited better inhibition activity of SARS-CoV-2 infection than that of ACE2 without μ tp. These results provide evidence that plant-derived ACE2 μ K can be used as an agent involved in the inhibition of SARS-CoV-2 and that fusion of the μ tp can enhance the function of the protein.

THE GENETIC ARCHITECTURE OF QUANTITATIVE TRAITS IN PLANTS

0204-A

GENETICS CONTROL OF PHENOTYPIC PLASTICITY IN RESPONSE TO WATER DEFICIT IN PEARL MILLET

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Phenotypic plasticity (PP) refers to any change in characteristics of an organism in response to environmental cues. Drought is a factor that influences the response of phenotypes. We looked at genetic variation in PP of agro-morphological and root anatomical traits in a pearl millet diversity panel grown under well-watered and drought conditions for two years. The proportion of variance attributed to phenotypic plasticity (E), and the variation among genotypes (GxE) were greater for agromorphological traits. The GxE effect was significant for metaxylem size and number of vessels. Relative distance plasticity index and linear regression analysis were used to calculate plasticity metrics. A large variability for these was observed. Finally, genetic association analyses revealed genetic loci related to phenotypic plasticity. These associations pave the way for the identification of genes and physiological associated with root drought-induced plasticity and adaptation to future climates.

0205-B

HIGH-QUALITY GENOME ASSEMBLY AND GENETIC MAPPING REVEAL A GENE REGULATING FLESH COLOR IN WATERMELON (CITRULLUS LANATUS)

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Genome assemblies and genetic maps explained many molecular mechanisms in watermelon. Here, we assembled two Korean inbred watermelon genomes with unique color and fruit-type characteristics and sequenced their 87 F2 descendants that identified 1539 single-nucleotide polymorphisms and 80 InDel markers. Based on genetic mapping, 15 quantitative trait locus intervals for watermelon fruit quality-related traits were detected. By investigating these mapped intervals, we identified 33 candidate genes containing variants in the coding sequence. Among them, PSY1 was annotated as a phytoene synthase with a single-nucleotide



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variant in the first exon at 9539129 bp of chromosome 1 that resulted in the conversion of a lysine to glutamic acid, indicating that this gene might regulate flesh color changes at the protein level. These findings not only prove the importance of a phytoene synthase gene in pigmentation but also explain an important reason for the color change of watermelon flesh.

0206-C

ASSESSMENT OF RETAMA GENETIC DIVERSITY USING ISSR, REP, AND ITS-RFLP AND PHYLOGENY

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In this work, we assessed the genetic diversity among and within species of *Retama*, using ISSR and rep markers, and ITS phylogeny. Hence, a total of 48 and 18 bands were scored respectively for ISSR and rep, of which 83.33% and 88.89% were polymorphic. The polymorphic information content values were 0.70 with ISSR and 0.78 with the rep. The combined data AMOVA revealed lower variations among (25%) than within (75%) *Retama* species. The ITS sequences analysis revealed that *R. dasycarpa* has 99.83%, 99.01%, and 95.53% similarities with *R. monosperma*, *R. raetam*, and *R. sphaerocarpa* respectively. *Retama raetam* has 98.84, and 95.20 similarities with *R. monosperma* and *R. sphaerocarpa*. The ITS sequences phylogeny confirmed the close relatedness between *R. monosperma* and *R. dasycarpa* which were regrouped in the same cluster related to *R. raetam*. The principal coordinate analysis (PCoA) and the cluster analysis assembled the different samples into three groups.

0207-A

PATTERNS OF GENETIC AND METABOLIC VARIATIONS OF NEPETA NUDA L. IN THE CENTRAL BALKANS

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Numerous species belonging to the genus *Nepeta* are appreciated producers of various phenolic and iridoid compounds that have tremendously vast applicative value in pharmacology and agriculture but are also highly esteemed as chemotaxonomical markers. *Nepeta nuda* is a widespread Eurasian species, found in forest edges and clearings. We have collected leaf samples from 12 populations across the central Balkan Peninsula and investigated their genetic and phytochemical variations. We used 3 genomic and 7



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transcriptome-derived microsatellite markers and revealed relatively low variation within the populations. Both qualitative metabolite profiling of methanol extracts (Q-TOFF LC/MS) and essential oils (GC/MS) analysis pointed out to high inter- and intra-population variations, especially regarding the content of iridoids. A UHPLC-QQQ-MS/MS approach targeted towards quantification of the most abundant iridoids and phenolics was highly efficient in the diversification of *N. nuda* populations.

0208-B

HIGH-RESOLUTION MAPPING OF FRUIT AND LEAF METABOLISM USING THE TWO NEWLY DEVELOPED *S. PENNELLII* BILS POPULATIONS

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Exotic germplasm represents an important source for the expansion of the allelic diversity in inbred crop species. Here we aim to dissect the primary, secondary, and lipid metabolism using two newly developed tomato BILs populations by Zamir's lab. The two BILs populations are of unprecedented size and created from a cross between a newly discovered self-compatible accessions of tomato species *S. pennellii* (5240) and two divergent modern cultivated inbred lines (*S. lycopersicum* cv. LEA and TOP). Fruit and leaf materials from over 3000 BILs were harvested and subjected to comprehensive metabolite profiling using both GC-MS and LC-MS analysis. QTL results indicated that the mapping resolution is extremely high, with several novel QTL mapped to a single candidate gene. To understand the molecular mechanisms of some of the novel loci, putative candidate genes were selected for further biological validation through CRISPR-Cas9, overexpression, and/or virus-induced gene silencing (VIGS).

0209-C

GENETIC BASIS OF FLOWER SIZE PLASTICITY IN *ARABIDOPSIS THALIANA*

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Plasticity, the ability of an organism to adjust its' phenotype in different environments, provides a way for rapid adaptation. Nevertheless, genes controlling plasticity are still largely unknown. We have investigated the impact of temperature on flower size. Flower size has a central role in the reproductive strategy and therefore fitness of the plant. We grew 290 *Arabidopsis thaliana* accessions at 17 °C and 23 °C and quantified them for flower size plasticity. While on average, flowers were smaller at 23 °C, some accessions had larger flowers at the higher temperature. Using GWA analysis and candidate gene characterization, we showed that the MAF2-5 gene cluster underlies the temperature-mediated flower size



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plasticity in *A. thaliana*. The MAF2-5 gene cluster is known to control flowering time, yet our study provides a novel role for this gene cluster in flowers. Currently, we are testing the role of alternative splicing in regulating flower size plasticity.

THE GENETICS OF NATURAL VARIATION OF PLANT- PLANT INTERACTIONS

0210-A

THE MAIZE-BEAN ASSOCIATION, FIRST INSIGHTS FROM INTERCROPPING EXPERIMENTS

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The need for more sustainable agriculture has led to renewed interest in intercropping. To investigate the genetic bases of potential synergies in the cultivated association of maize (*Zea mays ssp. mays*) and climbing bean (*Phaseolus vulgaris*), we performed two field assays in France and in Romania, where 200 bean lines – including 21 still traditionally associated with maize – were all associated with three maize landraces – including one still traditionally associated with beans. We measured traits related to shoot and root development, yield, and disease incidence. Preliminary analyses revealed that the associated maize landraces, have a significant effect on bean root architecture and development. Interestingly, the maize landrace traditionally associated with beans allows both a higher density and a greater mean area of bean root system while the bean varieties traditionally associated with maize displayed less disease and higher tap branching density than other bean varieties.

0211-B

FORWARD GENETICS STRATEGIES TO ELUCIDATE THE E-2-HEXENAL PERCEPTION PATHWAY

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Recently, we have identified plant- and insect derived (3Z):(2E)-hexenal isomerases that change the composition of GLVs by converting Z-3-hexenal to E-2-hexenal. This change in the Z-3-/E-2-ratio affects the behavior of foraging predators and host-seeking herbivores. Additionally, plants can respond very specifically to single GLVs, including E-2-hexenal. However, it is still unknown how plants perceive volatile compounds and how the specificity of the volatile signal is transduced in the plant. To identify volatile receptors and other players involved in the early signaling response of plants we have used a classical mutagenesis screen and assessed natural variation in the Arabidopsis HapMap population. We identify novel E-2-hexenal response mutants to understand the role of these key volatiles in the plant's self-



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recognition and its interactions with herbivorous insects and pathogens. This will increase our understanding of the adaptive ability of plants to environmental stressors.

0212-C

LEVERAGING THE EVOLVE & RESEQUENCE APPROACH COUPLED WITH DECENTRALIZED RESEARCH TO ELUCIDATE CO-ADAPTATION BETWEEN SPECIES IN INTERCROPPING SYSTEMS

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Intercropping (IC) has been recognized to provide several agroecosystem services, as well as to support yield stability through the exploitation of ecological mechanisms. However, genetic bases of phenotypic traits involved in the process of plant-plant interactions and whole-genome patterns of co-adaptation are still unknown, which demand for an integrated and tailor-made approach when breeding for mixtures.

Within the Horizon 2020 project RADIANT, we set up an adaptive evolution experiment to unravel co-adaptation mechanisms in a maize/bean intercropping system, combining experimental evolution, whole-genome sequencing of pool of individuals (PoolSeq) and Participatory Plant Breeding (PPB).

The integration of results derived from further population genomics analysis (selective sweeps, causative variants, allelic/genotypic frequencies) with ones from experiments of the H2020 INCREASE project will contribute to the elucidation of genomic patterns of co-adaptation and mixing ability.

0213-A

PRECISION PHENOTYPING OF NECTAR-RELATED TRAITS USING X-RAY MICRO COMPUTED TOMOGRAPHY

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Flower morphology shapes the accessibility to nectar and pollen, two major traits that determine plant-pollinator interactions and reproductive success. Melon is an important crop whose reproduction is completely pollinator-dependent and as such is a valuable model for studying crop-ecological functions. High-resolution imaging techniques such as micro-computed tomography (μ CT) have recently become popular for phenotyping in plant science. Here, we implemented μ CT to study floral morphology and honey bees in the context of nectar-related traits. Compared to 2D imaging, μ CT can greatly improve phenotyping precision and aid our efforts in characterizing gene networks controlling nectary development. By combining data on flower morphology, honey bee size and nectar volume, this method can



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be used to assess flower accessibility to pollinators in high resolution and readily carry out genotypes comparative analysis to identify nectar-pollination-related traits.