Abstract booklet
& more

CROPADAPT2026

Enhancing multi-stress tolerance for crop resilience

ILVO
October 14 & 15, 2026
Ghent, Belgium

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What to expect?

CROPADAPT2026 brings together researchers, students, and professionals from across the plant community to explore how we can understand, develop, and enhance crop resilience under increasing multi-stress conditions.

Over two days, participants will discover the latest developments in crop resilience through keynote lectures, research presentations, poster sessions, and networking opportunities.

The scientific program is organized into four sessions:

- Session 1: Soil Health & Stress Management
- Session 2: Crop Protection: Strategies against Pests and Pathogens
- Session 3: Building Resilience through Plant Breeding and Plant Modification
- Session 4: Understanding Plant Reactions to Tomorrow's Challenges

Participants can look forward to a dynamic poster session showing emerging research, alongside several awards recognizing outstanding oral and poster presentations.

Beyond the scientific programme, CROPADAPT2026 provides a forum for researchers at all career stages to exchange ideas, build collaborations, and connect across disciplines. On the evening of 14 October, participants are invited to continue these conversations – scientific or otherwise - at the CROPADAPT2026 Social Dinner in the heart of Ghent. Enjoy locally inspired cuisine, live music and an informal evening of networking and good company. Advance registration is required.

On 15 October, attendees will also have the opportunity to participate in an exclusive scientific visit to the Flanders Research Institute for Agriculture, Fisheries and Food (ILVO) in Merelbeke-Melle. The visit will provide a behind-the-scenes look at cutting-edge research facilities, including greenhouses, field phenotyping platforms, and other infrastructure supporting innovative research on crop resilience and sustainable agriculture. Registration in advance is required.

CROPADAPT2026 offers a unique platform to engage with a vibrant international network of young scientists working towards more resilient and sustainable agricultural systems. More information about the event can be found on the website: Adapt to thrive - Cropadapt2026

We hope you leave Ghent with new knowledge, new collaborations, and fresh inspiration for your research.

Organizing committee

The symposium is organized by a team of early-career researchers from ILVO who share a common goal: advancing research and collaboration in crop resilience. Together, the committee brings diverse perspectives on crop resilience, ranging from soil processes and plant health to breeding, biotechnology, phenotyping, and artificial intelligence.

Members of the committee: *Andries Hermans, Arno Kasprzak, Eline Bil, Elke Vereecke, Falke Engelbeen, Idrissa Traore, Jeppe Van den Langenbergh, Laura Strickx, Len Gruyaert, Marlies Peeters, Micaela Cosgrove, Rémy Willemet, Ruth Hofman, Viktor Devlieghere, Brecht Nissenne, Jozefien Demeulenaere*

With CROPADAPT2026 being a part of the global Corteva Plant Sciences Symposia Series, Corteva has been a very important partner in organizing this symposium, together with our other sponsors. More information about the Corteva Plant Sciences Symposia Series can be found here: Corteva Agriscience Plant Sciences Symposia Series.

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ILVO
Flanders research institute for agriculture, fisheries and food

Program Day 1

12:00-13:00: Registration & Reception

13:00-13:30: Welcome by Flanders Research Institute for Agriculture, Fisheries and Food (ILVO) and Vylor

13:30-14:40: Session 1: Soil health & stress management

Chairs: Rémy Willemet | Sarah Garré

13:30: keynote - Jean-Thomas Cornelis (University of British Columbia)
From fertilization to metabolic reprogramming: harnessing soil nutrient stoichiometry to redirect plant carbon belowground

14:00: Speaker - Inge Speeckaert (ILVO)
Disentangling the nitrogen and non-nitrogen effect of legume pre-crops

14:20: Speaker - Jamil Hossain (Ghent University)
Growth and Yield Responses of Grass pea (*Lathyrus sativus L.*) to Combined Waterlogging and Soil Compaction Stress

14:40-15:40: break / poster session (session 1 - session 2)

15:40-17:30: Session 2: Crop Protection: Strategies against pests and pathogens

Chairs: Viktor Devlieghere | Kurt Heungens

15:40: keynote - Corné Pieterse (Utrecht University)
The extended plant immune system

16:10: speaker - Ellen Vandenbussche (Ghent University)
Polymer-based dsRNA delivery systems for RNAi applications against *Phytophthora infestans*

16:30: speaker - Ward Boven (KU Leuven)
Integrating plant defense elicitors and ontogenic resistance for pear scab management

16:50: speaker - Jari Temmermans (Antwerp University)
From citizen science to microbial biocontrol: discovering phyllosphere-adapted lactobacilli for sustainable biocontrol

17:10: speaker - Ibe Naessens (Ghent University)
Revisiting the role of the jasmonate pathway in plant defense against *Meloidogyne graminicola* in rice

Evening: social dinner *(registration required)*

Program Day 2

8:00-8:45: Registration & Welcome with coffee

8:45-10:15: Session 3: Building resilience through plant breeding and plant modification

Chair: Elke Vereecke | Katrijn Van Laere

8:45: keynote - Dr. Amine Batnini (Corteva Agriscience)
From Field Signals to Durable Resistance: Turning Pathology Intelligence into Breeding Decisions

9:15: speaker - Senne Van Den Broeck (KU Leuven)
Transgene-free genome editing in banana through Agrobacterium-mediated base editing strategy

9:35: speaker - Muhammad Awais Zahid (Swedish University of Agricultural Sciences)
Parakletos links immune signalling, environmental stress tolerance, and future potato resilience

9:55 speaker - Lucas Phillips (KU Leuven)
Heat-induced meiotic alterations and unreduced pollen formation in European pear (Pyrus communis)

10:15-11:10: break / poster session (session 3 – session 4)

11:10-12:40: Session 4: Understanding plant reactions to tomorrow's challenges

Chair: Ruth Hofman | Peter Lootens

11:10: keynote - Benjamin Dumont (University of Liège)
Using digital twins to support the design of resilient and sustainable agicultural systems

11:40: speaker - Avilien Dard (VIB-PSB UGent)
Glow with the flow

12:00: speaker - Idrissa Traore (ILVO)
Scaling up soybean nodulation phenotyping with NodQuant

12:20-12:30: closing talk - Willem Desmedt (ILVO)

12:30-12:40: Awards

12:40-13:45: Lunch

13:45-17:00: Scientific visit @ ILVO *(registration required)*

Venue

The symposium will take place at the Virginie Loveling Building, located within the VAC Gent (Vlaams Administratief Centrum) in Ghent, Belgium.

Adress:
Virginie Loveling Building (VAC Gent)
Koningin Maria Hendrikaplein 70
9000 Ghent

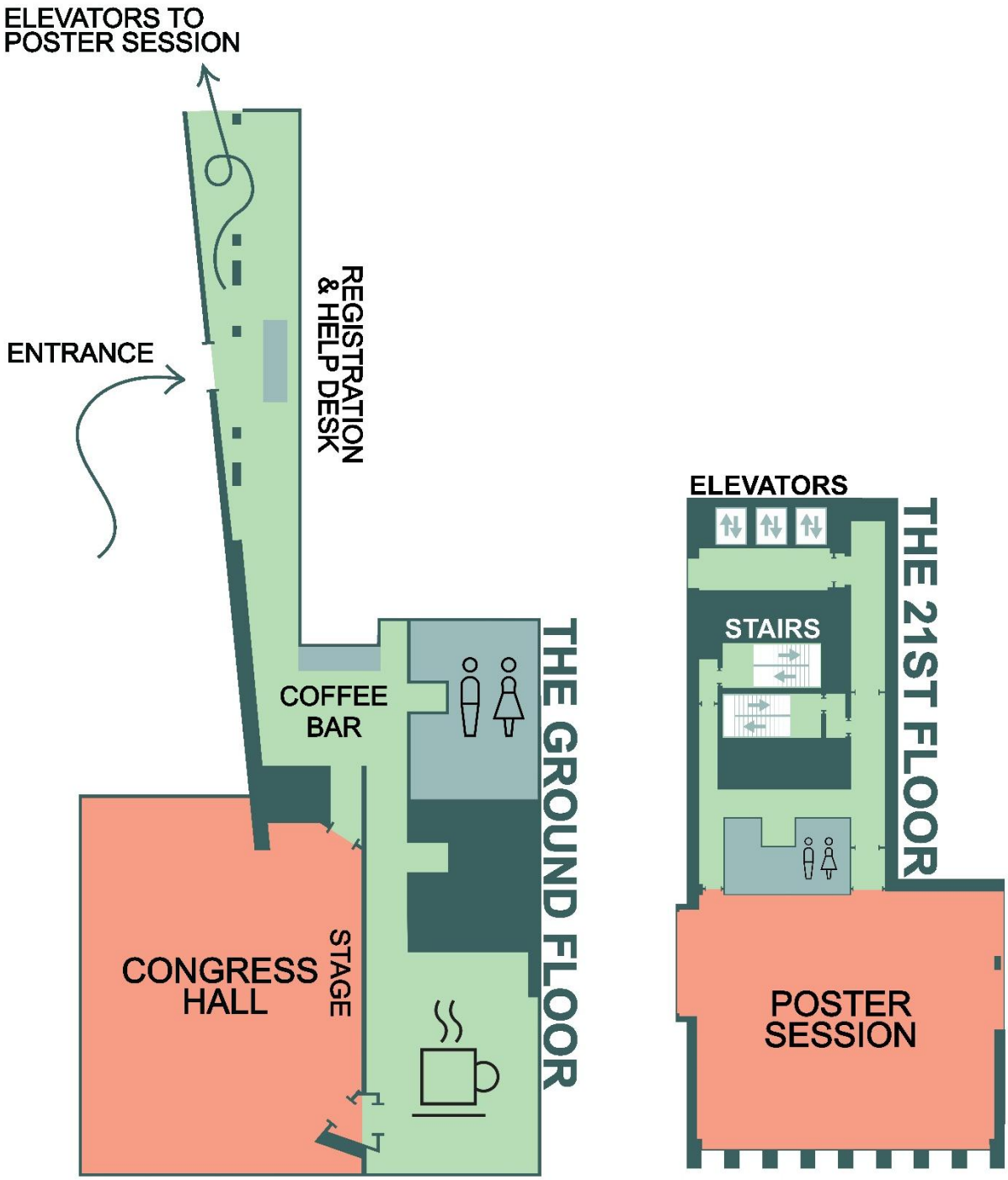
Entrance via the footbridge: You can reach the main entrance via the footbridge located above the bus and tram stops. Go through the revolving door, turn left, and follow the signs to the symposium.

How to get there?

By public transport:
This building is situated next to Gent-Sint-Pieters railway station, making it easily accessible either by train or by bus/tram (stop 'Sint-Pietersstation').

By car:
There is no free parking at the VAC. You can use the paid parking lot at the Gent Sint-Pieters station (electronic payment only).

Map of the venue



Social dinner

Only for the people who registered

The social dinner will take place at Madonna, located at **Poel 7, 9000 Ghent.** The reception **starts at 18:00**. We kindly ask you to arrive **no later than 18:30.**

If you are not travelling by car, you can either walk to the venue (± 40 minutes) or take the tram (± 25 minutes).

By foot:
We will walk together from the symposium venue to Madonna. If you would like to join us, please gather at the entrance of the auditorium at 17:45.

By tram:
You can take either tram 1 (T1) or tram 4 (T4). A tram ride costs €3. You can pay contactless with your bank card on the tram. Look for the white payment terminal inside the tram. Both tram lines operate in two directions, so please make sure you take:

T1 Gentbrugge Stelplaats

Take tram 1 from Gent Sint-Pietersstation, platform 2. The platform is located underneath the VAC building.
Get off at Gent Oude Houtlei. From there, it is approximately a 9-minute walk to Madonna.

T4 Gent Lange Steenstraat

Take tram 4 from Gent Sint-Pietersstation, platform 18. The platform is located directly in front of the station's main entrance.
Get off at Gent Theresianestraat. From there, it is approximately a 9-minute walk to Madonna.

By car:
You can park either on the street or in an underground car park. Please note that you need to pay in both cases. The closest underground car parks are Parking Ramen and Parking Sint-Michiels, which are both a 3-minute walk from Madonna.

ILVO visit

Only for the people who registered.

On the second day of CROPADAPT2026, participants will have the opportunity to visit the ILVO Plant Sciences unit and explore research facilities linked to the symposium's four scientific sessions.

After lunch, the group will travel by bus to ILVO, where participants will be divided into three groups for the visit.

The program will include two main stops:

- **ILVO P39** – focusing on Session 3: Building Resilience through Plant Breeding and Plant Modification and Session 4: Understanding Plant Reactions to Tomorrow's Challenges.
- **ILVO P109** – focusing on Session 1: Soil Health & Stress Management and Session 2: Crop Protection: Strategies Against Pests and Pathogens.

The visit offers a behind-the-scenes look at ILVO's research infrastructure and provides an opportunity to see how the themes discussed during CROPADAPT2026 are translated into hands-on research.

About ILVO

The Flanders Research Institute for Agriculture, Fisheries and Food, ILVO in short, is one of Belgium's leading scientific research institutes, dedicated to sustainable and innovative agriculture, horticulture, and food production. ILVO's research spans plant science, animal sciences, agriculture and society, and technology & food science which together cover the full breadth of challenges facing a sustainable and future-proof agri-food system.

The institute operates across multiple sites and shares an extensive research infrastructure, including over 200 hectares of trial fields, more than 15,000 m^2 of experimental greenhouses, and cutting-edge drone, robot, and sensor technology for precision agriculture. With over 650 employees, ILVO's Plant Sciences unit alone brings together nearly 220 researchers working across a range of disciplines.

Find out more at the ILVO website.

Abstracts: Session 1

Soil health & stress management

Keynote speaker (13:30 - 14:00)

From fertilization to metabolic reprogramming: harnessing soil nutrient stoichiometry to redirect plant carbon belowground

Jean-Thomas Cornelis (1)

(1) SoilRes3 Lab, Faculty of Land and Food Systems, University of British Columbia, Vancouver, Canada

Keywords: soil genesis, plant metabolism, root exudation, carbon flow

It is widely assumed that plant roots can locally respond to their soil nutrient environment by modulating the synthesis of bioactive chemicals, sometime referred as root local “sensing” or “signaling” abilities. Root development and activity can also be indirectly modulated through internal changes in shoot nutrient status and elemental stoichiometry, triggering systemic long-distance shoot-to-root signaling. These stoichiometric changes in the shoot induce cascading biochemical responses in shoot tissues, which in turn modulate the transfer of photosynthates from shoot to root. These shifts redirect metabolic fluxes toward the root system, promoting the exudation of compounds, the modification of root system architecture and/or the association with microorganisms that underpin beneficial plant–soil interactions. We propose that changes in root phenotypic and physiological responses are driven by shoot-level elemental stoichiometry that emerges from soil-forming processes and nutrient availability. These soil-shoot-root feedback loops offer promising avenues for targeting the stoichiometric nutrient balance in shoot tissues that triggers plant biochemical mechanisms optimizing root development and exudation processes. Those feedback mechanisms have been largely disrupted by conventional mineral fertilization practices designed to maximize grain production, often at the expense of root growth and activity that support plant resilience. Here we advocate for a shift from yield-maximizing fertilization toward a metabolic and stoichiometric framework, where soil nutrient availability and shoot elemental stoichiometry act as a regulator of plant metabolic pathways that partition carbon in root functions, thereby improving resilience in terrestrial ecosystem. Recognizing that phosphorus limitation can reconfigure central carbon metabolism through the activation of alternative, low-phosphorus-demand pathways that increase belowground carbon allocation and nutrient-acquisition processes, we build our framework on identifying the soil–plant stoichiometric conditions that favor such metabolic states. Rather than viewing these responses as purely adaptive optimization strategies, we propose that they emerge from fundamental biochemical constraints imposed by soil nutrient and water availability and elemental stoichiometry. We think the linkages between soil-forming processes and long-distance biochemical shoot-to-root signaling can help translate natural processes into land use practices that promote sustainability and resilience of terrestrial ecosystems. The primordial and critical step to achieve this goal is to target elemental concentration and stoichiometry that promote shoot-to-root fluxes of molecules that support root-microbial interactions.

Speaker (14:00 - 14:20)

Disentangling the nitrogen and non-nitrogen effect of legume pre-crops

Inge Speeckaert (1)(2), Joke Pannecoucque (2), Hilde Muylle (2), Steven Maenhout (1)

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(2) Plant Sciences Unit, Flanders Research Institute for Agriculture, Fisheries and Food, Melle, Belgium

Keywords: Legumes, pre-crop effect, nitrogen

Grain legumes play a key role in the transition towards more sustainable agroecological cropping systems. Their introduction into crop rotations provides both direct and indirect ecosystem services, commonly referred to as the 'nitrogen (N) effect' and the 'non-nitrogen (non-N) effect'. The N effect arises from the ability of legumes to increase N availability for subsequent crops through two main mechanisms: N-sparing, whereby legumes rely less on soil mineral N than non-legume pre-crops, leaving higher residual soil N after harvest, and the mineralisation of N-rich crop residues, which releases additional N during the growth of the subsequent crop. The non-N effect encompasses all non-N related benefits, such as an improved soil structure, enabling enhanced water retention and root penetration and an altered soil microbial community.

This study aims to quantify the relative contributions of N and non-N effects to the rotational benefits associated with grain legumes. At a conventional field site, cereals grown after legumes exhibited yield increases of 17-54% compared with cereals grown after cereal pre-crops, whereas no significant pre-crop effects were observed at an organic site. To estimate the N effect, the crop growth model STICS was used to simulate net N mineralisation during the growing season of the subsequent cereal crop following legume and non-legume pre-crops. Complementing this modelling approach, an N balance was derived from field measurements by accounting for changes in soil mineral N stocks, cereal N uptake, and fertiliser N inputs throughout the growing season. Components of the non-N effect were assessed by monitoring soil water stock using electromagnetic induction and characterising soil microbial diversity through metabarcoding. Variance partitioning will be applied to determine the relative contribution of N availability, soil water dynamics, and microbial community composition to the observed yield differences.

By disentangling the mechanisms underlying legume pre-crop benefits, this research will provide a better understanding of the relative importance of N and non-N effects of grain legumes as a pre-crop.

Speaker (14:20 - 14:40)

Growth and Yield Responses of Grass pea (Lathyrus sativus L.) to Combined Waterlogging and Soil Compaction Stress

Jamil Hossain (1)(2), Monirul Islam (1), Mohammad Mofizur Rahman Jahangir (3), Frank Van Breusegem (4)(5), Wim Cornelis (1)

(1) Department of Environment, SENSE Group, Ghent University, Ghent, Belgium
(2) Pulses Research Centre, Bangladesh Agricultural Research Institute (BARI), Bangladesh
(3) Department of Soil Science, Bangladesh Agricultural University, Mymensingh, Bangladesh
(4) Department of Plant Biotechnology and Bioinformatics, Ghent University, Ghent, Belgium
(5) VIB Center of Plant Systems Biology, Technologiepark 71, 9052 Ghent, Belgium

Keywords: Lathyrus sativus, waterlogging, soil compaction, yield

Grass pea (Lathyrus sativus L.) is an important climate-resilient grain legume widely cultivated in rice-based cropping systems of South Asia. However, unseasonal rainfall often causes waterlogging during the growing season, while the use of agricultural equipment for planting and harvesting under wet conditions and waterlogging increases soil compaction, exposing the crop to multiple abiotic stresses. Although the individual effects of waterlogging and soil compaction have been studied, information on their combined impacts on grass pea growth and productivity remains limited. This work aims to evaluate the combined effects of waterlogging and soil compaction stress on the phenology, growth, and yield of grass pea. Three genotypes (BK-2021, BARI Khesari-3, and BD-5635) were grown on two levels of soil compaction (SC) (1.4 and 1.6 g cm-3) with waterlogging (WL) and non-waterlogging (NWL) conditions, conducted in a pot experiment under glasshouse conditions at ILVO, Ghent, Belgium. Waterlogging was imposed for 8 days at 20 days after emergence. High soil compaction and WL stress significantly delayed flowering and maturity and reduced photosynthetic activity, dry matter accumulation, plant height, and the number of pods per plant compared with non-waterlogging and low soil compaction treatments. Consequently, seed yield was significantly influenced by waterlogging, soil compaction, genotypes, and their interaction. Among the tested genotypes, BARI Khesari-3 achieved the highest seed yield under low soil compaction, whereas BK-2021 exhibited the lowest yield under the combined stress of waterlogging and high soil compaction. These findings demonstrate that the combined waterlogging and soil compaction substantially reduce grass pea productivity and highlight BARI Khesari-3 as a promising genotype for cultivation and breeding in waterlogging-prone rice-based cropping systems.

Poster (P1)

Fertigation in potato cultivation as a sustainable irrigation and nitrogen fertilization strategy

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Keywords: Potato cultivation, irrigation, fertigation, nitrogen, climate change

1. Objectives

The trial evaluated whether fertigation and drip irrigation can maintain high potato yields and quality under drought and heat stress. Additional objectives were to reduce nitrate residues after harvest and improve nitrogen-use efficiency through targeted nutrient placement in the root zone.

2. Methods

2.1 Experimental setup

Fontane potatoes were planted on sandy soil on 28 April 2025. Six treatments were compared: a dry control, an irrigated control, split conventional fertilization, two fertigation strategies, and a reduced-fertilization treatment. Nitrogen rates ranged from 72 to 192 kg N/ha. Liquid nitrogen (Amnitra, 18% N) was applied through fertigation. All irrigated treatments received the same amount of water during the season.

2.3 Measurements and statistics

Every two weeks, plant sap and soil samples were collected to monitor nutrient status and soil nitrogen. Drone flights with a multispectral camera were performed to determine NDVI. At harvest, yield, underwater weight, tuber size distribution, and nitrate residues were determined. Data were analyzed with JASP.

3. Results

3.1 Nitrogen in soil and crop samples

Higher initial nitrogen applications resulted in higher soil nitrogen concentrations early in the season. Values converged from July onwards, except in the treatment receiving a late fertilizer application. Plant analyses showed no nitrogen deficiency in any treatment.

3.2 Crop yield and nitrate residue

Irrigated treatments produced higher yields (77–84 t/ha) than the dry control (62 t/ha), with no significant differences among irrigation strategies. Fertigation maintained yield with lower nitrogen inputs and resulted in the lowest nitrate residues (56–58 kg N/ha), while late nitrogen application increased residues (108 kg N/ha). Tuber quality was unaffected.

3.3 Normalized Difference Vegetation Index (NDVI)

Crops receiving all nitrogen at planting showed lower canopy vigor, while fertigated crops maintained greener and more vigorous foliage for longer.

4. Conclusion

Fertigation combined with drip irrigation maintained high potato yields while reducing residual soil nitrate. Targeted nitrogen applications improved nutrient-use efficiency and allowed lower fertilizer inputs without loss of productivity. In contrast, late fertilization increased nitrate residues. These results confirm fertigation as a promising strategy for sustainable and climate-resilient potato production.

Poster (P3)

Plant Growth-Promoting Rhizobacteria Strains Alleviate Lead-Induced Stress in Strawberry

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Keywords: Heavy metal, PGPR, Pseudomons sp., abiotic stress, bacterial mitigation

Lead (Pb) contamination is one of the major environmental constraints limiting sustainable strawberry production by impairing plant growth, physiology, anatomy, and fruit quality. This study investigated the detrimental effects of Pb stress and the potential mitigating role of three plant growth-promoting Pseudomonas strains (Pseudomonas fragi MS-7, P. lactis MS-12, and P. canadensis MS-13) in three strawberry cultivars (Rubygem, Kabarla, and YFL). Plants were exposed to 0, 500, and 1500 mg kg^{-1} Pb, and morphological, physiological, anatomical, pomological, and Pb accumulation parameters were evaluated.

Lead treatment adversely affected most of the investigated traits, reducing vegetative growth and fruit performance while increasing Pb accumulation in plant tissues. The severity of Pb toxicity differed among cultivars, with YFL exhibiting the highest susceptibility and greatest Pb accumulation. In contrast, Rubygem accumulated comparatively lower amounts of Pb, whereas Kabarla showed relatively higher Pb translocation to leaves. Bacterial inoculation alleviated Pb-induced damage across most evaluated parameters. Among the tested strains, MS-7 was the most effective in reducing Pb uptake, restricting its translocation to aerial tissues, and lowering the translocation factor. Meanwhile, MS-12 and MS-13 provided broader improvements in plant growth and physiological performance under Pb stress. These beneficial effects were also reflected in the partial restoration of leaf anatomical characteristics, indicating an overall enhancement of plant tolerance.

Overall, the findings demonstrate that Pb toxicity substantially compromises strawberry performance, whereas inoculation with plant growth-promoting rhizobacteria strains effectively mitigates its adverse effects. In particular, MS-7 showed superior potential for limiting Pb uptake and transport, while MS-12 and MS-13 enhanced overall plant performance under stress. The results highlight the potential of beneficial bacteria as an environmentally friendly strategy to improve strawberry production in Pb-contaminated soils and emphasize the importance of selecting appropriate bacterial strain–cultivar combinations for sustainable heavy metal stress management.

Poster (P5)

Enhancing fertilizer use efficiency: the potential of nature-based solutions

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Keywords: Plant metabolites, Nitrogen Use Efficiency (NUE), Biological nitrification inhibitor (BNI), High-throughput screening; Ammonia oxidation

Nitrification, the microbial oxidation of ammonia to nitrate, plays a central role in the agricultural nitrogen cycle, directly influencing fertilizer use efficiency and environmental nitrogen losses. Adequate nitrogen supply is essential to sustain crop productivity by promoting shoot development, maintaining plant vigor, and supporting a balanced carbon-to-nitrogen ratio required for chlorophyll biosynthesis. However, inefficient nitrogen use contributes substantially to nitrate leaching and greenhouse gas emissions. Synthetic nitrification inhibitors (SNIs), such as 3,4-dimethylpyrazole phosphate (DMPP) and dicyandiamide (DCD), are well-established tools that enhance nitrogen use efficiency while reducing environmental nitrogen pollution. Their effectiveness is widely recognized, including in policy frameworks that promote their use as mitigation strategies. Despite these benefits, concerns remain regarding their long-term persistence in soils, potential impacts on microbial communities, and inconsistent field performance. In this context, biological nitrification inhibitors (BNIs)—plant-derived metabolites that suppress nitrification—have emerged as promising, nature-based alternatives. These compounds offer potential for improving nitrogen management in a more sustainable manner. However, their effectiveness and functional relevance under realistic soil conditions remain insufficiently characterized. Therefore, this study aims to explore the potential of natural products as viable complements or alternatives to existing synthetic approaches. To evaluate the potential of nature-based solutions, we assessed 21 reported BNIs under soil-relevant conditions using dose–response and time-course assays. Most compounds only inhibited nitrification at unrealistically high concentrations, questioning their biological relevance and practical applicability. Several also showed notable toxicity toward A. fischeri, further limiting their suitability.

These results highlight the limited effectiveness of current BNIs and the need for renewed discovery efforts. We therefore performed a large-scale screening of 17,000 natural compounds, establishing a systematic pipeline to identify more effective inhibitors. Overall, this work refines our understanding of BNIs, reveals key limitations in existing candidates, and supports the development of improved, nature-based strategies to enhance fertilizer use efficiency and reduce environmental nitrogen losses.

Poster (P7)

Performance of climate resilient nutrient management strategies on sesame under Arid Western Rajasthan in India

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Keywords: Sesame, Vermi-compost, Panchagavya, Phosphate solubilizing bacteria

Sesame is one of the oldest cultivated oilseed crops, extensively grown in Asia and Africa for its high-quality nutrient-dense seeds. Due to its rich nutritional composition and associated health-promoting properties, sesame holds considerable importance in human nutrition. The rising cost and overuse of chemical fertilizers have created a nutrient demand–supply gap, limiting sesame productivity and soil health, while the indiscriminate use of synthetic inputs has further degraded soil fertility, reduced yields, and posed risks to human and environmental health.

The present experiment was conducted during rainy seasons 2023 to 2025 with eight different treatments combinations viz., T1: Application of vermi-compost on N equivalent basis (recommended dose of nitrogen), T2: Application of Neem cake on N equivalent basis, T3: T1 + foliar application of 3% Panchagavya at flowering & capsule formation stage, T4: T2 + foliar application of 3% Panchagavya at flowering & capsule formation stage, T5: T3 + soil application of Phosphate solubilizing bacteria (PSB) and Azospirillum @ 2.5 liter in 50 kg/ha FYM), T6: T4 + soil application of (PSB and Azospirillum @ 2.5 liter in 50 kg/ha FYM), T7: 100% recommended dose of fertilizer (50% N and 100% P2O5 and K2O as basal and remaining 50% N in 2 split doses), T8: Absolute control (No NPK) in randomized block design and replicated thrice.

The data revealed (2023 to 2025) that significant increase was observed in seed yield (590 kg/ha) by 87.3% in T5 [Application of vermicompost on N equivalent basis + foliar application of 3% Panchagavya at flowering & capsule formation stage + soil application of PSB and Azospirillum @ 2.5 liters in 50 kg/ha FYM]. Albeit, which was statistically similar to T7 (100% recommended dose of fertilizer) and T3 (Application of vermi-compost on N equivalent basis of RDN + foliar application of 3% panchagavya at flowering & capsule formation stage). Climate resilient nutrient management practices in sesame resulted in additional income ranging from 115.26% to 287.48% over absolute control.

Poster (P9)

Moisture conservation practices in pearl millet [Pennisetum glaucum (L.) R. Br.] under arid western Rajasthan in India

Ram Swaroop Choudhary (1), Manoj Kumar (1), C. Tara Satyavathi (1)

(1) ICAR-All India Coordinated Research Project on Pearl Millet, PC Unit, ARS Mandore, Agriculture University, Jodhpur (Rajasthan), India

Keywords: Pearl Millet, Super absorbent polymers, Microbial, Crop residue mulch

The farmers in drier areas of the India especially in the western Rajasthan of India extremely faced the drought situation during the cropping season and drought is the main constraint in the farming in these areas which entirely depends on the monsoon rains. Hence conservation and utilization of moisture is main aim during the crop growing period. The moisture conservation through super absorbent polymers is an excellent source and crop residue mulching helps in suppression of weed species and thereby we can minimize the water loss. The present experiment was conducted at ICAR-All India Coordinated Research Project on Pearl Millet, Mandor during rainy seasons of 2020 to 2022 comprising of ten different super absorbent polymers (hydrogel) and crop residue mulching treatments i.e. T1: Control (Recommended dose of fertilizer; RDF), T2: T1+Crop residue mulch @ 5.0 t/ha after 10-15 DAS, T3: T1+ Pusa Hydrogel dry application @ 5.0 kg/ha, T4: T1+ SPG 1118 dry application @ 5.0 kg/ha, T5: T1+ Pusa Hydrogel slurry application @ 5.0 kg/ha, T6: T1+ SPG 1118 slurry application @ 5.0 kg/ha, T7: T3+ Crop residue mulch @ 5.0 t/ha after 10-15 DAS and T8: T4+ Crop residue mulch @ 5.0 t/ha after 10-15 DAS, T9: T5+ Crop residue mulch @ 5.0 t/ha after 10-15 DAS and T10: T6+ Crop residue mulch @ 5.0 t/ha after 10-15 DAS with three replication under randomized block design. The data revealed that highest grain (18.57 q/ha) yield was recorded in T8 (T4+ Crop residue mulch @ 5.0 t/ha after 10-15 DAS), which was 82.5% higher over the control and stover yield was found maximum in T9 treatment (38.15 q/ha) and it was markedly higher by 58.6% over control. The data on microbial counts study revealed that dehydrogenase activity 3.98 µg TPF/g soil/day was recorded highest in the treatment T8 (T4+ Crop residue mulch @ 5.0 t/ha after 10-15 DAS) which was found statistically at par with T2, T7 and T10, but significantly superior over all other treatments. Whereas, alkaline phosphatase population 56.52 µg/g soil/hr was found significantly higher in T8 (RDF + SPG 1118 dry application @ 5.0 kg/ha + Crop residue mulch @ 5.0 t/ha). The MBC populations 140.51 (µg g-1 soil) were recorded highest in treatment T9 and it was at par between T8 & T10 treatments but significantly superior over rest of the treatments. Bacterial counts, fungal counts and actinomycetes counts were not affected significantly with the application of different treatments during the study period.

Poster (P11)

Influence of organic and natural farming on productivity of Pearl millet under drier part of Western Rajasthan in India

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Keywords: Pearl Millet, Vermicompost, Manure, Cow based formulation

The pearl millet (Pennisetum glaucum (L). R. Br.) crop is not only just a climate resilient crop but also it is an important source for other dietary requirements, especially rich in various micronutrients. It is cultivated in various state of India including Rajasthan and in arid, semi-arid tropical and subtropical regions of world.

The present experiment was conducted at since kharif 2022 to 2025 with nine treatments combinations viz., T1: Control, T2: 100% recommended dose of nitrogen fertilizer through farm yard manure, T3: 100% recommended dose of nitrogen through vermicompost, T4: 100 % recommended dose of nitrogen through goat/sheep manure, T5: 100% recommended dose of nitrogen through FYM and biofertilizer, T6: 100% RDN through vermicompost and biofertilizer, T7: 100% recommended dose of nitrogen through goat/sheep manure and biofertilizer, T8: Cow base bioformulation (250 kg/ha Cow Urine based solid organic Bioformulation/ha before sowing alone with sieved dry FYM@ 250 kg/ha applied into the soil before sowing and cow urine), T9:100 % recommended dose of fertilizer (RDF) along with P, K and ZnSO4 in randomized block design and replicated thrice.

The data revealed (2022 to 2025) that grain and stover yields were highest under the RDF treatment, recording 18.96 q/ha for grain and 35.73 q/ha for stover yield. The data also revealed that marked variations among different organic treatments were observed under root zone of crop enzymatic and microbial studies of the soil. The dehydrogenase and alkaline phosphatase activity were recorded highest in the T5 treatment (recommended dose of nitrogen through farm yard manure + biofertilizer) being statistically at par with T6 (recommended dose of nitrogen through vermicompost + biofertilizer). Acid phosphatase was found statistically at par in the T4 to T8 treatments but significantly higher than control. Urease population was found statistically at par among T5 to T7 treatments but showed their statistical superiority than all the remaining treatments. The soil microbial biomass carbon populations were recorded highest in treatment T5 and it was at par with T4, T6 and T7 treatments.

Poster (P13)

Plant microbe interactions in horticulture

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Keywords: Rhizosphere microbiome, metabolites, growing medium, light quality

Root metabolite secretion, or root exudation, plays a crucial role shaping the rhizosphere microbiome. In turn, this microbiome affects plant growth and nutrient uptake, and therefore it is important to analyse root-rhizosphere interactions. In vertical farming, controllable environmental factors include light quality and growing medium. The objective of our study was to (1) identify which root exudate metabolites shift with light quality and growing medium treatments, (2) identify which bacteria shift with these treatments and (3) find tentative correlations between metabolites and bacteria. Full-spectrum light, monochromatic light (660 nm) and growing medium were tested in a full-factorial design experiment in lettuce (Lactuca sativa) var. Expertise. Growing medium was potting soil and perlite (0.6-2.5 mm). Root exudates were collected in a hydroponic setup and analysed with gas chromatography coupled with mass spectrometry. Rhizosphere bacteria were collected from soil attached to the roots and analysed based on the 16S rRNA gene. Red light increased the diversity of metabolites in the exudate. Plants grown under red light showed a shift in root exudate metabolites depending on the growing medium. Growing medium strongly influenced bacterial community structure. We identified several metabolites for further research on root-rhizosphere interactions.

Poster (P15)

DISCOVERY OF NOVEL NITRIFICATION INHIBITORS THROUGH HIGH-THROUGHPUT SOIL SCREENING

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Keywords: Nitrification inhibitors, Nitrogen Use Efficiency (NUE), High-throughput screening, Ecotoxicity assessment

Nitrification is a key microbial process in the soil nitrogen cycle, in which ammonia (NH_3) is oxidized to nitrate (NO_3^-). In agricultural systems, accelerated nitrification enhances nitrate leaching, reduces nitrogen use efficiency, and contributes to eutrophication and nitrous oxide (N_2O) emissions. The use of nitrification inhibitors can mitigate these impacts by slowing the conversion of ammonium to nitrate, thereby decreasing nitrogen losses and improving fertilizer use efficiency.

However, only a limited number of nitrification inhibitors is currently available. Their efficacy varies across soil types and environmental conditions, they impose logistical constraints, and several are increasingly subject to regulatory scrutiny. Consequently, both in the short and long term, it is strategically important to develop and ensure access to alternative inhibitors with at least equivalent, and preferably superior, efficacy.

To address this need, a high-throughput (HT) soil screening assay was developed to identify novel compounds with robust inhibitory activity under realistic soil conditions. Because inhibitor performance observed in liquid culture assays often shows poor translatability to soil environments, all evaluations were conducted directly in soil matrices. Starting from a library of approximately 10,000 compounds, an integrated selection pipeline combining HT soil assays, time-course inhibition measurements, and parallel assessment of ecotoxicity and non-target effects was applied. This workflow enables the identification of candidate inhibitors with consistent activity and strong potential for further development, resulting in a current set of 33 promising compounds and providing a robust foundation for the development of next-generation nitrification inhibitors.

Poster (P17)

Climate-resilient tree nurseries - soil management strategies to increase organic matter for improved water dynamics

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Keywords: Soil management, Soil organic matter, Tree nurseries, Soil water dynamics, Climate resilience

In North-West Europe, intensive agricultural and horticulture practices, such as frequent tillage, monocultures and limited organic inputs, have resulted in soils with low soil organic matter (SOM) contents. Low SOM levels have a negative impact on soil resilience against climate extremes by affecting soil structure, water infiltration and water holding capacity. Increasing SOM contents in agri- and horticultural soils is therefore necessary to improve soil functioning and enhance crop resilience in periods of drought and excessive rainfall. In avenue tree production systems, increasing SOM is challenging. The long cultivation periods (4-6 years), limits the opportunities for the cultivation of green manure crops and for organic amendments. In addition, frequent mechanical weed control practices can potentially accelerate decomposition of SOM by disturbing the top soil. Tree harvesting also removes a substantial amount of belowground biomass, a potential source of organic matter to the soil. All of the above factors, limit natural SOM accumulation and therefore, reduces the climate resilience of tree nurseries. The objective of our study is to evaluate alternative soil management strategies that enhance SOM accumulation in tree nurseries, with the aim of improving soil water dynamics, while maintaining tree quality. In a first field trial, four weed management strategies are evaluated in avenue tree production systems (Quercus robur and Ulmus laevis), including inter-row cover cropping, frequent mowing of weeds, chemical and mechanical weed control. Their effects on SOM development, aggregate stability, nutrient availability, soil moisture dynamics, infiltration capacity and tree performance are monitored during a 4-year trial period. In a second trial, di□erent organic amendments, including compost, coarse fraction of compost and woodchips, are incorporated in the soil to evaluate their potential to increase soil structure and water-related soil properties. The same parameters will be monitored. This experiment was initiated in 2016 and is conducted with four avenue tree species differing in drought sensitivity: drought-sensitive Tilia cordata and Quercus robur, and drought-tolerant Castanea sativa and Liquidambar styraciflua. The combined results of these trials will be used to provide tree nursery growers with practical recommendations on soil management strategies to effectively increase their soils SOM content and enhance the climate resilience of their cropping systems.

Poster (P19)

Modeling Mulching Effects on Crop Multi-Stress Responses

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Keywords: Organic mulching, Mechanistic model, Soil processes, Crop productivity

Mechanistic soil–crop models integrate environmental conditions and management practices on crop growth and yield. By simulating climate, soil processes, and crop development, these models link process-level stress responses to crop productivity. However, their predictive capacity strongly depends on parameterization.

A modeling workflow was developed to investigate crop multi-stress responses under contrasting mulching practices using the Decision Support System for Agrotechnology Transfer (DSSAT). The workflow was developed using data from a 2025 potato field experiment comparing a bare-soil control with woodchip (86 t DM ha^{-1}) and grass–clover (21 t DM ha^{-1}) mulching practices, both applied as an initial 6 cm layer. Soil water tension and temperature were monitored hourly at three depths (−15, −25, and −35 cm), complemented by measurements of plant-available nitrogen in soil and crop, leaf area index (LAI), and yield. Morris sensitivity analysis was used to identify parameters controlling soil processes and crop productivity at both daily and seasonal scales. The most influential parameters were subsequently calibrated using a Simplex optimization against weighted observations. Parameter bounds were defined from field observations and their variability, complemented by literature-derived ranges.

Across the 62 initial candidate parameters, the sensitivity analysis identified 15 influential parameters, mainly related to crop development and soil and mulch physical properties. Simulations indicated reduced temperature and water stress under mulching, while nitrogen responses differed between mulch types, with greater late-season nitrogen stress under woodchips and higher nitrogen availability under grass–clover. Model verification against observed crop and soil measurements under contrasting climatic conditions will assess its validation capacity.

Overall, the workflow identifies key processes and quantifies multi-stress responses to mulching, providing a mechanistic basis for evaluating mulching as a crop adaptation strategy under changing climatic conditions.

Poster (P21)

More is not always better: smart irrigation in sweet cherry (Prunus avium)

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Keywords: Irrigation, sweet cherry, drought

Fruit production in Belgium is increasingly threatened by drought stress, as illustrated by the exceptionally dry conditions during the summer of 2026. In sweet cherry, the increasing adoption of rain covers further necessitates the need for efficient irrigation strategies to maintain yield and fruit quality while minimizing water consumption. In a multi-year field trial, we evaluated irrigation strategies for the sweet cherry cultivar 'Kordia' grafted on Gisela 5 to identify a balance between water conservation and the maintenance of yield, fruit size, and overall fruit quality.
Our results demonstrated that higher water availability did not consistently increase yield or fruit size. Maintaining a soil water tension of 35 kPa throughout the growing season did not increase fruit size and, based on multi-year observations, was associated with a tendency toward increased fruit cracking and reduced overall fruit quality. In contrast, a phased irrigation strategy maintaining 60 kPa from April until the 15th of June, followed by 35 kPa during 3 to 4 weeks preceding harvest, provided the most balanced response.
Based on the multi-year results, maintaining a soil water tension of approximately 60 kPa during the early and mid-growing season, followed by 35 kPa during the pre-harvest period, appears to be an effective irrigation strategy for 'Kordia' sweet cherry under the conditions of this study. This approach may contribute to more water-efficient cherry production without compromising yield, fruit size, or economic performance.

Abstracts: Session 2

Crop protection: Strategies against plant pests and pathogens

Keynote speaker (15:40 - 16:10)

Plant microbiome: The extended host immune system

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Keywords: Plant microbiome, Plant immunity, Coumarins, Defense signaling

Plants have evolved a sophisticated immune system that enables them to recognize and resist attack by a wide range of pathogens. This classical view of plant immunity, built on molecular mechanisms such as pattern recognition and effector-triggered responses, has provided a powerful framework for understanding how plants defend themselves. Yet plants do not act alone: they are embedded in complex microbial communities where beneficial, commensal, and pathogenic microbes continuously interact with one another and with their host. These interactions extend the boundaries of plant immunity beyond the individual organism, integrating microbial allies into a coordinated "extended plant immune system" that operates at the community level. Research in the Plant-Microbe Interactions group at Utrecht University exemplifies this concept. We showed that upon foliar infection with downy mildew, Arabidopsis roots recruit a synergistic microbial consortium that activates induced systemic resistance (ISR) and leaves behind a soil-borne legacy that protects the next plant generation. Root-exuded coumarins emerged as crucial chemical signals in this dialogue. Extending these insights to crops, we developed a microbiome-informed prediction model in potato, where seed tuber microbiome profiles accurately forecast plant vigor in the next growing season. Together, these findings illustrate how the extended immune system is grounded in genetically determined processes, from host-mediated microbiome recruitment to microbial traits that suppress pathogens and activate ISR. By linking classical plant immunity to modern plant-microbiome concepts, we highlight how plants deploy an evolutionarily integrated immune system that transcends the individual and offer a conceptual and practical foundation for developing microbiome-assisted cropping systems that produce more with fewer inputs.

Speaker (16:10 - 16:30)

POLYMER-BASED dsRNA DELIVERY SYSTEMS FOR RNAi APPLICATIONS AGAINST PHYTOPHTHORA INFESTANS

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Keywords: RNAi, polymer nanocarriers, cell uptake, cytotoxicity, pathogen control

RNA interference (RNAi) is a highly specific and environmentally friendly strategy for crop protection, offering strong potential for the control of plant pathogens such as Phytophthora infestans. A key limitation for broader application of RNAi-based approaches is the efficient delivery of double-stranded RNA (dsRNA) into plant and pathogen cells while maintaining RNA stability and biological activity.
In this study, polymer-based nanocarriers were evaluated as delivery systems for dsRNA in plant cell culture models, with the aim of developing platforms suitable for future RNAi delivery applications against P. infestans. Polyplexes were assessed for their biocompatibility, stability, cellular uptake, and ability to induce gene silencing in plant cells. The results indicate that polymer-based complexes enable effective dsRNA uptake with limited toxicity, supporting their suitability for RNAi-based crop protection strategies. Building on these findings, future research will focus on the application of dsRNA–polymer complexes against P. infestans, including studies using a GFP-expressing P. infestans strain to monitor dsRNA uptake and gene silencing efficiency. Additional work will investigate dsRNA delivery to P. infestans spores and protoplasts to further evaluate the potential of this approach for controlling late blight disease.

Speaker (16:30 - 16:50)

Integrating plant defense elicitors and ontogenic resistance for pear scab management

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Keywords: Transcriptome, GC-MS, HPLC

Common pear scab (Venturia pirina) is a major economic threat to pear (Pyrus communis) cultivation resulting in substantial crop losses if left uncontrolled. The widespread use of chemical plant protection products is increasingly challenged due to the buildup of pesticide resistance in the fungus, environmental concerns and the regulatory pressure to reduce chemical inputs. While 'green' plant protection products for scab control exist, their efficacy falls short of chemical alternatives, intensifying the challenges of scab control in pear cultivation. Research over the past decades, has primarily focused on apple scab (caused by Venturia inaequalis), leaving pear scab relatively understudied. As a result, apple scab management strategies have been applied to pear cultivation without necessary adaptations. Growers and auctions now call for a knowledge-based, sustainable approach to pear scab management.

In this research we want to find alternative products efficient against pear scab and understand their mechanisms. We are particularly interested in their mode of action and duration of the induced plant defense. The potential and mechanisms of plant defense enhancers (PDEs) were explored. Grafted plants were treated with PDEs and artificially inoculated with V. pirina-spores to (i) analyze a selected set of the plant's defense response genes through qRT-PCR and ii) to determine the effect on the development of V. pirina symptoms on leaves and twigs.

Secondly, the potential ontogenic resistance of pear leaves was investigated based on a similar approach previously applied to apple leaves. Leaves from different ages (1 week old to 8 weeks old) were sampled for transcriptomic analysis while their phenolic and cuticle compositions were characterized using HPLC and GC-MS, respectively. Together, these findings highlight the role of leaf developmental age in influencing the plant's natural resistance.

By integrating genomic, molecular, and phenotypic approaches, this study aims to contribute to a comprehensive understanding of the P. communis – V. pirina pathosystem, paving the way for sustainable and global scab control strategies.

Speaker (16:50 - 17:10)

From citizen science to microbial biocontrol: discovering phyllosphere-adapted lactobacilli for sustainable biocontrol

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Keywords: Lactobacillaceae, phyllosphere, biocontrol, adaptation

Yearly, up to 40% of crops are lost due to plant pests and diseases. While chemical plant protection products increase crop productivity, pathogen resistance, environmental and health concerns, and stricter policies have increased the need for alternatives. Microbial biological control agents (MBCAs) are regarded as sustainable alternatives, offering targeted suppression of plant pathogens while preserving ecosystem health. However, their performance on the plant can be variable. While this challenge is especially pronounced in the phyllosphere, the aerial surfaces of plants, this environment remains significantly less studied than the rhizosphere. Understanding why field performance is more challenging, particularly on flowers and leaves, is essential for guiding future research and product development. Key barriers to field efficacy include ecological factors, such as (a)biotic stressors, technical limitations, such as ineffective formulation or application, and structural constraints, including regulation, and stakeholder training.

We performed an MBCA isolation campaign on strawberry flowers, increasing the likelihood of natural phyllosphere adaptation, by employing a citizen science approach, involving 50 growers from four countries. We explored the strawberry flower bacteriome across a gradient of cultivation intensification, revealing that more intensive agriculture led to decreased diversity, the loss of core taxa, and greater variability. By actively involving growers we received early feedback, enhanced microbial literacy and fostered stakeholder partnerships. Furthermore, by focusing our MBCA isolation campaign on Lactobacillaceae, a large family of beneficial bacteria that have a niche in the phyllosphere and have not yet been commercialised as MBCAs, we aim to accelerate the registration process.

The acquired Lactobacillaceae isolates were screened for antipathogenic activity and survival in the phyllosphere by subjecting them to stressers and inoculating them on strawberry flowers. Notably, one isolate exhibited potent in vitro inhibitory activity against several plant pathogens, which was retained after formulation via spray-drying. Importantly, when sprayed preharvest on greenhouse-cultivated strawberry plants, this isolate significantly inhibited the growth of Botrytis cinerea. Ongoing and future work will focus on scaling up, elucidating the mode of action, and improving persitence in the phyllosphere.

Speaker (17:10 - 17:30)

Revisiting the role of the jasmonate pathway in plant defense against Meloidogyne graminicola in rice

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Keywords: Jasmonate, Root-knot nematodes, Rice, plant defense, induced resistance

Rice is an important staple crop grown in over 100 countries. As global rice consumption continues to rise with the growing world population, yield losses have increasingly severe consequences. One major threat is the root-knot nematode (RKN) Meloidogyne graminicola, which recently made its way to Europe and was added to the European and Mediterranean Plant Protection Organization (EPPO) Alert List. This pathogen alone can cause yield reductions of up to 70%, making it one of the most devastating pests in rice production. Conventional nematicides are an effective countermeasure to RKNs, but are often associated with adverse effects on human health and the environment. A potential alternative, environmentally friendly strategy is enhancing the plant's immune system through a mechanism called induced resistance (IR). Many candidates of induced resistance have already been described in the literature, including beta-aminobutyric acid (BABA), dehydroascorbic acid (DHA), piperonylic acid (PA), and benzothiadiazole (BTH). Desmedt et al. (2022) demonstrated that IR stimuli can elicit common defense response patterns. Notably, all tested compounds enhanced the expression of genes involved in jasmonate biosynthesis and signalling at 24 hours post-treatment (hpt). JA and its derivatives (collectively known as jasmonates) are plant hormones involved in chemical defense against biotic stressors in plants. Although the key enzymes of the JA pathway have been identified, the role of the pathway in plant defense against RKNs remains unclear. The study highlights common metabolomic signatures of different IR stimuli with a special focus on jasmonates. Additionally, the susceptibility of mutants with deficiencies in the JA pathway towards Meloidogyne graminicola was analyzed. Recent advancements towards unravelling the role of the JA pathway in plant defense against RKN will be presented.

Poster (P23)

Leveraging strawberry-associated yeasts for fungal disease protection

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Keywords: microbiome, strawberry, Botrytis cinerea, Podosphaera aphanis, SynComs

Strawberries are Flanders' most important berry crop. However, the cultivation is often hampered by the occurrence of numerous pests and diseases, most of which are still controlled by chemical plant protection products. The SynBioS project aims to develop synthetic microbial communities (SynComs) as a sustainable alternative to control strawberry fungal diseases. The SynComs will be designed to mimic the functions and structure of the phyllosphere microbiota of healthy plants and preserve the essential microbe–host interactions. To achieve this, leaves, flowers, and fruits were sampled across different cultivation systems. Using deep amplicon sequencing, we defined the composition, diversity, and richness of the microbiota across the different samples, followed by the identification of the core microbiome. From the same samples, a culture collection of this core microbiome has been established, with a focus on yeasts. The collection is being assessed for antimicrobial activity against Botrytis cinerea and Podosphaera aphanis, plant growth-promoting traits, and responses to environmental factors. For some yeast isolates and SynComs, we have already shown that they inhibit B. cinerea. In addition, we will perform whole-genome sequencing to fully characterize the potential of these microorganisms. Knowledge of these characteristics will allow us to select a specific set of microorganisms that are persistent under field conditions, do not outcompete each other, and strengthen plant health through their biocontrol potential.

Poster (P25)

Chemical and morphological defences against scale pests in custard apples

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Keywords: Annona, scale insects, plant defences

Crop losses caused by insect pests remain a major challenge for agricultural production worldwide. Understanding the plant traits associated with pest resistance is essential for breeding and for developing sustainable crop-protection strategies. In this study, we investigated variation in natural infestation by the scale insect Parasaissetia nigra, an important pest of cultivated Annona species. This insect reduces fruit marketability by damaging the fruit surface and, under severe infestations, may also affect crop productivity. Our aim was to identify chemical and structural plant traits associated with differences in susceptibility among Annona cherimola and its wild relatives.
To address this, we quantified natural infestation levels across accessions representing eight Annona species, including cultivated A. cherimola and wild relatives, and compared these patterns with untargeted leaf metabolomic profiles obtained by LC–MS analysis. We also characterized leaf-surface morphology using scanning electron microscopy (SEM) and examined internal leaf structure through light microscopy of stained cross-sections.
Overall, our results reveal a gradient of susceptibility to P. nigra within the genus Annona and identify metabolomic and structural traits that may contribute to this variation. These findings provide a basis for identifying candidate resistance-associated traits that should be validated through controlled infestation experiments. They also support the use of multiscale phenotyping approaches combining metabolomics with leaf structural characterization to improve our understanding of plant–insect interactions and to inform future breeding.

Poster (P27)

Distinct ecological drivers structure bacterial and fungal phyllosphere communities across cultivation systems

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Keywords: microbiome, phyllosphere, strawberry, synthetic communities

As soft fruit, strawberries are particularly susceptible to infections by pathogens such as Botrytis cinerea. Biocontrol agents using single strains of bacteria have been introduced to the strawberry market but are not widely used. This is likely due to cost and limited efficacy when compared to conventional chemical pesticides. Design of a strawberry-specific biocontrol product using multiple microorganisms in a synthetic community (SynComm) may serve as a more effective alternative. We aim to use bacteria and fungi naturally found in the phyllosphere (the aboveground portion of the plant) to create SynComms for future applications as biocontrol products. A sampling campaign was undertaken to collect samples from 27 farms using diverse cultivation strategies in the north of Belgium. Leaves, fruits and flowers were collected, and the bacterial and fungal communities were identified using 16S and ITS sequencing. Use of farmer questionnaire data enabled us to identify factors important for microbial communities. We hypothesized that (1) the phyllosphere microbiome would be depleted in the greenhouse compared to open field and tunnels, (2) cultivation factors determining community composition would be different between bacteria and fungi and (3) differential abundance testing would find specific microbial taxa enriched in the greenhouse compared to open fields and tunnels that could be used to design SynComms for biocontrol. Comparisons of alpha diversity using linear mixed models reveals that there is no difference in bacterial species richness between tunnels, open fields and greenhouses. Fungal species richness was, interestingly, higher in greenhouses compared to tunnels (Kruskal-Wallis; p ,0.05). Fungal communities show similar core community members and a comparable goodness-of-fit to the expected neutral model, indicating that they are less impacted a by increased agricultural intensity. Permutational analysis of variance was used to deduce the influence of specific cultivation factors on microbial community structure. Differential abundance analysis showed that fungal genera were enriched in the greenhouses and open fields compared to tunnels, while no clear patterns emerge for bacteria taxa. Overall, the unexpected divergence between fungal and bacterial trends underscores the importance of cross-kingdom analysis when designing phyllosphere-based SynComms for biocontrol applications.

Poster (P29)

The effect of microalgae-derived products on biotic and abiotic stress in fruit crops

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Keywords: Microalgae, biotic and abiotic stress, growth stimulation, biopesticide, biostimulant

Objectives: Microalgae are a promising source of bioactive compounds that may contribute to more sustainable crop protection and improved plant resilience. Within the Interreg IDEA+ project, bead-milled microalgal biomass and water and ethanol extracts were evaluated for their efficacy against several biotic and abiotic stress factors relevant to fruit production, as well as for their biostimulant effects on plant growth.
Methods: Microalgae cultivated on different side streams were processed into bead-milled biomass, water extracts and ethanol extracts. Their efficacy was assessed in laboratory and greenhouse experiments against Venturia inaequalis (apple scab), Phytophthora cactorum (strawberry crown rot), Cacopsylla pyri (pear psylla), drought stress and growth stimulation in apple seedlings. Depending on the bioassay, disease severity, pest mortality and plant growth were evaluated.
Results: Several microalgae extracts strongly inhibited ascospore germination of V. inaequalis, with efficacies up to 93.9%. In greenhouse experiments, selected extracts reduced apple scab severity by 39.2%, which was comparable to the reference copper based fungicide (36.5%). No direct inhibition of P. cactorum mycelial growth was observed in vitro. However, several biomass fractions and extracts reduced crown rot symptoms in strawberry plants by more than 60%, although these reductions were not statistically significant. Against pear psylla, the highest efficacy (38.5%) was obtained with a water extract of Nannochloropsis cultivated on permeate of process water. Under drought conditions, the water extract obtained from mixed pond biomass improved plant growth, increased leaf number and maintained higher chlorophyll levels compared with the drought-stressed control. Under normal water conditions, without drought stress, bead-milled Nannochloropsis grown on process water permeate led to increased growth in apple seedlings.
Conclusion: The efficacy of the tested microalgae products differed between the products, target organisms and stress factors. However some promising effects were observed for apple scab, strawberry crown rot, pear psylla, drought stress and growth. These findings indicate that microalgae-derived biomass and extracts can potentially contribute to sustainable crop protection and plant resilience. Further research is needed to identify the compounds responsible for the observed effects and to validate their efficacy under field conditions.

Poster (P31)

Insight into the role of Botrytis cinerea phytotoxins in infection niche establishment and virulence in host plants

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Keywords: Botrytis cinerea, Comparative genomics, Biosynthetic gene clusters ,Phyllosphere microbiome ,Secondary metabolites

Traditionally, sustainable crop resilience against fungal diseases has focused on binary plant–pathogen interactions. However, infection outcomes are not solely determined by this pairwise relationship; the broader ecological context also plays a crucial role in shaping disease progression. After penetrating plant tissue, Botrytis cinerea—a necrotrophic pathogen—releases a diverse array of specialized metabolites, including the sesquiterpene botrydial (BOT) and the polyketide botcinic acid (BOA), which induce host cell death. Yet, the ecological functions of these molecules within the phyllosphere microbiome during host colonization remain largely unknown.

To explore this perspective, the pathogenicity of 15 B. cinerea isolates was assessed on tomato and lettuce leaves, revealing substantial variation in virulence among isolates. To investigate genetic basis of these difference , whole genome sequencing followed by comparative genomics analysis was performed, with a focus on secondary metabolite biosynthetic gene clusters, particularly BOT and BOA clusters. Comparative analysis identified genetic variation within the BOA cluster, whereas the BOT cluster remained largely conserved. Variation within these clusters was then linked to the production of these phytotoxins both in vitro and in planta using LC-MS/MS,showing that toxin production was associated with isolate-specific virulence levels. Subsequently, we investigated their ecological roles by analyzing the phyllosphere microbiome diversity through metabarcoding and quantifying toxin production during infections at different time points caused by virulent and non-virulent strains. Finally, by linking genomics variation to toxin production, virulence level and microbiome dynamics during infection, this study reveals a novel pathogen strategy for niche establishment and provides an ecological framework to guide microbiome-aware biocontrol strategies.

Poster (P33)

Genetic diversity of rice-associated bacteria and their potential for biocontrol of major rice pathogens in Bangladesh

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Keywords: Genetic diversity, rice-rhizosphere bacteria, biocontrol, rice pathogens, Bangladesh

Rice-associated beneficial bacteria play an important role in plant health and disease suppression. Understanding how cropping season, geographical location, and host genotype shape these communities is essential for sustainable microbiome-based disease management. In Bangladesh, rice blast predominates during the Boro (dry) season, whereas bacterial leaf blight is highly prevalent during the Aman (monsoon) season. This study investigated the diversity, distribution, genetic relationships, and antagonistic potential of rice root-associated beneficial bacteria collected from Bangladesh during the Aman and Boro seasons. A total of 1320 bacterial isolates were recovered from healthy and diseased rice rhizospheres, of which 549 (41.6%) exhibited antagonistic activity against Pyricularia oryzae and Xanthomonas oryzae pv. oryzae. The abundance of antagonistic bacteria varied significantly among cropping seasons, geographical locations, and rice varieties, with the Aman season yielding a higher proportion of antagonistic isolates. Based on 16S rRNA gene sequencing, the antagonistic community was dominated by Bacillus, Pseudomonas, Burkholderia, Serratia, and Enterobacter. Bacillus and Enterobacter were associated with the Boro season, whereas Pseudomonas, Burkholderia, and Serratia predominated during the Aman season. Specific rice varieties exhibited selective bacterial recruitment: Gutishwarna, Horidhan, and Pajam were associated with Pseudomonas, while Hybrid-Vision and Madhobi were associated with Bacillus and Burkholderia, respectively. Geographical variation was evident, with Bacillus predominating in Gazipur and Pseudomonas in Jamalpur. Correlation analysis revealed contrasting associations between soil pH and disease incidence, with positive and negative correlations for blast and bacterial leaf blight, respectively. Representative isolates of Bacillus, Pseudomonas, and Burkholderia exhibited broad-spectrum antagonistic activity against major rice fungal pathogens, with several isolates producing >90% mycelial growth inhibition, whereas only a few showed strong antibacterial activities against Xanthomonas oryzae pv. oryzae. These findings demonstrate that cropping season, geographical location, and host genotype shape the diversity and composition of rice-associated beneficial bacterial communities. The identified native antagonistic isolates represent promising candidates for sustainable biological control of major rice diseases in Bangladesh.

Poster (P35)

Biocontrol Potential of Bacillus Strains Against Halyomorpha halys in Strawberry

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Keywords: Biological control, Induced resistance, Brown marmorated stink bug, Bacillus, Strawberry

The brown marmorated stink bug, Halyomorpha halys, is an invasive East Asian pest that attacks more than 300 plant species, causing substantial economic losses in diverse fruit, vegetable, and field crops worldwide. Sustainable management options for this pest are limited, highlighting the need for environmentally friendly alternative control strategies. One promising sustainable pest management strategy is the use of plant growth-promoting rhizobacteria (PGPR), which have been shown to enhance plant growth and induce resistance against pests and pathogens. In this study, we evaluated the biocontrol potential of three rhizobacteria of the genus Bacillus against H. halys on strawberry plants. Bacillus strains, isolated from strawberry plants, were identified and characterised on various in vitro PGP traits. Strawberry plants were grown under greenhouse conditions, and the soil was inoculated with the selected strains, either individually or as a consortium. After fruit ripening, fourth-instar nymphs of H. halys were confined on individual strawberry fruits for two days. Afterwards, insect relative growth rate, mortality, and the number of feeding sites were assessed. One strain (Bacillus safensis) significantly increased nymph mortality up to 35%, compared with 0% in the control treatment, and significantly reduced insect relative growth rate. The other bacterial treatments also increased mortality, although these effects were not statistically significant. By contrast, for none of the tested strains a significant reduction in the number of feeding sites was observed. Altogether, these findings identify this Bacillus safensis strain as a promising candidate for further characterisation and development as a microbial biocontrol agent against H. halys. Further research is warranted to elucidate its mode of action and evaluate its efficacy under field conditions.

Poster (P37)

Evaluation of novel fungicides against soil borne diseases of Cotton (Gossypium spp.) in arid western zone of India

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Keywords: Macrophomina phaseolina, Cotton, Fungicide, Disease management and Root rot

Cotton is one of the most important commercial crop grown in India as well as at global level, contributing significantly towards the agricultural economy and textile industry. However, the productivity of cotton is severely affected by several soil borne diseases caused by various pathogens such as Fusarium oxysporum, Rhizoctonia solani, Macrophomina phaseolina and Pythium spp. The root rot caused by Macrophomina phaseolina is one of the most serious disease of cotton. Therefore, the present investigation was aimed to evaluate the efficacy of novel fungicides against major soil borne diseases of cotton under current climate changing scenario of Indian agricultural conditions. The field experiment was conducted at DBRC, Agricultural Research Station, Mandor, Jodhpur, Rajasthan, India during rainy seasons of 2024-25 comprising three replications under Randomized Block Design with eight different treatment combinations of new-generation fungicides. The data on management of soil borne diseases of revealed that all the treatment were found markedly superior over untreated control. The data also depicted that the seed treatment with prochloraz 5.7% + tebuconazole 1.4% @ 0.03ml /kg seed was observed most effective in managing root rot (10.4% disease incidence) with maximum yield (2613 kg/ha) followed by seed treatment with tebuconazole 15% + zineb 57% @ 1.0 g/kg seed (12.1% disease incidence). However, the control showed maximum disease incidence of root rot (22.7%) with lowest yield (1537 kg/ha).

Furthermore, economics analysis of the seed treatment through prochloraz 5.7% + tebuconazole 1.4% @ 0.03ml /kg seed was found more economical with maximum B:C ratio (3.13) followed by seed treatment with tebuconazole 15% + zineb 57% @ 1.0g /kg seed (2.70). Whereas, the minimum B:C ratio (1.85) was observed in untreated control.

Poster (P39)

Deciphering Host–Pathogen Interactions Through Proteomics and Organelle Biology

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Keywords: organelle signalling, pathogen effector proteins, proteomics, interactomics, oomycetes

Plants rely on highly coordinated intracellular signaling networks to perceive and respond to the environment and biotic stress. Subcellular organelles are increasingly recognized as dynamic sensors of environmental and pathogenic cues, integrating signals that shape immune responses and stress adaptation. Our research focuses on the molecular mechanisms underlying organelle communication through membrane contact sites, as well as organelle-to-nucleus signaling pathways that regulate plant defense and resilience.

A major focus of our work is understanding how pathogens manipulate host cellular processes through effector proteins that target specific organelles. To address this, we develop and apply advanced proteomics-based approaches for the de novo identification of pathogen effectors and use proximity-labeling and interactomics technologies to uncover their host targets and mechanisms of action. By uncovering how pathogens reprogram organelle signaling and identifying the host proteins involved, our work provides mechanistic insights that can contribute to the development of novel and durable disease-resistance strategies for crop improvement.

Poster (P41)

Unravelling the molecular basis of plant immunity priming by bacterial cyclic lipopeptides

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Keywords: Immunity priming, bacterial cyclic lipopeptide, transcriptomics and metabolomics, plant-pathogen interaction

Plant immunity is continuously shaped by various environmental signals, including cues derived from both pathogenic and beneficial microorganisms. One promising outcome of these interactions is immune priming, a physiological state that enables plants to respond faster and more effectively to subsequent pathogen attack. Understanding how plants perceive and integrate these signals is essential for developing sustainable strategies to enhance crop health.
A well-studied inducer of immune priming is the root associated bacterium Bacillus velezensis, which protects plants against a broad range of diseases through induced resistance. A crucial component of this process is the cyclic lipopeptide surfactin, a bioactive secondary metabolite secreted by B. velezensis. Upon perception by plant roots, surfactin induces a primed state, enhancing the plant's ability to mount rapid defense responses. Previous research revealed that surfactin is not recognized in the canonical way as a microbial associated molecular pattern by the plant's pattern recognition receptors. Consequently, it does not trigger induced resistance through the conventional pattern triggered immunity pathway. Instead, it interacts directly with the plant cell plasma membrane, leading to atypical early immune responses and priming of the plant.
Despite its importance, the molecular basis of surfactin perception and the establishment of the primed state remain poorly understood. To address this, we use single-cell RNA sequencing in Arabidopsis thaliana roots to capture cell type-specific responses to surfactin. In parallel, we investigate the systemic effects of surfactin treatment through disease assays with Botrytis cinerea and Pseudomonas syringae, combined with transcriptomic and metabolomic analyses of leaf tissues. Preliminary transcriptomic analyses reveal extensive reprogramming of defense- and stress-related pathways in systemic tissues following surfactin treatment, highlighting the broad impact of this bacterial signal on plant immunity. By integrating these datasets, we aim to uncover the signaling pathways and cellular mechanisms underlying surfactin-induced immune priming, providing new insights into how beneficial microbes shape plant immunity.

Poster (P43)

MULTISPECTRAL IMAGING AS A TOOL TO STUDY dsRNA DELIVERY AND RNAi EFFECTS AGAINST PHYTOPHTHORA INFESTANS

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Keywords: RNAi, late blight, Solanum, multispectral imaging, gene silencing

RNA interference (RNAi) holds strong promise as a sustainable strategy to control plant pathogens such as Phytophthora infestans, the causal agent of late bright in Solanum species. However, efficient delivery of double-stranded RNA (dsRNA) to the pathogen and reliable methods to monitor uptake and biological effects remain key challenges. In this work, multispectral imaging is explored as a powerful, non-destructive tool to study dsRNA delivery in complex with carrier systems and to support the screening of dsRNA and complexes with nanocarriers.

Two complementary experimental setups are being developed. In an in vitro assay, P. infestans wild-type or GFP-tagged strains are grown from spores or mycelial plugs in the presence of dsRNA–carrier complexes. Multispectral imaging enables the monitoring of the fungal growth and GFP fluorescence as readouts for pathogen viability and potential gene silencing effects. This setup serves as a rapid screening platform to evaluate carrier performance and dsRNA activity.

In parallel, an in vivo detached-leaf assay is being established for preventive treatment studies, in which leaves are treated with dsRNA–carrier formulations prior to P. infestans inoculation. To assess the effect, multispectral parameters such as chlorophyll content, anthocyanin accumulation, and photosystem II efficiency (Fv/Fm) together with GFP and RFP fluorescence are used. Together, these approaches provide an integrated framework to evaluate dsRNA delivery strategies and their potential for RNAi-based control of late blight.

Poster (P45)

Leveraging single-cell transcriptomics to unravel the molecular interplay between strawberry and Botrytis cinerea

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Keywords: plant-pathogen interactions, single-cell and spatial omics, quiescent infections

Botrytis cinerea, the necrotrophic fungus that causes grey mold, poses a major pre- and post-harvest threat to the 1.2 million tonnes of strawberries produced annually in the EU. This pathogen can establish quiescent, asymptomatic infections in strawberry flowers and unripe fruit, which later progress to symptomatic disease as the fruit ripens. Despite its economic importance, the molecular mechanisms regulating the initiation and termination of B. cinerea quiescence remain poorly understood. Here, we aim to combine advanced microscopy with single-nucleus and spatial transcriptomics to investigate the cellular and molecular basis of quiescent infections in the B. cinerea-strawberry pathosystem. We are currently optimizing microscopy workflows and dual single-nucleus isolation from strawberry and B. cinerea to overcome challenges associated with the distinct cellular biologies of plants and fungi and the low abundance of fungal nuclei in infected tissues during quiescence. The optimized workflows will enable us to track infection progression from quiescence to active necrotrophic growth and profile host and pathogen transcriptomes at cellular resolution during key infection stages. Integration of these datasets through state-of-the-art bioinformatic analyses will reveal the diversity of host and pathogen cell types and states and elucidate how this cellular and transcriptional heterogeneity contributes to variation in disease outcomes. Together, this work will provide novel insights into the mechanisms governing B. cinerea quiescence and strawberry susceptibility.

Poster (P47)

Carrying the Control: Harnessing Epiphytic Bacteria for Improved Phage Biocontrol

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Keywords: Phage-based biocontrol, Bacterial canker, Pseudomonas syringae, Bacterial carriers

Bacterial canker, caused by Pseudomonas syringae, is a recurring disease in cherry orchards that causes major economic losses. Phenotypic screening and genomic analyses of P. syringae isolates from Flemish orchards revealed that copper resistance determinants are widespread, explaining the decreasing efficacy of copper-based treatments in the field. This highlights the need for sustainable alternatives. We therefore aim to explore the biocontrol potential of bacteriophages and evaluate whether non-pathogenic bacterial carriers can improve phage delivery and amplification, promoting the establishment of a stable phage reservoir on the plant surface.

Twenty new bacteriophages were isolated and screened for their host range against pathogenic Pseudomonas syringae strains and non-pathogenic epiphytes, resulting in the selection of a five-phage cocktail. Candidate carrier strains were evaluated for their ability to support phage replication while maintaining broad infectivity, with several strains producing phage titers of up to 10^{11} PFU ml^{-1}. The most promising carrier-phage combination was subsequently tested in a detached cherry fruit bioassay. Both the phage cocktail and the carrier strain individually reduced disease symptoms, whereas their combined application completely suppressed symptom development under the conditions tested.

These findings demonstrate the potential of carrier-assisted phage biocontrol as a sustainable strategy for managing bacterial canker in cherry. Furthermore, this work establishes compatible phage–carrier pairs for future studies on phage persistence and efficacy under field conditions.

Poster (P49)

Brown spot of pear unraveled: Study of the influence of abiotic stress and the infection cycle of Stemphylium vesicarium

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Keywords: Stemphylium vesicarium, pear; disease assays, abiotic stress

Brown spot of pear is a fungal disease caused by Stemphylium vesicarium. Since the early 2000s, it has led to severe yield losses in European pear production. In recent years, the occurrence of the disease has intensified significantly, and current mitigation strategies are proving increasingly inadequate. Growers are urgently seeking effective management strategies, particularly as the number of available crop protection products continues to decline and pathogen populations are developing resistance to commonly used fungicides.

Efforts to identify effective control strategies have been unsuccessful because critical steps in the pathogen's infection cycle remain poorly understood. In particular, both pathogenic and non-pathogenic strains of S. vesicarium coexist, yet the ecological and molecular factors determining pathogenicity have not been identified. Moreover, the mechanisms that trigger the transition from a saprophytic lifestyle on grasses and herbs to a necrotrophic lifestyle on pear tissue are still unknown. Pear trees are also increasingly affected by climate change, which plays an important role in brown spot development. Abiotic stressors are thought to significantly increase the susceptibility of pear trees to S. vesicarium.

The aim of this project is to advance our understanding of pear–brown spot interactions under different environmental conditions through a multidisciplinary approach. First, a methodological toolbox will be established to support studies on S. vesicarium. We will assess the pathogenicity of a collection of strains isolated from infected tissues and inoculation protocols for greenhouse-grown pear plants will be optimized. In parallel, a qPCR assay will be used to quantify inoculum levels in different orchard samples, providing insights into the seasonal population dynamics of the pathogen.

Building on these tools, the project will investigate how abiotic stress affects brown spot development. In greenhouse experiments, mature pear trees will be exposed to drought, waterlogging, salinity or UV radiation to determine whether these stressors influence the sensitivity of leaves and fruits to S. vesicarium. Ultimately, this research will contribute to a better understanding of the pear–brown spot pathosystem and provide a foundation for the development of more sustainable control strategies.

Poster (P51)

Exploring the potential of RCF-lignin as a plant defense elicitor for sustainable pest and disease control

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Keywords: Plant Defence Elicitor, Induced Resistance, RCF-lignin, Sustainable Agriculture

The production of high-quality food for an estimated 11 billion people by 2100 within the planet's sustainable boundaries is one of the greatest challenges of this century. Currently, up to 30% of global staple food crops are lost annually due to diseases and pests. To limit these losses, chemical plant protection products (PPPs) are widely used, but they may pose risks to human health and the environment. Therefore, sustainable alternatives are urgently needed. One promising group of sustainable alternatives is biological PPPs, particularly plant defense elicitors (PDEs). Rather than directly targeting pathogens or pest insects, PDEs activate the plant's immune system through a process known as induced resistance (IR), thereby reducing the plant's susceptibility to subsequent attacks. Previous research has shown that foliar application of Reductive Catalytic Fractionation (RCF)-derived lignin (RCF-lignin) enhances plant resistance, but its potential for practical application and the underlying mechanisms remain largely unknown. The main aim of this project is to asses the potential of RCF-lignin as a PDE against multiple diseases and pests on tomato, an economically important greenhouse crop. First, we will evaluate its ability to induce resistance against the pathogens Botrytis cinerea and Oidium neolycopersici, and the pest insects Nesidiocoris tenuis and Myzus persicae. Next, we will elucidate the underlying mechanisms induced by RCF-lignin by an in-depth mode-of-action study. Therefore, we will employ an integrated transcriptomic and metabolomic approach, followed by validation of key findings using reverse genetics. Finally, we will optimize the PDE efficacy by assessing its performance under varying parameters that closely resemble commercial greenhouse production. Altogether, this project will generate fundamental insights into the plant-protecting potential of RCF-lignin and support its further development as a novel biological PPP.

Poster (P53)

6G-PestDetect: AI-Driven Real-Time Detection of Aulacaspis tubercularis for Sustainable Management of Mango Orchards

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Keywords: Precision agriculture, Artificial intelligence, 6G, Edge computing, Aulacaspis tubercularis

Objectives
Early detection of insect pests is essential to maintain crop productivity while reducing pesticide use and supporting sustainable orchard management. This study presents 6G-PestDetect, an AI-driven real-time pest monitoring system for the early detection of white mango scale (Aulacaspis tubercularis) in mango orchards. By integrating autonomous field scouting with real-time data processing, the project aims to enable rapid, site-specific pest management. Advanced wireless communication and edge computing support timely analysis and decision-making under field conditions.
Methods
The system employs a guided vehicle equipped with high-resolution imaging sensors to survey orchard rows and acquire image data. Images are transmitted through a 6G-enabled communication infrastructure and processed at the network edge using a YOLO-based deep learning model for automated detection of A. tubercularis. Detected infestations are converted into georeferenced hotspot maps and real-time alerts, enabling targeted pest management. The integrated platform is being validated under commercial-like orchard conditions at the UMA La Mayora 6G testbed (Spain).
Results
The integration of the 6G-PestDetect platform is in its final stage, with the YOLO-based deep learning model successfully developed and integrated into the monitoring workflow. Field validation is currently underway at the UMA La Mayora 6G testbed to evaluate detection accuracy, processing latency, operational reliability, and robustness under realistic orchard conditions. Final validation results will be presented at the symposium.
Conclusions
The 6G-PestDetect framework highlights the potential of integrating artificial intelligence, autonomous sensing, and advanced communication technologies for real-time pest monitoring in perennial cropping systems. By enabling earlier detection of A. tubercularis, the approach can support site-specific interventions, reduce unnecessary pesticide applications, and contribute to more sustainable and resilient mango orchard production.

Poster (P55)

Potential of alyssum and predatory bugs as control strategy against onion thrips in leek

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Keywords: alyssum, predatory bug, thrips, leek

In this trial, conducted in a commercial leek field, the potential of planting Lobularia maritima (alyssum) as a banker plant, either alone or in combination with the release of the predatory bug Orius majusculus, was investigated as a strategy to reduce thrips damage in leek caused by Thrips tabaci (onion thrips).
In two spraying tracks within a commercial leek field, a 60 metre strip of alyssum was planted. Along the first 30 meters, predatory bugs were released weekly on three occasions starting on June 26th 2025. Just before the first release, the adjacent leek crop was treated with Tracer (a.i. spinosad), followed by a second application with Tracer in September.
The trial included four treatments: leek grown adjacent to alyssum; leek grown adjacent to alyssum combined with the release of predatory bugs; leek treated regularly with Tracer; and untreated leek. Each treatment consisted of several zones arranged in four replicates, which were assessed separately. The zones were located at different distances from the alyssum strips. This allowed us to investigate whether leek plants further away from the alyssum experienced more thrips damage than those growing closer to it.
Thrips damage on the leek crop was assessed regularly during the trial, and plant samples were collected to count the number of thrips (adults & larvae) using Berlese funnels. At harvest, an additional sampling was carried out to evaluate the thrips damage at the leek processing line (to wash and clean the plants).
Field observations did not reveal any clear differences in thrips damage between the different treatments. In addition, no reduction in the number of visible larvae was observed. However, the assessment at the processing line did reveal some limited differences. Leek grown in combination with alyssum as a banker plant in combination with predatory bugs showed, on average, the lowest percentage of damaged leaf area (11%), followed by leek grown with the banker plant alyssum without the release of predatory bugs (13%). In both the untreated control and the treated reference, the percentage of damaged leaf area was approximately 4-5% higher.

Poster (P57)

Unravelling the Genetic Basis of Pathotype Diversity in Puccinia horiana.

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Keywords: Chrysanthemum white rust, avirulence effectors, effectoromics

Chrysanthemum white rust (CWR), caused by the fungus Puccinia horiana, is a major disease in chrysanthemum production. As available fungicide options continue to decline, durable host resistance becomes increasingly important. However, resistance breeding is complicated by the presence of multiple pathogen pathotypes that differ in their ability to infect differential chrysanthemum cultivars, meaning that a variety resistant to one pathotype may still be susceptible to another. Recognition of a fungal Avr gene product by the corresponding resistance (R) gene product in a chrysanthemum cultivar triggers the plant immune response, eventually leading to resistance. This study aims to identify candidate avirulence (Avr) effector genes underlying these pathotype-specific interactions.

The ILVO P. horiana collection was expanded with additional isolates and pathotyped using a diverse panel of chrysanthemum cultivars. A total of 31 isolates were tested on 29 cultivars. Interaction phenotypes were used to construct a host-pathogen interaction matrix. Additionally, whole-genome sequencing was performed on 4 selected isolates, followed by pangenome construction as well as effector prediction.

Pathotyping revealed distinct virulence profiles among the collected. Comparative analysis of the sequenced genomes enabled the identification of multiple predicted effector candidates. A list of promising candidate Avr effector genes was selected for downstream functional validation in a chrysanthemum protoplast system.

Identification of Avr effector genes will improve our understanding of pathotype diversity in P. horiana and support the development of molecular tools for rapid pathotype characterization. These insights will facilitate more targeted and sustainable resistance breeding strategies for chrysanthemums.

Poster (P59)

Fruit-ReCuP: replacing copper (Cu) in biological fruit production

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Keywords: Fruit crops, Crop protection, Copper usage, Polyploidy, Fungal resistance

The production of perennial fruit crops relies heavily on copper-based fungicides for disease management especially in organic farming systems. However, repeated copper applications result in soil accumulation, causing environmental concerns and prompting increasingly stringent restrictions on copper use within the European Union. This work is part of a larger project which aims to develop sustainable ways to reduce the need for copper applications in apple and grapevine. On the one hand, we focus on developing cultivars with a high intrinsic resilience to biotic stresses, including fungal diseases, through the generation of triploid and tetraploid apple and grapevine genotypes. On the other hand, we investigate the effectiveness of polyphenols and other natural plant defence elicitors as environmentally friendly alternatives for disease control. The polyploid genotypes are being generated using in vitro and breeding approaches. Subsequently, they will be characterized through physiological and molecular analyses while simultaneously being assessed for resilience using in vitro disease assays focusing on apple scab for the novel apple genotypes, and on downy and powdery mildew for grapevine. Effectiveness of novel polyphenol compounds and natural plant defence elicitors will be evaluated in laboratory, greenhouse and field experiments. This project will thereby generate fundamental knowledge needed to develop strategies for sustainable disease management in the organic production of apple and grapevine and reduce the need for excessive copper usage. In doing so, we contribute to more sustainable apple and grapevine production while providing the alternative disease control strategies needed for growers to comply with EU regulations without compromising crop quality or yield.

Poster (P61)

Bitter substances from Chicory as biobased insecticides and targets for resistance breeding

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Keywords: Chicory, Sesquiterpene lactones, Biopesticides, Plant defense

Sesquiterpene lactones (SLs) are common secondary metabolites of Asteraceae such as chicory (Cichorium intybus). SLs are believed to play a major role in insect resistance because of their bitterness. Also for humans these metabolites are highly significant: they give Belgian endive (witloof chicory) its characteristic bitter flavor, while in industrial chicory they must be thoroughly removed to yield neutral-tasting inulin for food products. Several SL intermediates are also under investigation for their nutraceutical properties.
Low- or altered-SL chicory varieties are thus attractive for humans. However, preliminary research has shown that completely eliminating SLs by CRISPR/Cas transforms chicory from a robust crop susceptible to only few pests into a crop that is highly susceptible to generalist insect pests.
In this study we aim to identify which individual SLs are most important for plant resistance to insect feeding and to unravel their complex biosynthetic pathway. This knowledge would enable precision breeding: the development of chicory and witloof cultivars with improved agronomic and consumer traits while maintaining sufficient levels of bioactive SLs to ensure crop robustness. In addition, bioactive SLs might provide leads for novel bio-based insecticides. Such alternatives are increasingly needed, as the withdrawal of chemical insecticides from the European market poses growing challenges to deal with yield loss and insecticide resistance.
By developing a robust bioassay with Thrips tabaci, feeding damage and insect development can be systematically assessed on mutant chicory lines with different SL profiles. An image processing pipeline will be established to quantitatively measure thrips-induced feeding damage, enabling objective and high-throughput comparison of resistance levels among different genotypes. In parallel, different bioassays will be developed to evaluate the toxicity of chicory root extracts and purified SL compounds. Combined with transcriptome analyses, these experiments will clarify the specific contributions of individual SLs to chicory resistance against thrips and other economically important insect pests. This integrated approach will not only deepen our understanding of SL-mediated plant defence but also evaluate the potential of specific SLs as bio-based insecticides.

Poster (P63)

Chicory sesquiterpene lactones as bio-insecticides and targets for resistance breeding

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Keywords: circular bioeconomy, crop protection, industrial chicory, terpenoids

The declining availability of chemical insecticides in Europe, together with the limited number of new registrations, poses major challenges for effective pest control and resistance management. As a result, interest is growing in plant-derived natural compounds as alternative insecticides. Sesquiterpene lactones (STLs), a class of secondary metabolites produced by chicory (Cichorium intybus, L.) and other Asteraceae species, are particularly relevant in this context due to their contribution to plant defense. However, the specific STLs contributing to insect resistance in chicory remain unidentified and our understanding of their biosynthesis, mechanisms of action and chemical properties is still limited.

To address this, the SESQUICHIC project will perform CRISPR/Cas genome editing and natural variation screening to elucidate STL biosynthesis in chicory and generate pre-breeding material. In parallel, bioassays, toxicity tests and transcriptome analyses will provide insight into the role of STL metabolism in plant-insect interactions, while natural product chemistry will define their chemical properties and optimize their extraction and production. Together, these approaches will deepen our understanding of STL-mediated plant defense and deliver well-characterized bio-insecticide leads. These leads offer potential to support a circular bioeconomy by valorizing STL-rich chicory waste and reducing dependence on synthetic insecticides. Precision breeding may further enable the development of robust insect resistant chicory varieties with optimized STL profiles that facilitate downstream processing.

Abstracts: Session 3

Building resilience through plant breeding and plant modification

Keynote speaker (8:45 - 9:15)

From Field Signals to Durable Resistance: Turning Pathology Intelligence into Breeding Decisions

Amine Batnini (1)

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Amine Batnini is a plant pathologist and molecular biologist whose work brings together genetics, genomics, and crop disease research. He has contributed to research on plant resistance mechanisms and the genetic basis of host responses to important pathogens, with particular experience in soybean–Phytophthora sojae interactions and disease-resistance mapping. His background also spans molecular marker analysis and plant genetic diversity studies across crop systems.

Batnini's research centers asa pathology & trait discovery leader on the molecular and genetic dissection of disease resistance in crops, especially the identification of resistance loci, the use of genomics-enabled approaches for pathogen response studies, and the application of molecular tools to crop improvement. More broadly, his work sits at the intersection of plant pathology, quantitative genetics, and applied agricultural research aimed at supporting more resilient cropping systems.

For legal reasons the abstract of Amine Batnini can't be released.

Speaker (9:15 - 9:35)

Transgene-free genome editing in banana through Agrobacterium-mediated base editing strategy

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Keywords: Transgene-free, Banana, Agrobacterium, CRISPR/Cas9

Banana is the most important fruit crop globally, with an annual production of over 145 million tonnes. They are both a commercial export crop of important economic value as well as a staple food for over 500 million people in several regions with chronic food security issues. Their triploid nature and sterility limit their use in breeding programs, resulting in monoclonal cultivation and thus high susceptibility to pests and diseases. To introduce new characteristics in banana cultivars, Agrobacterium tumefaciens-mediated transformation is most often used for the introduction of full genes or gene edits, for which a protocol was recently established at our laboratory. However, given that outcrossing of the T-DNA cassette is impossible, gene-edited banana remains classified as GMO, even after loosening of the regulatory framework in the European Union. Therefore, transgene-free genome editing techniques are required for these sterile and vegetatively propagating crops.
Here we show that transient expression of a base editor and corresponding gRNAs through A. tumefaciens-mediated delivery can result in the regeneration of transgene-free gene-edited banana plants. Moreover, we established a mutation-dependent selection procedure, where a point mutation in the Acetolactate synthase gene results in chlorsulfuron resistance. Using this selection procedure allows for the capture of desired edits without T-DNA insertion, with approximately 20% of regenerated transgene-free plants showing edits at two desired target sites.

Speaker (9:35 - 9:55)

Parakletos links immune signalling, environmental stress tolerance, and future potato resilience

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Keywords: Parakletos, potato, susceptibility gene, multi-stress resilience, genome editing

Crop resilience increasingly depends on understanding how plants respond to overlapping disease and environmental stresses. Potato is strongly affected by late blight, early blight, drought, and salinity, yet many resistance strategies still focus on single stresses. Identifying stress-regulatory genes that shape responses across different challenges may therefore provide useful entry points for developing more resilient cultivars.

We recently identified Parakletos, a thylakoid-associated protein, as a potato susceptibility gene and negative regulator of stress resilience. Loss of Parakletos function enhanced early ROS and Ca^{2+} signalling and improved resistance to *Phytophthora infestans*, *Alternaria solani*, and bacterial pathogens. Parakletos-edited plants also showed increased tolerance to drought and salt stress. Importantly, two years of field trials showed reduced late blight disease development and increased yield in Parakletos-edited potato under non-sprayed conditions.

Here, we present Parakletos as a case study connecting immediate and future crop resilience. First, we discuss how Parakletos affects early stress signalling and disease outcome under current production-relevant stresses. Second, we present ongoing translational work aimed at moving Parakletos editing from a laboratory cultivar into six elite potato cultivars, with comparative phenotyping planned under controlled and field-relevant conditions. This will allow us to test whether Parakletos-based resilience is maintained across different genetic backgrounds.

Together, this work highlights how mechanistic gene discovery can be connected to plant modification and prebreeding. More broadly, Parakletos-based editing could be integrated with R-gene-mediated resistance strategies, providing an additional stress-regulatory layer rather than replacing pathogen-recognition-based resistance.

Speaker (9:55 - 10:15)

Heat-induced meiotic alterations and unreduced pollen formation in European pear (Pyrus communis)

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Keywords: European pear, meiosis, unreduced gametes, pollen development, polyploid breeding

The production of unreduced (2n) gametes is an important mechanism for polyploid formation and can be exploited in breeding programs for the development of novel germplasm. In European pear (Pyrus communis), the cytological mechanisms underlying stress-induced meiotic restitution remain poorly understood. This study aimed to characterize male sporogenesis in European pear and evaluate the effects of heat shock treatments on meiotic progression, pollen development, and the formation of putative unreduced pollen. A cut-branch experimental system was used to apply controlled heat shock treatments during male meiosis. Meiotic progression and outcome were analysed using chromosome spreads and aniline blue staining to assess chromosome behaviour, nuclear dynamics, and cell wall formation during microsporogenesis. Mature pollen was subsequently analysed by DAPI staining to quantify pollen diameter and nuclear area and to identify putative unreduced (2n) pollen. Heat shock induced a broad spectrum of meiotic abnormalities, including irregular chromosome segregation and defects in spindle organization and cytokinesis. These alterations resulted in the formation of dyads, triads, and polyads instead of normal tetrads. Heat-treated samples also contained enlarged pollen grains with increased nuclear area. A positive relationship between pollen diameter and nuclear area supported the classification of these enlarged pollen grains as putative unreduced (2n) pollen. However, the frequency of putative unreduced pollen remained relatively low compared with the frequency of meiotic restitution products observed during tetrad analysis, suggesting that many restitution-derived microspores fail to complete pollen development successfully. This study provides new insight into the cytological basis of heat-induced meiotic alterations in European pear and demonstrates that controlled heat stress can induce meiotic restitution associated with the formation of putative unreduced gametes. These findings highlight the potential of controlled heat treatments as a tool to generate unreduced gametes for polyploid breeding applications.

Poster (P2)

Conservation of pearl millet landraces for livelihood and nutritional security in India

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Keywords: Pearl Millet, Landraces, Seed bank, Conservation, Biodiversity

In the 21st century, climate changes, scarcity of water, population pressure, demand and price hike of food and other socioeconomic impacts are expected to generate great challenges to the agriculture and food security across the globe, especially for the low and middle income countries. Agrobiodiversity conservation is playing a key role in livelihood and nutritional security in present scenario of climate change. Millets are rich of nutrients and micronutrients and they are real answer to combat hidden hunger. Due to its nutritional superiority of they considered as nutricereal for human nutrition to ensure nutritional and food security. The present experiment was conducted during rainy season of 2019 to 2022. The pearl millet landraces were assigned codes through ClimMob App for recording of crop data. The trails were designed as mother trials and baby trials at three locations.

The best performing pearl millet landraces were taken in the record and listed for purpose of conservation, seed multiplication and promotion to the farming communities under seed chain concept at community level seed bank. Based on the results across the locations 7 pearl millet landraces viz. Sulkhaniya Bajri, Sundaram Verma Local, Moochwali Bajri, DR-1, DR-2, Pili Bajri and Chanana Bajri were found promising in yield as well as nutritional quality parameters. These pearl millet landraces has been registered under Protection of Plant Varieties and Farmers' Rights Authority (PPVFRA), New Delhi as farmer's variety.

As outcome of the farmers was producing quality seed of pearl millet landraces from 2021-22 onwards they started to earn extra income as sale of seed for their livelihood and nutritional security. The farmers were benefited through community seed bank and the quality seeds of different landraces were available for local farmers and other parts of the pearl millet growing areas to ensure the aim of mainstreaming of agricultural biodiversity conservation and utilization in agricultural sector to ensure ecosystem services and reduce vulnerability in Rajasthan, India. The seed bank concept is really a boon for the farmers to get additional income as well as they are playing an important role in conservation biodiversity. Therefore, conservation of pearl millet landraces are the solution to alleviate hidden hunger and ensuring nutritional security.

Poster (P4)

Breaking meiotic recombination barriers in soybean

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Keywords: meiosis, genome editing, plant breeding

Genetic variation through meiotic recombination is fundamental to crop improvement. However, the low frequency of crossovers (CO) in general and the tight regulation of the occurrence of crossovers in specific genomic regions restrict the efficient combination of beneficial traits. In soybean, meiotic recombination is limited, with typically only one to a few crossover events occurring per homologous chromosome pair during meiosis. Therefore, the MeioCOntrol project aims for the development of tools to visualize and enhance meiotic recombination in soybean, as a model for protein crops.

First, to be able to monitor CO events and determine the genome-wide CO landscape, we will optimize single-cell sequencing on soybean pollen. This approach involves the isolation of pollen nuclei, sorting individual nuclei using fluorescence-activated cell sorting (FACS), whole-genome amplification of single-cell genomic DNA, and subsequent low-coverage sequencing. The resulting data will enable the identification and mapping of recombination events across the soybean genome. Second, we will generate CO inducer lines to enhance meiotic recombination, with a particular focus on stimulating recombination in the typically suppressed pericentromeric regions and decreasing the effects of crossover interference. CRISPR/Cas-mediated genome editing will be employed to disrupt genes that suppress class I and class II CO formation, including genes involved in the suppression of (peri-)centromeric recombination. In addition, we will investigate the natural variation in key genes associated with CO formation. For this, hiPlex pooled amplicon sequencing and SMAP-based data analysis (Develtere et al. 2023) will be employed on a diverse number of soybean accessions, the EUCLEG collection (Saleem et al. 2021). Third, we will examine whether environmental factors, i.e. temperature and drought, influence the CO rate and enhance meiotic recombination in soybean.

By combining genetic and environmental strategies, the MeioCOntrol project aims to unlock previously inaccessible genetic variation and support the development of next-generation breeding approaches in soybean and other crop species.

Poster (P6)

Drought Tolerance in Cowpea (Vigna unguiculata): A Transcriptomic Analysis of Mutant Lines and Their Parents

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Keywords: Induced mutagenesis, Transcriptomic, Drought, Cowpea

Drought triggers complex anatomical, physiological and molecular changes in plants. In response, they alter their gene expression, physiology and leaf morphology. As these responses depend on genotype, it is important to identify the genetic mechanisms underlying drought tolerance. Induced mutagenesis in resilient crops such as cowpea enables the rapid generation of diversity for the characterisation of resistance mechanisms. This study employed high-throughput transcriptomics to identify genes that respond to drought in drought-tolerant cowpea mutant lines (12_20 and YND_7_9) and their parents (Melakh and Yacine). The greenhouse experiment included two conditions (control and stressed), with stress initiated 20 days after sowing and maintained for 15 days before sampling on 4 replicates. RNA was extracted from young leaves for RNA-seq. We used both pairwise comparisons and tests for interactions effects (~lines + treatment) to identify line-specific response to drought. These were further characterized with gene annotation, clustering by expression pattern, and KEGG pathway comparisons. On average, sequencing yielded 78 million high-quality reads per genotype with 98% of the reads were aligned to the reference genome. Under stressed condition, lines Melakh, 12_20, Yacine, and YND_7_9 showed 3360, 1862, 162, and 322 up-regulated genes, and 5362, 2396, 1997, and 590 down-regulated genes, respectively. The test for lineage specific interactions identified 6035 significant genes, indicating significant interactions between the genetic lines and the treatment. Of these, 5,875 were grouped into 23 clusters. The KEGG pathway diagram of the clustered genes shows that 37 pathways are significantly differentially regulated among the 1558 KOs identified. Two photosynthesis-related pathways were down-regulated in all lines, while pathways such as metabolic pathways, carbon metabolism, carbon fixation and glycolysis/gluconeogenesis were only down-regulated in Melakh, Yacine and 12_20. Conversely, genes in the biosynthesis of secondary metabolites pathway are down-regulated in the other lines and up-regulated in YND_7_9. Of the 16 genes in this pathway, only the drought-tolerance-related genes AT4G33150, DWF4 and SK1 are significantly overexpressed in YND_7_9. In sum, comparative transcriptomics of these four lines has revealed expressed genes associated with drought tolerance and identified further drought tolerance genes that are unique to each lineage.

Poster (P8)

Climate Resilient Crops via Multiplex Gene Editing

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Keywords: Multiplex gene editing, heat and drought stress, Climate resilience, CRISPR/Cas

As climate instability drives increased frequency of drought and heat stress, traditional breeding methods often fail to keep pace with the necessary rate of genetic gain for these complex, multigenic traits. The Gates Foundation project of Rainbow Crops aims to bridge the gap between simple genetic approaches and whole-genome selection by utilizing a sophisticated, AI-driven platform to perform highly multiplexed gene editing on regulatory elements.
The primary goal is to enhance early seedling vigor under heat and drought stress, which is a key indicator of long-term crop productivity and yield stability. Tropical varieties of three major crops, maize, rice, and sorghum are implemented into the pipeline to integrate climate-resilient traits into germplasm that is relevant to smallholder farmers in South Asia and Sub-Saharan Africa.
The project implements the "Trait Foundry™" platform that integrates AI-guided target discovery with high-throughput multiplex CRISPR/Cas editing, targeting regulatory elements rather than just coding regions to allow for dominant trait expression and minimized negative side effects. By focusing on non-coding DNA, gene expression can be modulated in a tissue-specific manner. Based on literature and public data, an AI knowledge graph is being built to predict gene-gene and gene-phenotype interactions. This knowledge graph will then be used to prioritize high value genetic targets for multiplex gene editing and phenotypic screening. As around 100 genetic targets need to be edited, regulatory elements of genes related to heat and drought stress tolerance, new strategies are being developed to increase the number of gRNAs in one transformation. Multiplex edited populations will undergo several generations of screening, using AI--guided crossings, with the ultimate objective of identifying statistically significant edit combinations that enhance heat and drought stress tolerance. A critical initial step involves creating platform-agnostic, automated phenotyping assays for maize, sorghum, and rice to measure seedling vigor under combined heat and drought stress, validated against manual measurements.
The findings of the project should yield a scalable toolbox for breeders, enabling the integration of any desired trait into elite germplasm.

Poster (P10)

Protecting Innovation in Plant Breeding: A Layered IP Strategy for the NGT Era

Cenens William (1), Logie Emilie (1), Lagaert Stijn (1)

Gevers

Keywords: Intellectual property, Patents, Plant Breeder's Rights, Trademarks, Freedom to Operate

The approval of the EU NGT Regulation marks an important and long overdue step forward for plant breeding. By treating plants obtained through novel genetic techniques similarly to conventionally bred plants with respect to safety (the so called NGT type 1 plants), the Regulation will open new commercial pathways for novel plant varieties to enter the EU market. As a result, a growing number of plant varieties containing NGT-derived edits is expected to be developed for the European market. In this increasingly competitive and fast paced landscape, it will be more important than ever to protect innovations effectively.

Plant variety protection through Plant Breeders' Rights (PBR) offers a natural starting point: it protects the variety as a whole. However, PBR does not extend to the underlying technology, the genetic modification process, or traits that go beyond individual varieties. In addition, NGT plants may face additional challenges, for example where their mono-parental origin leads to classification as essentially derived varieties (EDVs).

Patents can fill this gap and provide innovators with an acceptable scope of protection to stay in control of their innovation. Despite the exclusion of plant varieties and essentially biological processes for European patents, patents can still provide broad protection for NGT-related innovations. At the same time, faster breeding cycles and increasing reliance on shared or patented technologies are giving rise to a more complex IP landscape.

Finally, trademarks add a further layer of protection. By protecting the brand associated with a proprietary variety or seed line, breeders can build long-term consumer recognition that extends beyond the lifetime of both PBR and patent terms.

Together, PBR, patents, and trademarks form a layered and complementary IP framework. A well-designed strategy combining all three can provide broad, durable, and commercially robust protection for NGT innovations, covering the technology, the variety, and the brand across the full product lifecycle.

On the flip side, these different types of protection do raise important questions for breeders, growers and research institutes: who controls the valuable traits and technologies used in developing new varieties? Indeed, freedom to operate is a key consideration that needs to be embedded at an early stage of any research and development project, and this against the backdrop of developing European and international IP practices.

Poster (P12)

Variety Testing as a Platform for Validating Disease Resistance and Drought Adaptation in Novel Pome Fruit Cultivars

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Keywords: Fruit, variety testing, resistance, climate adaptation, drought

Developing fruit cultivars that remain productive and profitable under increasing biotic and abiotic stress is a major challenge for modern breeding programmes. While breeding generates novel genetic variation, long-term field evaluation is essential to identify cultivars that can translate this potential into robust performance under commercial conditions. Variety testing therefore represents a critical bridge between breeding and practice, offering a unique platform to validate stress-resilience traits under realistic production environments. For more than four decades, the experimental orchard for pome and stone fruits of pcfruit npo in Sint-Truiden, Belgium, has evaluated new apple, pear, cherry, and plum cultivars. In response to climate change, stricter regulations on plant protection products, and the increasing demand for sustainable production systems, the programme has evolved from a traditional focus on yield and fruit quality towards a broader assessment of resilience and adaptability.

In apple, resistance breeding has delivered cultivars with varying levels of tolerance or resistance to apple scab. To assess the practical value of these traits, scab-susceptible cultivars are evaluated under integrated pest management (IPM), while scab-tolerant and scab-resistant cultivars are tested across IPM, reduced-input, and organic production systems. This approach enables the validation of resistance traits under contrasting disease-management strategies and varying levels of external inputs. In pear, water availability is emerging as a key constraint for sustainable production. Candidate cultivars are therefore evaluated in parallel on irrigated and non-irrigated plots, allowing the identification of genotypes capable of maintaining yield and fruit quality under limited water supply.

This illustrates how variety testing can contribute far beyond cultivar recommendation. By integrating disease resistance and drought adaptation into routine evaluation protocols, variety trials become powerful field-scale platforms for validating breeding progress under real-world stress conditions. As environmental pressures continue to intensify, such testing programmes will play an increasingly important role in accelerating the selection and adoption of fruit cultivars capable of supporting resilient and sustainable production systems.

Poster (P14)

Generation of crossover reporter lines in Zea mays

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Keywords: Maize, meiotic recombination, T-DNA mapping

Chromosomal crossover is the process by which homologous chromosomes pair and exchange DNA segments, generating novel allelic combinations and promoting genetic diversity in offspring. In maize, the introduction of new traits is hindered by the suppression of crossovers across large genomic regions. In Arabidopsis, crossover frequency can easily be monitored using crossover reporter lines, carrying genetically linked fluorescent markers that enables visualisation and quantification of meiotic recombination events in pollen. However, such tools are not yet available in crops such as maize. Here, we report the generation of such fluorescent tagged lines (FTLs) in maize. We have generated 18 independent maize lines expressing GFP in pollen and 14 expressing mCherry. All selected lines contain high-quality T-DNA insertion events, defined by a single T-DNA copy integrated at a unique site in the genome. Precise localisation of these markers is essential, as FTL functionality depends on linkage between markers. However, T-DNA mapping is challenging in maize due to the complexity of the genome. We therefore established a novel approach for localising T-DNA insertions within the maize genome, enabling the development of functional FTLs. These FTLs will provide a tool to quantify recombination in maize with high precision and enable large-scale screens to identify genetic factors and environmental influences that shape genome variability.

Poster (P16)

Development of new KASP markers to detect Phytophthora infestans resistance in tomato

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Keywords: Phytophthora, tomato, KASP

Late blight, caused by Phytophthora infestans (Mont.) de Bary, represents one of the most destructive diseases in cultivated tomato (Solanum lycopersicum L.). Over the past decades, several late blight resistance genes have been identified in wild Solanum species and introgressed into cultivated tomato. It was shown that that the combination of Ph 2 and Ph 3 genes provides resistance against a broad spectrum of P. infestans races (Foolad et al., 2006)
In Belgium and the Netherlands, a participatory breeding program was initiated in VIVES in 2023 with the objective of developing robust outdoor resistant tomato varieties. Phenotypic selection for late blight resistance in the field is not always reliable. Several molecular markers linked to Ph-2 and Ph-3 genes have been described (Shekasteband et al, 2015; Zhi et al, 2021).
The objective of this study was to evaluate the applicability and robustness of Ph 2 and Ph 3 molecular markers in a participatory breeding context involving diverse tomato types. Particular emphasis was placed on (new) developed KASP (Kompetitive Allele Specific PCR) markers, that enables rapid and accurate detection of co dominant SNP polymorphisms and that can distinguish homozygous and heterozygous resistant plants.
For the Ph-2 resistance gene, two KASP markers (8854 and KASP-1) located in close proximity of the gene were evaluated and their performance was compared with that of the widely used CAPS-1 marker. A similar approach was applied to the Ph-3 resistance gene, where two KASP markers (63742 and 69874) were assessed and compared with the commonly used TG328 CAPS marker. All markers were applied to approximately 50 commercial tomato varieties with known field resistance. For the Ph-2 gene, the KASP-1 marker showed the highest concordance with the CAPS-1 marker, making it the most reliable KASP marker evaluated to date. For the Ph-3 gene, the KASP marker 69874 marker showed near-complete concordance with the TG328 marker. Subsequently, we also successfully developed the TG328 marker into a KASP marker.
In addition, we screened approximately 200 samples collected in 2025 from the participatory breeding program using all markers to assess the usefulness of our marker set. Our results highlight the importance of screening parental lines, as some varieties exhibited contradictory marker responses. An additional dataset from the 2026 breeding program is currently being analyzed.

Poster (P18)

Exploiting hybridization and polyploidy to improve drought tolerance in forage grasses

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Keywords: hybridization, polyploidization, transcriptomics

The increasing frequency of extreme weather events are negatively affecting the productivity of agriculturally important crops such as ryegrasses, underscoring the urgent need for more climate-resilient varieties. Hybridization can combine complementary traits to improve stress tolerance, while polyploidization increases gene dosage, thereby expanding the phenotypic space available for resilience under changing environmental conditions. This study aims to evaluate the effects of genetic diversity and polyploidy on drought stress and subsequent recovery within a well-characterized Lolium–Festuca–Festulolium system, with a focus on its potential for future crop improvement.

At the diploid level, interspecific hybrids were generated between the highly digestible, nutritious ryegrass species Lolium perenne and Lolium multiflorum, as well as intergeneric crosses between Lolium and the more drought-tolerant genus Festuca, resulting in Festulolium hybrids (Lolium × Festuca). These diploid hybrids were subsequently tetraploidized, establishing a model system that spans both intra- and interspecific genetic diversity across ploidy levels. Within this framework, we investigated the effects of hybridization and ploidy on drought tolerance by integrating physiological measurements with transcriptomic analyses. Using multi-allelic, haplotype-based markers, we further assigned gene expression profiles to specific subgenomes, enabling detailed characterization of expression dominance and allele-specific expression patterns.

These insights provide a deeper understanding of the molecular mechanisms underlying adaptive stress responses in polyploid hybrids and offer valuable perspectives for the development of more climate-resilient forage crops.

Poster (P20)

Two strategies for transgene-free gene editing of *Malus domestica*

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Keywords: CRISPR, NGT1, Transgene-free, apple

Powdery mildew, caused by the fungal pathogen *Podosphaera leucotricha*, leads to a major loss in apple fruit yield and quality. Although gene editing presents promising opportunities to develop resistant cultivars, its application in vegetatively propagated crops like apple remains limited, as elimination of CRISPR-encoding T-DNA after *Agrobacterium*-mediated transformation requires additional crosses. This project explores alternative approaches for transgene-free gene editing of *Mildew-Locus O* (*MLO*) susceptibility genes in apple (*Malus domestica*) to confer resistance to powdery mildew.

In a first approach, leaf- and meristem-derived protoplasts are transiently transfected with plasmid DNA or ribonucleoprotein complexes to induce targeted mutations. An efficient protoplast isolation protocol is developed for apple and a transfection efficiency of 22.7 % was obtained, after transfection of protoplasts with a GFP-expressing vector. In addition, first results of regeneration of apple protoplasts are promising, as multiple consecutive divisions have been observed. Edited protoplasts are subsequently regenerated via callus into whole plants, and outcomes are assessed by dPCR and multiplex amplicon sequencing.

In a second approach, we are optimizing *Agrobacterium*-mediated leaf transformation and regeneration in apple to transiently deliver tailor-made CRISPR destination vectors in leaf material. Preliminary GUS-staining results show that multiple *Agrobacterium* strains successfully transform leaf tissue. Transformed leaves will regenerate into shoots carrying targeted mutations, without stable T-DNA integration. Preliminary results show a leaf regeneration efficiency of 67 %.

Both strategies will enable the development of transgene-free apple cultivars with targeted *MLO* mutations for enhanced tolerance to powdery mildew.

Abstracts: Session 4

Understanding plant reactions to tomorrow's challenges

Keynote speaker (11:10 - 11:40)

Using digital twins to support the design of resilient and sustainable agicultural systems

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Keywords: Agroecology, digital twins, soil-crop model, cropping systems, climate change

Modern agricultural systems face the dual imperative of enhancing climate resilience and delivering long-term sustainability while maintaining productive capacity. Addressing these complex, interconnected challenges requires a shift from static, single-scale evaluations to dynamic, system-level approaches. Digital twins—virtual representations of agricultural systems, potentially powered by process-based soil-crop models, spatial datasets, and robust analytical indicators—offer a transformative framework to design, simulate, and optimize agroecosystems to sustain effective agroecological transition.

This keynote synthesizes recent advancements across landscape and field scales to demonstrate how harmonized digital twins bridge the gap between crop-soil processes and strategic decision-making.

We will present how, at regional level, conceptual digital twin applications linking food systems to cropping systems can help land use redesign across territory, in light of a dietary shift towards more sustainable and healthy food. From there, we will show how agronomic knowledge can further be transformed into decision rules to automatically design agronomically-sound and environmentally-optimized crop rotations.

Scaling down from farm and regional levels to individual fields, we will evaluate how cropping systems transformation allows for optimizing the provision of targeted ecosystem service delivery under changing environmental pressures, including climate change. Relevant approach mobilizing crop diversity indicators will be presented as tools to evaluate the potential for maximizing biological synergies, breaking pest cycles, and stabilizing nutrient flows.

Complementarily, high-resolution soil-crop modeling provides essential mechanistic insights into how innovative crop rotations alter carbon and nitrogen cycling, soil structure, and water dynamics. When projected across future climate scenarios, we will show how these dynamic models quantify long-term trade-offs between yield stability and ecosystem services, offering a virtual testbed for climate adaptation strategies.

By integrating decisional mechanisms, soil-crop processes, and spatial optimization into a unified digital twin, we can move from reactive management to proactive agroecological design. Digital twin technologies might indeed help empower researchers and agricultural stakeholders to build resilient, multi-functional agricultural systems able to navigate future global challenges and ultimately inform policy-makers more efficiently.

Speaker (11:40 - 12:00)

Glow with the flow

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Keywords: Plant, Heat, Stress, adaptation, redox, biosensors

Hydroxyl radicals (•OH) are highly reactive molecules that can cause severe cellular damage. Plants rely on a range of redox-based protective systems to limit oxidative stress, but how these processes are organized in living tissues remains poorly understood. One emerging component of cellular sulfur chemistry involves hydropersulfides (RSSH), small and highly reactive sulfur-containing molecules that are part of conserved sulfur redox networks present across all domains of life.

To investigate their dynamics in living plants, we developed PersIc (PERSulfide IndiCator), a genetically encoded fluorescent biosensor that specifically reports hydropersulfide dynamics in real time with high spatial resolution. After validation in mammalian cells, we adapted the sensor for plants (PersIcPlant), enabling visualization of hydropersulfide changes from cellular to organ scale.

Using this tool, we aim to determine how environmental stresses influence hydropersulfide dynamics and how these changes relate to plant stress responses and adaptation.

In parallel, we are developing complementary biosensors with distinct spectral properties to investigate how plant interactions with pathogens and symbionts affect redox processes associated with oxidative stress, including hydroxyl radical formation. Together, this work will provide a dynamic view of sulfur-based redox chemistry in living plants and its role in stress resilience, building on deeply conserved biochemical systems that are fundamental to cellular life.

Speaker (12:00 - 12:20)

Scaling up soybean nodulation phenotyping with NodQuant

Idrissa Traore (1)(2)(3), Connor Forsyth (2)(3), Riet De Weyer (2)(3), Lara Van Dijck (2)(3), Margo Vermeersch (1), Olivier Berteloot (2)(3), Helen Wilkinson (2)(3), Hilde Muylle (1)(3), Sofie Goormachtig (2)(3), Niel Verbrigghe (1), Steven Maere (2)(3)

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Keywords: deep learning, soybean nodulation, object detection, phenotyping, YOLO

Root nodules are specialized symbiotic organs in which rhizobia convert atmospheric nitrogen into plant-available forms. Nodulation is therefore a key determinant of soybean productivity, yet remains difficult to characterize thoroughly and at scale. Existing automated pipelines for nodule phenotyping typically image nodules while they are still attached to the intact root system, an approach well suited to pots or hydroponics, where root systems remain small and easy to manipulate. These techniques typically do not estimate nodule volume, and are difficult to scale to field trials with large genotype panels due to the time-consuming steps of root cleaning and image acquisition. We therefore detach nodules from the roots after collection and image them separately in Petri dishes under standardized conditions, decoupling nodule imaging from root architecture altogether and making the workflow portable and scalable across field sites and genotype panels. Building on this strategy, we developed NodQuant, an automated deep-learning pipeline for high-throughput nodule quantification. It combines two dedicated YOLOv11s models: the first locates and crops the Petri dish region, the second detects individual nodules within it, followed by SAM2-based segmentation of each detected nodule, enabling precise estimation of nodule size and volume. The models were trained on manually annotated data (197 images for dish detection; 374 cropped images totaling 3,645 nodule instances). Petri dish detection, used solely to isolate the relevant image region, performed near-perfectly (mAP50 = 0.995); nodule detection reached a precision of 0.964, recall of 0.925, and mAP50 of 0.972 on validation. In practice, this accuracy translates into a substantial gain in throughput compared to manual nodule counting, making large-scale phenotyping campaigns feasible. To date, NodQuant has processed over 14,000 images across several trials, including a GWAS panel of 315 genotypes and a genotype × strain screen of 20 soybean accessions against 7 Bradyrhizobium strains, extracting nodule number, size, volume and weight to build a richer symbiotic phenotype. It is now being applied to drought and low-temperature trials to identify soybean × Bradyrhizobium combinations that best sustain nitrogen-fixing symbiosis under stress.

Poster (P22)

Decoupling lignan content from salinity tolerance: microRNA-mediated regulatory control in flax (Linum usitatissimum L.)

Anirban Jyoti Debnath (1)(2)*, Ľubomír Harenčár (4), Matúš Kučka (5), Marek Kovár (1), Eva Ivanišová (3), Veronika Mistríková (3), Ján Gažo (1), Katarína Ražná (1)

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Keywords: Antioxidant response, MicroRNA regulation, Reactive oxygen species, ROS detoxification, Salt stress adaptation

Dissecting molecular regulators of salinity tolerance is vital for climate-resilient crops. Flax (Linum usitatissimum L.) is rich in stress-mitigating lignans, yet their role in salt tolerance remains unclear. This study compared the physiological, biochemical, and molecular responses to salinity stress on two flax genotypes: Astella (high lignan) and Flanders (low lignan). Three-week-old plants were treated with 100 mM NaCl stress for 7 days. Interestingly, the low-lignan Flanders genotype exhibited superior stress adaptation through a resource-conserving strategy of growth suppression. Flanders also demonstrated enhanced antioxidant capacity, higher osmoprotection, and elevated lignan-associated microRNA levels, resulting in efficient reactive oxygen species (ROS) detoxification, reduced cellular damage, and improved stress tolerance compared to Astella. Multivariate analysis indicated that superior salinity tolerance does not directly correlate with sheer lignan abundance. Instead, microRNAs likely play pleiotropic roles in this adaptation. These findings show flax salt resilience stems from regulatory network efficiency rather than mere metabolite abundance, and provide novel targets for improving crop stress tolerance.

Poster (P24)

Below-ground field phenotyping with Electrical Resistivity Tomography (ERT) in HYDRAS

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Keywords: agrogeophysics, hydras, ERT

Changes in precipitation distribution and frequency across Europe related to climate change are a challenge for agriculture. With more intense rainfall and more extended drought periods becoming more likely, agroecosystems need to be made more resilient. Breeding drought-resistant genotypes or adapting agricultural management practices are two aspects to improve the resilience of agriculture against drought. In this context, soil moisture is a key variable that will help crops bridge periods of drought. Hence, understanding what is happening in the hidden half of the crop, i.e., how soil moisture is being used, is essential to select resilient genotypes and develop suitable management practices. Practical breeding applications and developing soil moisture preserving management practices require field-scale studies to fully assess the crop phenotype in real soil conditions comparable to production fields. Soil moisture point sensors are useful to monitor soil moisture in the field, but their small volume of observation makes it difficult to obtain information at a high spatial resolution. In this research, we showcase the use of electrical resistivity tomography (ERT) as a means to monitor soil moisture in the root zone and this in experimental fields of 300 m² over the entire growth period and, hence, scale up, information from soil moisture point sensors. As such HYDRAS, the HYdrology, Drones and RAinout Shelter open access international research infrastructure provides both High-Throughput Field Phenotyping (HTFP) both above and below-ground. ERT uses surface electrodes to send current into the soil and measure the resulting voltage. In this way we obtain the resistivity of the subsurface, that can be related to soil moisture. By coupling above-ground and below-ground observations it is then possible to obtain a complete representation of the whole crop phenotype throughout the growing season. Automated ERT systems enable data collection at an hourly frequency, a time scale relevant to studying crop processes in the root zone. While the use of ERT to follow soil moisture content is not new, the implementation of ERT within a field phenotyping facility is. In this work, we present our latest findings and current challenges on the use of ERT to phenotype the hidden half of the crop within the HYDRAS field phenotyping facility.

Poster (P26)

Effects of drought and heat stress on pollinator-attracting floral traits and pollen viability

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Keywords: carotenoids, flower age, pollen viability, water holding capacity

Reproductive success is a major determinant of yield in many horticultural crops, which often depends on effective pollination and high fertility. However, drought and heat stress are major constraints to productivity in these crops. Yet, the mechanisms by which water deficit and elevated temperatures affect floral development, pollinator interactions and pollination success remain poorly understood. We hypothesize that drought and heat stress alter floral traits involved in pollinator attraction, including petal size and pigmentation, while also impairing pollen viability. To test this hypothesis, *Brassica napus* cv. Westar was grown under three soil water-holding capacities (70%, 30% and 15% WHC) and two temperature regimes (22°C/20°C and 30°C/22°C day/night). Both treatments were applied from the bud stage to flowering to examine their effects. Petal area was assessed by image analysis, petal carotenoid content was quantified spectrophotometrically, and pollen viability was evaluated using fluorescein diacetate/propidium iodide co-staining and fluorescence microscopy. Our data show that petal area was significantly reduced under drought and heat stress. Petal carotenoid content was not significantly affected by either drought or heat stress. Pollen viability was unaffected by drought but declined significantly under heat stress. Together, these findings indicate that floral traits differ in their sensitivity to different abiotic stresses, with heat affecting pollen viability more strongly than drought, while carotenoid content remained relatively stable. Future work will integrate these phenotypic studies with metabolite profiling, transcriptomics, and CRISPR/Cas gene editing to identify key regulatory pathways driving stress-induced floral changes and their consequences for pollinator attraction and yields.

Poster (P28)

Crop dependency on multiple ecosystem services: a global exploration

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Keywords: Pest control, plant traits, pollination, resource use, yield

Agricultural production is shaped by multiple processes that operate simultaneously, including pollination, natural pest control, soil nutrition, and water availability. However, crops differ substantially in their dependence on processes. The extent whereby these sensitivities vary across crops and how they relate with certain traits has not been explored. In this study we explore and quantify how crop traits influence sensitivity to ecosystem services and environmental stressors such as drought and nutrient shortages for 239 crops. Our first analyses highlight that yield loss due to lack of pollination is less (16% yield loss) compared to yield loss due to a lack of pest control (27%), and that there is a negative relationship between pollination dependence and pest control. We also conclude that pest control dependence does not vary with plant growth form, whereas pollination dependence is higher for woody crops compared to herbaceous crops. Pest control dependence does not vary for the part of the plant that we consume, whereas pollination dependence is higher for crops of which we consume the reproductive parts (fruits, seeds), compared to the crops of which we consume the vegetative parts. Subsequent analyses will further include more plant traits and information on resources uses, yet these first results provide a framework for predicting synergistic effects and tradeoffs between pollination and pest control services in crops.

Poster (P30)

Differential physiological, nutritional and molecular responses to lead stress in garden balsam and ornamental kale.

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Keywords: Garden balsam, Ornamental kale, Pb stress, Heat shock proteins, Phytoremediation, Proline

Lead (Pb) is one of the most toxic environmental pollutants and poses a serious threat to plant growth and ecosystem health. Ornamental plants are considered promising candidates for phytoremediation because they combine environmental remediation with aesthetic value and are not part of the human food chain. In this study, the physiological, biochemical, nutritional, and molecular responses of garden balsam (Impatiens balsamina) and ornamental cabbage (Brassica oleracea var. acephala) to Pb stress were evaluated following exposure to 0, 100, 200, and 400 ppm $Pb(NO_3)_2$.

Pb accumulation occurred predominantly in the roots, with ornamental cabbage exhibiting greater accumulation capacity. Although Pb exposure affected nutrient uptake, the magnitude of these changes varied among elements and species. Ion leakage and turgor pressure were only moderately influenced, while chlorophyll content and biomass remained relatively stable, indicating a high level of tolerance. Garden balsam accumulated proline under severe Pb stress, whereas ornamental cabbage maintained protein homeostasis through increased total soluble protein content and strong induction of heat shock proteins (HSP60 and HSP23). In contrast, garden balsam showed weaker molecular responses.

These findings demonstrate that ornamental cabbage possesses more efficient detoxification mechanisms and greater tolerance to Pb stress than garden balsam, highlighting its potential as a suitable ornamental species for the phytoremediation of Pb-contaminated environments. This study contributes to a better understanding of plant stress responses and supports the development of sustainable strategies for the remediation of polluted ecosystems.

The results presented in this abstract are based on our recently published study in Scientific Reports.

Poster (P32)

Elucidating the role of the plant circadian clock in latitudinal adaptation

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Keywords: Circadian clock, latitudinal adaptation, photoperiod, climate change

Our most productive agricultural zones are shifting polewards to evade rising temperatures due to global warming. It is critical to understand what the impact of such latitudinal migration will be on plant physiology to predictably breed and engineer climate-resilient crops. Past research by our lab and previous work in the field has found that the plant circadian clock genes are key to how plants adapt to the two major environmental factors that change with latitude: photoperiod (i.e. seasonality) and twilight length. To expand our understanding on how plants adapt to latitude via the circadian clock, we have used multiplexed gene-editing to create new alleles of plant clock genes in Arabidopsis thaliana, which may result in altered latitudinal sensitivity. We are now using custom-built growth chambers that can simulate real world latitudinal light changes to screen these clock mutants. Altered phenotypes, such as flowering time, together with molecular analyses (transcriptomics and transcription factor-DNA interactomics), will give insight into how plants fine-tune their reaction to light regimes at different latitudes. Discovering which clock alleles allow plants to adapt better or worse to latitudinal migration will enable the development of robust, climate-adapted crops in a warming planet with rapid geographical changes in agricultural productivity.

Poster (P34)

Harnessing Pulses for Climate-Resilient Organic and Natural Farming: Current Status, Challenges and Future Prospects

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Keywords: Pulses, Organic farming, Natural farming, Soil health, Climate resilience, Regenerative agriculture

Pulses are indispensable for sustainable agri-food systems owing to their high nutritional value, biological nitrogen fixation, and capacity to enhance soil health under low-input conditions. With increasing global emphasis on climate-smart and chemical-free agriculture, organic and natural farming have emerged as promising approaches for sustainable pulse production. The experimental findings synthesize current knowledge on the role of pulses in organic and natural farming, highlighting the contribution of indigenous bio-inputs to soil fertility, crop productivity and environmental sustainability.

Concerted field experiments were conducted to evaluate the regenerative advantages of pulse cultivation under organic and natural farming systems to mitigate the vagaries of climate change. Particular emphasis was placed on the agronomic and ecological functions of natural farming inputs including Jeevamrit, Ghanjeevamrit, Achhadan (mulching) and Dashparni Ark, together with their influence on soil biological processes, nutrient cycling and pest management. The evidence indicates that pulses are highly compatible with organic and natural farming because of their inherent nitrogen-fixing ability and adaptability to resource-conserving production systems. Natural farming inputs consistently enhance microbial activity, improve nutrient availability, strengthen soil organic carbon dynamics, conserve moisture, suppress pests through eco-friendly approaches and reduce dependence on synthetic agrochemicals. Despite these advantages, wider adoption remains constrained by lower productivity, inadequate access to quality seed, limited technical knowledge, certification challenges and restricted market linkages. Growing consumer demand for residue-free food, supportive policy initiatives and advances in pulse improvement provide substantial opportunities for expanding sustainable pulse production.

Pulses represent a strategic component of resilient and regenerative agricultural systems capable of simultaneously addressing food security, environmental sustainability and climate adaptation. Integrating pulse-based cropping systems with scientifically validated organic and natural farming practices can substantially improve soil health, reduce external input dependency and strengthen ecosystem services.

Poster (P36)

Putrescine Enhances Root Growth, Water Status, and Redox Homeostasis in Zinnia elegans under Drought Stress

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Keywords: Zinnia elegans, drought stress, putrescine, antioxidant enzymes, membrane stability

Objective: Drought severely restricts the growth and ornamental quality of bedding plants. This study investigated the effectiveness of foliar-applied putrescine in mitigating drought-induced physiological, morphological, and biochemical damage in Zinnia elegans 'ZinniaCut'.
Methods: Plants were grown under three irrigation regimes (100%, 70%, and 35% of full irrigation). Putrescine (0.1 mM) was applied as a foliar spray at the onset of drought stress and again two weeks later. Growth, water status, photosynthetic pigments, membrane stability, and antioxidant responses were evaluated.
Results: Progressive drought significantly reduced biomass production, relative leaf water content (RWC), and photosynthetic pigments while increasing oxidative damage. Under severe drought (35% irrigation), putrescine increased root fresh weight from 1.92 to 3.70 g and improved RWC from 61.8% to 77.4%. It also reduced ion leakage from 18.4% to 17.1% and enhanced superoxide dismutase activity from 2.86 to 3.91 U mg^{-1} protein, indicating improved membrane stability and antioxidant capacity. In contrast, chlorophyll a and total chlorophyll contents were not maintained by putrescine, suggesting that drought tolerance was achieved primarily through cellular protection rather than preservation of photosynthetic pigments.
Conclusions: Foliar application of putrescine effectively enhanced drought tolerance in Z. elegans by improving water status, membrane integrity, and redox homeostasis. These findings provide a foundation for integrating putrescine into sustainable drought management strategies and for future studies exploring the molecular networks underlying polyamine-mediated stress tolerance in ornamental species.

Poster (P38)

Agronomic Biofortification of Pulses: A Sustainable Strategy to Combat Hidden Hunger and Nutritional Insecurity

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Keywords: Agronomic biofortification, Pulses, Hidden hunger, Iron, Zinc

Objectives: Hidden hunger resulting from deficiencies of iron (Fe), zinc (Zn) and other essential micronutrients affects more than two billion people worldwide, particularly in developing countries. Pulses contain 18–28% protein and are important dietary sources of Fe, Zn, Ca and other micronutrients, making them ideal candidates for biofortification. The concerted experimentation conducted evaluates recent advances in agronomic biofortification of pulses and its potential to enhance nutritional quality and improve food and nutritional security.
Methods: Various experiments conducted to assess the effectiveness of agronomic interventions, including foliar fertilization, soil application, seed priming, seed coating and nano-enabled fertilizers, in improving micronutrient uptake, translocation and bioavailability in pulse grains. Their performance was compared with complementary breeding and microbial approaches.
Results: The analysed findings demonstrates that agronomic biofortification is among the fastest and most cost-effective strategies for enriching edible grains with micronutrients. Although breeding approaches of biofortification are stable and long lasting. Across field crops, foliar and soil application of micronutrients increased grain iron concentration by approximately 5–25% and zinc concentration by 10–25%, depending on crop, genotype, soil type and fertilizer management. Moreover, genotypic variations are also pre-dominant in the Fe and Zn concentration in the grain. Foliar application of Fe and Zn during flowering to early pod-filling stages consistently produced greater grain enrichment than soil application alone. Integration of balanced fertilization, micronutrient-efficient cultivars and next-generation fertilizers further enhanced nutrient-use efficiency, grain nutritional quality and production sustainability. Nevertheless, nutrient mobility within plants, genotype × environment interactions and anti-nutritional compounds affecting mineral bioavailability remain major constraints requiring further investigation.
Conclusions: Agronomic biofortification provides a practical, scalable and environmentally sustainable strategy to alleviate hidden hunger through pulse-based food systems. Combining precision nutrient management with improved pulse cultivars offers a viable pathway to enhance dietary micronutrient intake and support global food and nutritional security while contributing to the Sustainable Development Goals.

Poster (P40)

Using single-plant multi-omics in the field to uncover the molecular wiring of yield phenotypes in Brassica napus

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Keywords: single-plant data, lab-field gap, plant development, predictive modelling, trajectory inference

Historically, processes influencing plant phenotypes have been studied intensively under controlled laboratory conditions. However, the results of such controlled lab studies often do not translate well to more complex field settings. To help close this lab-field gap, we developed an experimental setup to study the molecular wiring of plant traits and their variability directly in the field, based on profiling the transcriptome, micro-environment and phenotypes of individual plants of the same genetic background grown in the same field. We used this single-plant omics strategy on winter-type rapeseed (Brassica napus) and built machine learning models predicting within-field variability of various phenotypes from autumnal leaf gene expression and environmental data layers such as soil nutrient profiles, microbiomes and micro-climate data. Autumnal leaf gene expression showed predictive power for both autumnal leaf phenotypes and final yield phenotypes in spring. Many of the top yield predictors are linked to developmental processes known to occur in autumn in winter-type B. napus accessions, such as vegetative-to-reproductive transitioning, indicating that the yield potential of winter-type rapeseed is related to autumnal development. We applied trajectory inference methods from the single-cell field on our single-plant data to further unravel these developmental effects.

Poster (P42)

Eyes in the sky: UAV imagery and deep learning for stress and anomaly detection in ornamental crops

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Keywords: unmanned aerial vehicle (UAV), artificial intelligence (AI), High-Throughput Field Phenotyping (HTFP), ornamental crops, crop management

In the horticultural sector, many tasks, including the detection of stress symptoms and growth anomalies, are still performed manually through field scouting. Given the scale of commercial cultivation areas, this approach is time-consuming and labour-intensive. In addition, it often relies on subjective visual assessments and requires expert knowledge for early and specific stress detection. With the declining availability of highly skilled personnel, rising labour costs and a growing demand for efficient production systems, reducing dependence on manual labour has become essential.

Automation and digitalisation offer promising solutions to these challenges. High-Throughput Field Phenotyping (HTFP) using remote sensing technologies enables the rapid and non-invasive monitoring of large numbers of plants. Within this context, unmanned aerial vehicles (UAVs) equipped with high-resolution imaging sensors are particularly well suited, as they can efficiently capture detailed spatial and temporal information across large cultivation areas. Combined with deep learning and advanced image analysis, these data can support automated phenotyping and enables data-driven crop management.

Several applications are currently being developed for both production and breeding purposes, including container-grown as well as open-field crops. In chrysanthemum cultivation, plants exhibiting growth deficits were detected by automatically estimating the diameter of individual plants using RGB UAV imagery and the Segment Anything Model (SAM). Compared with the traditional approach, this method substantially reduces measuring time while providing objective, field-scale information to support cultivation decisions. Similarly, the use of UAV imagery and deep learning (DL) are being explored for the early detection of diseases, ranging from powdery mildew in tree nurseries to Phytophthora infections in container-grown rhododendron production systems, with encouraging results reported across both applications. The adaptability of these approaches suggests that similar workflows could be applied to other crop species and monitoring objectives through crop-specific model training and fine-tuning.

Overall, the presented applications demonstrate the potential of UAV-based HTFP and DL to improve the efficiency, scalability and objectivity of crop monitoring, contributing to more sustainable and precise crop production in horticulture.

Poster (P44)

Plant-based sensing for understanding water use and hydraulic responses in pear orchards

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Keywords: irrigation management, sap flow, stem diameter variation, hydraulic stress, tree age effects

Atmospheric demand and soil water status are commonly used to characterise water availability and guide irrigation management. However, plant-based measurements provide complementary information by directly capturing the dynamic water needs of fruit trees. This study aimed to compare the water use, hydraulic stress and recovery of 8- and 28-year-old fully bearing pear trees exposed to comparable atmospheric demand and soil drying conditions during a heat event.

The experimental setup consisted of five plots, each containing three trees, located within a 9.2-hectare commercial pear orchard in Bierbeek, Belgium, on moderately dry silt loam soil. During the 2026 growing season, the sap flow rate, stem diameter variation and soil water potential of 'Conference' pear trees (Pyrus communis L.) grown under drip irrigation were continuously monitored. Sap flow was measured using the heat ratio method, stem diameter variation using a linear variable differential transformer, and soil water potential using TEROS 21 sensors. Daily water use, net stem growth, recovery ratio, and daily maximum tree water deficit were derived for each age class.

Despite similar evaporative demand and soil drying conditions, the two age classes had different responses in terms of tree water use during the heat event. Younger trees used less water and showed a smaller increase in sap flow rate during the heat event. In contrast, older trees showed higher water use and a stronger response to increased atmospheric demand. Younger trees exhibited stronger growth and overnight recovery, while older trees developed a larger tree water deficit.

These differences appear closely linked to tree age and size, although a contribution of other tree-specific factors cannot yet be excluded. Since age classes showed distinct hydraulic responses despite comparable atmospheric and soil conditions, irrigation scheduling based solely on soil- and climate-based indicators risks over- or under-irrigating specific groups. Incorporating continuous plant-based measurements into
irrigation decisions could tailor water supply to actual tree water status, improving irrigation efficiency under increasing heat and drought.

This work was carried out within the framework of the Interreg North-West Europe project HydroSoilWise (Enhancing Hydromanagement & Soil Health in Agriculture for a Climate-Wise Environment), which contributes to the programme priority "Smart Climate and Environmental Resilience for NWE Territories."

Poster (P46)

A conceptual framework for multi-stress in crops

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Keywords: multi-stress, priming, eustress, distress

Crop performance is increasingly challenged by combinations of abiotic and biotic stresses that occur simultaneously or sequentially throughout the growing season. While plant responses to individual stressors are often described through the classical eustress-distress paradigm, no generic framework currently exists to extend this concept towards multi-stress environments. Here, a conceptual framework is proposed that aims to link stress exposure, plant resistance mechanisms and crop performance across single- and multi-stress conditions.

In the single-stress case, stress exposure is represented along a continuous axis describing the effective stress pressure experienced by the plant. This pressure is determined by the timing, duration and intensity of the stress event relative to crop development. The resulting plant response curve reflects the crop's ability to cope with the stress through a combination of tolerance, avoidance and escape mechanisms. Crop performance therefore emerges from the interaction between the magnitude of stress exposure and the shape of the response curve.

The framework is subsequently extended to multi-stress systems. Exposure to a primary stress may alter the crop's sensitivity to subsequent stresses by modifying physiological, morphological or developmental responses. Beneficial interactions, such as stress memory or priming, may shift the response curve, allowing the plant to withstand higher stress exposure. Alternatively, compounding effects may shift the curve in the opposite direction and consequently increase vulnerability. These shifts provide a generic representation of positive and negative interactions among multiple stressors, irrespective of their abiotic or biotic nature. This approach ultimately profiles the integrated overall effect of multiple stress factors on plant performance.

The proposed framework offers a common language for describing multi-stress conditions and for linking mechanistic understanding to breeding, phenotyping and crop modelling. Furthermore, it offers a conceptual foundation for improving the design and interpretation of experiments, facilitating the translation of experimental findings into practical strategies for crop improvement and adaptation.