



IPAP 2026

International Plant & Algal Phenomics Meeting

June 25th – 28th

Program | Book of Abstracts



List of Participants

IPAP 2026 | International Plant & Algal Phenomics Meeting

June 25th – 28th | Brno, Czech Republic

OPENING LECTURES

25 th June	Thursday
9:00 – 14:00	Data management working group meeting prior official IPAP program (organized at PSI, Photon Systems Instruments, spol. s r.o.).
15:00 – 18:00	Registration. Poster and Exhibition setup.
18:00 – 18:20	Martin Trtílek (Photon Systems Instruments, Czech Republic) Pushing the Boundaries of Plant Phenotyping: Next-Generation Sensors, Automation, and Imaging Technologies from PSI.
18:00 – 18:40	Antony Bačič (Institute for Sustainable Agriculture & Food (LISAF), La Trobe University, Australia) Beyond Phenotyping: Delivering Impact Across the Agri-Food Value Chain.
18:40 – 22:00	Welcome Reception with pre-conference networking and poster session. Beer, Wine and Snacks.

Pushing the Boundaries of Plant Phenotyping: Next-Generation Sensors, Automation, and Imaging Technologies from

Martin Trtílek¹

¹ Photon Systems Instruments, spol. s.r.o., Drasov, Czech Republic

Recent advances in plant phenotyping increasingly depend on the integration of novel sensing technologies, automation, and high-throughput data acquisition systems. In this opening presentation, we will provide an overview of the latest developments from Photon Systems Instruments (PSI), highlighting a new generation of unique research instruments designed to address emerging challenges in plant, algae, and environmental sciences.

The presentation will introduce PSI's newest phenotyping platforms and advanced sensor technologies, including recently developed imaging, physiological, and environmental monitoring solutions that expand the capabilities of both controlled-environment and field-based phenotyping. Particular attention will be given to innovative sensor integration approaches enabling the simultaneous assessment of plant performance across multiple spatial and temporal scales.

We will further present the latest developments of the **AlgaScreen robotic platform**, an automated high-throughput system for cultivation and phenotyping of microalgae and other photosynthetic microorganisms. Additional topics will include PSI's newly developed **Raman spectrometer**, next-generation **lysimeter systems**, the latest advancements in the **Envilog environmental monitoring platform**, and recent progress in **hyperspectral imaging technologies**, including new camera architectures and sensing capabilities.

Together, these technologies represent a significant step toward fully integrated, data-driven phenotyping workflows and provide researchers with unique tools for studying plant performance, stress responses, productivity, and environmental interactions. The presentation will offer a glimpse into the future of phenotyping instrumentation and demonstrate how emerging technologies can accelerate discoveries in plant science, agriculture, and biotechnology.

Beyond Phenotyping: Delivering Impact Across the Agri-Food Value Chain

Antony Bačič¹

¹ Emeritus Professor at La Trobe Institute Of Agriculture & Food, La Trobe University, Australia

Abstract

Over the past four decades, plant science has undergone a remarkable transformation, from the molecular understanding of plant biology to the emergence of high-throughput phenomics and digital agriculture. As global agriculture faces the challenges of feeding a growing population under increasing climate and resource constraints, plant phenomics is becoming a critical enabler of innovation across food, fibre and forestry systems.

This presentation explores how phenomics is evolving beyond measurement to accelerate the discovery and deployment of traits that improve productivity, resilience, sustainability and quality. Drawing on examples spanning broad-acre agriculture, protected cropping and food systems, the talk highlights how phenomics can connect plant performance with farmer outcomes, consumer needs and policy priorities. Ultimately, the future success of phenomics will be defined not by the volume of data it generates, but by its ability to deliver tangible benefits across the entire agri-food value chain.

SESSION 1: Integrated Functional Phenotyping for Plant Performance and Stress Resilience

Chair: Sónia Negrão (School of Biology and Environmental Science, University College Dublin, Ireland)

26 th June	Friday
9:00 – 9:35	Thomas Altmann (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany) Plants – Dynamic Genetic Systems in Dynamic Environments: Assessment of (growth) performance through automated non-invasive Phenotyping.
9:35 – 10:00	Carl-Otto Ottosen (Department of Food Science, Aarhus University, Denmark) Plant responses to co-occurring heat and water deficit stress – are the modern wheat genotypes more resilient?
10:00 – 10:25	Marek Živčák (Slovak University of Agriculture, Institute of Plant and Environmental Sciences, Slovakia) A High-Throughput Phenotyping Approach to Screen for Genotypic Variation in Wheat Tolerance to Nocturnal Warming.
10:25 – 10:40	Muhammad Ahmad (Federal Research Centre for Forests, Austria) From pixels to pathways in trees: multi-scale phenotyping of drought response in seedlings of a widespread Oak.
10:40 – 10:55	Éva Darko (Agricultural Institute, Centre for Agricultural Research, Hungarian Academy of Sciences, Hungary) Utilisation of high-throughput phenotyping platform in Martonvásár.
10:55 – 11:20	Coffee Break
11:20 – 11:55	Jim Whelan (ARC Centre of Excellence in Plant Energy Biology, La Trobe University, Australia) Plant Phenomics for Discovery.
11:55 – 12:20	Jana Kholová (Czech Advanced Technology and Research Institute (CATRIN), Palacký University Olomouc) Genetic determination of physiological responses to drought stress in barley (<i>Hordeum vulgare</i> L.) landraces.
12:20 – 12:35	Mikuláš Kňazovický (Aarhus University, Denmark) Water-carbon trade-offs in contrasting <i>Lupinus angustifolius</i> cultivars under combined deficit irrigation, heat stress, and elevated CO ₂ .
12:35 – 12:50	Huma Majeed (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany) STRESS-STOPP: Increasing drought stress adaptation in oilseed rape - yield stability and stress tolerance as selection targets for optimization via physiological phenotyping.
12:50 – 14:00	Lunch

Plants – Dynamic Genetic Systems in Dynamic Environments: Assessment of (growth) Performance through automated non-invasive Phenotyping

Marc C. Heuermann¹, Rhonda C. Meyer¹, Dominic Knoch¹, Rongli Shi¹, Astrid Junker^{1,2}, Henning Tschiersch¹, Markus Kuhlmann¹, Salar Shaaf¹, Christiane Seiler^{1,3}, Narendra Narisetti¹, Evgeny Gladilin¹, Leonardo Caproni⁴, Matteo Dell'Acqua⁴, Amine Abbadi⁵, Jozephus Schippers¹, and Thomas Altmann¹.

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Abstract

Whole plant phenotyping integrated with genotyping and molecular profiling is used to uncover determining factors and mechanisms of plant (growth) performance. It relies on high-throughput platforms for automated cultivation, transport, and imaging of plants in environmentally controlled facilities equipped with multiple camera and illumination systems and a broad range of environmental sensors.

Non-invasive imaging-based assessment of shoot growth progression over time in maize, Arabidopsis, and rapeseed revealed strong temporal dynamics of the action of QTL detected through genome-wide association studies (GWAS). Integration of image-based assessment of growth related traits with transcript and metabolite profiling enabled the detection of prime candidate genes affecting vegetative growth in rapeseed. Furthermore, physiological traits assessed by kinetic chlorophyll fluorescence imaging (kChFI) also revealed temporal QTL expression dynamics and indicate links between photosystem II (PSII) efficiency and plant growth in maize. Expansion of the platforms to disturbance-free assessment of root growth and development enable simultaneous integrative analyses of root and shoot traits. Analysis of 72 distinct genotypes (lines) of 17 plant species revealed wide inter- and intra-specific diversity of root trait expression including large temporal dynamics. Very strong influence of environmental conditions on the genetic factors (QTL) relevant for the expression of performance-related phenotypes was observed, when vegetative growth was monitored in an Arabidopsis GWAS panel cultivated under constant or fluctuating light intensities, respectively. QTL detected for growth-, coloration-, and photosynthesis-related traits were predominantly light regime (condition) specific and displayed distinct temporal activity patterns. Condition- and phase-specificity of QTL was also observed in Mediterranean maize lines exposed to combined head and drought stress. These observations emphasize the need for detailed experimental analyses under well-defined field-like environmental conditions to effectively unravel the complexity of gene x environment interactions that determine the expression of important plant traits: In open fields, plants are exposed to ever-changing dynamic environmental conditions and they need to constantly adjust to these changes and optimize the use of available resources in order to sustain high and stable yields. Reproducible assessment of crop plant performance in simulated field-like environments is enabled in the unique Container/PhenoCrane-System of the IPK PhenoSphere. This was as shown through the assessment of growth and development of 11 diverse maize inbred lines in an emulated single season and in a simulation of an averaged season (across several years) in comparison to cultivation in four years of field trials and in a standard glasshouse. The use of this facility for detailed analyses of performance-related trait expression in plants stands exposed to weather conditions of current and anticipated future climate scenarios and elucidation of causal biological mechanisms will be outlined with examples of recent/ongoing projects.

Plant responses to co-occurring heat and water deficit stress – are the modern wheat genotypes more resilient?

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Abstract

Global climate change increases the likelihood of co-occurrence of hot and dry spells with increased intensity, frequency, and duration. Studying the impact of the combination of the two stresses provide a better understanding of tolerance mechanisms in wheat, and our study was focused on revealing plant stress responses to different severities of combined stress at two phenophases in older and modern wheat genotypes from our panel. During the stem elongation and anthesis stages, the plants were exposed to four treatments: control, deficit irrigation, combined heat, and deficit irrigation at 31°C and 37°C. The modern genotypes were less affected by deficit irrigation at stem elongation as they maintained higher photosynthesis, stomatal conductance, and leaf cooling than the older genotypes. When the 37°C stress was imposed during anthesis, the modern genotypes showed a superior performance compared to older genotypes, due to a higher photosynthetic rate resulting from improved biochemical regulation and a higher chlorophyll content. The plant responses differed in the stages of plant development under the combined stress exposure. In the plants subjected to 37°C stress during stem elongation, photosynthesis was mainly controlled by stomatal regulation, whereas at anthesis it was regulated by biochemical regulation. The findings improve the understanding of plant resilience in response to co-occurring stress conditions and could facilitate the development of new cultivars.

A High-Throughput Phenotyping Approach to Screen for Genotypic Variation in Wheat Tolerance to Nocturnal Warming

Marek Zivcak¹, Marek Kovar¹, Maria Barboricova¹, Dominika Mlynarikova Vysoka¹, Hamideh Ghaffari^{1,2}, Anindita Das¹, and Marian Brestic^{1,2}

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2 Shandong Agricultural University, National Key Laboratory of Wheat Improvement, Taian, China

Abstract

Climate change is characterized by an uneven pattern of warming, where nighttime temperatures are increasing more rapidly than daytime highs. These sustained periods of nocturnal heat cover larger regions and last longer than typical daytime heat events, meaning they can affect a crop throughout its entire developmental trajectory. Despite the danger this poses to the global wheat supply, scientific understanding of genotypic differences in heat tolerance is still underdeveloped. Specifically, there is a lack of data on how high-yielding wheat cultivars respond to the combined pressures of nocturnal heat and drought, a scenario predicted to become more frequent in future climates. The present study employed high-throughput phenotyping to systematically assess wheat cultivar responses to elevated night temperatures under fully controlled environmental conditions. The investigation utilized the PlantScreen™ platform at the Slovak University of Agriculture in Nitra, enabling comprehensive monitoring of plant development from emergence through grain ripening. A specialized temporary chamber was constructed within the phenotyping facility to simulate nocturnal warming, maintaining night temperatures 3–4°C above ambient controls while preserving identical daytime conditions for both treatments. This experimental design isolated the specific effects of nocturnal warming from confounding diurnal temperature variations. Time-series phenotyping integrated multiple complementary approaches: RGB imaging for quantitative assessment of growth parameters and morphological changes, chlorophyll fluorescence imaging for evaluating quantum efficiency and non-photochemical dissipation dynamics, and hyperspectral imaging (VNIR and SWIR) for calculating reflectance indices associated with physiological status. These automated measurements were validated and supplemented by manual determinations of photosynthetic rates and photochemical parameters, ensuring data reliability and biological interpretation. Results revealed pronounced phenological shifts under elevated night temperatures, characterized by accelerated leaf area expansion and earlier onset of senescence. Plants exposed to nocturnal warming achieved peak photosynthetic efficiency more rapidly than controls but subsequently exhibited accelerated functional decline. Critically, substantial genotypic variation emerged, with certain cultivars demonstrating markedly greater sensitivity to nocturnal thermal stress than others. These findings establish that high-throughput phenotyping under controlled conditions provides a robust and efficient framework for identifying climate-resilient wheat genotypes. The observed genotypic variation in thermal tolerance represents valuable genetic resources for breeding programs targeting adaptation to future warming scenarios, particularly for regions experiencing accelerated nocturnal temperature increases. The study was supported by the national grants APVV-22-0392, APVV-24-0586, VEGA-1-0639-26 and VEGA-1-0048-25.

From pixels to pathways in trees: multi-scale phenotyping of drought response in seedlings of a widespread Oak

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Abstract

Rising temperatures and increasingly frequent drought events are threatening forest persistence, with seedling establishment representing a critical bottleneck for forest regeneration. Identifying drought-resilient trees at the seedling stage, and resolving the molecular basis of stress response, has therefore become an urgent priority. Sugar metabolism plays an important role in seedling survival and may serve as a marker of drought resilience, yet its molecular underpinning remains largely understudied in forest trees. Progress in crop species has demonstrated the power of integrating high-throughput phenotyping with molecular profiling to uncover markers for drought resilience, but similar approaches remain largely unexplored in forest trees.

Here, we present an example of combined sensor-based and molecular phenotyping in pedunculate oak (*Quercus robur* L.), one of the most widely distributed Oak species in Europe. We characterized drought stress and stress recovery responses in seedlings of 17 families from a commercial seed orchard using chlorophyll fluorescence and thermal imaging across a 38-day drought-recovery cycle. Families differed significantly in physiological performance. We then selected 12 families covering the full spectrum of responses and profiled pooled samples by time-resolved transcriptomics and metabolomics in leaves and stems. A pronounced accumulation of sugars was evident in both tissues under stress and largely reversed upon rewatering, linked to activation and recovery of starch degradation pathway genes. Notably, leaf sugar levels tended to correlate with family-level physiological performance, highlighting their potential as candidate markers for drought resilience that warrant validation in unpooled data.

Together, these complementary approaches open new possibilities for rapid family selection, breeding, and conservation in forestry under rapidly changing climate.

Utilisation of high-throughput phenotyping platform in Martonvásár (Hungary)

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Abstract

In 2023, a new phenotyping system was installed in the Agricultural Institute, Centre for Agricultural Research (ATK), HUN-REN, Martonvásár by PSI. This new phenotyping platform consists of cc. 200 m² growth chambers and a measuring chamber. In growth chambers, 464-1856 plants can be cultivated simultaneously in 2 separately controlled chambers, where the environmental conditions can vary within a wide range: temperature can be controlled between 10 - 40°C light intensity from 0 to 1500 $\mu\text{mol m}^{-2} \text{s}^{-1}$ and spectral composition can be varied using white, red, blue, far-red and UV LED panels. The CO₂ level can also change till up to 1500 ppm. The growth chambers are equipped with an automatic watering system enabling to water the plants either with water or with mineral nutrition.

The sensors are placed in 3 boxes within the measuring chamber enabling separate detection of several morphological and physiological parameters. We have fluorescence detectors to detect chlorophyll a fluorescence signals and signals derived from fluorochrome dyes, such as DAPI, SYBR Green, YFP, GFP. RGB, IR and 3D laser scanning detectors enable to detect canopy temperature and plant structure. With the use of hyperspectral cameras (VNIR and SWIR), the light rays reflected from the plant surface in the 380-1700 nm spectral range, which can be used to characterize numerous metabolic processes.

In 2024, this phenotyping platform won the EXCELLENT RESEARCH INFRASTRUCTURE NETWORK in HUNGARY (3-133-e).

Within the ATK, we use this high-throughput phenotyping system for the cultivation of cereals including wheat, barley or maize. Our researches are focusing on studying the effect of adverse environmental conditions on the growth and development and stress response of cereals. As it will be presented, we use this phenotyping system to select genotypes having high abiotic stress tolerance and useful agronomic traits from wide genetic plant material. All this can contribute to increasing the efficiency of breeding.

On the other hand, the phenotyping platform is available for scientists and breeders outside the Institute. Further information is found at our webpage: <https://atk.hun-ren.hu/en/phenotyping-system/> or please be in contact with the head of the platform: darko.eva@hun-ren.atk.hu.

Plant Phenomics for Discovery

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Abstract

A variety of 'omic' technologies are widely used in discovery based science investigations, essentially uncovering the "unknown unknowns". We established a plant phenotyping pipeline to incorporate with our other 'omic' platforms, to complement them and to generate hypothesis for further testing. Here we will outline the establishment of this platform, how we are developing it for quantitative 2D and 3D imaging of plants. Finally, we will show how it is raising question and how we can apply it for practical use in functional genomics.

Genetic determination of physiological responses to drought stress in barley (*Hordeum vulgare* L.) landraces

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Abstract

Barley (*Hordeum vulgare* L.) is a globally important cereal crop, yet its productivity is increasingly threatened by the rising frequency and severity of drought events. Understanding the physiological and genetic mechanisms underlying drought adaptation is therefore critical for developing climate-resilient cultivars. In this study, we investigated a diversity panel of 121 spring barley landraces originating from Europe, Asia, and Africa, leveraging their broad genetic variation shaped by local adaptations. Plants were phenotyped under well-watered and drought stress conditions in two independent experiments using a high-throughput phenotyping platform (PlantScreen™), integrating RGB imaging, chlorophyll fluorescence, and thermal infrared measurements, complemented by manual assessment of agronomic traits.

Time-series of phenotypic data were filtered based on the phenological development, level of stress, number of valid observations, heritability ($H^2 > 0.7$) and CV ($< 21\%$) ensuring robust inputs for genome-wide association studies (GWAS). GWAS was conducted using 18,629 LD-pruned SNP markers and multiple statistical models were used. Across traits and conditions, a total of 434 marker–trait associations (MTAs) were identified, including 265 unique loci. Several MTAs co-localized with previously reported quantitative trait loci (QTLs) associated with key agronomic traits such as phenology, tillering, biomass accumulation, and plant height, confirming the biological relevance of the dataset.

Importantly, loci linked to physiological processes—including photosynthetic efficiency and stomatal regulation—were also identified, particularly on chromosomes 1H, 2H, and 6H. While some of these overlapped with known “breeder-relevant” QTLs, others appeared independent of major agronomic loci, suggesting novel sources of allelic variation for drought adaptations. This methodology for rapid screening of the water-use efficiency components (efficiency of photosynthesis, stomata resistance) might be considered to identify genetic stock for targeted enrichment of elite breeding material and/or complement conventional agronomy-based breeding pipeline with foresight-relevant traits and underlying allelic variation.

Water-carbon trade-offs in contrasting *Lupinus angustifolius* cultivars under combined deficit irrigation, heat stress, and elevated CO₂

Mikuláš Kňazovický¹, Eva Rosenqvist², Nagashree A. Nageshbabu¹, Ana K. M. Lobo¹, Negin Hashemi¹, Emmanouil Tsochatzis¹, Laura K. Lemvig¹, Carl-Otto Ottosen¹

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Abstract

Increasing heat and drought events threaten the productivity of grain legumes. To identify traits associated with future climate resilience, *Lupinus angustifolius* was used as a model high-protein crop to assess physiological, yield, and grain quality responses under elevated CO₂ and abiotic stress. The heat-tolerant 'Mirabor' and heat-sensitive 'Primabella' were grown under ambient and elevated CO₂ and exposed to deficit irrigation alone or combined heat plus deficit irrigation. Plant performance was evaluated using gas exchange, chlorophyll fluorescence, biomass, yield traits, and grain composition, including quinolizidine alkaloids.

The cultivars showed contrasting adaptive strategies under combined stress. 'Mirabor' maintained higher intrinsic WUE, particularly under elevated CO₂, supporting more stable biomass and yield despite lower photosynthetic rates. In contrast, 'Primabella' maintained higher photosynthetic activity, but at a greater water cost that did not sustain yield. These results indicate that water-use efficiency was a stronger indicator of tolerance than photosynthetic rate alone under complex stress conditions. Grain macronutrient composition remained relatively stable. However, the sensitive 'Primabella' showed marked increases in quinolizidine alkaloids, while 'Mirabor' maintained relatively stable grain alkaloid contents, highlighting the cultivar-specific stress effects on secondary metabolism.

Overall, this study demonstrates the value of integrative phenotyping for identifying resilient physiological profiles. Cultivars combining conservative water use, adequate sink strength, and stable grain chemistry may provide improved adaptation to future climates.

STRESS-STOPP: Increasing drought stress adaptation in oilseed rape – yield stability and stress tolerance as selection targets for optimization via physiological phenotyping

Huma Majeed¹, Rhonda C. Meyer¹, Amine Abbadi², and Thomas Altmann¹

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Abstract

The STRESS-STOPP project aims to improve drought adaptation in winter oilseed rape (*Brassica napus*) by identifying shoot and root morphological and physiological traits associated with stress tolerance and yield stability. Three Container/PhenoCrane experiments were conducted in the IPK PhenoSphere using 80 lines assessed under drought stress with a subset of 20 lines also grown under well-watered (control) conditions. The PhenoSphere, with large soil containers (54 used per experiment) and an integrated multi-sensor imaging system, enabled the simulation of field-like drought scenarios and allowed high-resolution temporal monitoring of plant responses. Plants were phenotyped using daily RGB imaging and 3D laser scanning, twice-weekly hyperspectral and chlorophyll fluorescence imaging, and manual measurements including leaf water content, SPAD/chlorophyll content, osmolarity, plant height, and porometer traits. Two Rhizotron experiments complemented the Container/PhenoCrane analyses by assessing root system architecture and single plant shoot phenotypes of the same genetic material, resulting in the extraction of 56 root traits and more than 30 shoot traits. The results showed that the measured traits differed in their sensitivity to drought. Maximum plant height showed no significant treatment effect, whereas SPAD/chlorophyll content showed significant differences at later developmental stages, indicating greater sensitivity to stress during advanced growth stages. In the second and third experiments, drought-stressed plants showed higher osmolarity than controls after fall drought, demonstrating osmotic adjustment as a physiological response to water limitation. Porometer measurements during spring and mild summer drought revealed treatment effects for stomatal conductance, transpiration rate, and leaf vapor pressure deficit, indicating altered stomatal regulation and water-use strategy under drought. Chlorophyll fluorescence traits such as operating efficiency showed genotypic variation under drought. Root phenotyping performed under control conditions revealed significant genotypic effects for several root architecture traits, including total root length, projected area, total volume, surface area, and number of branching points. These traits showed moderate heritability, indicating useful genetic variation for root-traits based selection. Overall, osmolarity, SPAD/chlorophyll content, porometer traits, 3D-derived shoot, and root architecture traits could represent promising indicators for drought-response screening in winter oilseed rape.

Ongoing work focuses on multivariate analyses to integrate shoot, root, physiological and agronomic traits from indoor and field experiments to identify key indicator traits ("features") suitable for use in genomic-phenomic selection models for drought tolerance.

SESSION 2: Innovative Phenotyping Technologies for Climate-Resilient Agriculture

Chair: Lukáš Spíchal (Czech Advanced Technology and Research Institute (CATRIN), Palacký University Olomouc)

26 th June	Friday
14:00 – 14:35	Astrid Junker (AJ Consulting, Halle, Germany) From Sensors to Decisions: Translating Plant Phenotyping Innovation into Breeding and Agronomic Value.
14:35 – 15:00	Kerstin Neumann (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany) High-Throughput Phenotyping Reveals Genetic Diversity for Climate Adaptation in Chickpea.
15:00 – 15:20	Tim van Daalen (Wageningen University & Research, Netherlands) Describing High-Throughput Plant Phenotyping experiments.
15:20 – 15:35	Marie Bloome (Ghent University, Belgium) Hyperspectral imaging as a non-destructive phenomics tool to guide the discovery of novel metabolites during tomato-Serendipita interactions.
15:35 – 15:50	Iñigo Saiz-Fernández (Czech Advanced Technology and Research Institute (CATRIN), Palacký University Olomouc) LOCOPOTS: a LOW-Cost high-throughput screening platform for in vitro POTatoes under abiotic Stress.
15:50 – 16:15	Coffee Break
16:15 – 16:50	Matthew Lewsey (La Trobe Institute of Sustainable Agriculture and Food, La Trobe University, Australia) Phenotyping on Earth and in Space.
16:50 – 17:10	Peter Pietrzyk (Fraunhofer Institute for Integrated Circuits IIS, Germany) Opportunities and Challenges of 3D Root and Shoot Phenotyping in Controlled Environments.
17:10 – 17:30	Alexey Shapiguzov (Department of Organismal and Evolutionary Biology, University of Helsinki, Finland) Exploring flash-induced chlorophyll fluorometry: from mitochondrial mutants to tomato production.
17:30 – 17:50	Phanchita Vejchasarn (Ministry of Agriculture, Thailand) Toward Climate-Resilient Rice: Integrative Genomic Approaches for Candidate Gene Discovery Under Drought-prone Environments.
17:50 – 19:30	Poster session
19:30 – ON	Dinner

From Sensors to Decisions: Translating Plant Phenotyping Innovation into Breeding and Agronomic Value

Astrid Junker¹

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Abstract

Plant phenotyping technologies have advanced rapidly, from controlled-environment platforms and field sensors to UAV, proximal, and remote-sensing approaches. However, sensors alone do not create impact. Their value emerges when data streams are transformed into reliable, interpretable, and timely outputs that address concrete breeding and agronomic decisions.

In this keynote, I will discuss how phenotyping innovation can move beyond technical proof-of-concept towards decision-grade workflows. This requires end-to-end thinking: from experimental design, sensor selection, calibration, trait extraction and analytics to uncertainty reporting, interoperability, and integration into operational decision processes. I will also highlight why pragmatic FAIR principles, data harmonization, and shared reference frameworks are essential for scaling phenotyping approaches across platforms, sites, and communities.

Drawing on experience from academic infrastructure development, corporate breeding R&D, and current consulting work, the talk will reflect on how the phenotyping community can close the translation gap between technology potential and practical value. I will also briefly touch on the role of European and international research infrastructures, including EMPHASIS, in supporting validation, standardization, and community adoption.

High-Throughput Phenotyping Reveals Genetic Diversity for Climate Adaptation in Chickpea

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Keywords: chickpea, biomass, photosynthesis, drought stress, combined heat and drought.

Abstract

Climate change increasingly threatens agricultural productivity through the rising frequency and intensity of drought and heat stress events, highlighting the urgent need for climate-resilient crop varieties. Grain legumes play a key role in sustainable agricultural systems due to their contribution to biological nitrogen fixation, soil fertility, and plant-based nutrition. Among these crops, chickpea (*Cicer arietinum* L.) is considered particularly promising because of its natural adaptation to semi-arid environments and its importance for future sustainable food systems.

Within the European INCREASE project, integrated physiological, phenotypic, and genetic studies were conducted to investigate stress adaptation mechanisms in chickpea under drought and combined drought-heat stress conditions. A genetically diverse panel of single-seed descent lines derived from genebank accessions, the so-called INCREASE T-Core, was genotyped using whole-genome shotgun sequencing. A subset of 200 lines was subsequently analysed using high-throughput phenotyping approaches under abiotic stress conditions to monitor plant growth dynamics, biomass accumulation, and stress progression based on color-related traits under controlled but field-relevant stress scenarios. In parallel, chlorophyll fluorescence imaging was used to evaluate three photosynthesis-related parameters (QY, Fv/Fm, and NPQ) associated with stress tolerance and recovery across the genetically diverse chickpea material. Two stress scenarios were investigated in independent studies: drought stress alone and combined drought and heat stress, both applied during the vegetative growth phase and followed by a recovery period.

The studies revealed substantial variation in stress responses among genotypes and highlighted the complex interactions between drought and heat stress effects on plant performance and productivity-related traits. The integration of high-throughput phenotyping with genomic analyses provides valuable opportunities for the identification of candidate genes and adaptive traits associated with abiotic stress tolerance, thereby supporting the development of improved breeding strategies for climate-resilient chickpea varieties. Overall, the findings contribute to a better understanding of legume adaptation to changing environmental conditions and demonstrate the value of plant genetic resources for future sustainable agriculture.

Describing High-Throughput Plant Phenotyping experiments

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Abstract

High-throughput plant phenotyping (HTPP) platforms generate large volumes of data including images, environmental measurements, and derived traits across time. These data have considerable potential for discovery, benchmarking, and reuse in other disciplines, yet they are rarely exploited to their full extent. At many facilities, hundreds of experiments are conducted each year, but only a small fraction of the resulting datasets is available for sharing, much less used beyond academia, and even fewer are reused beyond the context of the original study.

Our international, trans-disciplinary work-group (part of the IPPN WG Advanced Sensor Applications and data management) aims to narrow the important gap limiting data re-usability and, accordingly, aligns the effort required to systematically describe the metadata as per the FAIR principles; for example the experimental design, platform configuration, acquisition protocols, and processing steps. Although existing standards such as MIAPPE provide an important foundation for describing plant phenotyping experiments, they do not yet capture many of the specific metadata to interpret the experiment beyond original context (e.g. environmental information, sensor set-up, feature extraction process). However, these contextual metadata are essential to further use, or reuse data for AI training approaches, or to link them with other experiments to enable meta studies without a lot of manual effort. Without machine readable and machine actionable metadata, the dataset value deteriorates over time.

Building on MIAPPE, we propose to develop MIAPPE-HTP, an extension of FAIR data standards tailored to the needs of HTP users that aims to standardize the way platform-level and workflow-level metadata are represented, shared, and validated (Training sets for AI-Models, meta-analysis approaches linking several studies, validating data analysis pipelines, sensor degradation detection). Creating a community accepted standard that can be used to describe datasets, enabling the reuse of data. As a second step, we aim to lower the effort to create a metadata-rich dataset by automating the process as much as possible using the PSI systems as a demonstrator. This will also increase the completeness and consistency of metadata for high-throughput experiments. By making it easy to use, share and re-use, we hope to demonstrate enhanced value of the HTP datasets and encourage more researchers to organize and share their data.

Hyperspectral imaging as a non-destructive phenomics tool to guide the discovery of novel metabolites during tomato-Serendipita interactions

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Abstract

Serendipita is an endophytic fungus with plant growth promoting properties. During colonization, the host immune response is circumvented to prevent formation of extensive necrotic zones. Therefore it is hypothesized that Serendipita produces a variety of cryptic bioactive metabolites that contribute in altering the host's metabolism. The majority of these metabolites still await discovery as their biosynthetic gene clusters are often silent under laboratory growth conditions. To activate these gene clusters, a plant-based platform has been established. A multimodel approach was created to discover and characterize metabolic interactions between fungi and host, facilitating the identification of yet undiscovered metabolites.

Within this framework, tomato (*Solanum lycopersicum* cv. "Moneymaker") was used as the fungal host. In addition to wild type, several defenseless tomato lines that are compromised in salicylic acid (SA) and jasmonic acid (JA) dependent signaling pathways were included. By lowering the host immune response, we aim to modify the chemical dialogue between plant and fungus, to stimulate the production of cryptic secondary metabolites. Two complementary experimental systems were used: a plant- and a hairy root-based system. In both systems, high resolution phenotypic profiling, using multi- and hyperspectral imaging enabled the detection of subtle spectral shifts associated with plant-fungal interactions. Combining phenomics with fungal growth rates and root colonization assays will enhance our insight in tomato-Serendipita interactions. This will be the groundwork for subsequent transcriptomic and metabolomic profiling, ultimately gaining a deeper understanding of the Serendipita metabolome and the biochemical crosstalk between Serendipita and tomato.

Key words: Serendipita spp., defenseless tomato, tomato-Serendipita interaction, hyperspectral and multispectral imaging.

LOCOPOTS: a LOW-COst high-throughput screening platform for in vitro POTatoes under abiotic Stress

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Abstract

Potato crop is highly vulnerable to abiotic stresses like salinity and low nutrient availability. Rapid identification of stress-resilient genotypes is therefore essential for breeding, yet conventional phenotyping is often slow, space-demanding and expensive. We present LOCOPOTS – a LOW-COst high-throughput screening platform for in vitro POTatoes under abiotic Stress – which combines individual in vitro plant culture, low-cost RGB imaging and machine-learning-based automatic segmentation using a trained model of a convolutional neural network, based on U-Net architecture. LOCOPOTS enabled the automated extraction of growth, colour, and vegetation- index traits and demonstrated robust performance across independent phenotyping rounds. We screened 30 potato varieties under control, low-nutrient and saltinity conditions, identifying contrasting growth and physiological responses. Integrated traits such as final area and height, Area_AUC and height_AUC, together with GLL, Chol, cive and chlorophyll fluorescence parameters, discriminated genotype performance under stress. Metabolic profiling further revealed genotype-specific reprogramming in carbon and nitrogen metabolism under low nutrition and salt stress, including changes in fructose, myo-inositol, β -aminobutyric acid, γ -aminobutyric acid, proline, and certain polyamines, identifying them as specific chemical biomarkers of plant stress responses. LOCOPOTS provides a scalable, affordable and space-efficient platform for early screening of potato genetic diversity and identification of candidate traits associated with stress resilience.

Funded by the European Union under the grant agreement No 101084284 (PataFEST project).

Phenotyping on Earth and in Space

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Abstract

We study plant re-design and bioresource production to enable off-Earth habitation and to provide solutions that will improve on-Earth sustainability. This research is part of the Australian Research Council Centre of Excellence in Plants for Space, which brings together experts from the plant science, food technology, controlled environment agriculture and space sectors. We are studying a tomato cultivar, Micro-Tom, which has a dwarf growth habit suited to vertical farming and spaceflight heritage. High throughput phenotyping studies have enabled us to better understand the cultivation requirements of Micro-Tom, whilst functional genomic studies have begun to inform us about its potential as a chassis for synthetic biology. We have also been developing analysis protocols for use during space missions as part of NASA's Artemis Lunar Surface Science Team.

Opportunities and Challenges of 3D Root and Shoot Phenotyping in Controlled Environments

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Abstract

Developing resilient crops requires understanding how plant structure, growth and stress responses are linked across above- and belowground organs. Controlled-environment phenotyping platforms allow these relationships to be studied under reproducible and experimentally adjustable growth conditions. In this context, 2D imaging is highly valuable for high-throughput monitoring, but many biologically relevant traits are inherently three-dimensional. Shoot architecture, leaf shape, root system architecture and belowground storage-organ development cannot be fully captured from projected images alone. 3D phenotyping extends classical image-based phenotyping with structural information for interpreting plant growth, stress responses, genotype-dependent architecture and root-shoot interactions.

3D root and shoot phenotyping can contribute at several levels. Above ground, 3D measurements quantify shoot architecture, canopy volume, spatial leaf distribution and organ-resolved traits such as leaf area, angle, curvature or orientation. These traits inform light interception, growth dynamics and crop-specific responses to environmental conditions. Below ground, X-ray computed tomography can provide access to root system architecture, root depth distribution, branching patterns and root volume. For several crops, storage-root size, shape and development are also of direct agronomic relevance.

At the same time, 3D phenotyping introduces specific requirements for integration into controlled-environment experiments. Compared with 2D imaging, 3D shoot reconstruction and root X-ray CT are typically more complex, slower and more demanding in calibration, acquisition planning, data volume, segmentation and trait extraction. These aspects do not limit its usefulness, but define the conditions for robust and biologically meaningful information.

Drawing on experience from developing 3D measurement systems and operating a controlled-environment plant phenotyping platform at the Technology Center Phenotyping at Fraunhofer IIS/EZRT, we discuss opportunities and practical considerations for 3D root and shoot phenotyping. Demonstration cases from sugar beet, maize and single-leaf phenotyping of young citrus trees illustrate belowground root and storage-organ phenotyping, 3D shoot measurements and organ-resolved leaf analysis. By linking root, shoot and environmental information, controlled-environment 3D phenotyping can help translate complex plant architecture into traits relevant for crop improvement and stress adaptation.

Exploring flash-induced chlorophyll fluorometry: from mitochondrial mutants to tomato production

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Abstract

In flash-induced fluorometry, chlorophyll fluorescence (CF) is elicited by short (~1-3 s) multiple-turnover light flashes and recorded at high temporal resolution. The resulting polyphasic kinetics, known as OJIP, enable rapid assessment of photosynthetic functions. Here we discuss the applicability of OJIP measurements, in both single-channel and imaging formats, for various phenotyping approaches.

For example, our recent study suggested that the I-P rise of OJIP is sensitive to tissue O₂ availability. We demonstrated this in Arabidopsis mutants with enhanced mitochondrial respiration and higher rates of tissue oxygen consumption. The effect can be visualized by treating plants with methyl viologen, which catalyzes electron transfer from Photosystem I to O₂. In the above mutants, this electron transfer was suppressed under hypoxic conditions, indicating that OJIP may provide a new approach for probing mitochondrial respiration.

While the theory of flash-induced CF rise is relatively well established for the dark-adapted state, in light-adapted conditions the signal becomes a complex mixture of “structural” and “operational” signals from the photosynthetic apparatus. This limits mechanistic interpretation but offers potential as a holistic performance indicator. We “calibrated” light-adapted CF using Arabidopsis knockout mutants deficient in specific metabolic processes and subsequently translate this knowledge to crop species. We use machine learning approaches to compare kinetics and identify differences between the genotypes. We also define new OJIP parameters by analyzing the timing and relative intensity of key points in the kinetics.

Our recent experiments revealed that light-adapted flash-induced CF fluctuates during day-night cycles and is highly sensitive to ambient environmental conditions, making it a promising readout for real-time physiological monitoring. We conducted proof-of-concept in situ measurements of flash-induced CF in tomato across different seasons in a Finnish production-scale greenhouse. Using machine learning, CF-derived features were linked with climate variables. The results revealed dynamic, season-dependent correlations across diurnal cycles and support flash-induced CF as a useful readout for resource-efficient greenhouse control systems.

Toward Climate-Resilient Rice: Integrative Genomic Approaches for Candidate Gene Discovery Under Drought-prone Environments

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Abstract

Drought has affected many regions worldwide over the past few decades and has been exacerbated by climate change. Roots, the hidden half of a plant, are of primary importance for numerous functions including absorption and translocation of water and nutrients and structural support. Plant roots exhibit highly plastic responses to drought stress and have evolved a series of adaptive strategies to enhance water acquisition. This study aimed to define a drought-adaptive root ideotype in rice and identify the underlying genetic factors associated with improved performance under water-limited environments. Phenotypic analyses revealed that steeper root growth angles, together with larger meta-xylem and low density of lateral roots, exhibited higher grain yield under drought stress suggesting that reduced root branching combined with enhanced hydraulic capacity may improve drought adaptation. Genome-wide association studies (GWAS) combined with QTL mapping were conducted using high-density genomic markers to identify genomic regions associated with these traits. Several significant loci were detected, and integrative genomic analyses highlighted a candidate region similar to the deeper-rooting locus DRO1, suggesting the presence of a Dro1-like genomic region influencing root architecture. Candidate genes within this region are likely involved in the regulation of root growth angle and vascular development. These findings provide new insights into the genetic architecture underlying drought-adaptive root traits and define a root ideotype for rice grown in drought-prone environments.

Keywords: Rice, drought-prone environments, root traits, genomics.

SESSION 3: Algae biotechnology and phenotyping

Chair: Zuzana Benedikty (Photon Systems Instruments, Czech Republic)

27 th June	Saturday
8:45 – 9:20	Yagut Allahverdiyeva-Rinne (Department of Life Technologies, University of Turku, Finland) Connecting photosynthetic mechanisms to phenotypes across systems: from algae to plants.
9:20 – 9:45	Ondřej Prášil (Centre ALGATECH, Institute of Microbiology, The Czech Academy of Science, Czech Republic) AlgaScreen – phenotyping platform for microalgal biotechnology.
9:45 – 10:00	Jan Červený (CzechGlobe, Global Change Research Institute, The Czech Academy of Science, Czech Republic) AI-enabled digital platform for distributed microalgal phenotyping and real-time cultivation optimization.
10:00 – 10:20	Bernard Lepetit (Molecular Stress Physiology, University of Rostock, Germany) The contribution of various Lhcx proteins to Non-Photochemical Quenching.
10:20 – 10:35	Tomáš Zavřel (CzechGlobe, Global Change Research Institute, The Czech Academy of Science, Czech Republic) Phenotyping Ethylene-Producing Cyanobacteria: Deciphering the Interplay Between Culture Density, Light Availability, Size of Metabolic Sinks and Ethylene Productivity.
10:35 – 10:50	Tomáš Zlámal (CzechGlobe, Global Change Research Institute, The Czech Academy of Science, Czech Republic) Enzyme-Functionalized MIMS Probes for Expanded Analyte Detection.
10:50 – 11:15	Coffee Break

Connecting photosynthetic mechanisms to phenotypes across systems: from algae to plants.

Yagut Allahverdiyeva-Rinne¹

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Abstract

This presentation will explore how environmental conditions shape cyanobacterial phenotypes, linking observable traits to the underlying physiological and photosynthetic mechanisms that drive adaptation and productivity. The talk will further expand identifying robust algal strains suitable for cultivation in industrial effluents, enabling sustainable large-scale biomass production while supporting wastewater remediation. Finally, the presentation will discuss pathways for upgrading algal biomass into value-added agrichemicals and biostimulants, highlighting how advanced plant phenotyping approaches can be used to evaluate and validate their impacts on plant performance, and agricultural productivity.

AlgaScreen – phenotyping platform for microalgal biotechnology

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Abstract

AlgaScreen is a phenotyping robotic platform developed for high-throughput continuous cultivation, monitoring and selection of genotypes of photosynthetic microorganisms. It consists of four independent cultivators for cell cultures growing either as colonies on agar dishes or as liquid suspensions in microtiter plates. The automated robotic manipulator can position the cultured microorganisms into five sensor units that enable automatic: 1. recognition of colonies and their growth, 2. measurement of full absorption and 3. emission spectra in the VIS-NIR range, 4. 2D detection of expression of fluorescent proteins and chlorophyll variable fluorescence. In addition, non-invasive Raman microspectrometer (5) can analyze the macromolecular content of tested strains. Finally, liquid-handling station allows for robotic colony-picking and manipulation with the samples.

In the presentation, we will introduce the architecture and capabilities of the AlgaScreen system for cyanobacterial and algal biotechnology, as well as for basic research to select strains with desirable properties (mutations) using a high-throughput and fully automated approach.

AI-enabled digital platform for distributed microalgal phenotyping and real-time cultivation optimization

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Abstract

Microalgal biotechnology increasingly relies on high-throughput, information-rich phenotyping to optimize cultivation strategies and to assess ecosystem services such as nutrient removal, contaminant capture, and waste valorization. In this contribution, we present a digital platform that couples geographically distributed microalgal cultivation devices (bioreactors) with a unified infrastructure for secure data acquisition, centralized storage, and AI-driven analytics, enabling advanced physiological characterization and real-time optimization of microalgae. The platform integrates standardized communication protocols for robust and secure transfer of high-frequency sensor data from user end-point devices, a cloud-based environment for aggregation and systematic categorization of experimental datasets, maintenance and deployment of analytical and predictive models, and an interactive web-based frontend for monitoring key physiological indicators and managing models and experiments.

We will showcase a case study in which this pipeline is integrated with a specially designed microalgal cultivator and third-party accessories, all operated through a unified microalgal interface, to perform closed-loop optimization of cultivation conditions using a combination of AI techniques. The resulting datasets provide a basis for validating predictive models targeting (not exclusively) biotechnological applications. From a broader perspective, the platform supports the development and evaluation of microalgal solutions addressing global challenges such as eutrophication driven by excess nitrogen and phosphorus, removal of pollutants including heavy metals, antibiotics, hormones, and colorants, mitigation of marine microplastic residues, and the design of circular-economy processes that valorize microalgal biomass and recovered resources. By bridging distributed phenotyping hardware with a scalable digital and analytical backbone, this work illustrates how AI-enhanced phenomics can accelerate the translation of microalgal physiology research into operational environmental and biotechnological applications in line with the themes of IPAP 2026.

The contribution of various Lhcx proteins to Non-Photochemical Quenching

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Abstract

As phytoplankton, diatoms are exposed to intense fluctuations in light intensity requiring effective photoprotective mechanisms. One such mechanism is Non-Photochemical Quenching (NPQ), and here particularly its reversible and fastest sub-type high-energy-state quenching (qE). qE in diatoms not only requires specific xanthophylls, it compulsorily needs the presence of thylakoid membrane-associated Lhcx proteins. Previous studies have demonstrated that three out of the four Lhcx proteins found in *Phaeodactylum tricornutum* can individually confer qE. These three proteins share a distinct peptide motif that is supposedly essential for qE. Lhcx proteins that include this motif are highly conserved among diatoms as well as haptophytes and green algae. In this study, we investigated the individual roles of Lhcx proteins during light stress by generating CRISPR-Cas-induced knockouts of multiple Lhcx proteins in *P. tricornutum*. Additionally, we complemented a *P. tricornutum* Lhcx1 knockout strain with heterologous Lhcx proteins containing the distinct peptide motif from various diatoms, haptophytes and green algae, in order to investigate a potential universality of Lhcx proteins in conferring qE. Physiological experiments demonstrate that triple Lhcx knockout lines exhibit no qE capacity even under prolonged high light stress. In contrast, the single and double knockout lines revealed that Lhcx proteins contribute not only individually but also additively to qE, elucidating the individual contribution of each Lhcx protein to the overall qE capacity. Experiments with heterologous Lhcx proteins from other diatoms demonstrate that diatom Lhcx can easily restore qE capacity in *P. tricornutum*, whereas Lhcx from more distantly related algal groups seem unable to provide a functional qE system. Most of the mutants created exhibit a phenotype that is not a simple on/off response, but instead shows slight variations in qE. These variations can be exaggerated under various environmental stressors, but are easily cancelled out due to a lack of statistical power. Moreover, the large number of mutant lines created prevents an in depth-characterisation with classical photophysiological experiments. Our results indicate, on the one hand, the complex interplay of Lhcx proteins within the photosynthetic light-harvesting system to provide rapid, fine-tuned photoprotection. On the other hand, our mutant collection demonstrates the need for high-throughput phenotyping to exploit its full potential and reveal hidden implications.

Phenotyping Ethylene-Producing Cyanobacteria: Deciphering the Interplay Between Culture Density, Light Availability, Size of Metabolic Sinks and Ethylene Productivity

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7 Department of Life Technologies, University of Turku, Turku, Finland

Abstract

Cyanobacteria are promising 'cell factories' for the renewable production of bio-products from CO₂ and light, yet current light-to-product conversion efficiencies remain insufficient for industrial deployment. Here, we present a systematic phenotyping study of ethylene-producing strains of the model cyanobacterium *Synechocystis* sp. PCC 6803. Using quasi-continuous cultivation - turbidostat - we investigated how specific growth rate (μ), culture density (ρ), and light availability determine volumetric ethylene productivity ($P = \rho \cdot \mu$). Whereas maximal growth rates are typically achieved in dilute cultures under high light, maximal volumetric productivity often occurs at high cell densities where strong self-shading takes place. Unlike conventional batch cultivation, turbidostat cultivation enables quantitative analysis of metabolic steady states. We will present comprehensive phenotyping data across a wide range of irradiances and culture densities to understand physiological limits of phototrophic ethylene production. In addition, we investigated metabolic engineering strategies aimed at redirecting carbon and energy flux from native sinks, specifically glycogen and sucrose biosynthesis, toward ethylene production. The resulting metabolic trade-offs between growth, photoprotection, photosynthetic electron transport, and product formation will be discussed in the context of improving cyanobacterial production efficiency.

Enzyme-Functionalized MIMS Probes for Expanded Analyte Detection

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3 Central European Institute of Technology – CEITEC, Brno University of Technology, Brno, Czech Republic

Abstract

Membrane Inlet Mass Spectrometry (MIMS) is a powerful analytical tool for the qualitative and quantitative determination of dissolved gases and volatile compounds. It is widely applied in studies of aquatic biological activity and pollution, as well as in the characterization of volatile organic compounds and gas exchange kinetics in living systems, such as microalgae and plants.

To extend MIMS capabilities beyond membrane-diffusible species, we functionalized MIMS probe surfaces with immobilized enzymes, enabling the biocatalytic detection of non-diffusible analytes via enzymatic reactions that generate or consume membrane-permeable products or co-substrates monitored by the MIMS. An eggshell membrane wrapped around silicon-membrane MIMS probe serves as a gas-permeable, biocompatible interface enabling rapid and low-cost biosensor probe preparation while maintaining stable enzyme activity. This approach broadens the applicability of MIMS-based techniques and opens new opportunities for measurements in phenotyping applications, enabling selective quantification of a wider range of metabolites in complex matrices without prior separation or purification.

Glucose oxidase, a model biosensor enzyme, was used as a proof of concept, yielding a linear response range of 50–1000 $\mu\text{mol}\cdot\text{L}^{-1}$ glucose, a response time of approximately 120 s, and a sensitivity of 67.8 $\mu\text{mol}\cdot\text{L}^{-1}$ decrease in dissolved oxygen per $\text{mmol}\cdot\text{L}^{-1}$ of glucose. Samples of wines and fruit juices were analyzed, and results were benchmarked against a conventional glucose oxidase amperometric biosensor showing good agreement and validating the MIMS-based approach. The enzyme immobilization procedure was characterized by scanning electron microscopy, confirming successful deposition on the eggshell membrane surface.

SESSION 4: AI-Driven Imaging and Sensor Technologies in Plant Phenotyping

Chair: Robert D. Hancock (The Advanced Plant Growth Centre, James Hutton Institute, Dundee, Scotland)

27 th June	Saturday
11:15 – 11:50	Sónia Negrão (School of Biology and Environmental Science, University College Dublin, Ireland) The Road to Precision: Spectral Imaging for Abiotic Stress Responses—Are We There Yet?
11:50 – 12:10	Anshu Rastogi (Department of Bioclimatology, Poznan University of Life Sciences, Poznan, Poland) Integration of Hyperspectral Reflectance and Sun-Induced Fluorescence for Stable Estimates of Gross Primary Productivity in Peatlands.
12:10 – 12:30	Krystyna Rybka (Plant Breeding and Acclimatization Institute – National Research Institute, Poland) Monitoring yield-related spectral responses of spring cereals under contrasting hydrothermal.
12:30 – 12:45	Lamis Abdelhakim (Photon Systems Instruments, Czech Republic) Root-to-Shoot Stress Response Dynamics: A Case Study of Barley Drought Resilience.
12:45 – 14:00	Lunch
14:00 – 14:30	Nuria de Diego Sanchez (Czech Advanced Technology and Research Institute (CATRIN), Palacký University Olomouc) AI-Powered Digital Biomarkers for Stress Resilience and Genotype Classification.
14:30 – 14:50	Katarzyna Retzer (Institute of Forest Ecology, BOKU University, Austria) Affordable Infrared DIY Microscopy for Non-Invasive Root Phenotyping.
14:50 – 15:05	Zhibo Cai (Horticulture and Product Physiology Group, Wageningen University & Research, Netherlands) SP3D: A benchmark for systematic comparison of image-based 3D reconstruction methods of cucumber plants.
15:05 – 15:20	Rijad Sarić (ARC Research Hub for Protected Cropping, La Trobe University, Australia) Linking Rosettes to Leaves: An AI-Driven RGB Imaging Pipeline for Arabidopsis thaliana Phenotyping.
15:20 – 15:35	Sebastian Seitner (Plant Sciences Facility, Vienna BioCenter Core Facilities GmbH (VBCF), Austria) Enabling Reproducible Phenotyping: An Open-Source Python PlantScreen and Fytotron APIs.
15:35 – 16:00	Coffee Break

The Road to Precision: Spectral Imaging for Abiotic Stress Responses—Are We There Yet?

Sónia Negrão¹

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Abstract

This presentation explores the genetic potential of heritage barley (landraces and formerly bred cultivars) to cope with abiotic stress. We examine the potential of different imaging methods in controlled conditions (root and shoot) as well as in field trials. We developed a deep learning pipeline to segment hyperspectral images and used machine learning to classify feature importance. Neural networks were found to predict tolerance values and rank genotypes in field conditions. Several vegetation indices enabled stress prediction according to the experiment timeline (early, late stress and recovery). GWAS was conducted and a new longitudinal visualisation tool - 3DQTL-Vis- was developed to discover new genetic regions associated with waterlogging.

Integration of Hyperspectral Reflectance and Sun-Induced Fluorescence for Stable Estimates of Gross Primary Productivity in Peatlands

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Abstract

Peatlands are among the most important terrestrial carbon reservoirs worldwide, functioning as major carbon sinks while remaining highly vulnerable to climate change. Understanding how peatland carbon dynamics respond to changing climatic conditions is therefore essential. The diverse vegetation structure of peatlands, ranging from simple Sphagnum mosses to vascular shrubs, presents unique challenges for conventional remote sensing approaches.

To investigate the impacts of climate change on peatland ecosystems, we conducted a climate manipulation experiment in Poland using infrared heaters, open-top chambers (OTCs), and rain-exclusion curtains to simulate warming and reduced precipitation. Vegetation responses to these environmental manipulations were assessed using hyperspectral reflectance, sun-induced fluorescence (SIF), canopy-level gross primary productivity (GPP), and leaf-level chlorophyll fluorescence measurements. Our results show that short-term climate manipulation altered both plant community composition and physiological functioning, with responses varying among species. The findings further demonstrate that different peatland plant species exhibit distinct sensitivities to climate change. In particular, the projected shift toward greater dominance of vascular plants under warmer future conditions is associated with stronger seasonal variability in SIF, reflectance, and GPP. We also found that far-red SIF and spectrally integrated full-spectrum SIF were strongly correlated with GPP ($R^2 > 0.85$) across vegetation communities, temperature treatments, and precipitation regimes. These results highlight the potential of combining optical and fluorescence-based sensing techniques to monitor ecosystem functioning, assess peatland resilience, and track carbon budget dynamics in vulnerable ecosystems under a changing climate.

Acknowledgment: This research was supported by the National Science Centre of Poland (NCN) within grant No. 2020/37/B/ST10/01213.

Monitoring yield-related spectral responses of spring cereals under contrasting hydrothermal conditions using UAV-based phenotyping

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Abstract

Background: Climate change is increasingly reshaping cereal production in Central Europe, particularly in regions characterized by light soils and recurrent spring droughts. In Poland, approximately 60% of arable land is classified as soils with limited water retention capacity, amplifying precipitation deficits during critical developmental stages of spring crops. Long-term analyses showed that the country's central-western region, one of its most drought-prone cereal production areas, experienced droughts in ~ 60% of growing seasons since 1992, resulting in spring wheat yield losses of 16% in dry years and a decline to 1.2 million ha of spring cereals.

Objectives and experimental approach: to evaluate whether UAV-derived spectral indices can support early discrimination of yield-related responses in spring cereals exposed to contrasting hydrothermal conditions basing on field results from 2024 and 2025 in Strzelce (central Poland). DJI Phantom 4 Multispectral at five developmental stages was used for phenotyping. The analyzed vegetation indices included NDVI, GNDVI, NDRE, LCI, OSAVI, and EVI. Meteorological conditions were described by drought indices for the March–July growing period.

Results: Hydrothermal analyses confirmed strongly contrasting conditions between seasons. In 2024, a severe drought occurred during stem elongation, with the lowest values recorded in May (SPI = -1.39; HTC = 0.39). Negative SPI values persisted from March to July (-0.84 to -1.39), indicating prolonged precipitation deficit. In contrast, the 2025 season was characterized by lower temperatures and higher precipitation, including 47.6 mm in May and 123.7 mm in July. Grain yield differed markedly between years and species. Under standard agrotechnique, spring wheat plot yield increased from 3.1–5.9 kg in 2024 to 8.1–10.4 kg in 2025. In spring barley, from 2.1–5.1 kg to 8.2–11.3 kg. Oats showed lower interannual variation, from 5.3–7.6 kg to 6.7–9.2 kg. During the 2024 drought, red-edge and chlorophyll-related indices exhibited the strongest relationships with yield. Depending on the phenotyping term, correlation coefficients for spring barley ranged from $r = 0.47$ to 0.83 for both NDRE and LCI. In spring wheat, NDRE correlation was $0.44 \leq r \leq 0.77$, whereas for OSAVI, $0.04 \leq r \leq 0.72$. Oat exhibited more stable moderate correlations, yield-NDRE ($r = 0.4–0.5$). In 2025, indices–yield correlations were predominantly low-/insignificant except for the last term of phenotyping, for wheat more pronounced than for oat.

Conclusions and breeding implications: UAV-based spectral phenotyping captured biologically meaningful differences in yield formation under contrasting hydrothermal environments. Under drought, red-edge and chlorophyll-sensitive indices, particularly NDRE and LCI, provided more stable relationships with grain yield than conventional biomass-oriented indices. In contrast, in 2025, correlations: indices–yield were absent/weak with significant associations for the final phenotyping term. These findings indicate that no single spectral index is universally optimal across environments. Adaptive multi-index phenotyping integrating climatic context with stage-specific UAV measurements may improve early identification of high-performing genotypes and support breeding for drought resilience and yield stability in spring cereals.

Root-to-Shoot Stress Response Dynamics: A Case Study of Barley Drought Resilience

Klára Panzarová¹, Lamis Abdelhakim¹, Ivan Kashkan¹, Sajid Ullah¹, Katarzyna Retzer²

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Abstract

High-throughput phenotyping has substantially advanced the understanding of shoot-level stress responses; however, progress in root phenotyping remains limited. Traditional root studies are destructive, time-consuming, and unsuitable for dynamic monitoring. Here, we present applications of the PlantScreen™ Root System, an automated, non-invasive platform enabling parallel monitoring of root and shoot growth across multiple plant species. The system allows precise control of rhizobox soil moisture, facilitating either waterlogging or drought treatments, and supports the application of defined nutrient and biostimulant regimes. Within the framework of the BarleyMicroBreed project, root growth dynamics of ten barley genotypes were characterized at early developmental stages under optimized moderate drought conditions. Simultaneous analysis of root and shoot growth complements field-trial evaluations aimed at assessing the contribution of root traits to plant performance, particularly yield stability under drought. Morphological traits of shoots and roots were captured using RGB imaging, while multispectral and near-infrared sensors provided additional insights into physiological properties, including root water content. Automated image segmentation using a sensor-specific pipeline with a pretrained model, followed by trait extraction, enabled efficient quantitative trait analysis. The results revealed distinct, genotype-dependent responses to drought, reflecting diverse stress-resilience mechanisms. Importantly, our findings demonstrate that high-throughput phenotyping at early seedling stages can capture divergent root dynamic strategies that may be predictive of later field performance under drought conditions. Overall, the integration of above- and below-ground phenotypic data with advanced analytical approaches extends trait assessment beyond traditional methods, providing deeper insights into root-shoot regulation under stress and supporting trait selection for crop improvement.

AI-Powered Digital Biomarkers for Stress Resilience and Genotype Classification

Nuria De Diego¹, Jan Zdražil^{1,2}, Ivan Kashkan³, Pavel Klimeš¹, Iñigo Saiz-Fernández¹, Václav Snášel², Jana Kholová^{1,4}, Jan Masner⁴, Klára Panzarová³, Lukáš Spíchal¹

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Abstract

Modern plant phenomics produces high-dimensional data from optical sensors and automated phenotyping platforms, creating new opportunities to understand plant growth, genotype performance, and resilience under complex environmental conditions. However, these datasets remain difficult to interpret, especially when abiotic and biotic stresses combine, and plant responses are dynamic, multidimensional, and not yet visible. Machine learning (ML) can transform such data into biologically meaningful digital biomarkers for early stress detection and genotype classification. Here, I will present AI-based pipelines developed for plant phenomics across controlled and field conditions. AMULET is a modular supervised ML workflow for image-based phenotyping that combines plant detection, segmentation, prediction, and trait analysis. Using *Arabidopsis thaliana*, AMULET predicted *Pseudomonas syringae* infection before visible symptoms appeared, demonstrating how AI can reveal the latent phenom and support early disease diagnosis. SPROUT (AI-based Seedling PRedictiOn and trait extraction Using RGB Time-series) is a low-cost RGB pipeline for automated monitoring of seedling emergence dynamics. It combines instance segmentation, object-detection-based data reduction, and temporal deep learning to detect seedling emergence, reconstruct emergence curves, and extract associated emergence traits. MARIGOLD extends this concept to field phenotyping of *Calendula officinalis* L., a medicinal plant with high variation in flower colour and metabolite-related traits. By combining tractor-mounted hyperspectral imaging, handheld spectroscopy, RGB imaging, and ML, MARIGOLD classified genotypes under field conditions and identified stable spectral features linked to carotenoid and chlorophyll absorption. A shallow 1-D convolutional neural network provided robust hyperspectral genotype classification, while Random Forest models supported interpretation of spectral and RGB traits. For multifactorial stress experiments, unsupervised strategies based on Topological Data Analysis improve visualisation of complex phenomics datasets and uncover hidden relationships among genotypes, treatments, and time points. By combining contrastive learning with Euclidean and hyperbolic representations, including the Poincaré ball, this approach better preserves hierarchical and temporal patterns than conventional projections, revealing growth trajectories under stress. Together, AMULET, SPROUT, MARIGOLD, and topology-based learning demonstrate how complementary AI strategies can move plant phenomics beyond visible traits, enabling earlier diagnosis, deeper biological interpretation, and the identification of novel phenotypic markers for resilient crops and medicinal plants.

Affordable Infrared DIY Microscopy for Non-Invasive Root Phenotyping

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Abstract

Understanding root growth dynamics in soil remains technically challenging because conventional imaging systems frequently expose roots to visible light and require artificial growth conditions. Here, we present a low-cost, modular, and do-it-yourself (DIY) infrared microscopy platform designed for non-invasive imaging of root systems under dark conditions. The system is based on OpenFlexure microscopy components, infrared illumination, and 3D-printed modules, enabling affordable and scalable construction of multiple independent imaging units.

Infrared illumination was specifically implemented to avoid disturbing natural root growth and to minimize light-induced artefacts during long-term imaging. The compact and flexible design allows easy integration into standard growth chambers as well as outdoor environments. Using mini-rhizoboxes filled with soil, the system enables continuous monitoring of root growth dynamics under environmentally relevant conditions.

Different optical configurations were used depending on the biological question. High-resolution imaging with up to 10× magnification enabled visualization of epidermal cells and root hairs, while lower magnification objectives around 2× allowed tracking of gravitropic root tip adaptation and root foraging behavior across diverse plant species. Automated time-lapse imaging further enabled long-term analysis of dynamic root growth responses.

Within the framework of the EU Horizon BarleyMicroBreed project, laboratory-derived root phenotyping data were compared with shovelomics campaigns performed across five field sites located on two continents under contrasting environmental conditions. This allowed direct comparison between controlled infrared imaging and field-scale root system architecture, providing insight into the ecological relevance of laboratory-observed root traits.

The presented platform demonstrates how accessible infrared microscopy can bridge cellular-level root phenotyping and field ecology while remaining affordable, scalable, and adaptable for broad use in plant research and breeding applications.

SP3D: A benchmark for systematic comparison of image-based 3D reconstruction methods of cucumber plants

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Abstract

Introduction. Accurate reconstruction of three-dimensional (3D) plant structure is important for plant phenotyping. Despite a growing interest in the topic, there is no public benchmark that evaluates the accuracy of 3D reconstruction approaches for plant phenotyping under a unified dataset and evaluation framework. To this end, we present the Single Plant 3D Reconstruction (SP3D) benchmark for greenhouse cucumber. Unlike general-purpose benchmarks, SP3D uses leaves as the main evaluation target and evaluates both geometric accuracy and phenotypic accuracy at the leaf and plant levels. This leaf-centered design better reflects the evaluation needs of plant phenotyping.

Methods. SP3D comprises 36 individual cucumber plants sampled at six time points over seven weeks after transplanting, covering early crop phases (2 to ~27 true leaves; plant heights of 9–250 cm). For each plant, the dataset provides a large set of multi-view images with foreground masks, structured-light scanner references data with organ-level annotations, and destructive leaf-area measurements. We estimated camera poses using Structure from Motion (SfM), and registered all reconstruction point clouds to the scanner coordinate system. Using the proposed benchmark, we evaluated three reconstruction methods: a) multi-view stereo (MVS), b) Neural Radiance Fields (NeRF), and c) 3D Gaussian splatting (3DGS). Evaluation was conducted at the leaf level and at the plant level. Geometric accuracy was measured by comparing to reference data collected by a structured-light scanner and phenotypic accuracy was determined compared to manual destructive leaf-area measurements. For the geometric accuracy, the scanner data was used as reference and the phenotypic accuracy was calculated using manual reference measurements.

Results. At the leaf level, MVS reached an F1-score with a tolerance of 4mm of 91.7% (geometric reconstruction accuracy at 4 mm tolerance; higher is better, max = 100%), compared with 79.8% for NeRF and 72.7% for 3DGS. Leaf area estimation followed the same ranking at both leaf and plant levels, with MVS achieving the lowest mean absolute percentage error (14.0% at leaf level, 5.9% at plant level) and 3DGS the highest (30.6% and 24.2%); NeRF fell in between. All methods became less accurate at later sampling time points due to the increased complexity of the taller plants with more occluded canopies. NeRF and 3DGS showed systematic overestimation of leaf area, which was associated with partial double-layer surface artifacts.

Conclusion. SP3D is the first benchmark to compare MVS, NeRF, and 3DGS for plant 3D reconstruction with a unified, leaf-centered evaluation. In our evaluation, MVS consistently outperformed NeRF and 3DGS across both geometric and phenotypic metrics. It enables application-relevant comparison of reconstruction methods and supports downstream tasks such as leaf area estimation. For future work, we will extend SP3D to additional plant species and imaging conditions and use it to evaluate other reconstruction methods.

Linking Rosettes to Leaves: An AI-Driven RGB Imaging Pipeline for *Arabidopsis thaliana* Phenotyping

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Abstract

Image-based plant phenotyping is becoming increasingly important for studying how plants grow, develop, and respond to their environment. In controlled indoor experiments, red-green-blue (RGB) imaging combined with computer vision offers a practical and non-destructive way to measure plant traits over time. However, large image datasets require reliable tools that can turn images into biologically meaningful information. This work presents an AI-based image analysis pipeline for rosette and leaf phenotyping in *Arabidopsis thaliana*. The pipeline first performs whole rosette segmentation, allowing the plant canopy to be separated from the background at different growth stages. It then extends to leaf instance segmentation and sequential tracking, enabling individual leaves to be detected and tracked over the experimental period, even when they occlude or partially block one another. By preserving the identity of each leaf throughout development, fine-tuned models support more detailed and biologically meaningful time-series analysis, rather than whole-canopy assessment alone. From the segmented rosettes and leaves, the pipeline automatically extracts quantitative growth traits, together with colour-based traits linked to the plant's physiological condition. These measurements support further statistical analysis of growth patterns and phenotypic variation, while clustering of the morphological traits makes it possible to group ecotypes according to similarities in rosette and leaf development. Overall, this approach provides a scalable and interpretable workflow for RGB-based phenotyping of *Arabidopsis thaliana*. Future work will focus on extending this approach towards a universal leaf-tracking deep learning model that can generalise across multiple plant species through more diverse datasets and improved cross-species model adaptation.

Enabling Reproducible Phenotyping: An Open-Source Python PlantScreen and Fytotron APIs

Tim van Daalen¹, Sebastian Seitner²

1 Netherlands Plant Eco-phenotyping Centre (NPEC), Wageningen University & Research (WUR), The Netherlands.

2 Plant Sciences Facility, Vienna BioCenter Core Facilities GmbH (VBCF), 1030 Vienna, Austria

Abstract

Photon Systems Instruments (PSI) offers several products, including PlantScreen for phenotyping and Fytotron for climate control. For both systems, PSI provides application programming interfaces (APIs). As with any API, it requires substantial effort to turn the documentation into robust, working code, and to maintain it over time. Currently, this work is duplicated at each facility, leading to divergent, incompatible implementations that complicate collaboration, for example sharing data analysis workflows and creating reusable, comparable datasets across sites. To address these challenges, we developed open-source Python packages that provide common, tested, interfaces for the PlantScreen and Fytotron APIs, reducing redundant effort and promoting more consistent, interoperable workflows.

To achieve this, we first created OpenAPI specification files based on the existing PlantScreen and Fytotron API descriptions. OpenAPI provides a standardized way to describe HTTP-based APIs, and the resulting specification files provide an easy way to process changes to the interface. From these specifications, the Python client code and accompanying documentation are generated automatically, which simplifies maintenance and improves consistency. Automated workflows regenerate the clients and run tests whenever the specifications are updated, ensuring that changes are propagated reliably. This decouples client maintenance from local programming expertise and allows facilities to focus on the research questions rather than low-level integration details.

These packages enable facilities to integrate PlantScreen and Fytotron data directly into automated analysis pipelines, apply shared analysis workflows across sites, and more easily construct reusable datasets that combine measurements and instrument metadata. By providing a common, openly available implementation, this work lowers the barrier to collaboration on higher-level tasks in plant phenotyping and supports more transparent and reproducible use of PSI platforms. This lays the foundation for a broader ecosystem of tools, including analysis and data management, which can be built on top. We already have some plans for this and hope it inspires others to join forces.

PARALLEL WORKSHOP SESSION

16:00 – 18:00 WORKSHOP 1

Data Management Working Group round table discussion

16:00 – 16:45

Jana Kholová (Czech Advanced Technology and Research Institute (CATRIN), Palacký University Olomouc, Czech Republic)

Tim van Daalen (Wageningen University & Research, Netherlands)

Sebastian Seitner (Plant Sciences Facility, Vienna BioCenter Core Facilities GmbH (VBCF), Austria)

Welcome note, introduction and overview of WG activities.

16:45 – 17:15

Round table discussions

TOPIC 1: PLANTSCREEN TOOLS – Data management integration +APIs; Current approaches to data management within the PlantScreen™ user community will be discussed, including the tools and workflows used to manage datasets, connect metadata to imaging data, and support automated or manual data annotation. Participants will discuss experiences with making datasets openly available, compare PSI-provided and locally developed tooling, and identified key strengths, limitations, and opportunities for improved integration through data management platforms and APIs.

TOPIC 2: HTP-DATA PIPELINES – Discussion will focus on the current state of high-throughput phenotyping (HTP) data pipelines, with particular attention to technical integration challenges and the maturity of existing data management solutions. Focus tasks is on what is working well, identify persistent gaps and bottlenecks, and discuss opportunities for collaboration in the development, implementation, and adoption of interoperable data management pipelines.

TOPIC 3: DATA MANAGEMENT SURVEY FOR HIGH-THROUGHPUT PHENOTYPING DATA – This round table will review the outcomes of the community survey on data management and data analytics tools in high-throughput plant phenotyping, using the survey results as a starting point for a broader discussion of current practices, challenges, and priorities. We will discuss common needs identified by the survey and will explore opportunities for improving interoperability, FAIR data practices, analytics workflows, and community-driven tool development.

17:15 – 18:00

Sebastian Seitner, Tim van Daalen, Jana Kholová Summary of table discussions

PARALLEL WORKSHOP SESSION

16:00 – 18:00 WORKSHOP 2

Controlled Environment Plant Phenotyping (CePPG) workshop (Hybrid mode)

16:00 – 16:10 **Thomas Altmann** (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany)

Welcome, Introduction to CEPPG and WG meeting.

16:10 – 16:35 **Robert D. Hancock** (The Advanced Plant Growth Centre, James Hutton Institute, Dundee, Scotland)

The Advanced Plant Growth Centre: Climate Simulation and HighThroughput Phenotyping for Gene Discovery and Resilience Breeding.

16:35 – 17:00 **Marco Maccaferri** (Department of Agricultural and Food Sciences, University of Bologna, Italy)

Dissection of developmental and adaptive diversity in a Tetraploid Wheat Core Collection (online).

17:00 – 17:25 **Lamis Abdelhakim** (Photon Systems Instruments, Czech Republic)

Integrative phenotyping combined with modelling as a tool for predicting harvest-related traits.

17:25 – 17:40 **Thomas Altmann** (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany)

Round table discussion on WG activities.

17:40 – 17:55 **Philipp von Gillhaussen** (International Plant Phenotyping Network e.V. (IPPN), Juelich, Germany)

WG chair and vice chair person election – candidates and procedure; steering committee volunteers.

17:55 – 18:00 **Thomas Altmann** (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany)

Closing remarks.

19:00 – ON **Conference dinner**

The Advanced Plant Growth Centre: Climate Simulation and High-Throughput Phenotyping for Gene Discovery and Resilience Breeding

Robert D. Hancock¹, Raymond Campbell¹, Fraser Macfarlane², Benjamin Potts³, Kyriakos Varypatakis¹, Sanjeev Kumar Sharma¹ and Dominic Williams¹

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2 Informational and Computational Sciences, The James Hutton Institute, Invergowrie, Dundee DD2 5DA. United Kingdom

3 Division of Plant Sciences, University of Dundee, Nethergate, Dundee DD1 4HN. United Kingdom

Abstract

The Advanced Plant Growth Centre, the UK's most recently commissioned high-throughput crop phenotyping platform, was developed with a focus on understanding crop resilience to future growing environments. Here we present an overview of the rationale behind platform design, the platform capabilities and pipelines for data analysis.

We will illustrate the presentation with results from ongoing projects. Examples include a combination of infra-red gas exchange (IRGA), and high-throughput growth and physiological phenotyping in a lettuce population to identify markers and genes for light use efficiency in the context of breeding for indoor agriculture. We will also present results from work aiming to identify genetic diversity of response to elevated CO₂ (eCO₂) in barley. These data suggest that eCO₂ induces overproduction of tillers, but reduced grain yield caused by excessive grain abortion under eCO₂. Genetic differences were observed with more recently released cultivars exhibiting reduced sensitivity to eCO₂. We present results in the context of source-sink relationships.

Integrative phenotyping combined with modelling as a tool for predicting harvest-related traits

Lamis Abdelhakim¹, Hans Tietze², Barbora Pleskačová¹, Ayelet Kurtz-Sohn³, Eyal Fridman³, Klára Panzarová¹, Zoran Nikoloski²

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Abstract

Harvest-related traits are key agronomic traits for cereal crops. Understanding the influence of abiotic stress on yield and the ability to find the most predictive traits for final yield are important for understanding and characterizing crop resilience strategies. Using a high spatial and temporal phenotyping approach with multiple imaging sensors, we monitored growth dynamics of plants and assessed their physiological responses throughout development until reaching the maturity stage under control and drought conditions. Here we present a dataset comprising 145 traits over 70 time points under two conditions for six barley lines, including elite, cultivated, and wild lines. We applied advanced data analysis using machine learning approaches for effective integrative visualization and subsequent modelling. The main objectives of this study were to identify distinct traits that differentiate drought-stressed from well-watered plants and to accurately predict harvest traits. Using a classification model, we observed an accurate separation between control and drought treatments and ranked the tolerance levels of different lines. For the harvest prediction models, we evaluated all time points under different watering regimes compared with models using only early time points and determined the importance of traits. Finally, we analyzed the variance components of highly predictive traits and identified which traits are mostly driven by genetic, environmental or time components. With the applied modelling approach, we were able to predict the harvest-related traits and pinpoint the most predictive traits at specific time points. Identifying predictive traits early in the developmental stage can help breeders find stress-tolerant traits of interest.

POSTER SESSION

List of Abstracts

POSTER #1

Root-to-Shoot Stress Response Dynamics: A Case Study of Barley Drought Resilience

Klára Panzarová¹, Lamis Abdelhakim¹, Ivan Kashkan¹, Sajid Ullah¹, Katarzyna Retzer²

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2 Department of Ecosystem Management, Climate and Biodiversity, Institute of Forest Ecology, University of Natural Resources and Life Sciences (BOKU), Peter-Jordan Straße 82, Vienna, 1190, Austria

Abstract

High-throughput phenotyping has substantially advanced the understanding of shoot-level stress responses; however, progress in root phenotyping remains limited. Traditional root studies are destructive, time-consuming, and unsuitable for dynamic monitoring. Here, we present applications of the PlantScreen™ Root System, an automated, non-invasive platform enabling parallel monitoring of root and shoot growth across multiple plant species. The system allows precise control of rhizobox soil moisture, facilitating either waterlogging or drought treatments, and supports the application of defined nutrient and biostimulant regimes. Within the framework of the BarleyMicroBreed project, root growth dynamics of ten barley genotypes were characterized at early developmental stages under optimized moderate drought conditions. Simultaneous analysis of root and shoot growth complements field-trial evaluations aimed at assessing the contribution of root traits to plant performance, particularly yield stability under drought. Morphological traits of shoots and roots were captured using RGB imaging, while multispectral and near-infrared sensors provided additional insights into physiological properties, including root water content. Automated image segmentation using a sensor-specific pipeline with a pretrained model, followed by trait extraction, enabled efficient quantitative trait analysis. The results revealed distinct, genotype-dependent responses to drought, reflecting diverse stress-resilience mechanisms. Importantly, our findings demonstrate that high-throughput phenotyping at early seedling stages can capture divergent root dynamic strategies that may be predictive of later field performance under drought conditions. Overall, the integration of above- and below-ground phenotypic data with advanced analytical approaches extends trait assessment beyond traditional methods, providing deeper insights into root-shoot regulation under stress and supporting trait selection for crop improvement.

POSTER #2

Hyperspectral imaging in plant phenotyping for the early-detection of cereal diseases: A bibliometric and case-study review

Anna Rita Balingit¹, Riccardo Rossi¹, Michele Moretta¹, Marco Bindi¹, Marco Moriondo^{1,2}

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Abstract

In a context of increasing pathogen pressure, imaging sensors have become important tools for breeding stress-resistant varieties and for guiding field-targeted interventions. Among multimodal optical sensors employed to characterize biotic stress, hyperspectral techniques are particularly valuable for detecting subtle physiological changes before visible symptoms appear. However, discriminating among pathogens within the same crop remains challenging due to potential spectral overlap in plant responses. Consequently, the present study aimed to provide a structured overview of existing image-based approaches for disease detection and severity assessment in major cereals, with a specific focus on maize and rice. These case studies specifically investigate hyperspectral data to identify pathogen-specific spectral signatures, aiming to develop differential spectral indices capable of discriminating between fungal and bacterial diseases based on their distinct effects on host reflectance. Initially, a structured search strategy was implemented across the Scopus and Web of Science databases using selected keywords related to cereal disease detection. Retrieved records were screened against predefined inclusion and exclusion criteria, retaining only studies focused on the detection, discrimination, or severity assessment of diseases using multimodal sensors. Following this procedure, 218 documents were selected for systematic analysis. To map the research landscape, author keywords were cleaned, standardized, and subjected to co-occurrence analysis to identify dominant thematic clusters. Finally, a subset of studies on rice and maize was analysed to extract hyperspectral reflectance signatures associated with disease-affected leaf area. The spectral characterization of key pathogens, including blast, sheath blight (ShB), and bacterial leaf blight (BLB) in rice, as well as Southern corn leaf blight (SCLB), Northern corn leaf blight (NCLB) and Southern corn rust (SCR) in maize, served to define novel discriminant indices tied to the distinct physiological signatures of fungal and bacterial infections. Overall, the bibliometric analysis identified „hyperspectral imaging“ as the most frequently occurring keyword (71 occurrences), underscoring its central role in cereal disease research. In accordance with this trend, discriminant-band trends from hyperspectral images highlighted pathogen-specific signatures. In rice, the effects of Blast were characterised by a decrease in reflectance at both the red-edge and NIR wavebands. In contrast, ShB exhibited an increase in reflectance at both the visible-red and red-edge wavebands. BLB, on the other hand, demonstrated an increase in NIR reflectance. In the maize case-study, SCR was characterised by a distinct long wavelength interval decrease (~750–1300 nm), while SCLB and NCLB showed predominantly increases in the VIS–red-edge–NIR wavebands. These findings underpinned a novel discriminant index, providing a framework for future validation and subsequent implementation in field-scale, leaf-to-canopy disease monitoring.

POSTER #3

Polyamine-Based Biostimulants-Mediated Responses in *Arabidopsis thaliana* under Contrasting Water Regimes

Lisney A. Bastidas-Parrado^{1, 2}, Carlos E. Aucique-Perez¹, Francisco I. Jasso-Robles¹, Lukáš Spíchal¹, Nuria De Diego¹

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Abstract

Climate change is intensifying environmental pressure on agricultural systems, increasing the need for sustainable strategies that improve plant performance under both optimal and stress conditions. Among abiotic stresses, water limitation strongly affects plant growth and photosynthetic activity by altering water balance, cellular homeostasis, and developmental processes. In this context, small-molecule-based biostimulants, such as polyamines, have emerged as promising tools for modulating plant responses and improving stress resilience by regulating physiological and metabolic pathways.

In this study, we evaluated the effects of putrescine (Put) or 1,3-diaminopropane (Dap) on the early development of *Arabidopsis thaliana* under well-watered and water-deficit conditions. Morphological and physiological responses were assessed using automated, non-invasive high-throughput phenotyping based on optical sensors, enabling continuous and precise monitoring of plant performance. The wild-type accession col-0 and two derived mutant lines, *Atadc2* and *Atnata2*, were analysed to investigate the contribution of polyamine biosynthesis and catabolism pathways. The arginine decarboxylase 2 (*AtADC2*) gene encode a key enzyme involved in polyamine biosynthesis, and N-acetyltransferase 2 (*AtNATA2*) participates in polyamine metabolism through acetylation processes.

RGB-based imaging revealed that perimeter, compactness, and slenderness were among the most sensitive parameters for detecting treatment-dependent responses in both water regimes. Genotype- and treatment-dependent responses were observed under water-deficit conditions, with Dap generally promoting early plant vigour. In addition, the differential behaviour of *Atadc2* and *Atnata2* mutants confirmed that both genes mediate plant responses to Put and Dap applications, highlighting distinct roles of polyamine metabolism in growth regulation and stress adaptation.

Overall, our results demonstrate that high-throughput phenotyping is an effective approach for detecting early morphological responses to polyamine-based biostimulants and highlight the role of polyamine metabolism in regulating plant growth and adaptation to water limitation.

Acknowledgement

This work was supported by the project Interdisciplinary approaches for the development and application of new materials in industrial, agricultural, and medical practice, reg. no. CZ.02.01.01/00/23_021/0008909 of the ERDF Programme Johannes Amos Comenius.

POSTER #4

Integrating UAV phenomics into maize breeding pipelines for improved field based selection

Sofija Božinović¹, Jovan Pavlov¹, Nikola Grčić¹, Jelena Vančetović¹, Marko Mladenović¹, Aleksandar Kovačević¹, Sanja Perić¹ and Vlatko Galić²

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Abstract

Due to increasing climate variability, frequent extreme weather events, and consequently stronger genotype × environment interactions, maize breeding is becoming increasingly complex and can no longer rely solely on conventional visual scoring. High-throughput field phenotyping (HTFP) enables non-destructive, repeated, and scalable data collection across large breeding trials while capturing plant responses throughout the growing season. Initially developed as a supporting tool, HTFP is increasingly being integrated into breeding pipelines as an independent source of information for data-driven selection and decision making. Therefore, HTFP should not be viewed solely as an imaging technology, but rather as a practical decision-support framework for modern breeding programs operating under increasingly unstable environmental conditions. Within the PHENO_MaizE project, we investigate the potential of UAV-based RGB phenomics for maize breeding applications using several complementary approaches. The study integrates repeated drone imaging, extraction of image-derived traits, and phenomic prediction approaches in order to evaluate the applicability of digital phenotyping for selection of superior maize genotypes. Experimental material includes maize inbred lines and their corresponding testcrosses evaluated across multiple environments in Serbia. Multi-temporal UAV surveys conducted throughout the growing season enable monitoring of crop development dynamics and extraction of traits such as plant height, canopy cover, vegetation indices, and growth-related descriptors. We will demonstrate how UAV-based HTFP can support breeding activities through temporal monitoring of genotype performance, characterization of plant responses to environmental variability, and integration of image-derived traits into phenomic prediction models for agronomically important traits, including grain yield, flowering time, and grain moisture at harvest. Special emphasis will be placed on the development of a practical, cost-effective, and scalable HTFP workflow adapted to medium-sized breeding programs.

Acknowledgement

This research was supported by the Science Fund of the Republic of Serbia, Grant No 6672, High-throughput field phenotyping in temperate maize hybrid breeding: how can phenomics improve speed and accuracy of selection?
– PHENO_MaizE.

POSTER #5

Deciphering wheat stressresponses: Assessingnon invasive methods for abiotic stress phenotyping

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Abstract

Abiotic pressure driven by climate change renders crop productivity highly unpredictable. Ensuring food security for a growing global population, therefore, requires a deep understanding of the physiological and biochemical mechanisms that enable plants to tolerate abiotic stress. In this study, a spring wheat (*Triticum aestivum* L.) was subjected to different abiotic stresses, such as low light, soil acidity, low nutrition and drought stress, compared to Control plants grown under optimal nutrition and irrigation, neutral soil pH and high light intensity. The seedlings were kept in a climate-controlled chamber, and data were recorded using various non-invasive techniques, such as gasometry, chlorophyll meter, fast fluorescence kinetics (HandyPEA and pulse amplitude modulated analyses of PSII and PSI photochemistry measured simultaneously with electrochromic bandshift using a handheld multiparametric analyser. Fifteen individual plants per treatment were assessed separately, and the dataset was analysed using ANOVA and Duncan post hoc test. The gas exchange analysis indicated down regulation of photosynthetic rate, stomatal conductance, and internal CO₂ concentration triggered in drought, soil acidity and low nutrition due to closed stomatal response to minimize transpiration and sustain carbon assimilation. Elevated chlorophyll (SPAD) values were observed in low-light and drought-stressed plants, which may be due to reduced leaf expansion and increased chlorophyll concentration per unit leaf area, but their low dry weight value indicated that increased chlorophyll concentration does not necessarily translate into enhanced biomass. The low-nutrition plants showed an increase in their proton conductivity alongside a decline in PSI active centers and an increase in PSI over-reduced centers. The fast fluorescence kinetics analysis showed that low-nutrition plants had the most impaired PSII performance, which denotes a decrease in energy absorption and electron transport, which may result in oxidative stress. In conclusion, our analysis demonstrates that non-invasive methods allow rapid, real-time phenotyping of plants, providing deeper insights into physiological responses unique to different stress factors. Keywords: non-invasive methods, abiotic stress, photosynthesis, crop productivity.

Acknowledgement

This work was supported by the research projects APVV-22-0392, APVV 24-0586, VEGA 1-0048-25 and VEGA 1-0639-26.

POSTER #6

Foliar Potassium Nitrate Application Mitigates Chilling-Induced Photosynthetic Limitation in Maize by Restoring Stomatal Conductance and Protecting Photosystem II

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Abstract

Spring chilling stress represents a major constraint to maize (*Zea mays* L.) productivity in temperate regions especially in Northern Europe, disrupting stomatal conductance, carbon assimilation, and photosystem II (PSII) photochemistry during critical early vegetative growth stages. While delayed sowing is commonly practiced to avoid cold damage, it significantly reduces yield potential. Chemical strategies to protect maize photosynthesis under chilling stress remain largely unexplored. In this study, we investigated the efficacy of foliar potassium nitrate (KNO₃) application (0, 1 & 2%), applied either as pre-cold priming or post-stress via foliar spray, in mitigating chilling-induced photosynthetic limitation in maize (cv. Golden Bantam). One-month-old plants were subjected to sequential mild (4°C, 7 h) and severe (0.5°C, 7 h) chilling events. Physiological responses were assessed through gas exchange (net photosynthesis, stomatal conductance, and intercellular CO₂, electron transport rate), chlorophyll fluorescence (Fv/Fm, ΦPSII, OJIP transients, and JIP-test parameters), leaf area, and biomass measurements.

Cold stress substantially reduced stomatal conductance (gs), net CO₂ assimilation (A), ΦPSII, and biomass accumulation. Foliar or primed 1% KNO₃ effectively restored gs and A, maintained ΦPSII, reduced leaf temperature, and supported biomass recovery, with protective effects most pronounced at 1% concentration. JIP-test analysis confirmed that KNO₃ stabilized PSII reaction centers, moderated QA accumulation, and supported downstream electron transport. Light response curves further revealed improved light use efficiency and reduced photoinhibitory stress in KNO₃-treated plants, indicating better capacity to utilize incident light for photochemistry under chilling conditions. In contrast, 2% KNO₃ provided only limited protection, likely due to phytotoxic effects at higher concentrations.

These findings demonstrate that foliar KNO₃ effectively protects maize photosynthesis under chilling stress by restoring stomatal conductance regulation, sustaining CO₂ supply to the Calvin cycle, and preventing photoinhibitory PSII damage. This approach offers a promising and practical agronomic strategy for enabling earlier sowing and improving maize productivity in cold-prone regions.

Acknowledgment

Md. Intesaful Haque is supported through the National Science Centre grant no. 2021/43/I/NZ9/01356. This research was supported by the Innowator Plus project under grant number 02/2025/INN-PLUS.

POSTER #7

A whole plant scan: investigating the above and belowground effects of waterlogging in European heritage lines of spring barley through image based technologies

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Abstract

Waterlogging is an often-overlooked stress that hinders crop yields and is becoming more frequent and severe due to climatic changes. Spring barley is the most important cereal crop in many Northern and Central European countries, and the most waterlogging-sensitive cereal. This project's overall aim is to analyse the phenotypic differences on root and shoot growth of European heritage spring barley lines exposed to waterlogging through image-based technologies available at University College Dublin. We first focused on ten discriminate lines of spring barley selected from the European Heritage Barley collection (ExHIBiT) cultivated in a field trial at UCD Lyons Research Farm. Soil cores were taken a week before, during and after a waterlogging treatment to assess stress impact on the root system architecture. The cores were scanned using X-ray Computed Tomography (CT), and root washed and scanned using Rhizovision Explorer software. We are currently conducting a glasshouse-based trial to obtain comprehensive scans of selected spring barley lines by using a Photon System Instruments (PSI) imaging platform equipped with chlorophyll fluorescence, RGB and hyperspectral imagers. X-ray CT scanners will be used for belowground phenotyping. Our objective is to identify phenotypic traits displaying improved tolerance to waterlogging by analysing both below and above-ground physiological changes. This approach will generate a comprehensive dataset detailing the physiological effects of waterlogging on spring barley.

POSTER #8

Nordic Research Hub for Digital Plant Phenotyping (NordPheno)

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Abstract

The Nordic region faces unique agricultural challenges due to its diverse climates and geographies, where many crops grow at the edge of their cultivation zones. High-throughput plant phenotyping (HTPP) has the promise to facilitate screening for Genotype X Environment/Management X Phenotype interactions, but the demands on Nordic crop breeding are so high that even this approach is no longer adequate. The next step in enhancing the breeding efforts will be to engage predictive modeling to speed up the genomic selection of resilient and adapted varieties to the Nordic challenges of the changing climate and fluctuating weather events. To allow effective application of AI in the analysis of HTPP data and crop modeling there is a need to bridge the gap between crop research and computer sciences. Globally, “AI in agriculture” market is projected to grow at 25.5% CAGR (2023–2030), driven by the demand for precision farming tools. Similarly, Nordic IT service spending on IoT/edge solutions has increased by 22% in 2022, reflecting regional readiness for the adoption of these technologies. To answer to this call, eight Nordic Universities and research institutions from Finland (UH), Sweden (SLU), Norway (NTNU, NIBIO, UiO, UiT, NMBU), and Denmark (UCPH) have established a NordForsk-funded interdisciplinary Nordic Research Infrastructure (RI) Hub called NordPheno. <https://www.helsinki.fi/en/infrastructures/nordic-research-infrastructure-hub-digital-plant-phenotyping>. The network aims at enhancing knowledge transfer, facility sharing and educational efforts in the support of digitization of plant phenomics and breeding. The hub will foster a strategic communication framework and stakeholder interaction efforts across the region over five years (2026–2030). The network aims to strengthen the connection between plant biologists and scientists specializing in data digitalization and mathematics, and to address data analysis bottlenecks across Nordic plant phenotyping infrastructures. This initiative will facilitate more effective utilization of both new and existing data through the establishment of FAIR data management tools at the plant research facilities and actively integrate artificial intelligence as a valuable tool in plant phenomics. This approach will directly benefit crop research as well as future plant breeding efforts.

POSTER #9

Functional validation of the DHN₃ gene in winter wheat using virus-induced gene silencing and integrated phenotyping approach

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Abstract

High-throughput plant phenotyping platforms provide powerful tools for the functional characterisation of candidate genes involved in stress responses. This study focuses on the functional validation of the DHN₃ gene in winter wheat (*Triticum aestivum* L.), which, based on previous phenotypic observations, is associated with approximately a 6% yield improvement under drought conditions. The aim is to verify whether DHN₃ directly contributes to this yield-related effect by modulating plant response to drought and, if so, to identify the underlying mechanisms. To achieve this, we phenotyped four winter wheat varieties: Venturero, Viginta, Aladin and Annie and performed transient knockdowns of DHN₃ using virus-induced gene silencing (VIGS) based on siRNA-mediated gene suppression. The viral construct contains fragments of the 5' untranslated region (5' UTR) and a DHN₃ exon in antisense orientation, enabling targeted downregulation of gene expression. For the virus inoculation, plants are subjected to mechanical inoculation, in which the viral construct is applied to the leaf surface following gentle abrasion to facilitate viral entry into plant tissues prior to stress treatment.

The experimental design integrates non-invasive phenotyping using optical sensors, combined with transcriptomic and metabolomic analyses, to better understand the different stress response strategies and the mechanisms of action. During the phenotyping experiment, the four genotypes were exposed to contrasting water regimes, 30% and 60% of field capacity (FC). Phenotypic responses were monitored using automated RGB side-view and chlorophyll fluorescence (FluorCam) imaging, enabling assessment of growth dynamics and photosynthetic performance. In addition, transcriptomics and metabolomic profiling will be performed on the most photosynthetically active leaf at the tillering stage (BBCH 20-29) to capture biochemical changes associated with DHN₃ silencing. By integrating phenotypic data with other omics data, we aim to identify key traits and targeted pathways associated with the functional role of DHN₃.

This combined methodological approach is expected to enable the discrimination of gene-specific effects on plant performance under water-limited conditions. Furthermore, the presented framework provides a scalable and reproducible strategy for the functional validation of candidate genes involved in drought tolerance. We believe this approach will contribute to a better understanding of the molecular mechanisms underlying stress adaptation in wheat.

POSTER #10

An Interactive Dashboard for Exploratory Analysis of High-Throughput Plant Phenotyping Data

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Abstract

High-throughput phenotyping (HTP) platforms generate large, multifactorial and multiparametric datasets that capture plant responses to increasingly complex combinations of biotic and/or abiotic factors. The use of machine learning (ML) models in image analysis enables efficient extraction of quantitative traits from plant phenotyping systems that use optical sensors such as RGB and fluorescence cameras; however, the subsequent exploration and interpretation of these datasets has been identified as an area for improvement.

We present a custom interactive dashboard developed for internal use at CATRIN, specifically adapted to the structure and data outputs of our plant phenotyping systems. The tool is designed to support preliminary image analysis and trait extraction from high-throughput phenotyping experiments with a selection of visualisation and analysis methods. It enables rapid exploration of datasets through dynamic parameter selection, statistical analysis, and plots and visualisations. The interactive design supports intuitive analysis of multiparametric data, simplifying the interpretation of complex interactions. By transitioning from Python script-based workflows to a graphical interface, the dashboard lowers the technical barrier to data analysis and reduces the risk of user introduced errors.

Built in Python using the Shiny web application framework, the dashboard is highly extensible and adaptable to evolving data formats and analytical needs. It supports data input from local files, and a direct link to an online BrAPI-compliant database is in development in collaboration with CZU. The development process has been carried out in close collaboration with researchers at CATRIN, and the analysis platform is currently undergoing testing and refinement to ensure usability and alignment with experimental workflows.

POSTER #11

When Seeds Break Through: AI Tracks Crop Emergence

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Abstract

Early seedling emergence is a critical stage of crop establishment, yet it is still predominantly assessed manually, limiting scalability and temporal resolution in plant phenotyping experiments. In this study, we present an RGB-based image-analysis pipeline for automated detection and characterisation of crop seedling emergence from time-series data. The proposed framework integrates instance segmentation, object detection-based data reduction, and deep learning models to identify the precise timing of emergence at the level of individual plants.

The pipeline processes high-throughput image sequences by first segmenting individual wells within phenotyping trays, then localising emergence regions and constructing image time-series datasets. Emergence detection is performed using a convolutional neural network combined with temporal architectures (LSTM and Temporal Convolutional Networks), enabling robust identification of early developmental stages despite heterogeneous soil backgrounds and imaging variability. Automated post-processing further refines predictions and reconstructs emergence curves, from which key traits such as final emergence rate, time lag (EC50), and emergence synchronicity of each population are derived.

The system was trained and validated on two independent datasets comprising barley and wheat, captured using different RGB imaging platforms, allowing assessment of robustness under domain shift conditions. The best-performing models achieved high classification accuracy (up to 99.5% during training and >90% under realistic evaluation with temporal tolerance), demonstrating strong generalisation across experimental setups.

Overall, the proposed pipeline provides a robust and cost-effective tool for high-throughput phenotyping of plant emergence. By enabling automated extraction of emergence dynamics from RGB image sequences and traits-related extraction, our pipeline offers new opportunities for crop breeding, stress physiology studies, and digital agriculture applications.

POSTER #12

Assessment of drought resistance in buckwheat genotypes through high-throughput phenotyping

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Abstract

Buckwheat (*Fagopyrum* spp.), a prominent pseudocereal, is garnering increasing attention as a functional food matrix, owing to its superior profile of essential amino acids, vitamins, and phenolic constituents. Nevertheless, its cultivation is frequently challenged by a spectrum of environmental stressors, with drought representing one of the most multifaceted and deleterious abiotic constraints. In this study, the automated phenotyping PlantScreen™ unit was employed to collect a relatively large dataset to analyse the six genotypes of buckwheat subjected to WW (well-watered, 80% field water capacity FWC), MS (mild water stress, 50% FWC) and SS (severe water stress, 50% FWC) conditions. Despite originating on different continents in different climatic regions, the genotypes showed surprisingly similar growth responses to the drought. We observed a significant decrease in morphological parameters, most notably plant height, leaf area, and top-view perimeter, under severe stress conditions. Combined with the decreased growth rates, these data indicate the resource allocation shift toward survival strategies in response to water scarcity. Among six studied buckwheat genotypes, Panda and Silver Hull maintained their height under MS, whereas the plant area for these varieties under MS decreased the least in comparison to respective WW. As Panda and Silver Hull were observed to be the shortest and smallest genotypes by plant area in WW conditions, our results show the advantage of the shorter genotypes in coping with MS. The results regarding vegetation indices (NDVI, PRI, and Vig2) and biochemical markers (ANTH and CAR) highlight the complexity of assessing drought stress in buckwheat. The Vig2 index shows clear differences between control and water stress-exposed plants. As chlorophyll content did not vary under different water regimes, no significant differences in NDVI values due to limited water supply were observed. In our study, we observed a simultaneous significant decrease in CAR and an increase in PRI, only for Emka, La Harpe, Panda, and Zimbabwe under SS. All genotypes showed increased carotenoids level as a protective mechanism, while only Emka, Panda, Silver Hull, and Zimbabwe exhibited a significantly increased anthocyanins level (ANTH), possibly indicating their reliance on other mechanisms for coping with drought. The observed divergence in phenotypic responses underscores the pivotal role of genetic variability in modulating drought-resistance strategies within buckwheat.

The study was supported by the national grants APVV-22-0392, APVV-24-0586, VEGA-1-0425-23 and VEGA-1-0048-25.

POSTER #13

Beyond stress escape strategy: cuticular wax composition contributes to barley tolerance under combined drought and Fusarium stress

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Abstract

Combined abiotic and biotic stresses represent a major constraint for crop productivity under changing environmental conditions. Epicuticular waxes play an important role in limiting non stomatal water loss and forming a protective barrier against pathogen infection; however, their contribution to plant responses under simultaneous stress conditions remains insufficiently understood. In this study, we investigated the role of cuticular wax composition and leaf surface micromorphology in shaping stress responses in four spring barley doubled haploid lines differing in wax phenotype and heading time.

Epicuticular wax composition was analyzed using ultra-performance liquid chromatography – high-resolution mass spectrometry, while wax crystal density and distribution were examined by scanning electron microscopy. Stress-induced ultrastructural changes in mesophyll cells were evaluated using transmission electron microscopy. Plants were subjected to drought stress, Fusarium infection, and their combination.

Genotype-dependent differences in wax ester composition and crystal coverage indicated distinct wax biosynthesis strategies among the studied genotypes. Under drought conditions, the late-heading, glaucous genotype examined in this study showed increased leaf surface coverage by wax crystals and accumulation of longer-chain wax compounds compared with the early-heading, glossy genotype, which was characterized by higher levels of short chain wax esters. Fusarium infection led to the accumulation of large starch grains, likely due to impaired phloem transport of assimilates, and to the formation of structures between the cytoplasm and the primary cell wall, suggesting altered cellular organization. Combined stresses caused the most pronounced ultrastructural alterations, including starch depletion, chloroplast deformation, and structural changes at the cytoplasm-cell wall interface.

Despite its late-heading parental background, the glaucous genotype maintained greater chloroplast structural integrity under drought and combined stress conditions, suggesting enhanced cellular resilience associated with differences in cuticular wax composition. These findings highlight the importance of structural and biochemical defense mechanisms beyond phenological stress escape strategies in determining barley responses to multiple environmental stresses.

Acknowledgments

This research was funded by National Science Centre, Poland, grant no. 2021/41/B/NZ9/02373. TEM studies were performed in the Laboratory of Electron Microscopy of the Nencki Institute, supported by the project financed by the Minister of Education and Science based on contract No 2022/WK/05 (Polish Euro-Biolmaging Node “Advanced Light Microscopy Node Poland”).

POSTER #14

Phenotyping A Light-Driven Mutualism Between the Green Alga *Oophila* sp. And *Ambystoma maculatum*

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Abstract

Symbioses between algae and heterotrophs provide powerful models for bioengineering, revealing strategies that challenge conventional assumptions about autotrophic efficiency. While efficient growth is often equated with maximizing photosynthetic rates, the endosymbiosis between the green alga *Oophila amblystomatis* and *Ambystoma maculatum* embryos demonstrates that successful partnerships can operate under more complex physiological constraints. Transcriptomic evidence shows that *Oophila* continues to proliferate even while expressing genes typically associated with stress responses, and previous studies indicate that light (hence photosynthesis) is essential both for algal growth and for accelerating salamander embryonic development.

Our project examined whether photosynthesis is the primary driver of *Oophila* proliferation by measuring embryonic development, ammonia dynamics, and photosynthetic performance across different light intensities. Ammonia concentrations were 16 times lower in illuminated eggs than in dark-treated eggs, suggesting that *Oophila* assimilates or detoxifies embryonic ammonia into more useful metabolites. Chlorophyll a fluorescence measurements allowed us to predict Photosystem II efficiency and electron transport rates in the egg in a non-invasive manner. In parallel, imaging of algal abundance and embryo development showed correlation with high-light conditions, despite Photosystem II efficiency being lower than in low-light treatments. We interpret the observed reduction of photosynthetic efficiency as down-regulation of Photosystem II under strong illumination. Electron transport measurements showed that oxygen production in high light was 20-fold greater than in low light and exceeded embryonic oxygen demand threefold, whereas low-light conditions produced insufficient oxygen for the embryo. All these results illustrate a highly efficient system.

The innovative use of non-destructive optical methods to study the symbiosis of algae and vertebrates showcase the relevance of custom design phenotyping tools like the ones used in this work. Understanding how this alga simultaneously supports host development and regulates its own metabolism provides a technical foundation for novel engineering nitrogen-processing and photosynthetic strategies in synthetic systems inspired by this unique symbiosis. Developing of novel ways to study in a non-destructive manner this “green embryos is further discussed”.

POSTER #15

One Tool, Many Domains: Harmonizing FAIR Metadata Collection with the ISA-Wizard

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Abstract

The rapid acceleration of high-throughput technologies in the life sciences has created a paradox: while we are generating more data than ever before, the vast majority of it remains “dark data” defined by Gartner as the “information assets organizations collect, process and store during regular business activities, but generally fail to use for other purposes” [1]. In fields ranging from crop science to systems biology, the value of raw data is strongly dependent on the quality of its surrounding context. Without rigorous metadata, the most sophisticated genomic or phenomic dataset cannot be effectively integrated, compared or reused. This challenge sits at the heart of Research Data Management (RDM), representing the foundational hurdle between raw biological observations and reproducible science. The ISA Wizard [2] was developed specifically to bridge this gap, serving as an intuitive, user-centred gateway for researchers. By addressing the very backbone of the data lifecycle, it transforms the complex burden of FAIR (Findable, Accessible, Interoperable, Reusable) data stewardship [3] into a streamlined, guided experience for researchers. Rather than treating metadata as a final, bureaucratic step in the publication process, the tool integrates curation into the active research phase. It leverages the Investigation / Study / Assay (ISA) framework [4], a robust and established standard for describing the metadata of biological experiments. However, the true innovation of the ISA Wizard lies in its accessibility. Historically, the technical barriers associated with metadata syntax such as the details of ISA-Tab or the structural requirements of ISA-JSON have acted as a deterrent for scientists. By utilizing a survey-like interface, the wizard effectively abstracts these complexities. It guides the user through a logical progression of questions, ensuring that the resulting metadata is aligned with established community ontologies and minimum information standards.

The practical application of this tool is most clearly seen in the realm of plant phenotyping. Capturing the interplay between a plant's genetic makeup and its environmental conditions requires a high level of detail. The ISA Wizard simplifies this process by enforcing compliance with the Minimal Information About a Plant Phenotyping Experiment (MIAPPE) standard [5]. In doing so, it creates interoperable datasets, allowing for the seamless exchange of data across different laboratories and seasons by exporting into Annotated Research Contexts (ARC). This interoperability is further extended through the BrAPI4PSI project, where the ISA Wizard integrates with the Breeding API (BrAPI) [6] to prepare metadata for the experimental setup of the IPK Phenosphere and export into FAIR Digital Objects in form of ARC RO-Crates. ARC is a new framework for representing ISA structured datasets in machine-actionable units which combine data, metadata and the computational environment needed to reproduce an analysis.

Beyond plant sciences, the tool's versatility has been shown through its adoption in animal phenotyping studies. Arising from a collaborative ELIXIR BioHackathon project [7], the development of a dedicated animal study configuration demonstrates how the ISA Wizard fosters community exchange and interdisciplinary collaboration. This use case demonstrates how the

tool can be applied beyond the original domain of interest and cater to different user communities. By providing a scalable, cross-domain solution for data annotation, the wizard supports researchers who may not be experts in informatics.

Ultimately, the impact of the ISA Wizard lies in its capacity to support multi-omics and systems biology workflows. Modern life science projects frequently require combining distinct datasets such as genomic sequences, metabolomic profiles and phenotyping data. Because the ISA Wizard is domain-agnostic in its nature, it provides a consistent framework to integrate these diverse data types at the point of collection. Ensuring that metadata from different biological domains is standardized and mutually interoperable helps prevent the creation of isolated data silos. This cross-domain integration opens up unified data spaces, ultimately allowing for the generation of insights that are difficult to capture when data remains fragmented. By connecting standard research workflows with structured data engineering, the ISA Wizard assists in improving data literacy and supporting a clearer routine for long-term data stewardship.

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POSTER #16

Imaging barley root plasticity in response to waterlogging and recovery

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Abstract

Barley (*Hordeum vulgare* L.) is the fourth most important global cereal and Ireland's primary crop, where its production is affected by waterlogging. This research aims to characterize root responses linked to waterlogging resilience. Leveraging the European Heritage Barley Collection (ExHIBiT), a panel of 12 genotypes (5 tolerant, 5 susceptible, 2 references) was isolated for an in depth study. Using the PLANTSCREEN™ ROOT IMAGING SYSTEM (PSI, Czech Republic), non-destructive root phenotyping of rhizotrons-grown plants is being carried out to investigate root system architecture dynamics at high-resolution. Complementary destructive phenotyping is included to explore anatomical plasticity, specifically aerenchyma development in adventitious roots. Additional experiments using custom-made rhizoboxes are also conducted to sample plants at several time-points for hyperspectral VNIR-SWIR imaging using dedicated cabins of the PLANTSCREEN™ SC IMAGING SYSTEM (PSI), prior future shoot and root ionome profiling analyses to gain insights into the modifications in nutrients uptake induced by waterlogging stress.

POSTER #17

A Unified Data Architecture for Controlled Environment Agriculture Experiments

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Abstract

Plant experiments in Controlled Environment Agriculture (CEA) generate heterogeneous datasets, including structured experimental records, high-frequency microclimate sensor data, imaging outputs, and laboratory analyses. With the increasing adoption of advanced phenotyping instrumentation, data often accumulate across independently managed systems, limiting interoperability, reproducibility, and analytical potential. A domain-driven data architecture tailored to CEA research contexts has been developed at the controlled environment facility at La Trobe University to ensure data integrity and support downstream analysis.

The architecture introduces an experiment-centric model that unifies data across relational and object-store storage structures through a hierarchical experiment identity, ensuring consistent linkage across all data sources. The relational component captures structured experimental activities through control and observation data concepts. Operational data defines experimental design and configurations, including entities such as Experiment, Batch, Plant, Environment, and Treatment. Observation data captures experimental processes and outcomes, including cultivation activities (potting and feeding), plant measurements (morphology, development, health), harvesting events, sample tracking, and laboratory analysis results. To support large-scale phenomics data, the architecture extends into an object-store structure for semi-structured and unstructured datasets, with a standardized directory hierarchy organizing microclimate time-series measurements, spectral datasets, and image collections from mobile, DSLR, and drone cameras.

Although data are distributed across relational database and file-based platforms, unified governance is maintained through a single experiment identity, standardized file naming and consistent temporal alignment. Time-series structures enable synchronized integration and analytics, supporting phenomics workflows and provide a scalable foundation for cross-platform integration and data-driven applications.

POSTER #18

Evaluating leafy vegetable performance under shading conditions through image-derived phenotypic traits

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Abstract

Agrivoltaic systems (AVSs) maximize land-use efficiency by integrating agricultural and renewable energy production. Shade-induced morpho-physiological adaptations can either mitigate environmental stress or compromise plant development, particularly under the harsh climatic conditions typical of Mediterranean regions. For leafy vegetables, whose commercial value relies entirely on aerial biomass, these structural modifications have direct agronomic and economic implications. Identifying species optimally suited for AV shading gradients is therefore critical. Building on these premises, this study evaluated how AV-simulated shading intensities (control (T100), moderate (T50), and severe shading (T20)) affect four leafy vegetables, namely turnip broccoli (TB), Swiss chard (SC), lettuce (LE), and spinach (SP). By coupling high-throughput image-based phenotyping with comprehensive yield assessments, this research aimed to identify the most shade-responsive morpho-colorimetric traits, thereby supporting the strategic selection of species best adapted to the heterogeneous radiation environments of AVSs.

A greenhouse pot experiment was conducted using 15 replicates per species for each treatment. Throughout a 30-day experimental cycle, non-destructive monitoring was performed twice weekly using a high-throughput 3D phenotyping platform to capture top- and side-view images of each plant. Extracted image data, comprising nine morphometric and three colorimetric features, were subjected to univariate filtering followed by Partial Least Squares Discriminant Analysis (PLS-DA) to pinpoint the most responsive traits per species. At 34 days after transplanting (DAT), destructive sampling was carried out to quantify key yield parameters, including fresh and dry biomass weights, and Specific Leaf Area (SLA).

Overall, significant deviations in plant traits compared to the control were detected as early as 7 or 11 DAT, with differences amplifying over time in proportion to shading intensity. Across all evaluated species, increased shading consistently led to a higher SLA coupled with a progressive reduction in aboveground biomass. Furthermore, species-specific behaviours revealed that exclusively morphometric traits were the most responsive for TB (3 traits), SC (3 traits), and SP (1 trait), whereas LE exhibited both morphometric (2 traits) and colorimetric (2 traits) primary response patterns. Ultimately, Radiation Use Efficiency (RUE) under T50 increased significantly relative to T100, approximately threefold in SP and by 59.47%, 29.74%, and 15.38% in LE, SC, and TB, respectively, while no significant differences were detected in any taxa subjected to T20.

POSTER #19

Role of Seed Traits in Plant Development

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Abstract

Plants produce morphologically diverse seeds as an adaptive strategy to increase survival under fluctuating environmental conditions. Yet, the impact of individual seed traits on early post-embryonal growth and development remains largely unknown. Addressing this requires high-resolution phenotyping of large populations at single-seed level are necessary.

In *Arabidopsis thaliana*, we characterised up to 25 morphological seed traits. These traits are organised into structured feature libraries derived from a large-scale digital repository of *Arabidopsis* seeds processed in silico, forming the basis for developing machine learning approaches for AI-assisted seed sorting and classification.

Here, we investigate the functional relevance of selected traits during early post-embryonal development. Using both the Col-0 reference line and *Arabidopsis* lines enriched for specific trait, we assess how individual seed properties shape the growth dynamics and developmental programs. In parallel, the same analytical framework is being extended to crop species such as tomato and barley, where data availability is currently more limited. This ongoing work aims to test whether at least some of the described seed characteristics in *Arabidopsis* are conserved across species or are species-specific. This is of high importance to identify the most informative descriptors for robust seed phenotyping and future predictive modelling.

POSTER #20

Web-Based Platform for FAIR Phenotyping Data Management and Research Team Data Catalogue Integration

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Abstract

The increasing volume of phenotyping and experimental data in agricultural and biological research creates a demand for interoperable, secure, and user-friendly digital solutions (i.e., findable, accessible, interoperable, and reusable (FAIR) data). This contribution presents a web-based platform developed using Node.js technologies for FAIR management of high-throughput phenotyping (HTP) data and provides a centralised data catalogue with regulated, secure access control for research teams and collaborative projects.

The platform enables researchers to access, organise, and manage data obtained from standardised API (BrAPI) services through a unified web interface designed primarily for HTP domain specialists rather than IT professionals. The proposed solution supports management of datasets, experiments, metadata, and research outputs while facilitating interoperability and communication between research teams and heterogeneous research infrastructures.

The application architecture is built on modern Node.js technologies and modular web services, ensuring scalability, extensibility, and efficient integration with distributed data sources. Particular emphasis was placed on secure data handling, including authentication mechanisms, controlled access to resources, secure API communication, and protection of sensitive research data. These features contribute to reliable data exchange and improved collaboration among participating institutions and research groups.

In addition to data management functionalities, the integrated data catalogue improves discoverability, accessibility, and long-term organisation of research resources. The contribution also discusses implementation challenges related to API integration, metadata harmonisation, heterogeneous data structures, and security requirements in distributed environments. The proposed platform is part of the IPPNWG Advanced Sensor Applications and data management initiative and aligned with the ongoing EMPHASIS and ELIXIR efforts that aim to develop interoperable and secure digital ecosystems for agricultural and biological research by improving collaborative data sharing, streamlining research data management, and supporting efficient coordination among research teams.

POSTER #21

High-throughput phenotyping under biotic stress as a tool to identify the effect of single-gene mutants

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Abstract

Here, we examined single Arabidopsis mutants deficient in GABA biosynthesis (gad1–gad5) and catabolism (gaba-T) under biotic stress caused by the bacterial pathogen *Pseudomonas syringae* and the soil-borne fungal pathogen *Fusarium oxysporum*. *P. syringae* is a model hemibiotrophic leaf pathogen that triggers stomatal and immune responses, whereas *F. oxysporum* causes vascular wilt and represents a major root-invading pathogen.

Using high-throughput phenotyping based on RGB, fluorescence, and infrared imaging, we revealed that, in plants, disruption of GABA homeostasis elicits distinct physiological responses depending on the pathogen identity. Principal component analysis demonstrated a clear separation of mutant responses according to pathogen type, highlighting that GABA metabolism contributes to stress-specific adaptation to different pathogen lifestyles.

ROS burst assays and stomatal aperture measurements further revealed altered oxidative responses and impaired stomatal closure in several gad mutants. These findings support a role for GABA biosynthesis in coordinating stomatal defence and ROS signalling. Overall, our data demonstrate that GABA metabolism integrates immune responses, stomatal regulation, and environmental sensing, positioning it as a central hub in plant adaptation to diverse biotic stresses.

POSTER #22

Automated 3D Point Cloud Leaf-Level Analysis Across Multiple Plant Species

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Abstract

Accurate and scalable leaf-level plant phenotyping is essential for characterizing plant architecture in breeding and research programs. Traditional methods rely on manual measurements that are labor-intensive and limited in throughput. Here we present 3D Analyzer, a Windows-based software platform for automated analysis of 3D point cloud data acquired from SICK Ruler3060/3120 laser line scanners integrated into the PSI PlantScreen™ automated phenotyping system. The system automates 3D point cloud analysis from acquisition to trait export, delivering per-leaf measurements (leaf area, projected area, inclination angle, leaf index) and canopy-level metrics (digital biomass, height map, 3D convex hull) across three crop-specific segmentation models: soybean, maize, and a broad-species deep learning model. Validation against manual reference measurements with artificial 3D printed plant object yielded a mean absolute error of 3.30% and 2.90% for leaf area and projected leaf area, respectively. Applied to greenhouse-grown plants across multiple species, 3D Analyzer enables rapid, non-destructive phenotyping without manual intervention, providing a scalable solution for high-throughput plant analysis in commercial and research environments.

POSTER #23

Multi- and hyperspectral imaging as a non-destructive tool to study the biostimulant effects of *Serendipita williamsii* volatiles

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Abstract

Over the past years, there has been a growing interest in the role of volatile organic compound (VOC) signaling in plant-fungal interactions. However, knowledge on the composition of fungal volatilomes and how they affect plant physiology is scarce. The enigmatic genus *Serendipita* is a plant growth promoting endophytic fungus whose volatiles can enhance the plant's resilience upon abiotic stress. Growth-promoting effects such as increased biomass, a more efficient photosystem II and accelerated root growth were reported in *Arabidopsis thaliana* seedlings exposed to the volatiles of *Serendipita*, without any direct contact between plant and fungus. However, these effects are often masked, blended or blurred by the fertilization effect of CO₂ produced by the fungal metabolism. Furthermore, traditional destructive sampling limits our understanding of the dynamic physiological shifts induced by these VOCs.

To circumvent these limitations, we developed an innovative approach to assess the bioactivity of the *Serendipita* volatilome. We first used TD-GC-MS to identify qualitatively the most abundant VOCs emitted by in vitro grown *Serendipita williamsii*. Secondly, we compared the volatilome of *S. williamsii* with other fungi across the fungal kingdom, which showed several unique metabolites in the *S. williamsii* headspace. These unique compounds were individually tested in different doses for their bioactivity in plants under optimal and abiotic stress conditions (nutrient deficiency, salt and drought stress), where methyl benzoate was demonstrated as the most promising plant-growth promoting compound.

Central to our approach was the integration of multi- and hyperspectral imaging to monitor plant health non-destructively. Multispectral imaging provided tracking of vegetation indices and photosystem II efficiency (Fv/Fm), while hyperspectral imaging enabled a more detailed comparison of the full reflectance spectrum from 400 nm to 1700 nm. These non-destructive imaging tools allowed us to detect the impact of methyl benzoate.

POSTER #24

Deep Learning Segmentation of UAV-Acquired Hyperspectral Imagery for Field-Based Plant Phenotyping

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Abstract

Hyperspectral imaging from unmanned aerial vehicles (UAVs) is an increasingly important tool for field-scale plant phenotyping, enabling non-destructive monitoring of crop health, stress, and canopy structure. A critical bottleneck in realising its potential is accurate image segmentation, specifically the ability to reliably isolate and classify plant structures within complex hyperspectral data cubes. While deep learning approaches have shown strong performance in controlled glasshouse conditions, their generalisation to open-field UAV imagery remains limited, owing to variable illumination, complex backgrounds, and the scarcity of annotated field datasets.

A deep learning segmentation framework previously validated under controlled conditions on barley, maize, and *Arabidopsis thaliana* was extended to UAV-acquired hyperspectral field imagery. Open-source UAV hyperspectral datasets, including those available on Zenodo such as the FlexiGroBots blueberry dataset and a dataset of seventeen grapevine varieties, were used as benchmarks for field-based evaluation. To address the limited availability of annotated field data, a data augmentation pipeline was implemented to inflate training set size, encompassing geometric transformations, spectral perturbations, and synthetic noise injection. Segmentation was performed using a U-Net-based deep neural network architecture, selected for its established performance in biomedical and remote sensing image segmentation tasks.

Under controlled glasshouse conditions, the framework achieved segmentation accuracies of up to 99% (F1-score), representing a 15–20% improvement over leading commercial and open-source tools. Generalisation to a previously unseen external dataset yielded accuracy above 95%. Evaluation on open-source UAV hyperspectral datasets demonstrates that augmentation-assisted training substantially improves segmentation performance under field conditions relative to models trained without augmentation, with results across standard metrics (F1-score, IoU, precision/recall) showing strong performance and outperforming established algorithms.

These results indicate that deep learning segmentation frameworks developed in controlled phenotyping environments can be meaningfully extended to UAV-based field imagery through targeted augmentation strategies. The transition from glasshouse to field remains non-trivial, and continued work will focus on expanding species diversity in training data and optimising model inference for edge-deployed UAV hardware. This work contributes toward a generalisable, low-overhead segmentation pipeline applicable to high-throughput field phenotyping and precision agriculture at scale.

POSTER #25

Phenotyping of genotypic variation in buckwheat drought tolerance

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Abstract

Common buckwheat (*Fagopyrum esculentum* Moench) is a pseudocereal currently hardly cultivated in Germany and merely used as a cover crop. However, buckwheat's market share is recently increasing due to its health promoting properties and gluten-free grains. The project BIMOTEC contributes to strengthening buckwheat cultivation in Germany by pre-breeding for climate-resilient cultivars for food production and the extraction of valuable phytochemicals. Within this framework, we focus on exploring the genotypic variability in the drought response by phenotyping a global collection of 50 genotypes representing established cultivars and landraces from 22 different countries. To evaluate plant growth under drought, buckwheat seedlings were cultivated for 25 days under control and drought conditions in a greenhouse. Shoot phenotyping by repeatedly imaging the plants from four sides using a mobile plant rotator allowed quantification of shoot growth dynamics. Additionally, non-invasive measurements of photosynthetic performance were taken, followed by destructively harvesting the plants to assess morphological traits. In essence, we aimed to select drought-tolerant genotypes based on the combination of high growth performance under drought conditions and low relative growth reduction compared to control treatment. Preliminary results indicated substantial differences in shoot growth among the 50 buckwheat genotypes under both control and drought conditions. Genotypic differences in growth maintenance and biomass stability under drought relative to control suggest variation in drought tolerance among the studied genotypes. These findings will be complemented by root trait analysis using the novel phenotyping facility GrowScreen-Rhizo 3. This approach aims to provide a comprehensive understanding of the genotypic variation of buckwheat's above- and belowground growth dynamics– an aspect that has not yet been studied in depth and will contribute to breeding of local, climate-resilient buckwheat cultivars.

POSTER #26

The Niagara Region as a Biorefinery for Tropical Microalgae: Greenhouse Cultivation of *Spirulina* in Canada

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Abstract

Key words: *Spirulina*, Niagara region, Protein, Phycocyanin (C-PC), Greenhouse

Producing food in Canada's colder regions is an important challenge, as nutritious tropical imports are costly, and food insecurity remains a concern for a part of the population. Microalgae cultivation presents a promising alternative with the Niagara region offering favorable conditions for potential biorefinery development due to the availability of abundant freshwater and relatively low electricity costs in the region [1]. With approximately 70% protein content and high-value pigments [2], *Spirulina* represents a strong target for biomass production. In this study, eight strains from the UTEX algal collection were evaluated to determine which performed best under cultivation conditions representative of the Niagara region. Five strains showed promising growth (LB1926, LB1928, LB2340, 3086, and LB2342). Optimal temperature, light intensity, and growth media were first characterized for each strain; to then grow cultures in a greenhouse environment under these parameters for protein and phycocyanin (PC) content quantification. The cultures demonstrated total protein contents ranging from 58–67% of dry weight, with C-phycocyanin representing 10.86–16.33%. Biomass productivity ranged from 1.5 to 2.0 g/L, indicating that the production of high-protein *Spirulina* is feasible in the region. Among the tested strains, UTEX 3086 showed the greatest potential due to its fast growth rate under lower light intensity, adaptability to greenhouse conditions, and higher biomass yield. Additionally, each strain underwent a purification process that produced clean cultures using a novel high-alkaline salt treatment, which showed promising effectiveness compared with conventional antimicrobial agents.

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POSTER #27

Nondestructive 3D phenotyping method of plant fruits based on X-ray microcomputed tomography and deep learning

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Abstract

The phenotyping of plant fruits is critical for understanding complex genetic traits. High-precision analysis of internal fruit phenotyping traits can enhance modern crop breeding and post-harvest biotechnology research. Computed tomography (CT) imaging technology enables the noninvasive acquisition of three-dimensional images of fruit interiors, providing a robust data foundation for phenotypic analysis. A dataset named XrayFruitData was established, containing high-resolution images of over ten plant fruit varieties, with accurate annotations for orange, mangosteen, and durian. Accurate segmentation of internal fruit tissues is essential, directly influencing the accuracy and reliability of results. Current research often relies on traditional threshold segmentation or deep learning models designed for other data types, which are not optimized for the unique features of plant fruit images. This study introduced XFruitSeg, a general deep learning model for segmenting plant fruit CT images. Compared to four mainstream advanced models, XFruitSeg achieved superior segmentation performance. Furthermore, the method has been extended to coconut, passion fruit, and durian. Twenty-one key phenotypic traits of coconut and fourteen traits of passion fruit were automatically calculated through a designed trait calculation pipeline. Compared with the manual measurement, The R² values between the method and the manual measurement reached 0.98 (coconut volume), 0.96 (coconut water), 0.96 (passion fruit length) and 0.93 (passion fruit width). The method was also used to dynamically monitor the coconut seeds at the germination stage and the coconut fruits at the growth stage. The sarcocarp content and volume are key factors for assessing the quality of durian fruit. To enhance the efficiency in predicting the edible rate, a prediction model based on a single tomographic image was developed using machine learning techniques. Experimental results indicated that the SVR model enabled rapid and accurate prediction of the edible rate (R² = 0.917, MAPE = 4.03%). In summary, the method proposed in this study holds promise for extension to a wider range of fruit varieties, facilitating advancements in multi-omics association research and improved breeding strategies. In the future, photon counting CT technology, with its robust material decomposition capabilities and low-dose imaging potential, will be explored and applied to essential crop organs, such as seeds and fruits.

POSTER #28

Dynamic canopy temperature responses in wheat reveal context-dependent Phenotypic discrimination across time, stage and water regimes.

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Abstract

Canopy temperature (CT) is a widely used indicator of crop water and heat status in wheat phenotyping. However, it is almost always measured at a single time point. This approach treats CT as a temporally stable trait.

This study demonstrated that canopy cooling in spring wheat is a highly dynamic phenotype. Its expression is shaped by time of day, phenological stage, and environment. The study was conducted across two growing seasons (2024 and 2025) and two Mediterranean environments in Chile. These included a fully irrigated site (Santa Rosa, FI) and a rainfed water-stressed site (Cauquenes, WS). We used drone-based thermal imaging to measure CT at ten time points per day (09:00–18:00 h). Measurements were taken across three reproductive stages: anthesis (ANT), milk stage (MS), and grain filling (GF). The study involved a panel of 196 spring wheat genotypes.

A repeated-measures mixed model showed that all main effects (environment, stage, time of day, and year) and all their interactions were highly significant ($p < 0.001$). These factors together explain the dynamic nature of canopy thermal behavior. Variance-component analyses within each stage $\times$ environment $\times$ year combination revealed a substantial genotypic signal. The proportion of total CT variance due to genotypic effects ranged from 2.1% to 52.2% when pooled across hours. It reached up to 79.9% at the optimal hour of the day. The optimal phenotyping window depended on the context. Under water-stressed conditions, peak genotypic discrimination occurred consistently around 14:00 h across stages and years. Under full irrigation, the most informative hour varied between 13:00 and 18:00 h, depending on stage and year.

Genotype rankings were less stable across hours under water stress. Mean Spearman rank correlations between non-adjacent hours were as low as $\rho = -0.69$. This indicates substantial within-day re-ranking as atmospheric demand increased. Thermal threshold analyses showed that the proportion of genotypes exceeding the critical CT threshold of 32°C varied strongly with time of day, stage, and environment. At the milk stage in 2024, 100% of the water-stressed panel exceeded this threshold at midday, while the irrigated panel remained below it throughout the day. Hierarchical clustering of diurnal CT profiles consistently identified two main groups across all conditions. Cluster membership shifted substantially across stages, especially under stress.

Random regression of CT on concurrent vapor pressure deficit (VPD) confirmed that CT increases strongly with VPD (mean population slope = 13.27°C kPa⁻¹). However, genotypic variation in sensitivity to VPD was negligible. Environment, stage, year, and their interactions with VPD remained highly significant ($p < 0.001$).

These findings show that single-time-point CT phenotyping gives an incomplete and context-sensitive picture of genotypic canopy cooling capacity. They highlight the need for multi-temporal, stage-specific, and environment-aware phenotyping protocols in wheat breeding programs targeting drought and heat adaptation.

POSTER #29

High-Throughput Automated Phenotyping of Microalgae

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Abstract

Despite their small size, microalgae are photosynthetic organisms with broad practical applications in fuel production, nutrition, environmental remediation, and the production of high-value compounds. Their wider commercial deployment, however, is limited by the lack of scalable and standardized phenotyping approaches. To address this challenge, we developed PhenoSelect, an automated platform that combines robotics, spectroscopy, fluorometry, flow cytometry, and advanced data analytics to enable high-throughput, multi-parameter phenotyping of microalgae.

Using this system, five algal species including *Chlorella sorokiniana*, *Haematococcus pluvialis*, *Halospirulina tapeticola*, *Nannochloropsis australis*, and *Phaeodactylum tricornutum*, were analyzed across 96 environmental and chemical conditions. Key traits including photosynthetic performance, growth dynamics, and cell size were quantified with high reproducibility. Species-specific phenotypic plasticity was visualized using Ranked Spider Plots and heatmaps, while overall phenome breadth was assessed via convex hull volume. *H. pluvialis* displayed the largest phenotypic space, indicating high adaptability, whereas *N. australis* exhibited the smallest phenome, consistent with a more specialized ecological strategy. Optimal photosynthetic activity and growth conditions varied among species, with low light intensity and nutrient-rich environments generally promoting higher performance.

PhenoSelect is built on PSI's AlgaeScreen™ robotic platform and enables fully automated, daily measurements with minimal manual intervention, while allowing modular expansion through additional analytical instruments. This platform fills critical gaps in algal biotechnology by accelerating strain selection, enabling quantification of phenotypic drift, and supporting predictive modeling. By delivering reproducible, multi-trait phenotyping at scale, PhenoSelect represents a significant advance in algal research and bioprospecting, with direct relevance to sustainable industrial production systems.

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