EPPS

EUROPEAN **PLANT PHENOMICS** SYMPOSIUM

Abstract Book

Content

Oral presentations:

DPPN presentations

Screening of Mentha breeding material for drought stress tolerance using High-throughput Phenotyping (HTP) platform

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Drought stress poses a major constraint to Mentha productivity and biomass quality. The genus Mentha spp (mint) comprises economically important aromatic and medicinal plants cultivated worldwide for their essential oils, flavor, and pharmaceutical properties. This study aimed to identify drought-tolerant genotypes in a Mentha breeding program using a high-throughput phenotyping (HTP) platform at APPP-A platform at IPK through the framework of "DPPN-ACCESS". Sixty-nine Mentha accessions representing multiple species were grown under controlled environmental conditions and subjected to either well-watered or drought-stress treatments. Phenotypic traits were acquired through visible and fluorescence imaging using LemnaTec Scanalyzer3D over a 27-day period. Eighteen digital traits were extracted, encompassing morphometric, colorimetric, and physiological parameters. Principal component analysis and drought tolerance indices were used to evaluate genotype responses. Biovolume was selected as the primary trait for stress response. Drought-tolerant genotypes (e.g., ME009, ME027) showed stable performance across multiple indices and fluorescence efficiency (Fv/Fm), while sensitive genotypes (e.g., ME002, ME077) showed significant biomass loss and reduced photosynthetic efficiency. These results provide valuable insights for breeding drought-resilient Mentha cultivars.

Acknowledgment:

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Keywords:

Mentha, drought stress, high-throughput phenotyping, HTP, biovolume, fluorescence imaging, drought tolerance indices, LemnaTec, Fv/Fm, digital traits, medicinal plants, biomass quality, plant stress physiology, phenomics

Root and tiller phenotyping to identify new variation for barley breeding

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One major challenge of agriculture is maintaining food security in times of climate change. Generally, different climate models concertedly predict that precipitation events will decrease in quantity while they increase in intensity. This will lead to more extended periods of drought, followed by periods of heavy rainfall. Future plant breeding, therefore, has to account for the genotypes' survival during drought and a good recovery ability after rainfall events. Plants have evolved different strategies to adapt to these threats, for instance through different rooting or tillering strategies. Within two DPPN-ACCESS projects we investigated these two aspects in the wild barley nested association mapping population HEB-25.

By accessing the GrowScreen-Rhizo 3 system (FZ Jülich) we characterized the different root architecture of wild and elite barley. It turned out that elite barley shows a generally wider root system with lots of lateral roots, while wild barley focuses on fast vertical root growth with deeper seminal roots. Based on genome-wide association studies genetic regions involved in controlling root growth could be identified.

The re-tillering behavior of selected barley genotypes was investigated in five different (re-) watering regimes on the APPP-B platform for medium-sized plants (IPK Gatersleben). We were able to show a genotype-dependent (re-) tillering behavior with genotypes maintaining a stable tiller number independent of watering and others with massive additional tillering after re-watering. Notably, this high re-tillering was negatively correlated with harvest index.
Altogether, both experiments highlight the genetic regulation of root and tiller dynamics with valuable genetic variation being available for plant breeding in the wild barley gene pool.

Drought Resistance in Oat for a Changing Climate: High-Throughput Phenotyping as a Foundation for Systems-Level Insights

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Climate change is intensifying drought stress, threatening crop productivity and food security. Oat (*Avena sativa*), valued for its nutritional and sustainability benefits, remains sensitive to drought. *DROAT* employs the FitnessSCREEN high-throughput phenotyping platform at Helmholtz Munich to generate high-resolution morphological and physiological datasets from a genetically diverse oat panel, including elite cultivars, landraces, and wild relatives. Controlled drought experiments, combined with 3D multispectral imaging, will capture growth dynamics, canopy architecture, biomass allocation, water use efficiency, yield components, and stomatal density from early vegetative to grain-filling stages.

All phenotyped lines possess reference-quality genomes from the international PanOat initiative. Time-resolved phenotypic data will be integrated with transcriptomic, metabolomic, proteomic, and epigenomic profiles to identify resilience-associated traits, regulatory circuits, and biochemical pathways, with a particular focus on subgenome-level regulation in this complex polyploid crop. This approach bridges the gap between molecular understanding and agronomic performance, providing a foundational resource for trait–omics correlations, biomarker discovery, and the targeted breeding of climate-resilient oat varieties—contributing to sustainable cereal production under future drought scenarios.

Oral presentations

Introduction:

Impact of plant phenotyping

Astrid Junker

Syngenta

Oral presentations

Focus Sessions:

AI for plant phenotyping

Beyond Classification and Regression: Explainability, Uncertainty, and Generative Models in Plant Phenotyping

Ribana Roscher

Forschungszentrum Jülich, University of Bonn

Machine learning has already proven its value in plant phenotyping through classification tasks (e.g., disease detection) and regression problems (e.g., yield prediction). Yet, phenotyping can benefit from much more than producing labels or numbers. In this talk, I will introduce three emerging directions that go beyond conventional applications. First, I will show how explainable machine learning helps us understand why models make certain decisions, which can improve model development and increase reliability. Second, I will discuss approaches for quantifying model uncertainty, which are crucial for deciding when predictions can be trusted and when additional measurements are needed. Finally, I will explore the potential of generative machine learning to model crop growth over time, opening up possibilities to simulate development under different environmental conditions or management scenarios. Together, these perspectives illustrate how AI can support phenotyping not only as a measurement tool, but also as a driver of reliability and innovation.

Using Foundation Models for Agricultural Applications

Jens Behley

Universität Bonn

Recent advancements in self-supervised training of vision models made powerful so-called "foundation models" available, which can be employed as basis for developing image-based interpretation. In this talk, we will dive into this exciting novel pathways to start your research based on such foundation models for labeling and image interpretation.

Artificial Intelligence for crop health

Spyros Fountas, Borja Espejo García

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Precision agriculture and smart farming are experiencing a profound transformation, driven by the convergence of robotics, computer vision, and deep learning. Building on this momentum, the Smart Farming Technology Group (SFTG) envisions the next step: integrating diverse modalities (ranging from imaging and sensor data to textual and contextual knowledge) into unified AI frameworks that enhance the perception, reasoning, and decision-making capabilities of agricultural robotics, paving the way for scalable, adaptive, and sustainable smart farming solutions.

One significant advance has been the development of selective spraying for weed management, where early-stage weed identification enables substantial reductions in pesticide use. To mitigate data scarcity, SFTG developed a methodology that combines transfer learning with generative adversarial networks (GANs), achieving over 99% accuracy in weed identification and pioneering this technology in the EU project SmartDroplets. The group has also demonstrated the advantages of vision transformers over CNNs, capturing plant morphology more effectively and reaching over 98% accuracy on the DeepWeeds dataset while improving interpretability with Grad-CAM++. Beyond crop protection, SFTG has applied AutoML with NDVI and multisensor data for grape quality prediction, and leveraged transformer-based language models (e.g., Agri-BERT) to advance automatic agricultural knowledge extraction. Most recently, SFTG has investigated foundation models such as DINOv2, highlighting their ability to generalise across agricultural imaging tasks with minimal fine-tuning. All these technologies are tested in real-time conditions within the EDEN Library Viewer, a real-time vision system for disease and pest protection, which can be mounted on most tractors.

Management of AI-based projects

David Rousseau

University of Angers

In this talk, Prof. David Rousseau explores the challenges and best practices in designing, executing, and sustaining AI-based projects in the domain of plant phenotyping. He identifies and discuss with the audience an a panel of expert in the field key phases, risks, and strategies.

Oral presentations

Session 1.1:

Phenotyping for stress resilience and tolerance

Digital phenotyping of plant-pathogen-interactions - insights into research for plant breeding and plant protection

Anne-Kathrin Mahlein

IFZ

In plant phenotyping research, significant advances have been made regarding the detection and monitoring of biotic stress, such as plant diseases or damage caused by pests. The technological approach is based on the use of optical sensors, artificial intelligence, Internet of Things (IoT) sensor networks, and robotic platforms, leading to new applications in plant phenotyping routines. In the focus is the qualitative and quantitative assessment of individual plant traits and the rating of compatible or incompatible plant-pathogen-interactions as indicators for tolerance or resistance. Currently, sensors for detecting plant diseases are used at various scales, from the level of a single leaf to the level of a whole field and concepts that complement visual expert assessment are available. However, several challenges remain: the accuracy, specificity and timeliness of disease detection must be improved further, and transfer of models across field sites and years needs improvement. In addition, phenotypic information must be linked to genomic data. Data-driven artificial intelligence will probably contribute to solutions. In this context, the integration of agricultural expert knowledge of breeders and farmers is particularly important for the implementation. Thus, there is a clear need for interdisciplinary research, knowledge transfer, and education regarding the use of digital technologies for the characterization of biotic stress. This talk will provide recent insights from the digital experimental field site 'FarmerSpace' (https://www.farmerspace.uni-goettingen.de/) and the Cluster of Excellence 'PhenoRob' (https://www.phenorob.de/).

Genotype-specific shoot–root interactions and nitrogen-dependent plasticity shape wheat performance in intra- and inter-genotypic canopies

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The above- and belowground responses of plants to their neighbors are key for their performance in a canopy. These responses, so called plant–plant interactions, can occur within (intra-genotypic) or between genotypes (inter-genotypic), shaping competitive or cooperative responses that depend on genotype-specific strategies and resource availability. Here, we used the high-throughput rhizotron system "PhenoSphere" under controlled conditions to phenotype shoot and root plasticity in response to high (HN) or low nitrogen (LN) levels and different types of plant-plant interactions.

Using two winter wheat cultivars (Tobak and RGT-Reform) with contrasting shoot and root architecture, we designed a sophisticated experimental setup that allowed us to phenotype the dynamic responses of 127 root and shoot traits to intra- or inter-genotypic shoot competition at both canopy and individual levels, and their interactions with nitrogen.

Limited nitrogen availability amplified the effect of shoot competition on shoot dry weight at the canopy level by about 15%. To resolve dynamic plant responses, we used image-based phenotyping to track individual plants over time, revealing clear differences in organ-specific plasticity shaped by competition type and nitrogen supply. In intra-genotypic canopies, Tobak maintained its compact shoot architecture under high shoot competition, while RGT-Reform showed greater architectural plasticity but reduced stability. Root traits responded later than shoots, indicating sequential consequences of competition. Under high shoot competition, inter-genotypic mixtures enhanced vertical root growth under LN, suggesting increased foraging in mixed canopies. Nitrogen × competition interactions also shifted root and shoot allocation strategies over time, highlighting the coordinated nature of organ responses.

Using modern phenotyping techniques, our results provide the first evidence that shoot competition can trigger genotype-specific, nitrogen-dependent root responses. These findings highlight the potential for selecting genotypes with ideal and complementary root-shoot plasticity to optimize productivity in variety mixtures.

Botrytis lesion screening on strawberries using deep learning with zero-shot prompt-based annotation assistance

Dan Jeric Arcega Rustia; Maikel Zerdoner; Manon Mensink; Paul Arens; Richard GF Visser; Suzan Gabriëls

Wageningen University & Research

Efficient phenotyping of disease resistance is a major bottleneck in modern plant breeding, particularly for traits like susceptibility to Botrytis cinerea (gray mold), a pervasive fungal pathogen affecting strawberry production. This study presents a mobile deep learning-based phenotyping approach designed to accelerate resistance screening in strawberry breeding programs. We developed a coarse-to-fine detection and segmentation algorithm to detect strawberries and quantify Botrytis lesions on individual strawberries from images captured via smartphone cameras. A diverse dataset spanning multiple genotypes and lesion stages was used to train edge-optimized models, enabling secure, offline deployment in field settings. Training annotations were generated using pseudo-labels from zero-shot models, which were then manually reviewed to minimize labeling effort. Two models were trained for detecting individual strawberries (mAP=0.98; mIoU=0.90) and for segmenting Botrytis lesions (mIoU=0.82) on each strawberry, achieving an average total inference time of 4.8s per image on a smartphone. The algorithm can quantify traits including fruit size (mm2), lesion area (mm2), lesion diameter (mm) and lesion-to-fruit size ratio. The algorithm is integrated into a mobile application to enable scalable, objective, and standardized phenotyping, ultimately enhancing the selection efficiency for Botrytis resistance and accelerating genetic gain in strawberry breeding

Evaluation of microalgal extracts for enhancing stress tolerance in tomato and lettuce using high-throughput phenotyping

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Microalgae, as autotrophic microorganisms, possess remarkable adaptability, making them attractive candidates for developing sustainable agricultural inputs. This study investigates the potential of microalgal extracts (MEs) derived from Chlamydomonas sp., Chlorella sp., Scenedesmus sp., and Chromochloris zofingiensis, alongside a commercial biostimulant (AE), in supporting the growth of tomato and lettuce cultivated in pots with a sandy substrate. Plants were grown under controlled greenhouse conditions and subjected to either optimal or stress-inducing nutrient regimes, including limited nitrogen availability and elevated salinity. The analysis focused on key morpho-physiological parameters, assessed through high-throughput phenotyping and pigment profiling (chlorophyll, flavonoids, and the Nitrogen Flavonol Index [NFI]), while leaf mineral composition was also evaluated. Among the tested treatments, the extract from C. zofingiensis (ME 4) and the commercial product AE demonstrated the strongest positive effects. These included increased chlorophyll levels and NFI values, coupled with reduced flavonoid accumulation—suggesting a decrease in oxidative stress—under both nitrogen-deficient and saline conditions. Despite these physiological improvements, none of the biostimulant treatments significantly influenced shoot biomass (fresh or dry weight) or mineral nutrient concentrations in the leaves. However, nutrient solution type notably impacted mineral content. Phenotyping data revealed that ME 4 significantly enhanced digital biomass, plant height, 3D leaf area, NDVI, and projected leaf area in tomato plants compared to untreated controls, regardless of nutrient conditions. In contrast, no notable morphological changes were detected in lettuce. Overall, ME 4 emerged as the most promising extract, meriting further investigation for its potential in long-term abiotic stress mitigation strategies.

Oral presentations

Session 1.2:

Phenotyping for stress resilience and tolerance

Genetically controlled limitations to photosynthesis under real world fluctuating conditions: The OpenJII approach and platforms.

David M Kramer

Jan IngenHousz Institute

Photosynthesis is a complex and dynamic process that must constantly adjust to rapid changes in light, temperature, humidity, and the availability of water and nutrients. Achieving high productivity and resilience requires genetic regulation that fine-tunes these responses to maximize efficiency while minimizing trade-offs. In real-world conditions, multiple processes can limit photosynthesis, and these limiting factors can shift from moment to moment. Addressing such complex and context-dependent traits is a major challenge—one that demands new sensors, methods, shared datasets, and modeling approaches that can be scaled to field experiments. I will present the Jan IngenHousz Institute’s approach, highlighting new sensors, the OpenJII platform, and data analyses that reveal the genetic controls of complex photosynthetic processes and their impacts on crop performance.

Multi-generational impact of future climate conditions on Arabidopsis thaliana epigenome and phenotype

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Predicting the effects of climate change on plant life remains a significant challenge. While elevated atmospheric trace gases, rising temperatures and water scarcity are known to disrupt plant redox systems and impair physiology, the long-term phenotypic and regulatory effects of these factors across generations are not well understood. Most existing studies examine isolated stressors over a single generation, which limits their relevance to complex real-world scenarios. To address this, we exposed Arabidopsis thaliana to individual stressors (drought, heat, elevated ozone and CO_2) as well as to a combined climate scenario that more closely mimics the complexity of the natural environment. The plants were grown under these conditions for three generations, followed by two generations under control conditions. Whole-genome bisulfite sequencing and transcriptome analysis revealed general and treatment-specific responses, with notable variation across generations. Plants exposed to the complex scenario exhibited distinct transcriptomic profiles and phenotypic traits compared to those subjected to individual stressors or the control conditions. Epimutation rates also varied across generations under the complex treatment. Phenotypically, exposure to heat and the combined stress scenario resulted in accelerated growth that continued into the fourth generation, even after the stress had been removed, suggesting a transgenerational memory effect. However, growth rates declined in the fifth generation, returning to or falling below control levels. Similarly, seed weight decreased significantly during the first three generations under complex stress, but increased again by the fourth and fifth generations, indicating dynamic phenotypic plasticity.

Our findings suggest that complex environmental conditions can induce heritable phenotypic changes that persist beyond the period of exposure to stress. This reflects a form of transgenerational memory, whereby shifts in DNA methylation are passed down through the generations. Although the data analysis is ongoing, this approach provides valuable insights into the interaction between the environment, epigenetic regulation and phenotype. It emphasises the roles of these factors in shaping how plants respond to multifactorial climate stress.

Study on short-term high temperature stress on rice by combining high-throughput phenotyping and genome-wide association study

Liang Tang; Yonglin Wang; Yan Zhu; Weixing Cao

NANJING AGRICULTURAL UNIVERSITY

Under the context of global warming and increasingly frequent extreme weather events, heat stress poses a significant challenge to rice, one of the world’s most important staple crops. While numerous studies have focused on identifying heat-tolerant genes and breeding heat-resilient varieties, the application of long-term high-throughput phenotyping data to dissect the genetic basis of heat tolerance remains limited. In this study, 110 rice cultivars were subjected to a four-day high temperature (29°C-39°C) and ambient temperature treatment during the flowering stage in phytotrons. Daily canopy multispectral information and point cloud data were collected using a high-throughput phenotyping platform (FlantEye F500, Phenospex B. V., The Netherlands). After denoising and voxelization of the point clouds, multiple structural phenotypes, including canopy volume, inclination angle, surface area and height traits were estimated. Spectral indices were calculated from four-band reflectance data, including hue (HUE), normalized difference vegetation index (NDVI), plant senescence reflectance index (PSRI), and normalized pigment chlorophyll index (NPCI). Relative heat tolerance indices (RHI) were developed based on trait ratios between heat-stressed and control conditions. Genome-wide association studies (GWAS) were conducted to identify significant quantitative trait loci (QTLs) and candidate genes. Results showed that reconstructed canopy inclination angle was significantly higher under heat stress, with the difference increasing over time. Angle-based daily GWAS revealed a QTL on chromosome 4 repeatedly detected for 11 consecutive days (5–15 days after flowering), where a gene encoding an Hsp40 chaperone with a DnaJ domain was annotated, likely involved in the heat response. Canopy HUE was significantly elevated under heat treatment from day 1 to 15 after flowering. HUE-based GWAS results showed 9 co-localization days at the same QTL on chromosome 1 (8–25 days after flowering), where two candidate genes associated with abiotic stress were annotated. This study demonstrates that GWAS based on long-term high-throughput phenotyping facilitates the precise identification of heat tolerance candidate genes and highlights the great potential of integrating phenomics and genomics for unraveling the genetic mechanisms of heat tolerance in rice.

Phenotyping wheat varieties for heat tolerance – a case study from down under

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To meet global food security demands, wheat yields must increase by 2–3% annually—yet current gains fall short of meeting this goal. Climate-induced heat stress is a major constraint, especially in Australia's grain-growing regions. Our study presents a comprehensive phenotyping strategy aimed at developing novel, high-throughput tools to assess and improve heat tolerance in wheat.

Field trials were conducted across six distinct thermal environments using 200 wheat genotypes. A key innovation was the deployment of a robotic Q2 fluorophore system, which enabled high-throughput measurements of photosynthetic oxygen evolution and dark respiration. By replacing traditional, labour-intensive gas exchange methods, the Q2 system facilitated the rapid collection of physiological data at an unprecedented scale. Despite some challenges, its deployment marked a significant step forward in field-based phenotyping efficiency of photosynthesis traits.

Measurements were complemented with additional techniques including hyperspectral reflectance, gas exchange, and stomatal imaging. Together, these provided new insights into the physiological underpinnings of heat tolerance, such as variation in photosynthetic efficiency, respiratory acclimation, and stomatal conductance across genotypes and environments.

To translate these findings into scalable selection tools, we are developing machine learning algorithms capable of predicting heat tolerance traits from hyperspectral reflectance data. While initial models—particularly for dark respiration—showed promise, cross-season validation underscored the need for diverse training datasets to ensure broad application.

This integrative approach—combining field phenotyping, physiological trait analysis, and predictive modelling—advances the frontier of stress resilience screening. The tools and insights generated in this project lay the foundation for large-scale screening efforts in wheat and other crops, helping secure future yields in a warming climate.

Oral presentations

Session 2:

Phenotyping for innovative practices

Novel technologies for innovative practices: supporting crop diversification through digital agriculture

Frank Ewert[1,2] & Ehsan Rezaei[1]

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Agriculture is facing multiple challenges that require substantial changes in the way crops are produced. Numerous innovative practices have been developed but their adoption is slow and largely constrained by available technologies. Diversification of crops and cropping systems is increasingly propagated with advantages to improve the resilience and sustainability of crop production. Digitalization including sensing, data analytics, and modelling and robotics offers great potential to diversify production systems, but concrete solutions are still fragmented. A particular challenge refers to the understanding of plant traits needed in diversified systems. Based on selected examples, the advantage of traits targeted to specific environments, production situations and combinations of crops is presented. Advances in phenotyping, sensing and modelling for the identification of traits are highlighted and limitations for their application to diversified systems are discussed together with participatory approaches such as participatory selection and breeding helping to overcome such limitations. In concluding, the demand for joint efforts integrating agronomy, breeding, phenotyping and modelling is stressed to utilize the potential of diversified cropping systems and advances in digital technologies.

Digital canopy height measured with RGB-UAV drone revealed the time sequence activation of Rht and Vrn genes in bread wheat

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High-throughput phenotyping using Unmanned Aerial Vehicles (UAVs) provides new possibilities for capturing crop growth patterns with fine spatial and temporal detail. In this work, we applied UAV-derived canopy height data within a breeding-oriented approach for bread wheat (Triticum aestivum L.), combining remote sensing outputs with genetic mapping tools. Two distinct genetic materials were assessed: a panel of 173 elite Italian cultivars and a population of 164 recombinant inbred lines (RILs). Field experiments were conducted over two seasons under Mediterranean conditions, using an augmented design. Regular UAV flights were carried out throughout the crop cycle. RGB images were processed with Structure-from-Motion (SfM) techniques to create digital canopy height (DCH) models. Validation against manual canopy measurements confirmed the reliability of UAV estimates. Digital terrain models (DTMs) from early flights were used to normalize 3D point clouds for each plot. Quantile-based metrics extracted from DCH layers showed high predictive accuracy ($R^2 = 0.89–0.95$ for the diversity panel and 0.94–0.98 for RILs; RMSE = 0.07–0.20 m), with higher consistency at upper canopy percentiles. Time-resolved canopy height and growth rate profiles were then used for genome-wide association studies (GWAS) and QTL analysis. These revealed key growth-related loci, with temporal shifts in gene effects, including stage-specific activation of major loci such as Rht and Vrn. Our results highlight how UAV-based phenotyping combined with genetic analysis can effectively capture dynamic growth traits, improving the resolution of gene–phenotype relationships and supporting breeding for complex temporal traits.

Phenotyping canopy-level photosynthetic responses to intermittent shading: beyond the daily light integral in multilayered cropping systems

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Multilayered cropping systems such as agrivoltaics, agroforestry, and intercropping create spatiotemporal light variability, including daily shade intermittence. While its physiological impacts are recognised, shade intermittence remains understudied and is not accounted for in crop models, which typically consider a daily light integral (DLI) to calculate growth. Beyond photosynthetic adjustments to rapid light changes, it also affects integrative traits such as plant morphology and reduces radiation use efficiency (RUE) compared to constant shading. In a recent study across 14 rice genotypes, intermittent shading compared to constant shading with the same DLI, significantly reduced yield and aboveground biomass. Source limitations were driven by the nonlinear light-assimilation response combined with a decrease in photosystem efficiency (ΦPSII and electron transport rates) under both low and high light levels. Crop responses were consistent among genotypes, but biomass and yield varied widely. These findings emphasise the need to consider not just DLI but also shading dynamics when phenotyping crop responses in partial shade. Moreover, plant responses to shade intermittence vary with shading intensity, frequency, and duration. This raises a key question: how can shading dynamics be integrated into phenotyping and modelling approaches? To address this, we combined canopy assimilation measurements (flux chamber) under four daily shading patterns, created with removable shade nets, and leaf-level fluorescence and gas exchange measurements (Li-6800) on two rice varieties. Objectives include observing canopy assimilation dynamics under various shading patterns, identifying traits relevant for phenotyping rice photosynthesis under intermittent shading, and determining shading pattern variables that explain these responses for consideration into modelling. First results provide insight into key traits for phenotyping rice performance under intermittent shade and identify shading pattern indexes explaining assimilation variation. This novel approach to phenotyping photosynthesis traits under intermittent shading opens new possibilities for improving genotype selection and optimising multilayered system design.

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

Qian Liu; Lejun Yu

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 non-invasive 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 ($R^2 = 0.917$, 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.

Oral presentations

Session 3:

Phenotyping the hidden half

Root phenotyping aimed at crop breeding towards improved water and nitrogen use

Kristian Thorup-Kristensen

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There are a range of reasons for breeding towards better water and nitrogen use by crops, including crop productivity, environmental concerns and the challenges caused by climate change. Breeding requires phenotyping, and root phenotyping is severely challenged by the fact that roots and their function is well hidden in the soil. Several attempts of root phenotyping have tried to deal with this, by doing root phenotyping on young plants, with the root system growing under highly artificial conditions, to allow easier root observation. However, the link between results from this kind of phenotyping and the traits needed for improving real crops growing until maturity in field soil, is unclear. To achieve progress, we need to develop methods which allow us to quantify variability in root development and function under real field conditions. The number of root traits which can be phenotyped is endless, so we need to identify the root traits which are most promising for development of improved root system function.

For this purpose, we developed the RadiMax semi-field facility, which allow the measurement of root growth and function of up to 600 plant lines per season. For water and nitrogen use, we defined deep root growth as a main promising trait, as deeper rooting simply allows the exploitation of a larger soil volume. The facility is therefore designed to allow root phenotyping down to 3 meters soil depth. Root growth is observed through 5 meter long minirhizotrons in RadiMax. Root function is mainly phenotyped by deep placement of stable isotope tracers (15N and 2H2O) through drip lines installed at different depths throughout the facility. Also the natural 13C discrimination is measured as an indicator of crop water stress, and correlated with the root data and the uptake of deep placed 15N and 2H2O.

The facility was developed in 2015, and since then, we have done root phenotyping on genotypes of spring barley, potato, feed and lawn grasses and not least winter wheat. Currently we are phenotyping faba bean and white clover genotypes. A three-year phenotyping study of winter wheat has just been published, which will be used as a main example for the discussion of root phenotyping.

The results show, that we can identify considerable variations in deep root growth, as well as in deep root function. Even among current commercially available winter wheat genotypes grown in Denmark, which represent a rather narrow genetic variation, highly significant differences were observed. The results will be presented and used to discuss root phenotyping methods, identification of critical root traits and to suggest further research needs.

Odone A, Changdar S and Thorup-Kristensen K (2025) Winter wheat phenotyping for deep root growth and function, reduced water stress and increased uptake of deep N and water, Annals of Botany. DOI: 10.1093/aob/mcaf160/8220669

What can high-throughput root phenotyping and AI bring us?

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The root is an important organ for plants to absorb water and nutrients, and its structure and function directly affect the growth and adaptability of plants. However, traditional root phenotyping methods are inefficient, time-consuming, and destructive, which limits the progress of large-scale root functional genome study. To address this issue, this study designed a high-throughput hydroponic root phenotyping platform, a hydroponic root 3D scanning device, a high-throughput crop rhizo-box root phenotyping platform, and a micro scanning device for high-throughput automated collection of root phenotypes. The capability of high-throughput hydroponic root phenotype platform is up to 2000 plants and can complete 2000 plant detection tasks within 5 hours. The high-throughput crop rhizo-box root phenotyping platform can respectively achieve dynamic observation of the root systems of 2380 plants throughout their growth period and 1600 plants during their seedling stage. To efficiently process a large number of root images, we also developed an integrated root phenotyping toolbox (RPT), which can automatically and quickly extract 42 root phenotype traits such as root length, root area, and root angle. The micro root phenotyping device can complete the panoramic image acquisition of the root system of a single crop within 10 minutes, with a maximum image resolution of 0.5 µm/pixel and field of view with 30 cm×30 cm. It can dynamically extract the micro phenotype of root hairs such as development process, density, and length. In conclusion, this study developed a comprehensive high-throughput root phenotyping solution based on hydroponics and soil cultivation, from macro to micro and 2D to 3D, which has shown great potential in the exploration of functional genes for complex traits such as drought resistance in maize and rice, and also explore crops suitable for growing in Martian soil environments, providing a new method for root phenotyping improvement and crop breeding.

Deciphering key root traits involved in phosphorus tolerance in bread wheat (Triticum aestivum L.)

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Phosphorus is a crucial nutrient in agricultural systems, as it is both scarce in soil and difficult for plants to acquire. This makes it a key factor in ensuring optimal crop growth and development. Phosphorus deficiency has been demonstrated to have a detrimental effect on both the yield and quality of cereals. In particular, this deficiency has been shown to have a significant impact on bread wheat (Triticum aestivum L.), which is one of the most cultivated cereal crops in the world.

Plants adaptation mechanisms towards phosphorus use efficiency is determined by both genetic and environmental factors. In the presence of limited available phosphorus (P), crops such as wheat have been observed to undergo processes that restore their P status. This process involves the modification of root architecture, morphology, and functionality, resulting in the preferential development of the root compartment. In our study, in order to ascertain which of the root system architecture (RSA) traits or root system functions were modified according to the available phosphorus (P) and the role played by these in plant performance, the response of 26 different bread wheat genotypes to two different levels of phosphorus was evaluated on a large trial using a root phenotyping platform using RhizoTubes.

Rhizotubes allowed non-invasive deep root phenotyping, revealing significant genotypic effects on biomass production and root system traits. Dynamic modelling of architectural and morphological traits allowed determining various trait dynamics parameter and highlighted which ones were independent and their genotypic variability. Then, links between these traits and phosphorus acquisition and use efficiencies indicators were established.

This study allowed identifying contrasted strategies used by the different genotypes to either acquire or use the soil phosphorus. This paves the way to deliver P-efficient germplasm that may contribute to promote agroecological cultural practices in a context of low soil P availability.

Root phenotyping for drought tolerance traits in the underutilized crop plant buckwheat

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Buckwheat (Fagopyrum esculentum Moench) is a pseudocereal that was once a globally grown staple food. However, it was replaced by higher yielding cereals such as wheat. In Germany, it is nowadays only used as catch crop because of its beneficial effects on soil health. With an increasing interest in nutritious and gluten free products, buckwheat consumption is on the rise, and buckwheat must currently be imported. In the BMBF-funded interdisciplinary project Buckwheat Improvement by Modern Technologies for the Establishment of a Dual-Use Crop (BIMOTEC), we aim to support buckwheat re-establishment in Germany by additionally revealing its bioeconomic potential as multi-purpose crop. Besides the improved production of grains as food, the utilization of residual buckwheat biomass is investigated, i.e. extraction of the secondary metabolites like rutin from leaf biomass and seed hulls, as well as bio-based platform compounds from stem biomass. An extensive pre-breeding approach involving phenomics, transcriptomics, and metabolomics combined with the development of genome-editing technology will be a kickstart for breeding of new local cultivars, while improved agronomic models and industrial-scale metabolite extraction protocols will support the production of buckwheat and buckwheat-based products. As part of BIMOTEC, we initiated the first large-scale image-based phenotyping of buckwheat root traits. In high-throughput plant phenotyping experiments using the novel phenotyping platform GrowScreen-Rhizo III, we will quantify the genotypic variation in root development of buckwheat in response to drought. In a preliminary experiment, plants of the cultivar 'Devyatka' were grown under control and drought conditions, which were achieved by adjusting the soil water potential to 0.2 MPa and 0.7 MPa, respectively. Here, buckwheat revealed a widely branched taproot system with many very fine roots. Based on the established protocol, we will phenotype a panel of buckwheat genotypes under control and drought conditions and combine our results with earlier analyses of water-use strategies. In addition, we will establish a root washing procedure to determine root traits of buckwheat destructively. With this high throughput phenotyping approach, we will provide new insights into buckwheat drought tolerance and bring forward breeding of local climate-resilient buckwheat cultivars.

Oral presentations

Session 4:

Phenotyping for improvement of yield and quality

Smart data for smart crops: predicting performance with high-throughput phenotyping and modeling

Pierre Matre

INRAe

Crop breeding programs are designed to develop new varieties suited to particular environments, but progress can be constrained by genotype-by-environment (G×E) interactions and the significant resource requirements of multi-site, multi-year trials. Crop growth models (CGMs) address these challenges by using ecophysiological principles to simulate genotype performance under varying conditions. These models depend on both species-level and genotype-specific parameters, with the latter requiring calibration for each new genotype using controlled conditions or field data. However, estimating genotypic parameters for large populations is difficult due to the necessity for extensive and often destructive manual phenotyping.

High-throughput phenotyping (HTP) technologies provide scalable, non-invasive methods for gathering comprehensive, multi-modal data from numerous plots. This presentation outlines how HTP data—collected in both controlled and field settings—can improve parameter estimation, model accuracy, and offer insights into trait values that affect varietal adaptation. The biological accuracy and structural features required of CGMs to predict G×E interactions and trait performance are also discussed. The integrated approach is examined for its role in supporting more efficient breeding decisions and the development of crop varieties with increased resilience to climate variability.

Phenomic approaches to aid agri-system transformation: X-ray systems to scale-up operations in crops breeding and commodity value-chains

Jana Kholova[1]; Stefan Gerth[2]; Janila Pasupuleti[3]; Martha Domhoefer[2]; Tharanya Murugesan[3]; Mareike Weule[2]

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Agricultural systems are under increasing pressure to meet growing global food demand, driving, among others, the need for faster and more efficient crop improvement. Novel imaging technologies, combined with advanced image analysis, offer a promising path to accelerate breeding progress. Same tools can also enable the fairer commodity pricing for primary producers while incentivizing higher-quality grain production in the related value-chains.

In this study, we present a successful example from the pan-India peanut breeding system, which has adopted X-ray imaging for routine evaluation of breeding lines. This required the collaborative efforts of transdisciplinary team who identified the key phenotyping bottlenecks in breeding pipeline (i.e. everaging Multitemporal UAS-Based Data for Growth Analysis in Winter Wheat Breeding evaluation of grain number, grain size, grain size distribution and shelling %) and then addressed them with suitable technology (X-ray system; CTportable160.90). This phenotyping innovation enabled cost-effective (~50% reduction) and faster (months reduced to weeks) evaluation of whole peanut pods. As a result, breeding programs can now assess critical peanut pod traits such as shelling %, pod weight, pod count and even the very labor-intensive traits like grain size distribution, much earlier in the breeding pipeline (as early as the F4 generation instead of F5/F6). This system is now routinely used to evaluate more than 6,000 samples per season across India as part of nationwide multi-location testing of advanced breeding lines.

We will also briefly discuss emerging concepts aimed at supporting rice breeding programs and highlight ongoing efforts to empower primary producers through in-field grain quality assessment technologies.

Intercropping in Europe: Demonstrated higher land use efficiency over monocultures

Madhuri Paul

University Bonn

Intercropping (IC) is the cultivation of multiple species in a single field in close association, either simultaneously or in incomplete temporal overlap as in relay IC. IC outperforms monocultures in terms of grain production per unit area. Meta-analyses, drawing on a wide range of studies in different production situations, have consistently shown that IC enhances land-use efficiency. On average, IC allows land to be used 17 to 30% more efficiently than when growing single crops alone. Cereal–legume IC, is known for delivering high yields particularly under low N conditions largely due to the synergistic use of N sources. Legumes contribute by fixing atmospheric N through symbiotic N_2 fixation while IC systems also promote better P uptake & more effective utilization of soil water.

Despite its numerous benefits, the use of IC has declined in Europe since the 1950s. In particular, European farmers have favored monoculture for food production due to managing the complexity of IC. While monocultures offer an economic benefit in the short term, there is concern about long-term sustainability of this practices. Given the growing challenges of current agricultural practices, reintroducing diversified IC systems is seen as a pathway for promoting sustainable agriculture in Europe.

Meta-analyses have been conducted using worldwide data or for specific regional contexts however no specific meta-analysis has been done to synthesize the yield benefits of IC for Europe. But the quantitative syntheses in this comprehensive review focus on experimental data from France. As there is uncertainty on the yield benefits of IC across the whole of Europe, & the factors driving it, we are conducting a meta-analysis on the relative performance of IC systems under European growing conditions. Our focus is on grain-producing cereal–legume IC, which have attracted the most research interest due to their potential to deliver higher grain yields under organic growing conditions & with lower environmental impacts. Particularly, this study seeks to answer the following key question:What is the average land equivalent ratio (LER) of cereal-legume IC systems by identifing key factors driving LER in Europe.

To address this, we conducted a literature search & selected more than 80 studies for preliminary analysis. Our initial results show a median LER of 1.16. This indicates that, on average, IC uses land 16% more efficiently than equivalent areas dedicated to sole crops in EU.

Development of a Machine Learning model to predict sunflower seed humidity

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Optimizing harvest timing and enhancing breeding for climate resilience require accurate and non-destructive estimation of seed development in agronomic context. Within the framework of the European HelEx project, a multi-site experimental protocol was implemented to generate a reference dataset for developing a predictive model of seed moisture as proxy for development, based on drone imagery.

Field trials were conducted across four environmentally contrasting sites (France, Spain, Romania, and Chile) using four commercial sunflower varieties and the gms83HR4xXRQ hybrid used as reference in the HelEx project. At each site, 15 micro-plots were monitored at six key seed developmental stages via repeated drone flights. Destructive sampling was performed in parallel: A total of 180 capitula per site were harvested, photographed, and their seed moisture content determined by fresh-to-dry weight comparison.

Drone images were processed using a deep learning model to detect and isolate sunflower capitula with bounding boxes. Each capitulum was paired with a ground-truth moisture value obtained through gravimetric moisture determination. A neural network architecture combining a Vision Transformer and a Masked Autoencoder was used to extract visual features, followed by a linear regression model to estimate moisture at the capitulum level. Plot-level values were obtained by averaging individual predictions.

The model showed high predictive accuracy across the diverse environmental conditions, with a coefficient of determination (R^2) of 0.91, a root mean square error (RMSE) of ±6%, and a Pearson correlation coefficient of 0.96. These results confirm the effectiveness of drone-based phenotyping for non-invasive seed moisture and provide a proxy for seed developmental stage.

Future work could focus on improving yield prediction by leveraging accurate 3D reconstructions of the capitulum, which is likely correlated with seed count and potentially with thousand kernel weight. Neural Radiance Fields (NeRFs) offer promising avenues for such detailed structural analysis. Seed oil content could also be estimated via time-series models like V-JEPA, capturing environment-driven dynamics through drone imagery.

Keywords: seed humidity, deep learning model

Focus Session:

AI for phenotyping

Poster presentations

Session 1:

Phenotyping for stress resilience and tolerance

Poster location: S01

Field assessment and specificity of Fusarium Head Blight detection on wheat using Near Infrared Hyperspectral Imaging

Damien Vincke[1]; Damien Eylenbosch[1]; Anne Chandelier[1]; Vincent Baeten[1]; Benoît Mercatoris[2]; Philippe Vermeulen Ir.[1]

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Recent reviews identified research gaps in hyperspectral imaging (HSI) for plant stress detection. Among these gaps is the limited number of HSI applications in field conditions. Another gap is that studies often focus on a single stress, but the specificity of the detection is rarely tested on other stresses. This study is a contribution to filling both gaps by applying near infrared hyperspectral imaging (NIR-HSI) in the field to detect Fusarium Head Blight (FHB) and assess the ability of this technique to differentiate FHB and Take-all infections. The differentiation of both diseases is of great interest as they show similar symptoms on the ear, but their respective pathogen agents are well distinct.

A field trial with 6 winter wheat varieties was sown outdoors in a cultivation bed. The trial was inoculated at flowering with Fusarium graminearum. The plants were scanned using NIR-HSI in the field at 7 dates during grain maturation. A Take-all infection occurred simultaneously with the FHB infection which provided an opportunity to test the method’s ability in classifying both stresses.

A dichotomous classification was developed to detect both stresses with Partial Least Squares Discriminant Analysis (PLS-DA). Method validation at pixel level showed accurate classification of pixels of healthy and diseased ears (accuracy > 90%). However, classifying between FHB and Take-all did not provide satisfactory results. At plot level, the models were evaluated by comparing the predicted disease severity (% coverage on the plot) with the field-observed disease incidence (% of infected ears). The models did not allow disease discrimination, but the sum of both diseases’ predictions showed good correlation with the observed overall stress incidence ($R^2 \geq 0.80$). These results suggest that the models assess the symptoms rather than the disease itself and further developments are needed to accurately discriminate individual stress types, including spatial information analysis.

Poster location: S02

A multi-scale phenotyping approach to unveil the biostimulant potential of Serendipita

Noémie De Zutter[1]; Jolien Venneman; Geert Haesaert[1]; Jan Verwaeren[1]; Danny Vereecke[2]; Kris Audenaert[1]

[1] Ghent University; [2] Howest

As climate change accelerates and the use of chemical fertilisers is being reduced, abiotic stresses such as prolonged drought and nutrient limitations are becoming critical bottlenecks for global crop production. This growing challenge calls for innovative strategies to support and maintain plant growth and yield. Biostimulatory microorganisms are rapidly emerging as sustainable agents to enhance crop performance and resilience under abiotic stress. Although many microorganisms have been explored for their biostimulants activity, their consistency is often poor. The enigmatic root endophytic fungus Serendipita has proven its potential as a promising microbial biostimulant, but its complex interactions with host plants remain poorly understood. To capture the biostimulant impact of Serendipita across organisational plant levels, we employed a multi-scale phenotyping strategy encompassing morphological, physiological and yield-related traits. Using RGB- and multispectral imaging techniques in high-throughput phenotyping platforms, we quantified plant responses from early cellular changes in Arabidopsis thaliana, to whole-plant performance in maize under greenhouse and field conditions.

This integrated phenotyping approach showed that Serendipita affected multiple levels of plant development. At the cellular level, the visibly larger rosettes of Arabidopsis plants exposed to Serendipita were be linked to increased cell size suggesting a role in cytoplasmatic cell expansion. The shoot effect was mirrored below-ground, where we observed that Serendipita enhanced and changed the root architecture, characterized by longer primary roots and an increase in lateral root density. Physiological and biochemical parameters revealed that Serendipita-treated Arabidopsis plants exhibited higher photosynthetic efficiency and increased accumulation of photoprotective anthocyanins compared to control plants. To extrapolate our data to an agricultural relevant context, greenhouse and field trials were performed on maize plants under drought conditions. These confirmed the growth promoting effect of Serendipita, which coincided with enhanced yield potential.

This multi-scale phenotyping approach reveals how Serendipita boosts plant development and stress responses, supporting its potential as a microbial biostimulant for sustainable agriculture. Moreover, it highlights how phenotyping pipelines can help uncover untapped microbial biostimulants for the agriculture of tomorrow.

Poster location: S03

Interactive effects of elevated CO$_2$ and Cercospora leaf spot on photosynthesis and yield traits in field-grown sugar beet characterized using passive and active chlorophyll fluorescence

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Climate change, characterized by rising atmospheric CO2 levels and shifting disease patterns, poses significant challenges to agricultural systems worldwide. Current atmospheric CO2 concentrations surpassed the 400-ppm threshold and is expected to reach 650 ppm CO2 equivalents during this century (Moss et al. 2010). Elevated CO2 directly alters photosynthetic activity impacting both the incidence and severity of fungal pathogens on crops (Luck et al. 2011). However, there is a lack of understanding of the underlying processes like photosynthesis and yield formation of sugar beet under CO2 elevation, especially under biotic stress.

In this study, we conducted trials in two growing seasons (2023 and 2024) at experimental fields at Campus Klein-Altendorf, Germany using two sugarbeet genotypes with different susceptibility to cercospora infection (high and low) under elevated CO2 concentration (600 ppm) and ambient CO2 concentration. Half of the trial was inoculated by the fungus Cercospora beticola (CLS), and the other half was treated with fungicide to prevent CLS. Two field-based chlorophyll fluorescence methods were employed, an active Light-Induced Fluorescence Transient (LIFT) (Keller et al. 2022) device to obtain the operating efficiency of PSII (Fq’/Fm’) and FloX system passively measuring reflectance-based vegetation indices and solar-induced fluorescence (SIF Red and SIF Far-Red) (Porcar-Castell et al. 2021) to evaluate photosynthetic activity of sugar beet. Leaf area index, yield, and quality parameters were also measured to estimate and to understand the interaction of factors on yield formation for entire crop season.

Across both the years seasonal developmental variations in Fq’/Fm’ and SIF were observed in response to elevated CO2 when CLS was controlled with fungicide. After the appearance of disease symptoms, there is a significant decrease in Fq’/Fm’ and SIF in both ambient and elevated CO2 conditions under inoculation in the high susceptible genotype. Fq’/Fm’ and SIF shown responses to disease progression and elevated CO2 earlier than traditional indices like NDVI. Elevated CO2 increased beet yield in both the years and genotypes even under the inclusion of biotic stress. The sugar content was not much effected by elevated CO2 with slight increase in 2023 and slight decrease in 2024. Our results reveal complex interactions between elevated CO2 and disease progression, showcasing effects on photosynthesis and growth that vary in nature

Poster location: S04

RAphids: Rapid phenotyping of plant resistance to aphids using smartphone imaging and deep learning

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The demand for pest-resistant crops is rising in response to increasing pest pressures, climate variability, and the need to reduce chemical pesticide use in sustainable agriculture. In plant breeding programs, traditional assessment of resistance to insects by quantifying their presence on different plants, using microscopes and hand lenses is labor-intensive, time-consuming, and prone to human error. Accurate and digitalized phenotyping of plant-insect resistance is necessary, not only for faster screening, but also for extracting richer data and insights. This work aims to develop a mobile-based phenotyping method that leverages smartphone imaging and deep learning to enable rapid assessment of plant resistance to aphids. A dataset composed of aphid-infested leaf images was prepared under laboratory conditions using standard smartphone cameras, with varying lighting setups and shooting distances. The dataset includes three aphid species: Aphis gossypii, Aulacorthum solani, and Myzus persicae, with both nymphs and adults that are found on the adaxial and abaxial surfaces of sweet pepper, pumpkin, and potato leaves. The dataset was split by species to train individual object detection models. Each model was optimized by applying image tiling and incorporating multi-scale training, maximizing accuracy while finding the least inference time. The models demonstrated high testing F1-scores (A. solani = 0.98; M. persicae = 0.86; A. gossypii = 0.94) with an average inference time of 2.3s. The algorithm was deployed in a cloud environment to process the data obtained using a mobile application called RAphids. RAphids is now being tested in internal breeding trials to act as a support tool for managing trials and screening aphid resistance. The results from the trials show that automatic counting results can reach an average R2 of 0.86 compared to the manual counts obtained with the help of a microscope. This approach offers a scalable solution for integrating artificial intelligence into pest resistance breeding and supports the broader adoption of digital phenotyping in precision agriculture.

Poster location: S05

Biological control of Phytophthora infestans in Solanum tuberosum by volatile organic compounds

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For decades, biological control as a plant disease management strategy has been undervalued. However, European initiatives such as ‘the Green Deal’ and ‘the Farm-to-Fork strategy’ are driving a paradigm shift. As many chemical phytopharmaceuticals are phased out in Europe, phytopharmaceutical companies are now adding biocontrol products to their portfolios. This shift is challenging for a crop such as potato (Solanum tuberosum L.), where chemistry has historically been the only effective strategy against Phytophthora infestans, the major potato pathogen.

A specific biocontrol strategy involves harnessing the plant's innate immune system through a phenomenon known as priming, which puts the plant in a state of alertness prior to infection. Priming agents such as beta-aminobutyric acid (BABA) have been known for some time. In our research group, we have provided proof-of-principle that the green leaf volatile Z3-hexenylacetate (Z3-HAC), which is released from plant cell membranes under stress, is a potent priming agent against P. infestans in potato.

In the present work, both the direct antagonism of Z3-HAC against P. infestans and its efficacy to control the pathogen via a plant-mediated manner have been determined. The direct antagonism was assessed in vitro, where mycelial growth and biomass were quantified using hyperspectral imaging. The dose-response effect of Z3-HAC was evaluated, in which both the minimum inhibition concentration (MIC) and minimum mortality concentration (MMC) were determined.

The priming capacity of Z3-HAC was evaluated in planta by consecutively exposing plants to Z3-HAC and inoculating these plants with P. infestans. Disease symptoms and progression were evaluated through multispectral imaging, enabling us to pre-symptomatically detect P. infestans disease progression in potato. The chlorophyll fluorescence (Fv/Fm) and chlorophyl index (ChlIdx) were two relevant proxies for evaluation of increasing or decreasing susceptibility of potato plants to P. infestans. Our research underscores the promising priming effects of Z3-HAC, however indicates that this priming effect only affects a certain leaf-layer.

In order to understand the mechanisms related to the immune response resulting from Z3-HAC priming, a mode of action study was performed including both mRNA and sncRNA.

Poster location: S07

Technology Center for Phenotyping in Merkendorf: Integrating Above- and Below-Ground Trait Analysis

Peter Pietrzyk; Cora Weippert; Günter Lehretz; Thomas Malzer; Fabian Keil; Christian Hügel; Stefan Gerth

Fraunhofer Institute for Integrated Circuits IIS

High-throughput plant phenotyping has become an essential tool for deepening our understanding of plant responses to environmental stimuli and for optimizing crop breeding strategies. However, a common limitation of existing phenotyping approaches is their inability to observe above- and below-ground plant traits simultaneously. Such observations are crucial for understanding how these traits interact under varying environmental conditions and for identifying correlations between below- and above-ground processes, which can serve as useful proxies in field phenotyping. Our newly established controlled environment facility at the Technology Center for Phenotyping in Merkendorf directly addresses this challenge by enabling comprehensive 3D phenotyping of plant structures in highly controlled settings.

Our facility consists of three automated growth chambers that accommodate up to 400 plants and offer control over environmental variables such as light intensity and spectrum, irrigation, fertilization, temperature, humidity and carbon dioxide levels. To enable detailed phenotypic analysis, we have integrated three measurement stations. The first, our PhenoCT station, equipped with the XEye camera, uses X-ray computed tomography for non-destructive 3D reconstruction of root systems and tubers. Our second station uses the CEye system, consisting of twelve RGB cameras that facilitate 3D reconstruction, along with laser light sheet technology for above-ground 3D phenotyping. Finally, the third station is equipped with high-resolution RGB cameras that capture top and side views, enabling rapid data collection and color analysis.

Our primary goals are to enable the development of new phenotyping methods and to provide both scientists and breeders with access to this technology. The versatility of our controlled environment is crucial for investigating complex synergies among plant traits and their responses to environmental changes. Furthermore, the modular design of our sensing technology allows for integration of new sensors and technologies, such as hyperspectral imaging. By bridging above- and below-ground phenotyping, our facility not only advances plant science but also contributes to the breeding of more resilient and productive crops. We welcome collaborators to unlock the transformative potential of our phenotyping capabilities, exploring traits such as root length, leaf area, biomass, and more.

Poster location: S08

Field-Ready Compressive Spectral Imaging for High-Throughput Plant Phenotyping: Insights from the PRO-PIX Deployment at PhenoFIELD

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Hyperspectral imaging (HSI) is a cornerstone of high-throughput plant phenotyping, yet its widespread adoption is hindered by high costs, data overload, and complex interpretation. In response, we present the first field deployment of a compressive sensing-based spectral imaging system—PRO-PIX—on the PhenoField® platform, a robotic field phenotyping infrastructure designed to assess genotype-environment interactions under controlled water stress. PhenoField® is part of the French Plant Phenotyping Network named PHENOME-EMPHASIS.

PRO-PIX leverages single-pixel imaging with structured light modulation via a digital micromirror device (DMD), enabling spectral acquisition with drastically reduced data volumes. Three acquisition strategies were evaluated: full Fourier Integral Scanning (FIS), Maximum Energy Fourier sampling (MEF), and Homogeneous Area Sampling (HAS), the latter using real-time RGB-based segmentation to target specific spatial classes (e.g., vegetation vs. soil). This modularity allows for real-time computation of vegetation indices (NDVI, PRI, MTCI, MCARI2) and spectral signatures, directly onboard the sensor.

63 hyperspectral cubes were acquired across three maize cultivars. Results show strong consistency between embedded and conventional NDVI measurements, with HAS enabling near-instantaneous trait extraction. Notably, anthocyanin-related stress symptoms were detected via spectral fingerprinting around 550 nm, demonstrating the system's sensitivity to early physiological changes.

Compared to traditional HSI systems, PRO-PIX offers a modular, resource-efficient and data-frugal spectral imaging system. Its embedded processing pipeline reduces data transfer needs and carbon footprint, while maintaining compatibility with existing phenotyping workflows. We propose collaborative development of adaptive acquisition strategies and open-source tools to further integrate compressive spectral imaging into multi-scale phenotyping networks.

Poster location: S09

Integrative Phenomics Accelerates the Development of Engineered Crop Root Systems

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Climate change threatens agricultural productivity by altering and intensifying environmental conditions. Plants are central agents in the earth's carbon cycle, fixing enormous amounts of CO2 each year and transferring some of the fixed carbon into the soil. Root System Architecture (RSA) is a key climate-smart trait, as the spatial configuration of roots in the soil determines not only a plant's stress resilience but also its capacity to sequester durable carbon below ground. Here, we present an integrated phenomics approach that combines high-throughput 3D imaging, automated root trait extraction, and genome-wide association studies (GWAS) to identify genetic loci and candidate genes that control RSA across multiple crop species. Using the Root Architecture 3D Imaging Cylinder (RADICYL) platform and automated data analysis tools, such as SLEAP and U-Net++, we phenotyped hundreds of plants daily. Through GWAS, we discovered several candidate genes associated with RSA in both model and crop species. In sorghum, we identified an ATPase gene associated with primary root length. We also found that a conserved gene (deep rooting "DR1") regulates lateral root angle distribution in soybean and canola, favoring narrower angles, higher root network length at the lower region, and promoting deeper root systems. Traits such as narrow lateral root angles, increased root branching, and density in lower soil horizons are key features of deeper and more robust root systems. Our current efforts focus on the functional validation of the DR1 gene at crop maturity using a novel Depthwise Root Biomass (DRB) tube system. This modular stackable system comprising cylindrical units (25 cm dia. X 15 cm L) enables the easy extraction of root length density and root mass distribution across depth layers (up to 90 cm), which will be used as a "trait proxy" for translating them from controlled to natural field conditions. In summary, our integrative phenomics tools, powered by cutting-edge imaging systems and automated analytics, not only accelerate the discovery and functional validation of root traits but also provide a scalable strategy for translating ideal RSA phenotypes into breeding programs.

Poster location: S10

Bioristor: a novel in-vivo Functional Phenotyping tool to decipher tomato drought response dynamics

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Extreme weather events, water scarcity, and heatwaves are increasingly disrupting agricultural systems, leading to a shift in cultivation zones and posing a serious threat to global food security. In this context, the identification of more resilient and adaptable crop varieties and deciphering the mechanism leading to drought tolerance is crucial.

In this study, we describe the application of the Bioristor, an in-vivo electrochemical sensor, as a high-resolution in vivo phenotyping tool to plant phenotyping.

Its ability to accelerate the characterization of tomato (Solanum lycopersicum) varieties under drought conditions and tracing the in vivo dynamics of the drought response under drought in tomato is described taking in consideration three tomato cultivars, Mariner, Faber, and Red Setter. Based on Bioristor-derived indices, a data-driven model, based on machine learning techniques and capable of characterizing and classifying tomato varieties according to their drought tolerance, was developed.

Moreover, the use of Carbon dots nanomaterials to improve drought resilience has been explored through bioristor characterization.

Our findings highlight the potential of the bioristor in-vivo sensor-assisted phenotyping as a scalable and cost-effective strategy to support breeding programs and basic research to face climate change.

Poster location: S89

Evaluation of complex root traits towards plasticity in barley under Salt stress for improving climate resilience and productivity.

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Soil salinity, impacting over 60 million hectares of irrigated land, is a growing threat to global crop production. This study focused on evaluating root plasticity under salinity stress in 100 barley germplasms, emphasizing phenotypic traits critical for salinity tolerance. Significant variation was observed in root fresh weight (FW), root-to-shoot biomass partitioning, and overall growth responses. Highly tolerant germplasms maintained stable root FW and balanced biomass allocation under salinity stress, demonstrating robust adaptability and efficient resource utilization. These traits supported sustained growth despite adverse conditions. Moderately tolerant germplasms exhibited partial reductions in root FW and slightly altered biomass ratios, indicating intermediate resilience. In contrast, susceptible germplasms showed marked reductions in root FW and disrupted biomass partitioning, reflecting poor adaptability to salinity stress. The phenotypic diversity observed underscores the importance of root plasticity as a key factor in salinity adaptation. These findings provide valuable phenotypic data for genome-wide association studies (GWAS) to identify genetic loci regulating root plasticity under salinity stress. Such insights are crucial for breeding programs aimed at developing barley cultivars with enhanced root traits and improved salinity tolerance. This work contributes to Climate-Smart Agriculture

Poster location: S14

Innovative Phenotyping for Salinity Tolerance in Taro: A Scalable Model for Orphan Crops

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Many orphan crops, despite their cultural and nutritional importance, have received limited breeding investment and remain vulnerable to accelerating climate change. Taro (Colocasia esculenta) is one such staple, widely cultivated across the Pacific, Asia, Africa, and the Americas. In the Pacific, taro production is increasingly threatened by salinisation due to rising sea levels, changing water tables, and more frequent coastal inundations events. As these challenges intensify, there is an urgent need for innovative phenotyping approaches that can reliably assess stress tolerance and unlock the potential of conserved genetic resources.

In response, we have developed a high-throughput, cost-effective, and size-adjustable phenotyping system to screen taro for salinity tolerance, addressing common challenges in stress screening. Traditional systems often struggle with scalability, consistency across regions with limited resources, and suitability for vegetatively propagated crops like taro. Our design overcomes these issues by using readily available materials – easily sourced from most hardware stores – to create a system that simulates salinity stress through tidal-like brackish water cycles. Crucially, it supports the use of farmer-preferred headset planting material, ensuring relevance to real-world cultivation practices, while enabling precise monitoring of both above- and below-ground physiological traits.

This phenotyping platform is designed not only for taro but also as a transferable model for other vegetatively propagated orphan crops. When integrated with genotypic data generated through DArTseq Genotype-by-Sequencing (GBS) of over 1,100 globally conserved taro accessions, this system enables the identification of candidate genotypes with salt-tolerant traits. Physiological response data can be linked to genomic regions of interest, forming the basis of a phenotyping-to-genomics pipeline that bridges pre-breeding and applied breeding efforts.

This pipeline represents an innovative approach to characterising stress resilience in crops that have been historically overlooked in mainstream breeding programs. It also provides a scalable, practical solution to phenotyping under complex environmental conditions – one that holds particular promise for building climate resilience in the Pacific and beyond.

Poster location: S16

High-throughput state-of-the-art technology in phenotyping of wheat genetic resources growing under drought

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Accurate quantification of traits and the entire plant phenotype represents a bottleneck in the process of selecting wheat (Triticum sp.) genetic resources characterized by increased production performance and tolerance to stress situations. High-throughput phenotyping platforms enable rapid and non-destructive whole-field imaging of large amounts of plant biological material and quantification of structural, functional and chemometric traits. The automated phenotyping platform PlantScreenTM, which is installed at the AgroBioTech Research Center, represents an advanced research tool, connecting knowledge about physiological processes of plants with different tolerance to abiotic stress with bioinformatics and statistics. In this paper, we quantify 27 phenotypic traits divided into five classes (production, structural, functional, chemometric and water regime parameters) on 35 wheat genotypes with different ploidy, grown under conditions of optimal water supply and drought. We evaluate the stability of traits and their heritability, as well as phenotypic plasticity realized under drought conditions. The calculated phenotypic plasticity (PhP) of a trait indicates the ability of an organism to undergo reversible morphological, biochemical or physiological changes in response to environmental conditions. In the study, we show that production parameters directly related to the total biomass mass, but also some geometric traits of the plant, such as height (H), width (W) and isotropy (Izo), exhibit relatively low levels of drought-induced PhP ranging from 0.21 to 0.45. Conversely, we identified high levels of PhP for the traits harvest index (ZI) and thousand-grain weight, as well as for minimum fluorescence intensity (Fo) and Fv/Fm. The high level of phenotypic plasticity of the trait was accompanied by high heritability (H2).

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Poster location: S17

panomiX Enables Integration of Phenomics and Multi-Omics Data to Reveal Molecular Drivers of Plant Traits

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High-throughput phenotyping and multi-omics technologies generate vast, complex datasets, making it difficult to connect molecular changes to observable plant traits. To address this, we present panomiX—an accessible, user-friendly toolbox for integrating phenomic data with transcriptomics, metabolomics, and other omics layers. panomiX streamlines the entire workflow, from data preprocessing and variance filtering to multi-omics prediction and interaction modeling using machine learning. We demonstrate its utility on a tomato heat-stress dataset, combining image-based phenotyping, transcriptomic profiles, and FTIR metabolite measurements. The analysis uncovered condition-specific interactions, including links between photosynthesis-related phenotypes and stress-responsive kinase expression under elevated temperatures. By simplifying complex analyses and enhancing interpretability, panomiX empowers researchers to uncover key molecular drivers of trait emergence and prioritize candidate genes for downstream studies.

Poster location: S18

Distinguishing drought and salt stress in grapevine through functional and image-based phenotyping

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Grapevine is a relevant socio-economic crop species requesting new digital and precision approaches to face current environmental constraints. Early and accurate recognition of abiotic stress types is essential for accelerating the selection of stress-tolerant varieties and implementing effective management strategies. Hence, stressor-specific fingerprint(s) is increasingly demanded to support reliable identification of stress type (e.g., drought or salinity) within a high-throughput plant phenotyping domain.

This work presents a reanalysis of two independent experiments pooling physiological and phenotyping data in Vitis vinifera under drought and salt stress aiming at identify trait(s) enabling stress type identification.

Physiological traits included maximum photosynthetic efficiency (Fv/Fm) measured with portable chlorophyll fluorometer (FluorPen FP 100, Photon Systems Instruments, Drasov, Czech Republic). Other traits were net photosynthetic rate (Pn), stomatal conductance (gs), transpiration (E) (Li-Cor 6400, Li-Cor, Inc., Lincoln, NE, USA), and stem water potential (SWP) (Scholander type pressure chamber (Model 600, PMS Instruments, Corvallis, OR). They were combined with phenotyping traits (i.e., R, G, B and Dark Green color of leaf) retrieved through image analysis. These colorimetric traits were determined with a robotized LemnaTec 3D Scanalyzer phenotyping platform (LemnaTec GmbH, Aachen, Germany)

Results suggest that salt-stressed vines might suffer additional (non-stomatal) limitations curbing Pn severely as drought stress does at equivalent gs levels. Through a Principal Component (PC) Analysis, physiological and colorimetric response variables were decomposed revealing that Fv/Fm and Dark Green dominates the non-stomatal PC (□80%) clustering data between salt and drought experiments. Confusion matrices reveal that model based on Fv/Fm and Dark Green performed better (accuracy = 1, precision =1) than that based on Pn, gs, transpiration, and stem water potential. This study supports the potential use of Fv/Fm and Dark Green for early and non-destructive stress type identification discussing their limitations.

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Poster location: S19

Enhancing Botrytis cinerea Detection and QTL Associated Resistance Evaluation Through Imaging

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Botrytis cinerea is a generalist fungal plant pathogen that causes significant economic losses in a wide range of crops. Resistance to Botrytis is quantitative, making breeding efforts complex and heavily reliant on accurate phenotyping. However, current phenotyping methods often depend on visual assessments that are subjective, labor intensive, and difficult to standardize. To support resistance breeding and genetic marker development, there is a pressing need for high-throughput and objective phenotyping tools. In this study, detached leaves from eight introgression lines and their parental genotypes—Solanum lycopersicum ‘Moneymaker’ and S. habrochaites ‘LYC4’—were manually inoculated with B. cinerea and monitored every 24 hours up to 72 hours using multispectral and chlorophyll fluorescence imaging. These imaging techniques enabled precise, quantitative assessments of lesion development and plant responses over time. Changes in lesion size, shape, and fluorescence signals offer promising phenotypic markers for understanding plant–pathogen interactions and improving selection in resistance breeding programs.

Poster location: S20

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

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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 visualisation 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 analysed the variance components of highly predictive traits and identified which traits are mostly driven either 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 location: S21

Decoding wheat stress responses using hyperspectral imaging and machine learning techniques

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Climate change-induced stressors such as drought and cold increasingly threaten global wheat production, undermining food security. Early detection of these abiotic stresses is critical for timely intervention and resilient crop management. This study explores the integration of hyperspectral imaging and photosynthetic metrics to assess stress responses in spring (Longfumai1) and winter wheat (Jimai22) seedlings under controlled glasshouse conditions. Plants were subjected to cold and drought stress for 2, 4, and 6 days. Photosynthetic parameters, including maximum quantum yield of PSII (Fq′/Fm′), maximum efficiency of PSII photochemistry (Fv′/Fm′), photochemical quenching (Fq′/Fv′), minimal photochemical quenching (1–qP), and non-photochemical quenching, were measured using a chlorophyll fluorescence imager. Leaf spectral reflectance was captured using a hyperspectral camera (SPECIM IQ). To decode stress signatures, we applied machine learning algorithms including Random Forest (RF), Support Vector Machine (SVM), and Partial Least Squares Regression (PLSR). Spring wheat exhibited higher Fq′/Fm′ under cold stress compared to winter wheat, but showed reduced Fv′/Fm′. Hyperspectral imaging revealed distinct spectral responses across stress types and varieties. RF classification models achieved high accuracy (0.79–1.00), while regression models demonstrated robust predictive performance ($R^2 = 0.78–0.92$) with low prediction errors. Key vegetation indices, including the Ratio Vegetation Index (RVI), Simple Ratio Index (SR1), Sum Green Index (SGI), Normalized Difference Vegetation Index (NDVI), Transformed Chlorophyll Absorption in Reflectance Index (TCARI), and Normalized Difference Moisture Index (NDMI), were identified as the most informative features for classifying and quantifying stress responses. These indices likely reflect short-term physiological changes, particularly in gas exchange. This study highlights the potential of combining physiological and spectral phenotyping with advanced machine learning for early, non-invasive detection of abiotic stresses in wheat. Our findings contribute to the development of precision phenotyping frameworks for stress-resilient crop management in the face of increasing environmental challenges.

Poster location: S22

Drought tolerance prediction in potato based on phenotypic traits

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Climate change model predict altered precipitation patterns and increased drought risks. Sustainable agriculture thus requires drought-tolerant crops. Potato, the most important non-cereal crop, has a high crop (calories) per drop (water supply) ratio. However, its low drought tolerance requires improvement by breeding. Breeding by selection in arid environments takes decades. The modern approach of genomic selection can tap into growing sequence information for tuber-bearing Solanum spec. However, the generation of the drought tolerance data that are required to train the models remains a bottleneck. We therefore tested whether data derived from continuous shoot phenotyping of two potato population with a PlantEye (Phenospex) laser scanner can predict yield response to reduced water supply. The ground-truth drought tolerance data for the populations were derived from tuber starch yield data gained in multi-environment trials that represent Central European drought stress scenarios. For phenotyping, potatoes were cultivated in a container system on natural soil; drought stress was imposed by increasing the time interval between the irrigations. The continuous shoot monitoring under control and stress conditions yielded multiple growth curves for the features plant height, leaf area and digital biomass plus time resolved information for leaf movements. Growth curves were evaluated by logistic regression and yielded the parameters initial slope, inflection point and maximum for plant height, leaf area and digital biomass. For leaf angle, means were estimated for six intervals of the diurnal cycle in three developmental intervals. Analysis by general linear model revealed significant genotypic variation for all features. Leaf movement and growth curve parameters for plant height were significantly affected by the environment, while leaf area curves were stable over years. Decision tree analysis for the first potato population selected the inflection point of the leaf area curve under stress as the most important feature for tolerance class prediction. Additional decision tree parameters were the maximum of plant height and the leaf angle before noon. Multiple regression analysis on data from the genetically more diverse validation population confirmed leaf area and leaf position parameters as predictive tolerance traits. Tolerant genotypes maintained leaf movement and continued to increase the leaf area under stress.

Poster location: S23

Digital Phenotyping of Drought Tolerance in Brassica carinata

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Drought is an increasingly critical environmental challenge for agricultural sustainability in the Canadian prairies. Brassica carinata, recognized for its climate resilience and biofuel potential, remains understudied in terms of drought tolerance. This research aimed to identify digital phenotypes associated with drought tolerance in B. carinata. Forty-seven Nested Association Mapping (NAM) founder lines of B. carinata and two B. napus checks were evaluated under irrigated and rainfed conditions in replicated trials during 2023 and 2024. Phenological and agro-morphological traits were systematically measured throughout the growing season. Additionally, weekly UAV flights equipped with multispectral, RGB, and thermal sensors captured digital phenotyping data from the rosette stage to maturity.

The study identified the Stress Susceptibility Index as the most reliable indicator of drought tolerance, demonstrating a strong correlation (R^2=0.9) with seed yield reduction. UAV-derived vegetation indices proved useful for drought assessment, with effectiveness varying based on drought timing. Lasso regression models revealed NDVI at BBCH stages 65-69 and plant height at BBCH stages 69-79 under recurring drought (2023), and days to flowering initiation, NDYI (BBCH 50-60), NDVI, and NDWI (BBCH 60-65) under terminal drought (2024), as key predictors for drought tolerance. The developed models successfully distinguished genotypes exhibiting extreme drought tolerance and susceptibility. Our findings underscore the value of integrating UAV-based imaging technologies and agronomic data to effectively characterize drought tolerance in Brassica carinata.

Poster location: S24

Optimizing Canopy Architecture for High-Density Planting in the Sahel: Linking 3D Laser Scanning to Field Performance in Sorghum

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Food security for people and cattle is a major cause of ethnic and political conflicts in the Sahel and crop intensification is a way to curb current threats. Pearl millet and sorghum are critical staple foods in these environments, being well adapted to high temperature. However, they are sown at low densities, ~ 30, 000 plant/ha, owing to the memory of the droughts of the 70's and low soil fertility.

Our field experiments show that increasing sowing density from 10 to 20 plants m-2 significantly enhances biomass and grain yield, by 25 to 50% across trials and genotypes, with some genotypes showing 70-90% increase. Genotypes with the strongest response to high density had higher water use efficiency (WUE), had the strongest transpiration response to the evaporative demand (assessed by the Penman-Monteith reference evapotranspiration equation, ETref), and allowed more light to penetrate inside the canopy under high density.

To explain these differences in light distribution, we assessed 3D canopy architecture traits using a 3D laser scanner (Phenospex PlantEye), including leaf angles, ground-projected leaf coverage, and canopy light penetration depth. Besides the 3D scanner, we developed complementary analysis tools to extract other 3D traits, including the vertical distribution of leaf area. Thirteen genotypes of sorghum, tested under high density in the field and for WUE, were scanned in the glasshouse.

Genotypes with the strongest density response had: (i) more leaf area in the bottom part of the canopy; (ii) fuller leaf coverage; (iii) deeper light penetration. Genotypes with the strongest transpiration response to the evaporative demand also had fuller leaf coverage and steeper leaf angles, which was also related to higher WUE.

In the current limitation of field-based tools able to routinely measure 3D canopy traits, our ability to phenotype relevant architectural features in controlled conditions in a scalable and cost-effective way is exciting. This will enable the breeding of cultivars suited to high-density planting, paving the way to intensify staple food crop production in semi-arid regions.

Poster location: S26

Impact of GABA Pathway Disruption on Stomatal Defense, ROS Dynamics, and Metabolite Profiles under Biotic Stress

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γ-aminobutyric acid (GABA) is a conserved signalling molecule important in both animals and plants. In animals, it acts as the main inhibitory neurotransmitter, while in plants, it regulates development, stress responses, and adaptation to environmental conditions. Playing a role in plant stress adaptation, GABA modulates responses to biotic stress or environmental factors such as humidity. To explore this, we investigated Arabidopsis mutants impaired in GABA biosynthesis (gad1–gad5) and catabolism (Gaba-T) under Pseudomonas syringae (Pst) infection, as well as under controlled low (50%) and normal (70%) humidity regimes. Using high-throughput phenotyping techniques and metabolite profiling, we identified distinct physiological and metabolic response patterns associated with altered GABA homeostasis across humidity conditions.

Analysis of targeted metabolites, including amino acids and polyamines, revealed a clear separation of mutant lines according to stress type and humidity. Biotic stress responses were tightly linked with changes in GABA and polyamine levels, confirming crosstalk between GABA signalling and defence-related metabolism. Using ROS burst assays and stomatal aperture measurements, we identified divergent oxidative burst patterns among GABA-related mutants in response to flg22 and Pst treatments. Stomatal measurements further confirmed impaired closure in some gad mutants. These findings point to a role for GABA in regulating stomatal defence, particularly under low humidity or during Pst infection.

Altogether, these traits contribute to altered stress resilience in GABA pathway mutants. Our results support that GABA metabolism integrates immune signalling, environmental conditions (humidity), and metabolic adaptation as a key node in shaping plant responses to biotic stress under fluctuating atmospheric conditions.

Poster location: S27

High-throughput phenotyping reveals early immune dynamics in Arabidopsis accessions under Pseudomonas syringae infection.

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Understanding the early dynamics of plant immunity requires integrative phenotyping approaches that can capture spatial and temporal resolution without disrupting physiological processes. In this study, we combined high-throughput phenotyping (HTP), ultra-weak photon emission (UPE) imaging, and molecular analyses to characterise the early immune responses of three Arabidopsis thaliana accessions, Columbia (Col-0), Landsberg erecta (Ler), and Wassilewskija (Ws) upon infection with Pseudomonas syringae pv. tomato DC3000. Plants were screened in 24-well plates using a high-resolution RGB-based HTP platform across large biological replicates. A detailed time-course assessment captured dynamic phenotypic traits at 3, 6, 9, 12, and 24 hours post-inoculation (hpi). UPE imaging enabled non-invasive, real-time monitoring of reactive oxygen species (ROS) distribution under in vivo conditions. All accessions exhibited an early ROS spike between 3 and 6 hpi, but patterns diverged thereafter. Ler exhibited the most robust immune response, with rapid ROS bursts, early stomatal closure, and strong upregulation of AtPR1, likely mediated by salicylic acid (SA) signalling and AtRBOHF expression. Ws, in contrast, showed heightened susceptibility, with delayed yet prolonged ROS production, elevated non-photochemical quenching (NPQ), and higher ABA-linked responses. Col-0 displayed an intermediate phenotype, characterised by differential expression of AtNHL10 and AtPDF1.2, indicating a SA–JA interaction. This work demonstrates the power of integrating automated phenotyping and UPE imaging with molecular markers to study genotype-specific immune strategies. Our findings identify Ler as a promising model for resistance studies and chemical screening, providing a scalable framework for advancing plant immunity research and enhancing crop resilience under biotic stress.

Poster location: S28

DiPredict – AI based optimization of selection under drought stress in wheat breeding

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Wheat (Triticum aestivum L.) is one of the leading staple crops around the globe. Abrupt changes in the climate are causing concerns for its production. Drought stress is becoming increasingly prevalent – Saxony-Anhalt in Germany is particularly affected due to the rain shadow of the Harz mountains in the Central German dry region. Simultaneously, advances in technological, statistical and computational domains have opened avenues for sustainable crop improvement. With DiPredict, a research network has been established in Saxony-Anhalt that sets the course for future-oriented, digitalized plant breeding in times of climate change and its associated challenges. The research network includes Martin Luther University Halle-Wittenberg (MLU), Anhalt University of Applied Sciences (HSA), the Julius Kühn Institute, Institute for Resistance Research and Stress Tolerance (JKI), Quedlinburg and the breeding company RAGT 2n S.A.S. with its wheat breeding station in Silstedt. The focus of DiPredict is to promote digitalization in agriculture through AI-based optimization of selection under drought stress in wheat breeding. For this, a diversity panel of 50 relevant bread wheat genotypes has been selected that will be screened for agronomically interesting traits regarding their response to drought at multiple drought-prone locations across multiple years. Unmanned aerial vehicles (UAVs) with various types of sensors such as RGB, hyper-/multispectral, thermal, and LiDAR will be used to capture sensor data in high-throughput to predict the traits of interest for wheat research and breeding. A novel hyperspectral FTIR imager will also be used onboard of a survey aircraft to collect data of all field trials. In addition, the PlantArray system (Plant-DiTech) will be used for an automated functional phenotyping of the same genotypes under control and drought conditions to collect detailed data on transpiration dynamics and water use efficiency. By applying the same sensor techniques in the controlled PlantArray experiments and in field trials, we aim to identify proxies that allow improved phenotyping for water use efficiency related traits in the field. This way the knowledge gathered for the 50 reference genotypes will be extrapolated to thousands of plots in breeding nurseries to close the gap between research and breeding for the targeted use of UAVs to develop drought-tolerant cultivars.

Poster location: S29

High-throughput phenotyping approach for study of wheat nitrogen use efficiency under drought

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Laboratory high-throughput phenotyping tools provide repeated, accurate measurements and accumulation of a huge amount of data on a large number of traits. Water and nitrogen are the two main limiting factors of wheat yield. Complex tolerance to drought is an attribute, constituted by many traits and realized at all hierarchical levels of the plant. Automatic and high-throughput phenotyping approach renders new possibilities for insight into the interplay between N limitation/excess and the alterations in the growth and photosynthetic responses in plants subjected to drought. High-throughput protocols using PlantScreenTM phenotyping installation in the Slovak University of Agriculture in Nitra were optimized for wheat phenotyping. Plants of one modern genotype (two Rht genes and N-responsive) and one old Bulgarian variety (tall stature and N-non-responsive) of wheat (Triticum aestivum L.) were grown in fully controlled environmental conditions (light, temperature, humidity, water and nutrient content). Experimental treatments contained three levels of nitrogen (0 ppm, optimal 100 ppm and high 250 ppm) and two water levels (well-watered and water stress, followed by rehydration). During plant ontogeny, the structural, functional and chemometrics quantitative phenome traits were determined using three types of optical sensors (RGB, fluorescence, hyperspectral reflectance). In total, 200 different traits were measured. The level of phenotypic plasticity of wheat plants to water stress under different N supply allowed the characterization of key structural and functional traits. Finally, the evaluated traits expressed significant genotype × environment interactions. Significant differences were identified between the modern semi-dwarf variety (carrier of Rht-genes) and the old local high-growth variety. A powerful approach for large-scale screening of plant stress responses allowed us to gain a deeper insight into the strategy of plants to cope with drought at different levels of N depending on the genotype.

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

Poster location: S30

Cytokinin-regulated DIRIGENT13 enhances root architecture and abiotic stress tolerance via lignan biosynthesis in Arabidopsis

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DIRIGENT (DIR) proteins mediate stereoselective coupling of monolignols during lignan and lignin biosynthesis, yet their roles in development and stress adaptation remain poorly characterized. Here, we investigate DIRIGENT13 (DIR13), a cytokinin-responsive gene in Arabidopsis thaliana, and its role in root growth, lignan biosynthesis, and abiotic stress resilience.

DIR13 is expressed in the root endodermis and margins of lateral root primordia. While not required for Casparian strip formation, DIR13 promotes both primary and lateral root growth. Metabolomic profiling and imaging mass spectrometry showed that DIR13 facilitates (neo)lignans biosynthesis.

Functional analysis of overexpression (OE) and mutant lines revealed that DIR13 enhances salt and drought tolerance. Under salinity, DIR13 OE maintained root growth, delayed leaf chlorosis, and exhibited higher photosynthetic efficiency. Chlorophyll fluorescence imaging (PlantScreen™ SC Root System, Photon System Instruments) showed higher Fv/Fm values indicating better photosystem II (PSII) quantum efficiency in DIR13 OE compared to wild type under stress. DIR13 OE plants also accumulated more reactive oxygen species (ROS) under both control and salt stress, especially in the presence of cytokinin, linking DIR13-mediated lignan metabolism to ROS signalling and stress response. Under drought, DIR13 OE plants had better survival, larger shoot area, and faster recovery upon rewatering. These phenotypic traits were supported by physiological data, including sustained Fv/Fm values during stress and recovery phases and indicating improved stress acclimation. Based on our findings we propose that DIR13 integrates cytokinin signaling, lignan metabolism, and ROS homeostasis to promote abiotic stress resilience.

Orthologs of DIR13 are present in economically important Brassica species (B. napus, B. juncea, B. oleracea), widely cultivated for canola and mustard oil. These crops are rich in lignans such as pinoresinol and lariciresinol, compounds with antioxidant, anti-inflammatory, and cardioprotective properties. The presence of multiple DIR13 homologs and high endogenous lignan levels suggest a conserved functional role in Brassica. Our results in Arabidopsis offer a molecular basis for enhancing stress resilience and nutritional value in oilseed crops, contributing to phenomics-driven strategies for climate-smart, health-promoting agriculture.

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Poster location: S31

PHENOMIC TOOLS FOR ENHANCING WHEAT TOLERANCE TO VARIOUS ABIOTIC STRESSES

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Climate change and the degradation of soil and water resources have led to the need to minimize agriculture's dependence on high inputs of fertilizers, water, and pesticides, promoting more sustainable farming practices. Against this backdrop, our objective is to identify wheat varieties that perform best under challenging abiotic conditions achieving higher yields, improved grain quality, and more efficient use of resources in stress-prone environments. Over the past decade, we have assessed the effects of drought and its interactions with other abiotic stresses, such as salinity, heat, and nitrogen availability on wheat growth and development, utilizing advanced phenomic tools. Our findings have shown that the Serbian cultivar NS 40S demonstrated strong water use efficiency, while NS Avangarda exhibited a good balance of both water and nitrogen use efficiency. In our investigation of the combined impacts of drought and salinity, among 5 investigated wheat cultivars from Serbia, NS Avangarda achieved the highest grain yield under salt stress alone, while cv. Balkan had the best performance in water limited conditions. The highest level of tolerance when both water and salt stress were applied simultaneously was recorded in cv. NS 40S. Building on these insights, we expanded our research to examine wheat responses to heat stress during two critical growth phases: flowering and grain filling. Two Serbian cultivars outperformed even the known heat-tolerant control variety under elevated temperatures. Cultivar NS Rani otkos had the best performance when increased temperatures were applied in one of the selected stages (anthesis or mid-grain filling), while under conditions of combined heat stress at the both stages, cv. Subotičanka showed the highest yield. The outcomes of all these studies provide valuable knowledge for wheat breeders aiming to enhance tolerance to abiotic stresses.

Poster location: S32

A new facility to bridge plant phenotyping and remote sensing for environmental impact assessment

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CIRA - Centro Italiano Ricerche Aerospaziali

In recent decades, growing global concern about the health of ecosystems has driven scientific research toward the use of plant species as bioindicators of ecological criticalities for environmental monitoring. However, the phenotypic change of plant bioindicators in response to an adverse growth situation is influenced by several factors that generate a certain uncertainty in the measured traits, particularly in remote observations. Within this framework, high-throughput plant phenotyping facilities allow the acquisition of a large amount of data by simultaneously analyzing hundreds of plants with advanced equipment, either in controlled environments or open field, quickly providing useful information for revealing plant response to unfavorable climatic conditions. Additionally, experimental infrastructures that exploit structures such as mesocosms and lysimeters are nowadays available to test the effects of chemicals in both aquatic and terrestrial environments from an ecological perspective. Despite this, there is still a lack of multifunctional sites that are able to simulate realistic scenarios of anthropogenic contamination impact on plant, contemporary investigate which phenotyping traits are influenced and how such traits can be effectively measured by remote sensing tools/algorithms. To face these challenges, the Italian Aerospace Research Centre (CIRA) is designing an experimental facility to support the Bioscience for Earth Observation project's goal of synergistically using plant phenotyping and remote sensing technologies to develop innovative services in the field of environmental monitoring. For this multifunctional infrastructure, a gantry-type solution is currently being studied that would be equipped with both plant phenotyping and remote sensing cutting-edge sensors, designed for high-frequency acquisitions from variable heights up to 20 meters. The same test area will also be overflown with drones and other aerial platforms to obtain data at higher altitudes, while ground-based instrumentation will be used for validation measurements. Finally, the experimental field will be further equipped with a lysimetric station to isolate a certain volume of contaminated soil (both naturally and experimentally), thus monitoring the effect of xenobiotics on crops in semi-natural conditions. Overall, the CIRA facility could represent a bridge between different scientific disciplines such as plant phenotyping, remote sensing and bioindication.

Poster location: S33

Photonics-Assisted Fertilization of Cauliflower

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Fertilization of cauliflower consists in multiple applications of nitrogen-based inputs to agricultural soils during the crop growth. This approach aims to optimize the dynamic nutrient needs before the harvest time and to minimize the risk of nutrient loss through leaching or run-off, typically during the winter months. Indeed, when excess nitrogen is applied (or poorly timed), the fertilisers can leach into the soil, reaching groundwater and thus contributing to nitrate pollution. In addition, this nitrogen excess can lead to the production of nitrous oxide.

In the frame of a collaborative project, Biophotonics Group (Photonics Bretagne) worked on the development of a decision support system enabling to predict the crop nutrient status in cauliflower and, then to make data-driven decisions in real time. For this, the spectral signatures of cauliflower leaves were collected in the field using a lab-made plant clip (VIS – SWIR spectral ranges) during agronomic trials in 2024 – 2025 (Experimental Station CATÉ, France). The agronomic trials focused on the differentiation of the nitrogen status in the cauliflower leaves after fertilization. Spectral database (i.e. around 4000 reflectance spectra) was built on nine measurement campaigns over three months and included multiple variabilities such as type of cultivars and measurement areas.

First, a statistical analysis of both the chlorophyll absorption coefficient Cab [Remote Sens. Environ. 177, 220 (2016)] and the REIP index was implemented, showing that the effect of fertilization is observable and detectable 23 days after nitrogen application. Then, a prediction model allowed to determine if a fertilisation was applied to cauliflower plants regarding the sowing date. The precision of the model reached 75% with less than 20 repetitions. Currently, Biophotonics Group is working on the improvement of the model by predicting the need (or not) to apply fertilisers.

Poster location: S34

HYDRAS: Innovative Phenotyping for Drought Resilience

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ILVO

The recent report by the European Environment Agency (2024) identifies drought as a significant risk that leads to crop failures and reduced yields. Guaranteeing food security necessitates understanding and improving crop resilience to climate stress. Here, we present HYDRAS, a state-of-the-art open access research infrastructure enabling High-Throughput Field Phenotyping (HTFP) of above- and below-ground plant responses to drought in a realistic crop production environment. HYDRAS combines HYdrology, Drones and RAinout Shelters to address key challenges in plant breeding, evaluate water saving crop management strategies, investigate interactions between abiotic and biotic stresses, etc. HYDRAS allows investigating below-ground crop functioning and the translation of research findings from controlled conditions to field settings. While techniques to assess the above-ground phenotype are readily available; below-ground plant traits are not as accessible due to the opaque nature of soil. Recent advances in non-invasive hydrogeophysical techniques allow for effective indirect monitoring of water depletion in the root zone. A fully automated electrical resistivity tomography (ERT) installation is implemented in HYDRAS, supplemented by frequent drone-based measurements using various sensors and mobile rainout shelters to simulate periods of drought. In 2023, we conducted a proof-of-concept experiment with three soybean varieties. Results show that the resolution achieved with the ERT system installed in HYDRAS is sufficient to detect inter-variety below-ground differences. Drone-based phenotyping revealed differences in reflection patterns, leaf temperature and onset of senescence between the drought (sheltered) and control (irrigated) fields (Blanchy et al. 2025). By combining aboveground and belowground observations, HYDRAS is perfectly suited to identify important crop traits for breeding purposes and evaluate water-saving management strategies. HYDRAS (https://hydras.ilvo.be/en) is an open access facility available to research institutions and industry, supporting collaboration and data sharing. It aims to improve research capabilities in crop breeding and climate adaptation in Europe.

HYDRAS is funded by Emphasis-Belgium projects (I002121N, I001725N) and the Flemish Government's FutureAdapt project (VV028).

Blanchy et al. (2025). Closing the phenotyping gap with non-invasive belowground field phenotyping. Soil, 11, https://doi.org/10.5194/soil-11-67-2025

Poster location: S35

Decoding Plant Intelligence in Curved Space for Sustainable Agriculture

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Ensuring food security in global agriculture is critical for sustaining populations and promoting environmental resilience, yet it faces significant challenges due to increasingly variable and stressful environmental conditions. AI-assisted tools hold promise for providing deeper insights into plant responses to these conditions, but their efficacy is limited by the complex interplay of multifactorial data and the need to preserve the geometrical structure of plant-related datasets. In this work, we focus on visualizing and understanding large data sets generated during experiments with plant data. We use topological data analysis to understand these data. Drawing on the mathematical principle that concepts with broad interdisciplinary impact merit independent study, we reframe the traditional Euclidean-based agricultural monitoring problem, with its inherent constraints, as a manifold optimization task. We propose the hyperbolic Topological Data Analysis technique, referred to as Manifold Mapper, and denote it as HTDA-Mapper, a novel method that employs Poincaré space to visualize and analyze dynamic interactions among key variables: compound concentration, growth timeline, nutrition level, and compound type, to infer plant growth wellness. Applied to Arabidopsis thaliana under multifactorial stress conditions, our approach was validated using a dataset of >27,000 images, corroborated by expert agricultural analysis. The results demonstrate that HTDA-Mapper eliminates the need for labor-intensive post-processing, facilitates robust clustering of compound–concentration effects, and preserves the temporal and hierarchical structure of plant growth. This scalable framework offers significant advancements for phenomics, omics, and data-driven decision-making, paving the way for sustainable agricultural practices

Poster location: S36

The Irreplaceable Role of Field Phenotyping in Climate-Resilient Crop Development

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Buckwheat (Fagopyrum esculentum Moench) is increasingly gaining recognition as a climate-resilient crop that is well suited to low-input and organic farming systems due to its adaptability, nutritional value and relatively short growing cycle. As part of the H2020 ECOBREED project, a set of 53 different buckwheat accessions was evaluated under field conditions in Austria and the Czech Republic in three consecutive growing seasons (2019–2021). Standardized morphological descriptors were used to evaluate key traits including plant height, flowering time, 1000-seed weight as well as seed quality parameters such as protein content, antioxidant activity and polyphenol composition.

The field-based experimental design captured significant genotype-environment interactions, with notable differences in temperature and rainfall between years and locations significantly affecting both morphological and nutritional traits. For example, the accumulation of phenolic compounds such as rutin and epicatechin varied widely, with the highest rutin levels observed in years with increased environmental stress. This suggests that abiotic stress, particularly drought and heat, stimulates the synthesis of antioxidant compounds as part of plant defence mechanisms. This emphasizes the importance of evaluating genetic resources under real-world conditions to discover functional traits relevant to climate resilience.

Despite the inherent variability of field environments, such data provide a unique and irreplaceable basis for identifying stable and high-performing accessions. Furthermore, the study confirmed strong correlations between agronomic and biochemical traits, providing valuable insights for breeding programmes aiming to combine yield potential with nutritional quality.

These results highlight the urgent need to develop cost-effective, digital tools that can support real-time data collection and enhance traditional field evaluation methods. However, without reliable data sets from the field, the application of AI and other advanced digital phenotyping tools is severely limited. These technologies rely on comprehensive, ground-tested data to learn, validate and function in a meaningful way. In this context, field phenotyping is not only irreplaceable, it is fundamental.

This work was financially supported by the ECOBREED project, European Union’s Horizon 2020 research and innovation programme, grant agreement No. 771367.

Poster location: S37

Continuous optical dendrometry as a non-invasive indicator of grapevine drought resistance

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An increased risk of drought stress is a major constraint for plant productivity in wine-producing regions. For grafted crops like grapevine, rootstocks mitigate environmental stresses by improving rootstock x scion interactions choosing cultivars with rapid root growth, increased rooting depth, better hydraulic conductivity and adaptions to a variety of physical-chemical soil properties and biotic stresses. In our study, we evaluated drought responses of three commercial grapevine rootstocks: Börner, Selection Oppenheim 4 (SO4) and Vinto with continuous monitoring of stem diameter variability using low-cost Raspberry Pi optical sensors. We linked high temporal resolution RGB images with leaf reflectance to describe physiological and morphological traits associated to plant hydric status. Our time series analysis showed distinctive drought responses among rootstocks. Börner mean width stem areas were 2.95 mm and exhibited highly dynamic area fluctuations going above and below the overall rootstocks mean with rapid shifts during peak summer temperatures. Vinto mean width stem areas were 2.92 mm and maintained stable stem area across the experiment with an abrupt area decline towards the last three days of our experiment. In contrast, SO4 stem area was significantly smaller than those of Börner and Vinto (2.73 mm, $p < 0.05$). The dendrometry trends were confirmed by the leaves pigment content, as SO4 showed smaller chlorophyll content and NDVI, and largest flavonoid content compared Börner and Vinto. Furthermore, we found positive associations ($p < 0.05$) between stem width with chlorophyll content ($r = 0.59$), vegetation indices such as MCARI ($r = 0.83$), NDVI ($r = 0.67$), NPQI ($r = 0.67$) and SIPI ($r = 0.7$); and negative trends with flavonoid content ($r = -0.72$), NPCI ($r = -0.69$) and TCARI ($r = -0.55$). These findings suggest that rootstock water status can be linked to spectral signatures collected in the leaves, that vegetation indices are excellent proxies of rootstock drought responses and that chlorophyll and flavonoid associations highlight the role that physiologically active leaves can have to buffer drought effects. This study showcases the importance of integrated phenotyping approaches for drought phenotyping and demonstrates that continuous monitoring of plant traits can advance our understanding of genotype plasticity and adaptation to future climates.

Poster location: S38

High-Throughput Phenotyping Reveals Genotypic Variability in Wheat Responses to Elevated Night-Time Temperatures

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Global warming is characterized by an asymmetric increase in night-time temperatures, which poses a significant, yet understudied, threat to crop production. The presented study addresses the critical knowledge gap regarding the genotypic variability of wheat in response to elevated night temperature, a persistent stressor that can impact the entire crop cycle. To investigate this, we conducted controlled environment experiments using a high-throughput, automated phenotyping platform (PlantScreenTM). Ten wheat cultivars of different origin were subjected to either a control or a high night temperature treatment, where a custom-built chamber increased the ambient temperature by 3-4°C during the night, while daytime conditions remained identical for both groups. A suite of non-invasive imaging techniques, including RGB, chlorophyll fluorescence, and hyperspectral imaging, was used to continuously monitor plant growth, color, and key photosynthetic parameters from seedling emergence to maturity. The results revealed that elevated nighttime temperature significantly altered plant phenology. Treated plants exhibited accelerated development, reaching full leaf area and maximum photosynthetic efficiency more rapidly than controls. However, this was accompanied by a premature onset of senescence and a shorter overall growing season. As an important finding, we observed significant intervarietal differences in sensitivity, with some cultivars demonstrating markedly greater tolerance to night-time warming than others. These high-throughput findings were validated and supported by conventional measurements of photosynthetic rates and photoprotection-related parameters. In conclusion, our study demonstrates that high-throughput phenotyping is a powerful and effective approach for dissecting the complex physiological effects of elevated night temperatures on wheat. Applied methodology successfully identified genotypic variation in tolerance, providing a valuable tool for screening and selecting climate-resilient wheat varieties. The study was supported by the national grants APVV-22-0392, VEGA-1-0425-3 and VEGA-1-0048-25.

Poster location: S39

Identification of resistance to abiotic stress in potato varieties using a novel high-throughput in vitro phenotyping method

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Potatoes (Solanum tuberosum L.) are a staple food in many cuisines worldwide. Each year, around 380 million metric tons of potatoes are produced globally, and the value of their global market is estimated to be 120 to 140 billion USD, counting both fresh and processed products. To meet the rising global demand for tubers, plant breeders need to continuously develop new varieties with increased productivity and resilience against abiotic stressors, such as drought, salinity, or mineral imbalances. However, due to their long live cycles, the phenotyping and selection of the most promising varieties prior to their introduction in the market can be time-consuming. Moreover, their larger size compared to model plants like Arabidopsis makes them unsuitable for conventional high-throughput phenotyping (HTP) systems, highlighting the need for new approaches that address the specific requirements of modern biotechnology.

Here, we employed a novel high-throughput (HTP) method for in vitro potato plants in order to assess differences in intervarietal resistance to abiotic stress. Micropropagated potato plants were grown in 5 mL flat square tubes, which minimized optical aberration of the pictures, and subjected to either salinity or low nutrient availability. RGB images were obtained using a custom-built phenotyping chamber, equipped with LED light stripes, which ensured uniform image composition and lighting conditions. A set of Python scripts were used for automatic background removal, colour segmentation of images, and subsequent quantification of plant height and various colour indices. This setup allowed the rapid identification of varieties with varying levels of resistance to the selected abiotic stresses. This breakthrough technology will allow the simultaneous screening of many potato varieties and support the selection of genotypes based on their resistance to various abiotic and biotic stressors.

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Poster location: S40

Application of Image-Based High-Throughput Phenotyping to Assess Genetic Variation for Combined Drought and Heat Stress Tolerance in Chickpeas

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Climate change has intensified the occurrence of drought and heat stress, posing significant challenges to global agriculture. In arid and semi-arid regions, these stresses often occur simultaneously, highlighting the need for climate-resilient crop cultivars with combined drought and heat (DH) tolerance. Chickpea (Cicer arietinum L.), a legume valued for its high nutritional content and ability to thrive under low-input conditions, is a key candidate for such improvement.

Efficient phenotyping of chickpea plant genetic resources (PGR) is essential to assess the genetic variation available for breeding DH-tolerant cultivars. High-throughput phenotyping (HTP) systems offer a rapid and precise approach for evaluating dynamic traits related to DH tolerance.

In this study, 200 single-seed descent-derived chickpea genotypes from the INCREASE T-Core diversity panel (Rocchetti et al., 2022), consisting of an equal number of kabuli and desi types, were evaluated using an RGB image-based HTP system. Plants were subjected to DH stress followed by a recovery phase under optimal conditions. The 61-day experiment spanned from early vegetative to early reproductive stages, with final yield parameters collected at maturity outside the platform.

The study aimed to: (i) assess the impact of DH stress on chickpea growth, physiological, and reproductive performance, and (ii) compare the responses of kabuli and desi types under DH stress. Traits such as biovolume, projected area, plant height, fluorescence-based indicators, and colour-related parameters were recorded using the HTP system, while yield traits and final plant height were measured manually at maturity.

Preliminary results revealed that DH stress significantly reduced growth performance, particularly biomass accumulation, plant height, and canopy area. The red-to-green colour ratio exhibited considerable genotypic variation under stress, suggesting its usefulness as a selection trait for breeding. Desi type showed a higher proportion of brown and yellow pixels under DH stress compared to kabuli, potentially reflecting a stress protection strategy. Photosynthetic efficiency, measured by the operating efficiency of photosystem II (ΦPSII) and maximum quantum yield (Fv/Fm), declined under DH stress but recovered under optimal conditions. Notably, desi types were less affected in terms of ΦPSII, indicating a greater capacity to dissipate excess excitation energy than the kabuli type.

Poster location: S41

Active and Passive Chlorophyll Fluorescence Sensing to Access Photosynthetic Traits

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Measuring photosynthesis at field remains a challenge, as it requires resolving both rapid physiological dynamics and structural effects at multiple spatial scales. Chlorophyll fluorescence is known as a promising sensitive and non-invasive proxy for probing photosynthesis. Several fluorescence measurement protocols exist to retrieve physiological traits.

Passive fluorescence measurement (SIF) relies on sunlight as the excitation source. It is already used by the remote sensing community to measure at large scale. In particular, the upcoming ESA FLEX mission aims to retrieve chlorophyll fluorescence from space to monitor vegetation function globally. However, SIF interpretation is limited due to its strong dependence on the canopy structure. As a result, the use of SIF measurements as a direct indicator of photosynthetic efficiency at the canopy scale is questionable. A better understanding of SIF could open new possibilities for satellite-based phenotyping.

Active fluorescence measurements are characterized using artificial light sources for excitation. Modulation of the light source allows the application of illumination protocols like OJIP, PAM and FRR. They provide access to physiological traits often used as proxy of the larger scale response. Active fluorescence is usually performed with leaf clips, limiting its ability to represent canopy-scale physiology due to low spatial coverage.

By combining both technique with 3D canopy structural measure, it becomes possible to disentangle physiological signals from structural effects. It enables the retrieval of more accurate, spatially resolved photosynthetic phenotyping traits across heterogeneous canopies such as light use efficiency (LUE) and photoprotection capacity.

We present here a system able to measure both passive and active chlorophyll fluorescence at canopy scale and organ-level resolution. The system combines a LiDAR, a 3D canopy camera, and a solar induced fluorescence imager which can be integrated on phenotyping platform. First measurements were conducted in controlled environment on maize, showing detectable diurnal variation in fluorescence yield. A field campaign is underway on maize try, at PhenoField a plein field Platform of PHENOME-EMPHASIS, to evaluate the system's ability to measure outdoor and produce physiotyping traits at field. This work aims to provide tools to make the chlorophyll fluorescence used, useful and usable for the high throughput physiotyping.

Poster location: S42

Objective real-time biotic stress quantification using RGB images and deep learning models

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Plant phenotyping is a cornerstone of modern agricultural research, providing critical insights into plant growth and development in relation to external stresses, such as the presence of pest insects and/or plant diseases. To objectively compare the experienced biotic stress of these insects/pathogens across experiments and time, a frequent, non-destructive and objective quantification method is needed. Therefore, an objective real-time pest/disease biotic stress quantification method, which tracks the infected plant area over time, was developed using RGB images and recent deep learning models. The common ornamental plague Tetranychus urticae (spider mite) and disease Golovinomyces orontii (powdery mildew) were selected as biotic stressors.

To construct a heterogeneous and balanced RGB image dataset, two species of young Hedera plants (Hedera helix and Hedera hibernica) were mixed and evenly split into a control and an infected group (112 plants/group). Using previously infected Hedera plants, the latter group was subsequently inoculated with spider mites. Both groups were cultivated over summer in separate greenhouses at Viaverda (Destelbergen, Belgium). Analogously, two groups of one Viola cultivar (variety ‘Cool Wave’ | 50 plants/group) were created: a control group and a group infected with powdery mildew. Over the course of several weeks to months, all plants were weekly photographed using a high-resolution (42 MP) DSLR-camera with macro lens inside a white light-controlled phenotyping cabinet. All images were subsequently corrected (white balance and lens correction), split into smaller image patches (320x320 pixels | pixel resolution: Viola = 60 µm; Hedera = 70 µm) and manually labelled based on the presence or absence of pest/disease symptoms. Next, a balanced dataset of 1,000 labelled image patches per pest/disease type was homogeneously selected across all acquisition dates and split into 70% training, 15% validation and 15% testing data. Apart from this, also an additional independent test dataset was gathered using independent plant images across all acquisition dates. Lastly, various small size YOLOv11 classification models were trained per pest/disease type using Python and tested on both the original and independent test datasets. Future research should focus on including more biotic stressors, a quantitative evaluation of stress severity and other imaging techniques such as multispectral or chlorophyll fluorescence.

Poster location: S43

Phenotypic Profiling of Waterlogging responses : An Image-Based Study of Barley Accessions under controlled conditions

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Climate change projections indicate an increasing frequency of waterlogging due to intensified rainfall, severely impacting barley yield, as the most waterlogging sensitive cereal, by limiting soil oxygen and disrupting plant development. This study aims to assess the waterlogging tolerance 10 barley genotypes (seven 2-row and three 6-row) in controlled glasshouse conditions. We employed image-based phenotyping, to quantify the physiological effects of waterlogging on growth, greenness and plants' health status throughout barley life cycle. We used top down and side view RGB (Red-Green-Blue) images, as well as VNIR images from a top-down Hyperspectral camera on the PSI PlantScreen™ platform, using a protocol of 14 days of waterlogging, followed by 7 days of recovery time, and weekly imaging profiling. Additionally, final productivity and its components were measured. Waterlogging drastically affected all image-based growth and health traits, suggesting a longer recovery period (14 days) is needed for comprehensive assessment. Flowering was delayed by an average of 5 days in most accessions, though GDB-0572 and Refsum flowered faster under stress. Overall, waterlogging reduced productivity by a mean of 56% and plant height by 23%, alongside decreases in total dry weight, spike length, and seed number. Using an overall performance stress score incorporating productivity, plant height, and total dry weight from both treatments, we classified genotypes based on their waterlogging response. Accessions Refsum and Olli emerged as waterlogging tolerant, representing valuable genetic material for breeding schemes aimed at the development of barley waterlogging tolerance, mitigating one of the future climate major yield constraints.

Poster location: S44

Selecting drought-tolerant ‘crioulo’ common beans through root phenotyping

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Climate change has significantly increased plant stress levels, with drought being one of the most critical abiotic stresses limiting crop productivity. Root system architecture (RSA) plays a crucial role in drought adaptation; however, it remains an understudied trait. Phenotyping studies can help our understanding of crop ecophysiology and abiotic stress resilience by establishing a connection between root architecture and drought resilience. The common bean (Phaseolus vulgaris L.) is one of the oldest cultivated plants in the world and holds great economic and social importance in many parts of the world. ‘Crioulo’ common beans are ancient landraces cultivated by farmers, and represent a valuable source of genetic diversity, putatively for drought tolerance. Our objective was to implement a simple and cost-effective root phenotyping methodology based on 2D-RSAT to select ‘crioulo’ common bean accessions with resilience to drought stress.

A total of 12 ’crioulo’ accessions from Brazil were grown semi-hydroponically in germination paper pouches under control (water) and drought stress (PEG; -1,5 bars) conditions for eight days under a 16h/8h (25 ± 1°C). At the eighth day of experiment, root images were acquired, pre-processed and analysed using the RootNav software to extract key parameters, including total length of the root system, average length of all roots, average length of lateral roots, lateral root count and the length of primary root. Root and shoot weight were also determined.

Differences in root parameters were observed between the two treatments, indicating that RSA is affected by drought stress. An integrate analysis of all evaluated parameters allowed the classification of accessions according to different levels of drought resilience, with three accessions identified as highly tolerant. This root phenotyping study demonstrates that the use of innovative technology (digital imaging) to identify ‘crioulo’ common bean accessions resilient to drought stress is a robust approach. These results provide valuable data to support breeding programs focused on improving drought resilience in grain legumes.

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Poster location: S46

Hyperspectral Phenotyping of Genetic Diversity in Scots Pine (Pinus sylvestris L.): Spectral Insights into Forest Resilience Across Environmental Gradients

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Scots pine (Pinus sylvestris L.) is a foundation species in European forest ecosystems, where its resilience to increasing biotic and abiotic stresses is critical under changing climate conditions. Yet, the physiological basis of its adaptive potential remains poorly characterized. Understanding intraspecific variation in key functional traits is essential for identifying genotypes capable of coping with environmental pressures.

In this study, we combined hyperspectral phenotyping with genomic data to assess needle functional traits (NFTs) linked to foliar structure, water regulation, and pigment composition—traits closely associated with stress tolerance. Measurements were conducted across two growing seasons in clonal seed orchards using high-resolution hyperspectral sensing at needle and canopy levels, integrated with genotyping via a newly developed 50K SNP array. Linear mixed models revealed considerable genetic variation, with heritability estimates reaching 0.38 for structural and water-related traits, and up to 0.29 for pigment ratios such as carotenoid-to-total-chlorophyll—an indicator of oxidative stress response.

Significant genetic correlations between stress-relevant NFTs and canopy-level reflectance highlight the potential of spectral data as a scalable proxy for selecting resilient genotypes. Low genotype-by-environment interactions and stable clonal performance across years further support the robustness of these traits for long-term adaptive breeding.

Our findings underscore the utility of hyperspectral phenotyping and NFT-based selection for accelerating the identification of Scots pine genotypes with enhanced resilience to drought, heat, and pathogen pressures—offering a powerful strategy to support forest adaptation in the face of intensifying environmental challenges.

Poster location: S47

Assessing the response of lentil genotypes to progressive drought stress under a highthroughput phenotyping lysimeter platform in Morocco

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Lentil (Lens culinaris Medik.) is a cool-season legume with high nutritional, agronomic, and environmental value. It is a rich source of dietary fiber, complex carbohydrates, high-quality proteins, and essential micronutrients playing an essential role in food and nutritional security. Lentil is crucial for sustainable agriculture because of its capacity to fix atmospheric nitrogen, which improves soil fertility and lessens the need for chemical fertilizers. However, drought and heat stress compromise lentil productivity, especially under current climate change scenarios. Therefore, the selection of genotypes adapted to these stresses is important to improve and stabilize lentil productivity. The objective of the current study is to investigate the genetic variation for drought tolerance among 45 lentil genotypes, including varieties, landraces and interspecific advanced lines. The experiment was conducted at INRA-ICARDA's Precision Field Phenotyping Platform at Sidi El Aidi INRA Morocco experimental station which includes an automated lysimeter system (PhysioTron) allowing regular pot weighting and irrigation according to preset parameters for the calculation of the amont of water to add for each pot for the estimation of transpiration in a dynamic way. Regular data acquisition from LIDAR sensor and a Multispectral camera allowed the estimation of some plant canopy parameters. In addition, several morphological and phenological traits were assessed. Following initial field capacity maintenance at 100%, plants were subjected to two stress levels: 40% at 52 and 20% at 78 days after sowing. The results indicated that early flowering is a drought and heat stress-adaptive trait. Late flowering genotypes were adversely impacted by drought and high temperature. Among tested genotypes three interspecific advanced lines and the Moroccan cultivars "Chakkouf" "Extra" and "Bakria" performed better under increasing water deficit. The cultivar "Bakria" produced the highest grain yield and could be recommended for drought-prone environments.

Poster location: S48

High-Throughput Phenotyping Enables Comprehensive Analysis of Stomatal Morphology

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Limited data on stomatal morphology across environments constrain our understanding of genotype–environment interactions, despite stomata's critical role in regulating plant water use and gas exchange under varying light, temperature, and water stress (WS). To address this gap, we used high-throughput handheld microscopy (ProScope H5) to phenotype stomatal morphology across more than 50 winter wheat genotypes grown in growth chamber (GC), greenhouse (GH), and field conditions, generating ~27,300 images. We investigated the effects of light, temperature, and WS on stomatal traits across adaxial (AD) and abaxial (AB) surfaces of 3rd, 6th, and flag leaves. To facilitate large-scale phenotyping, we developed a YOLOv8-based detection pipeline trained on 560 annotated images and optimized to improve the detection of blurred and partially visible stomata achieving a mean average precision (mAP) of 0.78 and a root mean square error (RMSE) of 0.002 mm^2 of objects sizes using 240 validation images. This enabled the extraction of 12 traits per image that incorporate various measurements related to size, variation, coverage related traits and traits describing stomatal spatial patterning. Across all environments, stomatal density (SD; stomata count per μm^2) was consistently higher on the adaxial (AD) surface than the abaxial (AB) surface, with median values of 71.3 and 53.6 under field condition, 67.3 and 48.8 (high light/temperature), while the lowest SD were 31.9 and 20.3 (low light/temperature). This pattern suggests an adaptive strategy to optimize gas exchange, particularly under stressful high light/temperature conditions. In addition, the correlation between SD on AD and AB surfaces was strongest (r=0.85) under high light/temperature but weakest under WS (r=0.44), indicating surface-specific regulation to balance stomatal demand and minimize water loss. Broad-sense heritability (H^2) estimates for size-related stomatal traits—including stomatal length, width, and coverage—were high across both field and GC environments (0.83 to 0.94), indicating strong genetic control over these traits. In contrast, H^2 of these traits dropped sharply under WS (0.12 to 0.37), reflecting increased environmental influence on size-related traits under WS. Leveraging this trait variation could support breeding wheat cultivars with improved stomatal adaptability for sustainable production under climate stress and maintain productivity in resource-limited environments.

Poster location: S49

Development of a rapid field-laboratory method to assess wheat freezing tolerance and acclimation level during winter

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Climate change poses major challenges for wheat cultivation to maintain high and stable yields. Progress needs to be made to accurately characterize the phenological development of future wheat varieties. Ideally, a wheat variety well adapted to a certain environment should show a high tolerance to abiotic stresses, particularly during phases at which the stress of interest is most likely to occur. Among these, freezing temperatures can cause significant damage. As winters become milder, the timing and intensity of freezing events may change. This shift requires breeders to adjust the varieties to these new conditions, but they must also balance improved growth with frost tolerance in case of extreme events (e.g. sudden drop in temperature affecting non-acclimated or deacclimated plants, or absence of snow cover usually insulating plants from very low temperatures).

We aim to develop a field-to-laboratory protocol to assess the freezing tolerance of field-acclimated plants. The main purpose of this protocol is to calibrate our field imaging methods established in the Field Phenotyping Platform (FIP) at Eschikon (Switzerland). Using the platform, we aim to monitor canopy cover development throughout winter and to quantify leaf damage. To assess winter hardiness independently of actual freezing conditions in the field, a diverse set of 12 winter and facultative wheat varieties was sampled during the season 2024-2025. Leaves were collected throughout the winter, aligned on plates, and gradually frozen at temperatures ranging from -3 to -24°C. Fluorescence Quantum Yield (QY) was recorded before and after freezing to estimate frost damage. The values collected for different freezing temperatures should make it possible to calculate an LD50 value for each genotype.

The data will help us track changes in frost tolerance as a function of climatic conditions and provide indirect insight into the processes of acclimation and de-acclimation of different varieties. Here we present the preliminary results from the first season of leaf freezing tests.

Poster location: S50

Harnessing High-Throughput Phenomics and Root Architecture Analysis to assess the drought response of Tunisian durum wheat varieties

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Climate change is projected to intensify drought stress, which is one of the major limiting factors for crop productivity around the globe. Wheat is worldwide cultivated to provide staple food for the growing population and is among the most economically, ecologically, and socially important cereal crops in Mediterranean agriculture. Addressing these challenges requires the development of drought-tolerant wheat varieties with shorter breeding cycles. This objective can be achieved through the integration of advanced breeding strategies with high-throughput phenotyping (HTP) technologies.

This work conducted in the framework of the European Twinning project INPLANTOMICS, aims to study the response of several Tunisian durum wheat varieties to drought stress. To this end, we leveraged the high-throughput phenotyping platform at Helmholtz Zentrum München (HMGU), to perform a comparative analysis of biomass accumulation under both control and drought conditions, alongside physiological measurements such as carbon content, nitrogen content (N), and carbon isotope discrimination ($\delta^{13}C$) to estimate intrinsic water use efficiency (iWUE) as a proxy for drought tolerance. In addition, root architecture analysis has been initiated using RootPainter as an image annotation tool followed by root image analysis using the Rhizovision platform. Overall, the data presented revealed genotype-specific effects of water stress, with the landraces seemingly outperforming the breeding lines. This comprehensive analysis lays the groundwork for identifying key genes controlling the apparent phenotypic plasticity of Tunisian durum wheat varieties under drought stress.

Poster location: S51

Sensing the dynamic response of photosynthesis to abiotic stressors with oscillating light

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Fluorescence emission from chlorophyll a (ChlF) is extensively used as a proxy to study photosynthesis in plants and monitor its performance. The most common methodologies adopt Pulse Amplitude Modulation (PAM) fluorometers and the saturation pulse method to measure ChlF parameters related to photosystem II activity. For measurement of stress-related parameters such as Non-Photochemical Quenching (NPQ), this approach requires initial measurements in a dark-adapted state, which is not always feasible in greenhouse or field conditions. To overcome this limitation, we established novel experimental protocols based on a frequency-domain analysis approach. This method allows to investigate photosynthesis dynamics in light-adapted states by applying actinic light that is forced to oscillate at specific frequencies and amplitudes. Here, we demonstrate the utility of dynamic ChlF signature emerging in oscillating light, without dark adaptation, to detect stress and acclimation responses of plants exposed to high temperature and/or high light.

The ChlF measurements were performed with a novel macroscopic fluorescence imager on plants exposed to four different treatments: control, high temperature, high light, and combination of high temperature and high light. All treatments had a duration of three days, and measurements were conducted at a specific timepoint daily. First, light saturation coefficient (Ek) was determined for each treatment and day based on the light-response curve of relative photosystem II electron transport rate. Subsequently, frequency scans were performed between 1/128 Hz and 1 Hz by applying oscillating light with the mean light intensity of 2.5 Ek to assess the frequency response of photosynthesis in a light-saturated state. The oscillation amplitude was kept at ± ¼ Ek. The obtained ChlF data were analysed with the Fast Fourier Transform to extract amplitudes and phase shifts, and by plotting these as a function of oscillation frequency (Bode diagrams). Furthermore, we explored the potential of machine learning algorithms to categorise ChlF fingerprints of the different treatments. The results from Arabidopsis thaliana and tomato will be presented and discussed.

Poster location: S52

The IPSA high-throughput plant phenotyping platform, delivering services from experimental design to plant trait extraction at large scale.

Bart Van Gansbeke; Stijn Dhondt

VIB

The VIB Agro-Incubator has developed a high-throughput phenotyping pipeline to support large-scale plant research and innovation. The Integrated Phenotyping Platform for Sustainable Agriculture can accommodate over 1,920 large plants or up to 20,000 small plants, enabling scalable and reproducible experimentation. Pot size is dependent of the crop size and length of the experiment.

The platform follows a fully integrated, project-based workflow, beginning with a tailored experimental design aligned with the client's research goals. It supports both automated phenotyping and combined treatment studies, including spray applications of biostimulants, novel compounds, and herbicides.

The camera system consists of high-resolution cameras covering both front and top imaging for morphological feature extraction, including root imaging for small plants. Hyperspectral imaging and high-resolution multispectral imaging across six channels enables detailed spectral analysis of plant traits. Image processing is handled by in-house developed software that extracts phenotypic features from RGB and multispectral data.

The pipeline also includes specialized data analysis tools for efficient data management and interpretation, resulting in a comprehensive report. Typical projects involve population screening or assessing abiotic stress, such as drought tolerance assays and nutrient deficiency tests. The IPSA pipeline demonstrates the platform's versatility in addressing the challenges posed by climate change in the agricultural sector.

Poster location: S53

Applications of drone-based estimates of canopy temperature in the evaluation of wheat and soybean varieties

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Canopy temperature (CT) is a key indicator of the relative fitness of crop genotypes to their environment and is correlated with several primary traits. It has been proposed as a method for phenotyping stress tolerance in field crops. Thermal cameras mounted on drones can measure large experiments quickly. However, confounding effects limit the interpretability and applicability of the results of these surveys. These confounding factors include thermal drift, spatial field trends, viewing geometry, and changing environmental conditions.

We evaluated several protocols for collecting and analyzing thermal images from drones in two winter wheat variety performance experiments during two consecutive growing seasons (2020–2021 and 2021–2022) in Switzerland. The trials comprised more than 30 modern registered European winter wheat varieties and candidate lines for inscription in the Swiss list of recommended wheat varieties. Soybean variety trials were conducted over three years.

In winter wheat, a mixed model approach that accounted for temporal drift and viewing geometry by including temporal and geometric covariates improved the consistency and genotype specificity of CT measurements compared to approaches relying on orthomosaics. The correlations between measurements from different flights at intervals of no more than 30 minutes reached 0.99, and heritabilities were 0.95. Applying this approach to 99 flights showed that confounding factors could be statistically accounted for, and on average, more than 96.5% of the variance could be explained. Accounting for these confounding factors led to sound conclusions about phenotypic correlations of CT with traits such as yield, plant height, and fractional canopy cover.

In soybean, which was exposed to more severe drought and heat stress conditions, strong correlations were found between CT and ground assessments. Measurements were consistent regardless of the sensors used (Flir ZXT and Micasesne Altum) and across different assessment periods.

Based on extensive and diverse data, we developed protocols to collect high-quality CT measurements using drones for variety testing, breeding, and field crops research.

Poster location: S54

IN-FIELD HIGH-TROUGHPUT PLANT PHENOTYPING TO STUDY THE IMPACT OF WOOD VINEGARD ON SAFFLOWER RESPONSE TO WATER LIMITATION

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In the last year the Institute for Sustainable Plant Protection (IPSP) of the National Research Council of Italy (CNR) has developed a novel and comprehensive phenotyping Research Infrastructure (RI): the Digital Ecosystems for MEtabolomics, plant Trait Research, and Imaging Systems-Hub (DEMETRIS-Hub). This RI includes a range of state-of-the-art platforms as well as advanced field-based systems, offering an integrated approach to plant phenotyping. In this contribution, we present the first results obtained using the DEMETRIS-Hub RI to evaluate the effects of wood distillate (WD, also known as pyrolytic acid or wood vinegar) on safflower (Carthamus tinctorius L.).

WD, a byproduct of the pyrolysis process of lignocellulosic matrices to produce biochar and syngas, is considered a green alternative to synthetic chemicals in agricultural production. Owing to its content of bioactive compounds, particularly phenolic derivates, WD can function as a root biostimulant, promoting plant growth, improving nutrient availability in the soil, and increasing tolerance to abiotic stress.

To this end, an open-field experiment was conducted at the ALSIA Metapontum Agrobios in Metaponto, Southern Italy, to investigate the interaction between two irrigation treatments (well-watered and suboptimal) and fertirrigation with two WDs and a tannin-enriched extract on the physiology and productivity of safflower plants (cv. CW99OL) compared to control plots irrigated with water only. To achieve a full factorial design, each plot was subdivided into two subplots to apply the different irrigation regimes, enabling assessment of their interaction. Throughout the experiment, remote and proximal sensing measurements were performed to monitor plant physiological performances. Finally, qualitative analyses will be conducted on the oil extracted from the seeds.

The results explore the potential utilization of WDs and tannin extracts in agriculture, suggesting a possible reduction in the use of chemical fertilizers and, consequently, a lower environmental impact. At the same time, these findings support the development of a circular economy supply chain aimed at producing high-value crops rich in bioactive compounds for multiple industrial applications.

Project Funded by Missione 4, Componente 2, Investimento 1.4: “National Research Centre for Agricultural Technologies (Agritech)” - Spoke 8 Circular economy in agriculture through waste valorisation and recycle

Poster location: S55

NON-DESTRUCTIVE ASSESSMENT OF THE PHYSIOLOGICAL STATUS OF WHEAT MUTANT LINES IN THE OPEN FIELD

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The productivity of wheat (Triticum aestivum L.) is increasingly challenged by global climate change, particularly rising temperatures and drought stress. Enhancing stress resilience through conventional breeding is limited by the complex nature of abiotic stress tolerance, making the development of innovative breeding strategies to overcome these challenges a global priority. Accordingly, winter wheat variety NS40S developed at the Institute of Field and Vegetable Crops in Serbia was chosen for production of mutant populations to potentially improve abiotic stress tolerance and yield. Within the project RER/5/024 “Enhancing productivity and resilience to climate change of major food crops in Europe and Central Asia” 2000 seeds were exposed to the dose of 210 Gy gamma irradiation in the International Atomic Energy Agency (IAEA), in 2021. The obtained M0 seeds were sown in a bulk at the experimental field at location Rimski Šančevi, Serbia, in 2021/22 growing season, and during the 2024/2025 growing season M4 generation, comprising of 200 lines, was obtained. The aim of this study was to assess physiological status of 50 mutant lines and variety NS40S by using non-destructive portable devices. For measurements of chlorophyll, flavonols, anthocyanins and nitrogen balanced index, optical leafclip meter DUALEX was used. Normalized Difference Vegetation Index was determined with GreenSeeker crop sensor. ANOVA showed significant differences between lines regarding analyzed parameters. Lines were separated into different groups using PCA whereby a certain number of lines were grouped together with the variety NS40S, while the other lines were in distinct groups, which may be a consequence of the effects of gamma irradiation. These results, as indicators of photosynthetic activity, health status of plants and stress response, coupled with further analysis of yield components and quality will be used for selection of new high-yielding varieties with enhanced abiotic tolerance.

Poster location: S56

Spectral Reflectance Indices as proxies for pigment composition in spring wheat under drought and heat stress.

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Leaf pigment composition is closely associated with photosynthetic capacity, stay greenness (chlorophylls), and with photoprotection from excess light (carotenes and xanthophylls), which increases under abiotic stresses. Both stay greenness and photoprotection are desirable traits, providing tolerance to drought and heat stress. Phenotyping pigment composition can be approached by using Spectral Reflectance Indices (SRIs) as a non-destructive and high-throughput phenotyping (HTPP) tool. However, SRIs must be validated against actual leaf pigment concentrations to be effectively incorporated in breeding programs for drought and heat stress resilience. Sixteen spring wheat lines selected from the Best Physiological Traits Panel developed by CIMMYT were grown in the field in North-west Mexico during three consecutive seasons under well-watered, drought, and heat stress conditions. Seeds were planted in late November to early December for the control and drought treatment. Control plants were irrigated throughout at regular intervals, and drought was imposed by irrigating at sowing and at 50% seed emergence. Heat stress was imposed by sowing in late February to early March, and irrigation was as in the control. Reflectance data were collected at 0.5 m at the nadir of the canopy with an ASD Field Spectroradiometer at the heading and grain filling stage. Leaf samples were taken, frozen in liquid nitrogen, and pigments quantified by HPLC. Significant effects of genotype, treatment, growth stage, and the interaction with growth stage were observed for SRIs related to carotenoids, crop water status, wax, and chlorophyll-related indices. Genetic variability in chlorophylls and carotenoid composition was detected. Heat and drought increased leaf carotenoid concentrations, xanthophyll pool size, and their de-epoxidation state, but the increase was higher under heat stress than under drought. We found strong linear associations between carotenoids and chlorophyll-related SRIs and the actual pigment composition derived from HPLC analysis at both stages and treatments. Our results suggest that SRIs have the potential to be used as a reliable HTPP platform for assessing pigment composition and their response to heat and drought in wheat, as they could detect genotypic variability, were responsive to stress conditions, and were closely correlated to actual leaf pigment composition.

Key words: High-throughput phenotyping, photoprotection, climate change, photoinhibition

Poster location: S57

Automated Detection of Fusarium Head Blight symptoms on wheat ears using Deep Learning on field RGB imaging

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Fusarium head blight (FHB) is a fungal disease that affects various cereal species worldwide, and particularly winter wheat (Triticum aestivum L.). Infection by Fusarium species Discolor section leads to significant yield losses and can result in the production of mycotoxins, which are harmful to human and animal health. Currently, as part of the registration process for varieties in the European Catalogue, field resistance to FHB is mainly assessed through visual observations by expert evaluators. This process can be time-consuming due to the large number of varieties to be evaluated across a multi-site network. With the launch of the European Phenet project, an innovative method based on RGB imaging has been developed by GEVES to automate and enhance the evaluation of winter wheat resistance to FHB in field conditions. Approximately 3,000 images of wheat ears, with and without symptoms, were acquired between 2021 and 2024 by CRA-W, GEVES, and Agroscope, at various phenological stages on different winter wheat varieties using several RGB imaging devices (camera, smartphone, Literal stick). These images were used to train a deep learning model specifically designed to detect Fusarium head blight. The model accurately identifies and quantifies infected areas on wheat ears, providing an infection FHB percentage for each tested variety. From this dataset, 1,113 images were annotated using Roboflow. Annotations were carried out using three methods (manual, semi-automatic, and automatic) for two classes: healthy ear / FHB-infected ear. Two modelling approaches were tested: the first one was based on a binary classification model distinguishing healthy and FHB-infected areas and the second involving preliminary detection of wheat ears using the model from the Global Wheat Challenge 2021. In both cases, a deep learning model (YOLOv8) produced strong correlations (> 0.8) between FHB predictions and field visual scores. This study aims to validate the use of RGB images and deep learning as an alternative to manual counting for classifying varietal resistance to FHB for breeding and registration in the European Catalogue. It opens the way for automated and objective monitoring of varietal resistance, potentially accelerating the breeding process while reducing the workload for experts. The next steps will involve transferring or adapting the methodology to other cereal crops for detecting other ear diseases or foliar diseases.

Poster location: S58

EXPLORING THE POTENTIAL OF WHEAT LANDRACES FOR DROUGHT RESILIENCE: A SCREENING OF MORPHOPHYSIOLOGICAL TRAITS

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Bread wheat plays a key role in ensuring food security, as it is the most widely cultivated crop globally. While early innovations, such as selective breeding and the introduction of reduced-height genes during the Green Revolution, dramatically increased yields, today's climate challenges, particularly the rising frequency and intensity of droughts, are causing significant yield reductions. The most promising strategy to mitigate these challenges is the development of wheat varieties with high and stable yields across variable environments. It is estimated that the vast genetic diversity stored in genebanks, particularly landraces, represents a valuable source of alleles associated with drought tolerance. However, their use in developing new varieties has been limited, primarily because pre-breeding is both time-consuming and costly. In addition, much of the material conserved in genebanks remains poorly characterized. Recent advances in plant phenotyping and genotyping have led to the development of innovative breeding approaches that facilitate the more efficient use of genetic resources. In this context, 38 Serbian hexaploid wheat landraces were evaluated under rainfed conditions during the 2024/25 growing season at the experimental trials at Rimski Šančevi, Serbia. The evaluation was conducted at three growth stages, using 14 traits associated with yield and water use efficiency. Meteorological data were recorded, and the following non-destructive phenotyping devices were used: the LI-600 porometer/fluorometer, the DUALEX optical leaf clip meter, and the Literal sensor (Hiphen). ANOVA revealed statistically significant differences among landraces for the analyzed traits, enabling the identification of promising candidates for further high-throughput phenotyping under drought conditions using advanced platforms.

Key words: climate change, drought, wheat landraces, phenotyping

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Poster location: S59

Hyperspectral Imaging: A Non-Invasive Approach for High-Throughput Monitoring of Plant Responses to Various Treatments

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In the pursuit of sustainable agriculture, the need for innovative monitoring techniques has never been more critical. Hyperspectral imaging emerges as a powerful tool, enabling the non-invasive observation of plant responses to various treatments. This cutting-edge technology allows researchers to detect non-visible, early, and subtle effects that traditional methods may overlook, providing a comprehensive understanding of plant health and development. By supplementing existing techniques such as RGB and fluorescence imaging, hyperspectral imaging enhances our ability to assess the physiological status of plants. It facilitates precise measurements of pigments content, water content, and structure characteristics which are essential indicators of plant vitality and stress response. Integrating hyperspectral imaging within automated greenhouse systems, coupled with an automated analysis pipeline, streamlines the monitoring process and significantly increases efficiency and throughput. This advancement not only supports researchers and agronomists in making informed decisions but also paves the way for a more sustainable agricultural future. Join us in exploring how hyperspectral imaging can revolutionize plant monitoring and contribute to the sustainable agriculture of tomorrow.

Poster location: S60

Development of deep learning models to detect Barley Yellow Dwarf Virus in barley using RGB images

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GEVES

Following the withdrawal of neonicotinoids, the genetic resistance of barley varieties to the aphid-borne Barley Yellow Dwarf Virus (BYDV) has become a key factor in the development of new cultivars. To support the phenotyping of BYDV-tolerant varieties for registration in the French Catalog, GEVES aims to develop robust artificial intelligence models using RGB images to replace traditional visual scoring in the field.

As part of the European Phenet project (2023-2027), within the “Plant Health” use case, GEVES has explored the development of deep learning models to detect BYDV in barley using RGB images. This work presents an automated pipeline based on deep learning techniques to replace conventional visual scoring methods.

RGB images of barley cultivars were acquired in BYDV-infected fields using a zenithally positioned RGB camera mounted on a 1.80 m literal stick, achieving a resolution of approximately 0.55 mm/pixel. For each plot, one or two images were collected.

A total of approximately 2,700 images were collected over four campaigns (2021–2024). Each image underwent a preprocessing pipeline that included cropping, normalization, brightness adjustment, rotation, contrast enhancement, and flipping. Three annotation strategies were explored on a subset of 569 images: manual, semi-automatic, and automatic.

Two deep learning models were independently trained:

- YOLOv11: for instance segmentation into two classes (‘healthy’ and ‘BYDV’), using annotated masks, providing fine-grained detection.
- ResNet18 CNN: for classification into five severity levels (from 1: no symptoms to 9: severe mortality), based on expert visual scoring, without requiring pixel-level annotation.

Both models demonstrated strong performance. YOLOv11 achieved a high mean average precision (mAP ≈ 0.8) and bounding box precision up to 0.88. The ResNet18 CNN also yielded high precision (P = 80%) and showed strong predictive capability for field-based scoring, with an R^2 of 0.94.

The results indicate that YOLOv11 is well-suited for detection and quantification of infection, while ResNet18 offers advantages in speed and does not require annotation.

Future work (2025–2026) will focus on testing these models under more diverse conditions and integrating them into broader initiatives to support scalable, automated plant health assessment.

Poster location: S61

Assessing fruit tree vigor in peach and apple orchards through wood segmentation in ground-based RGB images

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Vigor is an important trait for fruit tree breeding and orchard management, representing annual tree growth. Vigor is classically assessed measuring, once a year, trunk circumference manually, which is slow, laborious and potentially with low reproducibility. In this study, we propose a high-throughput phenotyping method that combines RGB imaging and deep learning to segment woody parts in fruit trees in the absence of leaves. Difference in the segmented wood area, before and after shoot pruning, could be seen as a proxy of vigor, here defined as the wood biomass loss after pruning.

A dataset of 2,278 RGB patches of 512x512 pixels was collected, including several tree species, years and sites. These images were mostly acquired using a LITERAL light phenotyping system under natural light, or the PHILOMENE unmanned ground vehicle under active illumination (flashes). Both LITERAL and PHILOMENE do stereovision, which allows the distance camera/scene to be computed in every pixel. Wood pixels were manually annotated in every patch, and seven UNet-based models were trained to segment woody parts. These models were trained using either original images or images enhanced with artificial flash effects or a combination of both. These flash effects were proposed as a solution to decrease the background influence and to improve the consistency between LITERAL and PHILOMENE images. These effects were simulated using depth maps derived from the IGEV stereovision algorithm. The best model was the one based on enhanced images only, and, when tested on independent test datasets, it achieved F1 scores of 0.93 on LITERAL images and 0.88 on PHILOMENE images.

These segmentation results were then used to estimate pruned wood biomass. In January 2025, PHILOMENE images were acquired before and after pruning on 36 peach and 37 apple trellised trees planted in 2023 in Avignon, France. Wood pixels were segmented and the ones belonging to the central tree in the image that was detected using a YOLO model were kept to calculate the projected wood area. Differences in wood area before and after pruning showed strong linear correlations with experimentally measured weights of pruned branches for apple ($R^2 = 0.90$) and combined apple-peach data ($R^2 = 0.86$). The correlation was weaker for peach alone ($R^2 = 0.41$), likely due to thinner shoot removed by pruning being harder to detect. This study thus demonstrates the potential of image-based phenotyping to estimate vigor-related traits.

Poster location: S62

A different beerspective: imaging barley under stress with AI help

Sonia Negrao

UCD

In Ireland, spring barley is the most cultivated cereal, and production must meet an increased demand of a flourishing malting industry. Modern barley cultivars have been bred under optimal conditions, leading to a reduced stress tolerance. In contrast, robust stress tolerance can be found in heritage germplasm. Here we explore the genetic potential of Heritage barley (landraces and formerly bred cultivars) to cope with abiotic stress. Climate change is causing extreme weather events such as flooding and droughts. Barley is the most susceptible cereal to waterlogging with yield losses of approximately 20-25% and improving waterlogging tolerance has been flagged as a major goal for future breeding programs. To investigate waterlogging tolerance, we imaged a germplasm collection of heritage barley using RGB, chlorophyll fluorescence and hyperspectral sensors as well as in field conditions using Unmanned Aerial Vehicles (UAV) coupled with RGB and multispectral sensors. 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).

Poster location: S63

Genotypic variation in root and shoot traits of wheat suggesting an indirect effect of breeding on nitrogen efficiency

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Wheat (Triticum aestivum) production in Europe relies heavily on nitrogen fertilizer inputs, negatively affecting soil, air, and water quality. An approach to reduce agriculturally caused nitrogen emissions is breeding of nitrogen-efficient crop cultivars. To investigate whether breeding approaches in recent decades have already indirectly targeted nitrogen efficiency in wheat, a collection of winter wheat cultivars released over a period of 50 years was examined under control and nitrogen-deficient conditions. Selected cultivars were grown in soil-filled rhizotrons for 15 days under greenhouse conditions to enable phenotyping of root and shoot growth at the seedling stage. During the experimental period, plants were phenotyped every two to three days for root and shoot traits. Additionally, physiological measurements were taken once before the end of the experimental period to quantify chlorophyll content, leaf-level spectral reflectance and the photosynthetic trait quantum yield of photosystem II. After the plants were harvested, root and shoot biomass were assessed destructively. Generally, all cultivars showed a reduction of shoot growth in favor of root growth in response to nitrogen deficiency. Genotypic variation was observed for physiological parameters under both control and nitrogen deficiency. Multivariate analysis, considering morphological and physiological shoot and root traits, revealed clustering of the cultivars roughly according to their year of release. In summary, our phenotypic data hint towards improved nitrogen efficiency in younger cultivars, which implies an indirect selection of genotypes with high nitrogen efficiency in wheat breeding progress over the last few decades.

Poster location: S64

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

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In light of the increasing frequency and severity of climate change-induced abiotic stresses, our research aims to unravel the drought stress response mechanisms in oilseed rape (Brassica napus), contributing to the development of more resilient cultivars for sustainable agriculture. We combine high-throughput phenotyping with advanced data analysis and machine learning to evaluate genotype performance under drought conditions.

We conducted three experiments using 80 genetically diverse rapeseed lines, cultivated under drought stress, alongside a subset of 20 lines as well-watered controls, within the state-of-the-art PhenoSphere facility at IPK Gatersleben. This highly controlled environment, featuring 108 large soil containers (1 m^3 each) and an integrated multi-sensor, multi-camera system, enables precise simulation of field-like stress conditions and high-resolution temporal monitoring. Daily RGB imaging, 3D laser scanning, plus twice a week hyperspectral imaging and kinetic chlorophyll fluorescence measurements were employed to capture morphological and physiological traits indicative of stress response. Manual measurements including osmolarity, porometry, chlorophyll and leaf water content, and maximum plant height were integrated with automated phenotyping data.

To complement the shoot phenotyping, we conducted two Rhizotron experiments to investigate root system architecture of the same 80 lines. Traits such as total root length, root depth, and lateral branching patterns can be extracted and used for further analyses.

By combining datasets from both shoot and root phenotyping platforms, we aim to identify key indicator traits for drought tolerance. Ongoing multivariate analyses aim to refine trait-based selection models and inform future phenotyping strategies for field conditions.

Our comprehensive approach lays the groundwork for improved understanding of drought tolerance mechanisms in B. napus and provides actionable insights for breeding programs targeting yield stability under water-limited conditions.

Poster location: S65

Divergent Photoprotective Strategies in Eastern White Pine and Spruce Under Moderate Drought

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The northern hemisphere forest is warming rapidly, with some regions facing up to 11°C of warming by the end of this century. As the climate shifts, moderate droughts are becoming frequent and prolonged, especially in southern boreal zones where conifers already face heightened stress and mortality. Unlike extreme drought, which can trigger immediate hydraulic failure, moderate drought imposes chronic, recurring stress that is expected to dominate future boreal growing seasons. This study investigates how moderate summer drought shapes photoprotective strategies and electron transport regulation in two co-occurring boreal conifers: eastern white pine (Pinus strobus) and eastern white spruce (Picea glauca), which may differ in drought acclimation responses. We hypothesized that moderate drought would shift non-photochemical quenching (NPQ) components, enhance cyclic electron transport (CET), alter PSII regulation, and elicit species-specific photoprotective responses. Seedlings were grown under controlled conditions. Controls were watered to maintain field capacity, and drought was applied progressively in three phases: light (~60% of field capacity), mild (~30%), and moderate (~0%), followed by rewatering. Chlorophyll fluorescence showed stable Fv/Fm under mild drought and a slight decline at moderate drought, while ΦPSII decreased progressively, especially in spruce. Dynamic NPQ rose with drought, with spruce showing higher sustained NPQ (Φf,D). Pine maintained stronger CET and PSI stability. Spruce had greater ΦNA and ΦND but remained stable in pine; likely contributing to its greater photochemical decline. All parameters, including PSII efficiency, PSI yield, ETRII, ETRI, CET, and ΦND/ΦNA, fully recovered after rewatering. Spectral reflectance indices followed similar patterns: PRI and CCI declined with drought and recovered with rewatering. Pigment analysis showed pine accumulated more zeaxanthin and had larger VAZ pools, while spruce had a higher carotenoid-to-chlorophyll ratio. Immunodetection revealed greater drought-induced D1 loss in spruce, while pine maintained higher levels of PsbS, PsaD, and Lhcb1, consistent with its enhanced dynamic NPQ response. These findings suggest that pine copes with drought through dynamic photoprotection and PSI stability, while spruce relies more on the sustained component of NPQ and pigment restructuring. This highlights distinct acclimation strategies to moderate drought in co-occurring boreal conifers.

Poster location: S66

High-Throughput Phenotyping as a Decision-Support Tool for Dynamic Sampling in Multi-Omic Analysis of Drought tolerance in Hordeum vulgare.

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Understanding how genetic variation translates into macro-phenotypes under environmental stress requires precise integration of molecular and phenotypic data over time. However, developmental heterochrony (variation in the timing of developmental transitions across genotypes) poses a major challenge to effective experimental planning. In this study, we propose a dynamic framework for sampling in multi-omic experiments integrating time-resolved phenotypic, environmental, and molecular data using multivariate linear mixed models. We develop real-time classification of developmental stages through deep learning-based analysis of the image data generated by high throughput phenotyping platforms and validate our tools on contrasting barley accessions under drought stress. In our case study, we selected 12 contrasting barley accessions based on (Dhanagond et al. 2019) which were well characterised in terms of drought resistance phenotypes and were grown on the IPK medium sized phenotyping system for high throughput imaging and photosynthesis efficiency measurements. Leaf tissue samples from the drought treatment and control for each genotype were collected at ten fixed time points for transcriptomic analysis. By further comparing fixed-time and developmental stage aligned sampling strategies, we aim to demonstrate enhanced statistical power for detecting genetic effects on the observed phenotype. This research would also enable developing a scalable decision-support system for optimizing sampling in multi-omic experiments, facilitating improved experimental design and deeper insights into temporal dynamics of stress responses.

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Poster location: S67

Detection of Nutrient Deficiencies in Arabidopsis thaliana Using Deep Learning for Smart Farming

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Detection of Nutrient Deficiencies in Arabidopsis thaliana Using Deep Learning for Smart Farming

Macronutrient deficiencies such as nitrogen (N), phosphorus (P), and potassium (K) have detrimental effects on plant growth, productivity, and overall crop quality. Early and accurate detection of these deficiencies is essential for sustainable nutrient management and enhanced agricultural efficiency. In this study, a deep learning-based image analysis pipeline was developed to detect and classify nutrient deficiencies in 20 genotypes of Arabidopsis thaliana, a widely used model organism in plant research. High-resolution RGB images were captured under controlled growth conditions, and two main methodological frameworks were implemented: (1) feature extraction using pre-trained convolutional neural networks (CNNs) in combination with traditional machine learning classifiers, and (2) transfer learning approaches that fine-tuned existing deep learning architectures with structural optimization. Despite observable variations in phenotypic responses among genotypes, including differences in leaf color, morphology, and pigment accumulation, the models successfully identified nutrient deficiencies with high precision. Individually, deep learning models achieved an average classification accuracy of 98.96%, while an ensemble model integrating multiple architectures reached perfect accuracy (100%). The proposed approach offers a non-invasive, cost-effective, and scalable solution, providing a significant advantage over conventional laboratory-based diagnostic techniques. By enabling timely detection of nutrient stress, this study contributes to the advancement of precision agriculture and supports the integration of AI technologies into smart farming systems for improved decision-making and resource efficiency.

Keywords: Arabidopsis thaliana, nutrient deficiency, RGB imaging, deep learning, image classification, plant health, precision agriculture,

Poster location: S68

Integrated Phenotyping Of Single And Combined Stress Responses In Contrasting Lupin Varieties Under Ambient And Elevated CO2

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To address the dual challenge of climate change and nutritional security, we employed Lupinus angustifolius as a model high-protein legume to investigate physiological, biomass, and yield responses to abiotic stresses under future climate scenarios. Using an integrated approach, we examined heat-tolerant (Mirabor) and heat-sensitive (Primabella) varieties—selected based on their contrasting heat stress tolerance—grown under ambient (400 ppm) and elevated (800 ppm) CO_2, and subjected to single (drought) and combined (heat + drought) stress. Physiological traits were assessed through gas exchange, chlorophyll fluorescence (PAM), and temperature differentials, while yield components and grain nutritional composition—including quinolizidine alkaloids (QAs)—were analysed at harvest.

A key objective was to determine whether heat stress tolerance in lupin also provides an advantage under combined heat and drought stress. Our results indicate that the heat-tolerant variety showed a degree of cross-tolerance, maintaining higher water use efficiency (WUE) under combined stress at both CO_2 levels compared to the heat-sensitive variety. Furthermore, the varieties appeared to employ distinct coping strategies: the heat-tolerant variety prioritized water conservation at the expense of some physiological traits, while the heat-sensitive variety maintained physiological activity but at a higher water cost. Our findings suggest that under combined heat and drought stress, the strategy of conserving water is more advantageous for sustaining biomass and yield traits. This work underscores the value of integrative phenotyping for identifying climate-resilient legume cultivars to support sustainable plant protein production in future environments.

Poster location: S69

Climate-ready pastures: Role of nitrogen-fixing bacteria in a field climate simulation experiment for assessing adaptation and mitigation strategies

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Human-induced climate change is causing the Earth's temperature to rise, and models indicate that this increase will continue in the coming years. Temperature is a crucial factor regulating the carbon flux of both natural and managed ecosystems. In recent decades, the use of plant growth-promoting bacteria (PGPB) in crops has emerged as a significant alternative for mitigating the negative impacts of abiotic factors on plant metabolism, growth, and forage nutritional quality. In this study, we utilized the T-FACE (Temperature-free air-controlled enhancement) facility to raise the plant canopy temperature by +2°C. We investigated the effects of this warming on photosynthesis, plant water status, growth, and nutritional quality in a managed pasture of Brachiaria (syn. Urochloa) Mavuno, both with and without inoculation of Azospirillum brasilense and Pseudomonas fluorescens. We implemented a multifactorial design to evaluate two temperature conditions (ambient and elevated) alongside two inoculation treatments (inoculated and non-inoculated). Our results demonstrated that inoculation enhanced root growth and increased photosynthetic rates by improving stomatal conductance and photosystem II performance. This, in turn, led to higher productivity, increased crude protein content, and better forage digestibility, along with a reduction in lignin and fiber fractions. Warming has been observed to increase non-photochemical quenching and the electron transport rate during the wet season. However, it reduces efficiency of PSII photochemistry, relative water content, productivity, forage quality, and digestibility during the dry season. The positive effects of inoculation fully offset the negative impacts of warming on photosynthesis, growth, nutritional quality, and digestibility and improved heat dissipation capacity. Our findings indicate that co-inoculation with A. brasilense and P. fluorescens is a sustainable solution to mitigate the adverse effects of elevated temperatures on tropical grass pastures. Additionally, this approach has significant environmental benefits, as biological nitrogen fixation can lead to a reduction in the use of nitrogen fertilizers, thereby decreasing N_2O emissions. These results emphasize the potential of PGPB to enhance forage resilience and productivity under climate stress, promote sustainable agricultural practices, and improve food security in the face of climate change. Financial support: FAPESP (Grant 2022/15021-2).

Poster location: S70

Phenotypic characterization of barley drought responses using high-throughput imaging reveals genotype-specific adaptation strategies

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Understanding the mechanisms underlying barley adaptation to drought is essential for the development of resilient cultivars. Plants from distinct ecotypes employ diverse strategies to cope with water-limited environments, resulting in substantial variability in their physiological and morphological responses. Barley landraces originating from regions characterized by challenging climatic conditions near the centers of crop domestication represent valuable sources of drought tolerance traits.

In this study, we evaluated five barley genotypes differing in cuticular wax characteristics (glossy vs. glaucous) and heading time under drought and subsequent recovery phases. The experiment utilized high-throughput imaging-based phenotyping, including integrating RGB, infrared thermography, and chlorophyll fluorescence assessments, in conjunction with yield measurements. Machine learning analysis, specifically Random Forest modeling, was employed to identify key traits contributing to treatment and genotype differentiation. Notably, delta canopy temperature (ΔT), leaf slenderness (SOL), plant compactness, and fraction of ‘open’ PSII centers (qL), among others, emerged as principal indicators.

In our experiment CamBW1 (a glossy line) performed well under early drought conditions, although a reduction in biomass was observed. In contrast, LubBW1 (a glossy line) and CamWa2 (a glaucous line) proved highly sensitive, struggling to effectively convert biomass into grain yield under drought stress. Notably, LubWa1 (a glaucous line) emerged as the most drought-tolerant genotype, efficiently allocating resources to maintain both biomass and yield. Meanwhile, CamWa1 (a glaucous line) achieved the highest grain production under control conditions, but under drought it exhibited low canopy cooling efficiency and a reduced biomass tolerance index. These findings underscore the necessity of integrating morphological and physiological phenotyping to elucidate the complex mechanisms of drought tolerance in barley, thereby informing targeted breeding strategies.

Poster location: S71

High-throughput phenotyping of sunflower responses to heat and drought stress using the Heliaphen platform

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The response of plants to their abiotic environment is highly complex, as it involves the integration of multiple factors, all of which interact dynamically. To elucidate the mechanisms and their genetic, it is essential to simulate these stress conditions within controlled environments and to develop phenotyping tools that are aligned with the scientific objectives and plant species under investigation.

INRAE developed the Heliaphen platform, an outdoor platform designed for high-throughput phenotyping to apply abiotic stress scenario. With a hosting capacity of 1300 plants growing in pots, it allows automated management of drought scenarios on plants throughout their lifecycles. A robot moving between plants monitors water status and perform images acquisition. A model has been developed to estimate whole plant leaf area from these images. A recent upgrade has been setup to apply heat stress. These features allow to evaluate plant response to abiotic stress in field-like conditions. Here, we describe the methodological framework of Heliaphen to detail how the drought and heat stress scenarios are applied and illustrate these features through two experiments conducted on sunflower (Helianthus annuus).

In the first experiment a drought stress has been applied during vegetative stress on a set of hybrids. The plant responses to this stress is characterized by two parameters developed for the SUNFLO crop model (Casadebaig et al., 2011 Agric. For. Meteorol.) through leaf expansion and transpiration rate. Computational tools to estimate them automatically have been developed and will be presented.

In the second study, we illustrate a new feature: managing heat stress using convectors in outdoor conditions while maintaining drought scenario. For this, a panel of sunflower inbred lines was subjected to drought and heat stress from flowering stage until full maturity. Final phenotyping of a 3rd SUNFLO crop model parameter (harvest index and its stress response) could be measured on all plants to validate genetic control of drought tolerance identified in multi-environmental trials.

Overall, our results demonstrate the potential of the Heliaphen platform to phenotype genotype × environment interactions and to identify key physiological traits for drought and heat stress tolerance. The ability to apply precise stress scenario and to automatically compute trait dynamics is a great opportunity for genetic resource evaluation.

Poster location: S72

Probabilistic atlases and mean individuals: spatial statistical methods for phenotyping traits associated with stress and tolerance.

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Plant phenotyping synthesizes high-resolution data into a few scalars, such as mean greenness or leaf area. Doing so obscures where trends and variations occur inside organs, plants, or fields. In this work, we derive methods from neuroimaging (Shattuck et al., 2009) and plant developmental biology (Neumann et al., 2022) to map the details of population trends and variations in plant phenotyping experiments. The maps are obtained by aligning the observations within a reference geometry to compute pixel-wise probabilities or intensity mean and variance across the population. This approach turns any 2D or 3D (+t) dataset into a visual statistical description of phenotypic populations. We demonstrate its applicability to plant phenotyping on three datasets covering abiotic and biotic stresses:

1. Sahel Faidherbia-Mil agroforestry (2D, drone): Aerial images of 72 Faidherbia albida trees (leguminous companion tree) were aligned and resampled to a common resolution. The mean map of the surrounding crops enables the impact of the Faidherbia on the growing millet to be characterised.

2. Grapevine wood disease (3D+t, MRI): Grapevine cuttings were manually infected with aggressive fungal pathogens and monitored with MRI for three months. The 3D time series were registered and flattened along their surface, then averaged across the population (40 cuttings). The atlas captures the mean moving fungal front and shows cultivar-specific rates of radial and tangential progression.

3. Rice aerenchyma networks (3D, µCT): Whole rice plants were imaged in vivo using X-ray µCT, 10 µm resolution. The leaf and root system architectures were reconstructed, and a pipeline was trained to estimate the aerenchyma ratio along the organs' central lines. This target trait (related to anoxia stress) was averaged across the dataset to study the correlations between root and shoot aerenchyma profiles, and to identify relations that do not appear in plant-wise global ratios.

Across cases, atlases provide intuitive visual summaries, enabling the comparison of heterogeneous samples to characterise stress responses. By combining statistics and image geometry, probabilistic atlases add an extra dimension to plant phenomics: mapping not only how much, but where variation occurs. Commonly used in neuroscience, these methods can likewise accelerate plant trait discovery, refine assessments of stress resilience, and help unlock the full potential of plant phenotyping.

Poster location: S73

Dynamics of Transcriptional Modulation of Phenylpropanoid Pathway Genes in Grapevines Under Variable Irrigation Regimes: Insights from a Controlled Irrigation Study

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Grapevines modulate the phenylpropanoid biosynthetic pathway in response to water availability, affecting plant resilience, and understanding how gene expression adapts under different amounts of available water can support irrigation practices. It is hypothesized that the intensity of water stress triggers distinct transcriptional responses in grapevines throughout moderate irrigation levels. This study aimed to understand: i) how irrigation levels of crop evapotranspiration (ETc) affect the expression of myba, myb14, myb15, abcc1, chs, dfr1, fls1, mate1, pal1 and ufgt1 genes and ii) how the phenylpropanoid biosynthetic pathway is modulated in response to water deficit during the early grape maturation period. The experiment was conducted in a greenhouse under controlled conditions using three irrigation regimes (10%, 30%, and 100% ETc) and three sampling points during maturation. The assay lasted 21 days, with 14 days of exposure to the defined irrigation levels. One week before the start of the experiment, the grapevines were irrigated to achieve water comfort. In Week 1 (WK1) of the experiment, evapotranspiration was calculated for each condition, with the first irrigation and foliar collection being performed, followed by the second irrigation and foliar collection in Week 2 (WK2), and the last foliar collection being performed in Week 3 (WK3). Gene expression was quantified using RT-qPCR. Results showed that both water availability and developmental stage dynamically modulate gene expression. In WK1, several genes (myba, ufgt1, dfr1 and mate1) showed higher expression under 30% ETc, suggesting early adaptive activation. In WK2, most genes remained at basal levels except under 10% ETc, where myba and ufgt1 involved in the flavonoid and anthocyanin pathways, respectively, showed an increased expression, indicating an initial stress response. By WK3, this pattern became more pronounced, with significant upregulation ($P \leq 0.05$) of myba and ufgt1 under severe stress (10% ETc), reinforcing their role in drought response and antioxidant defense at critical stages. The myba is a transcription factor in the anthocyanin and flavonoid pathways, contributing to stress protection. The ufgt1 is involved in the glycosylation of anthocyanidins, forming stable anthocyanins. Results suggest that pathway activation depends on stress intensity and phenological stage, contributing to more sustainable and climate-resilient viticultural practices (e.g. irrigation).

Poster location: S74

High-throughput phenotyping in future climate simulations elucidates genotype-specific responses towards elevated CO2

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By the end of this century, carbon dioxide (CO2) levels are predicted to continue to rise. On the one hand, increased CO2 concentrations could offer substantial plant growth improvements. On the other hand, it re-enforces climate change. We are confronted with abiotic stresses of both higher intensity and longer duration, negatively impacting crop health and yield. Therefore, there is a need to increase resilience and sustainability of our agricultural systems. One solution to do so is to increase biodiversity on the field to keep the balance between stress tolerance and productivity. Especially the use of climate-smart varieties, being varieties with increased tolerance or benefitting the most from future climates, hold major potential.

Globally, gene banks conserve these valuable resources, but phenotypic data is lacking. The International Musa Germplasm Transit Center (ITC) harbors over 1,700 Musa accessions from all over the world. The BananaTainer, a 40 FT hydroponics-based growth container, offers a solution to elucidate genotype-specific growth responses towards future climates in a high-throughput manner (Gambart et al 2025). In one run, 504 plants consisting of 16 different genotypes are grown and phenotyped. By simulating future climates through tight control over temperature, humidity, light intensity, CO2 concentrations and nutrient content, 4 climate-smart varieties have been discovered. In this study, 16 genotypes were screened for their growth potential towards elevated CO2 concentration. Further physiological evaluation of plant gas exchange with an infrared gas analyzer of contrasting genotypes elucidated differential effects of elevated CO2 on photosynthesis, decline in stomatal conductance and transpiration. These results highlight the importance of mining germplasm to discover climate-smart varieties with enhanced growth, photosynthetic capacity and water use efficiency.

Keywords: BananaTainer, Biodiversity, Climate change, climate-smart varieties, High-throughput phenotyping

Poster location: S75

Agro-physiological response of different lentil genotypes to phosphorus application under drought stress

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Lentil crop (Lens culinaris) is an essential food legume, recognized for its nutritional value and its role in sustainable agriculture. It is mainly cultivated in arid and semi-arid regions in Morocco, where drought stress limits its growth and yield. On the other side, phosphorus, a key nutrient for plant growth and development, plays a crucial role in the lentil's ability to tolerate the unfavorable conditions. However, its availability and use efficiency become particularly critical under drought conditions, where biological activity and soil phosphorus mobility are severely reduced. For this purpose, optimizing phosphorus use efficiency (PUE) by selecting the best performing genotype could be a key agronomic strategy to improve lentil tolerance to drought stress.

This study was conducted in a conditioned greenhouse located at the Regional Center of Agricultural Research of Settat (INRA, Morocco). The trial was structured according to a factorial design with three replications. It serves at evaluating the effect of different phosphorus applications (P0: check, P1: low level, and P2: high level) on different lentil genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, and G10) exposed to different water regimes (30% and 50% of pot capacity). The measurements included several physiological and agronomic traits.

The results showed that, phosphorus application, particularly at convenient optimal doses in each water regime, led to a significant improvement in chlorophyll content, NDVI index, and plant cover. Furthermore, each lentil genotype responds differently depending on the phosphorus dose and the water regime. For instance, some genotypes, promoted greater root and shoot development as well as active nodules under moderate to high phosphorus doses. Regarding yield, P0 dose was the most appropriate for G3, G4, G6, G7, G8 and G9, genotypes and P1 dose was the most suitable for G1, G3, G10 and G10 genotypes, and P2 dose was the most suitable for G2, G5, and G4 genotypes under stressed regime. This variability highlights the importance of adapting phosphorus fertilization management according to genotype and water regime to optimize growth and water use efficiency, opening up promising prospects for the selection of more efficient genotypes and the adoption of targeted fertilization strategies.

Poster location: S76

Automated Spittlebug Foam Detection using YOLOv11 for Xylella fastidiosa Vector Management

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Xylella fastidiosa (Xf) is the major ongoing threat to olive orchards in the southern Italian region of Apulia. This bacterium is known to infect olive plants, colonizing them and obstructing their xylem, therefore blocking the water flow to leaves and, ultimately, leading to the death of the plant. This bacterium is carried by a specific insect, Aphrophoridae, commonly known as the spittlebug, which should therefore be properly handled, preferably using a non-destructive method, without the use of harmful chemical pesticides. To this end, the proposed system focuses on non-invasive pest management, leveraging the latest developments in deep learning to automatically detect the foamy substance, i.e., spittle, produced by spittlebug nymphs. This is performed on images taken in the wild and is then potentially used to lead a robot to perform pest removal via air flows. To evaluate the most effective model for this task, we first compared the baseline versions of the latest two iterations of YOLO, that is, YOLOv11 and YOLOv12. Then, we evaluated the introduction of an architectural modification on YOLOv11, by incorporating a Convolutional Block Attention Module (CBAM) within the neck of the architecture. This addition was designed to enhance the capability of the model to focus on critical regions and channels of the image for the final classification step. The experiments, conducted under real settings in a field with tall, wild grasses, demonstrated the feasibility of the methodology, with the integration of the CBAM attention mechanism yielding significant improvements over the baseline models, thus highlighting the potential for effective deployment in resource-limited scenarios.

Poster location: S77

Uniform Colour Space for Evaluating Tomato plant Drought Stress Resilience

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Global food security faces several challenges, mainly related to severe threats from the extreme impacts of climate change and steadily increasing population growth. To deal with these issues, innovative methods for developing crops that can provide optimal yields even under stressful scenarios are mandatory. One possible solution is to assess the impact of genotypical mutants on the overall resilience of a plant; to this end, it is possible to exploit the large quantity of data generated by high-throughput phenotyping platforms (HTPPs) to analyze its phenotypical traits and isolate variants that demonstrate greater resilience to stresses such as drought or pests.

However, the amount of data generated by HTPPs is often large enough to pose a significant challenge in the analysis if carried out manually by human experts. Therefore, to overcome this issue, we propose an automated image processing pipeline specifically aimed at accelerating the evaluation of drought stress response in tomato plant mutants, thereby providing domain experts with statistically robust tools for large-scale data analysis and genotypical assessment.

The core of our proposed methodology is an efficient pipeline based on lightweight processing and uniform color spaces, modifying the CIELab standard to reduce the dependence of the chromatic components on illumination and ensure statistical uniformity. The system was validated on a dataset comprising 388 tomato mutations, gathered at three different stages of the plant's growth. The results confirm that the proposed pipeline is highly effective and provides an optimal tool for identifying drought-resilient variants.

Poster location: S78

Assessing transpiration kinetics to evaluate drought tolerance of winter oilseed rape (Brassica napus L.) in a semi-automated phenotyping platform

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Winter oilseed rape (WOSR) yield is expected to decline due to increasing drought events caused by climate change. In this study, 40 doubled haploid (DH) WOSR genotypes were tested in a high-resolution phenotyping platform (PlantArray). Two weeks after sowing, plants were grown under well-watered (60% field capacity) and limited-irrigation (40%) regimes, with an automated irrigation system controlled by the gravimetric platform. Plant weights were recorded every three minutes to estimate the transpiration rates along with ambient vapor pressure deficit (VPD) and air temperature over a six-week experimental cycle. To evaluate variations in drought-induced responses, discrete traits were extracted from the time-series transpiration rates recorded during the final two weeks before harvest, capturing daily water use patterns. The traits included daily total transpiration, transpiration rate peak values and water use efficiency (WUE) calculated as the ratio of dry shoot biomass to cumulative transpiration. In addition, transpiration-VPD interactions were assessed where transpiration-VPD breaking points were identified, at which genotypes would restrict the transpiration despite increasing VPD, yet other genotypes did not show this restriction. The analysis showed clear variations in transpiration kinetics among genotypes. Genotypes with stable water use patterns and higher WUE under limited irrigation were considered potentially drought-tolerant candidates for further testing in the field. Another assessment criterion was the identification of genotypes with earlier transpiration restriction at lower corresponding VPD values, reflecting efficient stomatal regulation under increasing VPD values. The results showed significant genotypic variations in water use behaviors under drought conditions across independent experimental cycles. Approximately 30% of the screened genotypes maintained higher WUE under limited irrigation, producing higher biomass with lower cumulative transpiration. High-resolution phenotyping and daily dynamic transpiration traits provided a proxy for selecting WOSR genotypes with high WUE. Integrating the dynamic transpiration traits into breeding strategies contributes to the development of drought tolerant WOSR cultivars that maintain stable production facing the challenging climate change.

Poster location: S79

Spectral traits phenotyping in Scots pine seedlings under drought stress and dissection of genetic variability

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Scots pine (Pinus sylvestris L.) is an important timber species, spanning across a wide ecological range, with local adaptations contributing to its extensive genetic diversity. Nursery-raised seedlings account for nearly 80% of Scots pine forest regeneration versus 20% from natural regeneration in the Czech Republic. Early-season drought represents a major bottleneck for the growth and survival of pine seedlings.

To investigate population-specific short- and long-term drought responses, we conducted a drought and recovery experiment on seedlings from open-pollinated families from three seed orchards in the Czech Republic, representing contrasting provenances. Seedlings were cultivated under semi-controlled conditions and monitored for 164 days using a high-throughput imaging platform capturing chlorophyll fluorescence and hyperspectral reflectance. Plants were then outplanted to a forest site and further monitored.

A custom image-processing pipeline and machine learning approach enabled the detection of population-level variability and early drought effects based on spectral profiles. All 810 individuals were genotyped using the PiSy50K SNP array, which allowed reconstruction of genomic relationships and exploration of genetic variability in drought-related responses. We applied univariate linear mixed models to partition trait variance, estimate narrow-sense heritability, and quantify population-level differentiation (QST) across measured regions of the hyperspectral spectrum and experimental phases. The analysis across experimental stages revealed dynamic patterns of genetic variance linked to both family and population effects in hyperspectral traits.

By integrating genomic data with physiological imaging, we observed population-specific responses and underlying genetic variability, suggesting regionally adapted variation that could aid Scots pine breeding for climate resilience and forest adaptation.

Poster location: S80

Field evaluation of BIO_STML_0061 biostimulant for enhancing tomato drought tolerance: physiological responses and water use efficiency

Elisa Mascanzoni[1]; Marta Polimeno[2]; Marco Acciai[2]; Valentino Bosco[1]

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Climate change is intensifying drought frequency and severity, posing critical challenges to tomato cultivation worldwide. Biostimulants represent a promising, sustainable strategy to enhance plant stress resilience, but their effectiveness must be validated under realistic field-like conditions.

This study evaluated the efficacy of the biostimulant BIO_STML_0061 in improving drought tolerance in tomato (cv. Datterino di Sicilia) using a greenhouse trial with the PlantArray System® (Agrigeos, Italy). A factorial completely randomized design tested three irrigation levels (100%, 80%, 60% water retention capacity) and two biostimulant treatments (BIO_STML_0061 at 0.7 L/ha vs untreated control). Multiple physiological and agronomic parameters were measured, including SPAD chlorophyll content, PRI, fruit set, fruit weight, biomass, leaf area, and water use efficiency (WUE).

BIO_STML_0061 significantly improved plant performance under moderate and severe drought. Under 80% irrigation, treated plants showed higher fruit set (28.7% vs 17.8%, $p < 0.10$), greater fruit weight (33.05 g vs 24.12 g), and a 30% increase in WUE (0.0026 vs 0.0020 g/L). SPAD values and biomass remained more stable in treated plants. Residual effects were also observed under 60% irrigation, and recovery measurements indicated faster physiological restoration in treated plants.

These findings demonstrate that BIO_STML_0061 enhances tomato drought tolerance by improving water efficiency and maintaining reproductive performance, offering a practical tool for climate-resilient tomato production.

Poster location: S81

Utilization of an image-based high-throughput phenomics platform to explore the time-resolved drought resilience responses of a faba bean germplasm collection

Docent Kristiina Himanen[1]; Sylvain Poque[1]; student Muhammad Omer[1]; Ulrika Carlson-Nilsson[2]; Dr. Hamid Khazaei[3]

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Climate change will increase the prevalence of weather fluctuations, calling for resilience crop breeding. Faba bean (Vicia faba L.) has great potential to contribute to sustainable agriculture and protein security globally. However, it is known to be very sensitive to drought. Uncovering the response patterns of drought-resilient germplasm is critical for understanding the mechanisms underlying the stress acclimation and breeding for resilience. In this study, we analysed genotype specific drought responses for growth and physiology of 44 faba bean accessions. Utilizing image-based time series analysis of growth by visible light RGB, allowed identification of early and later responding genotypes. The early and late responders were then correlated with their final size in plant height, canopy area, and digital biomass. In the second stage, the physiological responses were analysed by chlorophyll fluorometry and water use efficiency. The genotype specific responses, will again be correlated with the timing of the growth responses. Our hypothesis is that correlation between the growth signatures and the physiological signatures will be indicative of drought resilience in the germplasm. We demonstrate here, the potential of an indoor phenotyping facility for screening a relatively large faba bean germplasm collection under defined watering levels. Accessions that were shown to maintain growth and physiological performance under water deficit conditions have potential as pre-breeding materials for the development of drought-resilient faba beans.

Poster location: S82

Drones and Artificial Inteligence to optimize Portuguese Rice Cultivation

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Rice cultivation in Portugal faces several challenges, mainly promoted due to climate change, such as prolonged and severe drought events and outbreaks of rice blast disease. The advent of field imaging technologies, such as ground-based phenotyping platforms and drones equipped with high-resolution hyperspectral cameras, in combination with artificial intelligence-based models, present innovative solutions to tackle these issues. This poster showcases a doctoral research project aimed at providing rice producers with a digital tool, based on these technologies, for efficient irrigation of upland rice and early detection of rice blast disease, thereby helping to prevent production losses, optimize water use and promote a more sustainable future in rice farming.

Poster location: S83

Dynamic relationship between above ground and below ground in barley (H. vulgare L.) traits under different water regimes

Anna Backhaus[1]; Zeineb Dagdad[1]; Safaa Ouahid[1]; Miguel Sanchez-Garcia[1]; Andrea Visioni[2]

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Root system architecture plays a crucial role in drought stress tolerance therefore exploring patterns of root development under different water regimes is crucial to understand crop adaptation to drought prone environments. ICARDA’s PhysioTron, is a state-of-the-art semi-controlled environment designed for precise manipulation of growing conditions. It consists of a fully automated rainout shelter lysimeter with 700 pots and a mobile bridge equipped with a high-throughput phenotyping system. It can simulate various environmental stresses such as drought, heat, and salinity for studying plant responses to stress under semi-controlled conditions. During cropping season 2023-24, 70 barley genotypes enclosing modern cultivars, elite lines, landraces and H. bulbusum introgression lines selected from the germplasm available from the BarleyMicroBreed HorizonEurope Project were tested in the Physiotron. Full field water capacity was maintained in both treatments until the booting phase then plants were exposed to a dry down phase and finally two contrasting water regimes were applied during recovery phase (80% and 40% of water field capacity, 5 reps per treatment). Agronomic data, high-throughput phenotypic data along with key physiological metrics (fraction of transpirable soil water, total transpiration, transpiration corrected by plant architecture traits and vapor pressure deficit) were collected during the whole cycle of the 700 pots. Furthermore, treating each pot as root core (divided into 5 sections), below ground biomass was measured for all genotypes under different water regimes. Interestingly, root plasticity seems to play a major role for drought adaptation. Drought treatment had a clear effect on biomass, grain yield and grain width that were all lower than the in the irrigated treatment. Interestingly, root total weight and root biomass in the lowest layer were increased under drought. We also found a positive correlation between total root biomass and biomass at harvest and green cover, suggesting that plants with more extensive root systems were able to sustain better canopy cover and accumulate more above-ground biomass even under drought stress.. Correlation between the treatments was lowest for the root biomass in the bottom layer, suggesting that root biomass production at the lowest section has higher plasticity response among genotypes upon drought treatment.

Poster location: S84

Explore root phenotyping techniques to select cowpea drought resilient accessions

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Drought is one of the most important consequences of abiotic stresses posed by climate change and negatively affects crops production. Root system architecture (RSA) is an underexplored trait probably due the dense nature of soils which makes phenotyping roots in situ challenging. RSA has been reported as an important trait to better understand the crops ecophysiology and abiotic stress resilience. The main objective of this study was to explore the classical non-destructive 2D phenotyping techniques and to implement a suitable digital imaging acquisition system to screen cowpea genotypes drought resilient. Cowpea (Vigna unguiculata L. Walp.) was used as crop model because it is considered one of the legumes crops most adapted to high temperatures and drought conditions.

Three different techniques (agar, germination pouches or rhizoboxes) were developed for phenotyping the cowpea RSA under controlled conditions. Three cowpea accessions, previously described as drought stress resilient were submitted to two water treatments (control and drought). The root digital images underwent pre-processing for analysis with RootNav, which delivered information on various root parameters, such as total root length, seminal root length, number of lateral roots and lateral roots length. Differences in the RSA were observed among these cowpea accessions, suggesting diverse drought responses and putative resilience patterns. As reported in other studies, variability in the development of well-developed and deeper roots and increase of root biomass were observed between genotypes under drought stress and are important mechanisms for protecting plants against water deficit.

The implementation of novel approaches using new high throughput technologies, such as image acquisition and analysis, represents an excellent tool for providing valuable data to identify promising germplasm based on RSA traits. These results aim to increase crop production, while simultaneously mitigating the effects of climate change.

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Poster location: S85

Monitoring salt stress in different plants specie of the Mediterranean maquis: an “in vivo” and real time study by Digital Plant Phenotyping

Meri Barbafieri; Daniela Di Baccio; Andrea Scartazza; Eliana Tassi; Irene Rosellini

CNR-IRET National Research Council

The Digital Plant Phenotyping (DPP) technology has been employed to assess the effects of salinity stress on representative plant species from the Mediterranean maquis, a key component of coastal and sub-coastal ecosystems. This research addresses an increasingly urgent ecological issue: the rising salinity levels in soil and groundwater associated with sea level rise—one of the most pressing consequences of global climate change. By integrating advanced phenotyping tools with traditional instruments and measurements for plant environmental monitoring, this study aims to enhance our understanding of plant physiological and morphological responses to saline stress conditions.

The research focuses on the application of DPP for real-time, non-invasive monitoring of plant health, development, and stress adaptation mechanisms. Preliminary findings provided valuable insights into the tolerance thresholds and adaptive strategies of Mediterranean evergreen species when exposed to the progressive increasing salt concentration. The study targets both gymnosperms and angiosperms commonly found in the Mediterranean basin, particularly those dominant in maquis vegetation. Selected gymnosperms included Pinus pinaster, Pinus halepensis, and Cupressus sempervirens, while the evergreen angiosperms assessed were Myrtus communis and Arbutus unedo. These species were subjected to controlled salinity treatments over a six-month period within semi-controlled greenhouse growth conditions designed to simulate field-relevant conditions. This contribution presents method and preliminary findings on plant responses and functions under saline stress, focusing on Mediterranean maquis and environments.

We monitored a range of plant traits, including growth parameters, chlorophyll fluorescence, pigments, water use efficiency, leaf morphology, vegetation indices and canopy architecture. These phenotypic traits were analyzed to detect early stress symptoms and to quantify the degree of salt-induced damage or adaptation. Data generated from high-th

Poster location: S87

Decoding stress specific transcriptional regulation by causality aware Graph-Transformer deep learning

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Cells respond to environmental stimuli through transcriptional reprogramming orchestrated by transcription factors (TFs), which interpret cis-regulatory DNA sequences to determine the timing and location of gene expression. The diversification of TFs and their interactions with cis-regulatory elements (CREs) underpins plant adaptation to stress through the formation of gene regulatory networks (GRNs). However, deciphering condition-specific GRNs and identifying transcription factor binding motifs (TFBMs) for spatio-temporal gene expression remain major challenges in plant biology. To decipher the conditional networks governing TF-Target gene interactions, we developed CTF-BIND, a novel computational framework designed to reason about the spatio-temporal dynamics of TF activity. Leveraging over ~23TB of multi-omics data (ChIP-seq, RNA-seq, and protein-protein interaction data), we constructed Bayesian causal networks capable of explaining TF activity across diverse conditions. These networks, validated against extensive experimental data, were then integrated into a Graph Transformer deep learning system. This system uses expression information of network components to quantitatively determine TF activity levels. Models were developed for 110 abiotic stress-related TFs, enabling accurate condition-specific detection of TF binding directly from RNA-seq data, eliminating the need for separate ChIP-seq experiments. CTF-BIND achieved a high average accuracy of ~93% when tested against experimentally established data from various conditions. It is implemented as an interactive, open-access web server, it not only provides TF binding profiles but also facilitates downstream functional analysis. Furthermore, we developed CTF-BIND-DB, (https://hichicob.ihbt.res.in/ctfbind/) a database capturing dynamic shifts in regulatory pathways, providing information on TGs, network ontology, and binding motifs. CTF-BIND and CTF-BIND-DB represent a transformative approach for understanding and determining TF activity in plant stress responses, offering a powerful tool for crop improvement and bypassing the limitations of traditional methods and extensive experimental validation

Poster presentations

Session 2:

Phenotyping for innovative practices

Poster location: I01

Dictaphen: Accelerating Field Phenotyping Using Automatic Speech Recognition and Large Language Models

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Phenotyping of plants in the field traditionally requires considerable manual labor, often involving multiple peoples to accurately annotate observations. This process, which includes manual transcription, interpretation, formatting and digitalization of collected data, significantly delays analysis and decision-making. To address these limitations, we introduce Dictaphen, a novel mobile application designed to streamline phenotypic data annotation through the integration of advanced speech recognition and large language models (LLMs).

Dictaphen enables users to perform plant annotations efficiently by verbally describing phenotypic traits directly into their smartphones. The recorded annotation speech is automatically transcribed into text and immediately applies LLM-driven information extraction techniques to convert this unstructured text into structured data formats, such as JSON or CSV. This process substantially reduces annotation time, minimizes human-induced errors, and eliminates the requirement for additional personnel or post-processing.

Our key contributions to the field of plant phenotyping are threefold: an application that accelerates phenotyping workflows, enhancing data reliability and consistency by utilizing LLMs, Dictaphen's streamlined, a low cost solution accessible to broader research communities, including small-scale and resource-limited programs.

The novelty of Dictaphen is its integration of domain-specific large language models with speech-to-text functionality robust for field conditions that can improve and accelerate phenotypic data collection. The application has already been tested by tens of research teams across France and is still in active development, continuously evolving to meet diverse phenotyping needs.

Poster location: I02

How to Capture Within-Field Heterogeneity Across Multi-Year Crop Rotation: High-Resolution Insights from Sentinel-2 Imagery

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To identify optimal combinations of species, genotypes, and management practices, plant scientists are increasingly considering the transition from controlled environments to real-world agricultural conditions. A key challenge in this shift lies in capturing the spatial and temporal variability of within-field environmental conditions that strongly influence crop development. In this study, we (1) develop a method to quantify spatial heterogeneity in crop growth across multiple seasons, (2) define a heterogeneity score at the parcel level, (3) identify the main explanatory variables of this score, and (4) examine the temporal dynamics of heterogeneity patterns.

Time series of Sentinel-2-derived Leaf Area Index (LAI) were used to generate annual indicators of spatial crop growth heterogeneity and corresponding heterogeneity scores for over 110,000 agricultural parcels in Wallonia between 2017 and 2024. These scores served as response variables in both a linear mixed-effects model and a random forest regressor to assess feature importance. Predictor variables included crop type, year, and parcel-level topographic and soil characteristics.

Temporal persistence of spatial heterogeneity patterns was evaluated by calculating pixel-wise correlation coefficients across pairs of annual heterogeneity maps for each parcel. Higher correlation values indicate consistent spatial patterns over time. A second linear mixed-effects model using these coefficients as response variables revealed that correlations were significantly higher when the same crop was grown in both years.

This temporal analysis supported the delineation of within-field management zones by aggregating annual heterogeneity maps for similar crops. Resulting zones reflect (1) high-productivity stable areas, (2) low-productivity stable areas, and (3) unstable areas with fluctuating productivity across years. This concept was originally proposed by Blackmore (2000) using multiple yield maps; the approach developed in this study overcomes the common limitation of scarce or low-quality yield data and extends the analysis to fields managed under diverse crop rotations.

The proposed approach is scalable and cost-efficient, making it suitable for various cropping systems and regions. The generated maps have the potential to support dynamic, site-specific agricultural management towards greater sustainability and offer a valuable tool for in-field phenotyping under real farming conditions.

Poster location: I03

Mapping Bean-Wheat Mixture Effects with Solar-Induced Fluorescence and Hyperspectral Imaging

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Intercropping, the practice of cultivating two or more crops together, enhances resource acquisition and can result in higher and more stable grain yields. The physiological mechanisms driving positive mixture effects of growing a legume crop next to a cereal are however understudied. Hyperspectral and solar-induced fluorescence remote sensing offer promising tools to analyse canopy structural and physiological factors that influence crop performance in intercropping systems. This study explores multiple crop parameters related to radiative, structural, and physiological features, derived from remote sensing data collected in a three-year field experiment. These parameters were further used to establish a scheme for downscaling canopy measurements of solar-induced fluorescence to leaf and photosystem levels. By combining radiative transfer models with machine learning techniques, our method efficiently predicts key crop parameters, including leaf area and chlorophyll content. We successfully predicted crop growth parameters from field-sensor and image data and revealed significant differences not only between crop types but also among treatment combinations. Our results indicate that intercropping enhances biomass, light absorption, and grain yield and increases SIF at photosystem levels, although far-red SIF efficiency is reduced in mixtures. For the first time, our study successfully used novel remote sensing approaches in a mixed cropping field experiment.

Poster location: I04

Advancing monocot grafting through AI-driven phenotyping

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University of Copenhagen

Grafting is a widely used horticultural technique, yet its application in monocot crops has been limited due to anatomical constraints. Recent breakthroughs have demonstrated that monocot grafting is feasible when the shoot of an embryo (plumule) is replaced with analogous tissue from another seed, opening new avenues for cereal crop improvement.

To support this emerging field, we are developing a phenotyping platform for early-stage screening of grafting compatibility in monocot species. Our system integrates time-lapse imaging with machine learning to monitor and classify graft success. This approach can enable high-throughput, non-destructive assessment of graft union formation, offering a scalable tool for identifying and optimizing compatible scion-rootstock combinations.

We tested grafting unions between annual cereals, wheat (Triticum aestivum) and barley (Hordeum vulgare), and perennials, intermediate wheatgrass (Thinopyrum intermedium) and bulbous barley (Hordeum bulbosum). Preliminary observations suggest potential compatibility between species. While analysis of the machine learning model is ongoing, early results indicate promise for automated classification of graft success.

By combining imaging and AI-driven analysis, our work contributes to advancing grafting techniques in monocot crops, offering a novel approach for identifying compatible scion–rootstock combinations and improving graft success rates.

Poster location: I05

Model-assisted high-throughput approach to phenotyping biochemical capacity of photosynthesis

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Quantifying photosynthetic acclimation is essential for breeding climate-resilient crops, but remains challenging due to the low-throughput and labour-intensive nature of gas-exchange measurements. To overcome these limitations, we developed a model-assisted, high-throughput phenotyping framework that enables dynamic estimation of photosynthetic capacity and its underlying physiological mechanisms based on hyperspectral measurements. By modelling protein turnover, the approach captures synthesis and degradation dynamics in three key photosynthetic protein pools: light harvesting, electron transport, and carboxylation. The model focuses on three interpretable parameters—maximum synthesis rate (Smax), degradation rate (D), and an aging effect (td) that reduces synthesis over time. The pipeline was tested on 60 winter wheat genotypes, grown under three contrasting environmental conditions: constant light and temperature, fluctuating light, and fluctuating temperature. SPAD measurements on the third leaf were used to estimate investment in the light-harvesting pool, while hyperspectral reflectance was used to predict gas-exchange parameters via partial least squares regression, substantially increasing throughput while effectively capturing the temporal dynamics of the functional protein pools.

Environmental fluctuations distinctly regulated protein turnover across the pools. Fluctuating light enhanced both Smax (>30%) and D (~15%) in the light-harvesting pool, while fluctuating temperature primarily reduced Smax in the carboxylation pool (~15%). In the electron transport pool, both fluctuating conditions increased Smax (8-17%) and D (23-30%) with respect to constant conditions. Breeding-related differences were observed only in the light-harvesting pool, consistent with known progress on stay-green traits. These findings highlight how integrating physiological modelling with high-throughput spectral data enables robust dissection of photosynthetic acclimation strategies, offering a scalable approach to identify traits usable in selection strategies for climate-resilient breeding programs.

Poster location: I10

Integrating solar induced fluorescence with high throughput plant screening for advanced phenotyping of plants

Keren Moshelion

PlantDi-Tech

There is an urgent need to address the escalating impacts of climate change, particularly the exacerbation of drought conditions, which pose significant threats to global food security and agricultural sustainability. Innovative solutions are imperative, and one such solution involves integrating advanced technologies like the "PlantArray" system to monitor and enhance plant physiological responses to water scarcity. The "PlantArray" system enables the precise measurement of critical whole-plant physiological traits such as transpiration rate, canopy stomatal conductance, and growth rate with an exceptional spatiotemporal resolution. Augmenting this system with photosynthesis measurements offers an additional layer of information, facilitating a more focused interpretation of the system parameters. To overcome the limitations of single-leaf photosynthesis measurement techniques, this study employs a remote sensing approach to rapidly scan numerous samples at multiple time points, revealing insights into drought stress responses of S. lycopersicum lines. An ultra-spectral spectroradiometer mounted on a mobile cart was positioned above an experimental matrix comprising drought-stressed S. licopersicum obsolete and mutagenic lines.

Our findings reveal that the vegetation index Photochemical Reflectance Index (PRI) exhibited greater sensitivity to drought stress compared to other vegetation and photosynthesis remote sensing indices. Photosynthesis indices demonstrated increased sensitivity to daily biomass accumulation and served as predictors of final plant yield. Interestingly, Solar-Induced Fluorescence (SIF) parameters, solely indicative of photosynthesis-emitted fluorescence, exhibited no correlation with stress levels or final biomass production. This study articulates the potential to monitor plant responses to agricultural stressors through real-time physiological tracking across complete diel cycles, thereby enriching our understanding of plant-environment interactions.

Ultimately, this integrated system shows promise in screening and developing crop cultivars with ideal physiological and photosynthetic traits, vital to cultivating resilient crops in extreme droughts and weather conditions.

Poster location: I11

Environments: Enhancing Screening, Profiling Applications and Data Quality Through Digital Phenotyping

Sina Roth

Bayer Crop Science

As the agricultural landscape evolves under the pressures of climate change and resource constraints, the need for innovative approaches in controlled environments becomes paramount. Within Bayer Cropscience R&D cutting-edge strategies have been developed that accelerate screening processes, enhance candidate selection, and improve data quality in the realm of crop science. A central theme of our research is the utilization of digital phenotyping technologies, which provide comprehensive insights into plant physiological changes across various applications, including herbicides, fungicides, entomology, breeding, and biologics.

Digital phenotyping from the scale of a well to a pot, enables the collection of high-resolution, real-time data on plant responses, facilitating the early classification of candidates up to the in-depth profiling of physiological changes. By employing advanced imaging techniques and data analytics, we can effectively monitor phenotypic traits and their correlations with environmental factors and treatment interventions. This capability not only deepens our understanding of plant behavior but also fosters the development of precise management strategies in Crop Science.

Poster location: I12

Flying Towards Sustainability: Soybean HoloTypes for Climate Resilience

Oliver Knopf[1]; Thea Mi Weiss[1]; Beat Keller[2]; Andreas Hund[2]; Patrizia Zamberletti[3]; Nicolas Vuille-Dit-Bille[4]; Juan Herrera[4]; Claude-Alain Bétrix[4]; Boulos Chalhoub[4]; Christoph Barendregt[1]

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European soybean (Glycine max L.) cultivars are gaining importance as a sustainable protein source for food and feed, supporting agricultural self-sufficiency and reducing environmental impact, particularly in Switzerland (Keller et al., 2024). While rising temperatures due to climate change may expand cultivation potential, soybean production also faces increasing climatic risks, including hydrological stress and heat extremes. Breeding efforts must therefore focus on improving yield, protein content, early vigor, and resilience to stress.

The PhenoSoy project addresses these challenges by developing a UAV-based high-throughput phenotyping (HTP) platform to enhance response to selection, particularly in early breeding generations where high genotype numbers and low seed availability constrain traditional phenotyping. Building on prior research demonstrating the predictive potential of UAV-derived canopy traits for defining soybean ideotypes (Roth et al., 2022), PhenoSoy implements a systematic UAV-based workflow combined with advanced NIRS methodologies. This workflow leverages standardized, scalable image-processing pipelines developed collaboratively by DSP, Hiphen, ETH Zurich, and Agroscope, enabling efficient phenotyping across diverse environments.

By integrating phenotypic, genomic, agronomic, and meteorological data, PhenoSoy seeks to move beyond static ideotypes toward a flexible multi-environment framework — the HoloType. Rather than aiming for a universal genotype, HoloTypes represent sets of holistic, improved, multi-trait ideotype profiles tailored to specific agro-climatic conditions and defined by distinct trait combinations.

While preliminary UAV imagery analysis indicates promising results, comprehensive analyses and modelling remain ongoing. PhenoSoy aims to improve precision in early-stage selection, accelerate breeding cycles, and enhance the development of cultivars with reliable yield and protein performance under Swiss conditions. By integrating advanced phenotyping into routine breeding, PhenoSoy provides a forward-looking framework for climate-resilient soybean improvement. The PhenoSoy project anticipates significantly improving the precision and efficiency of early-stage soybean selection decisions, ultimately enhancing yield stability, protein quality, and contributing to sustainable crop improvement.

Poster location: I13

Non-invasive imaging to monitor crop performance in Cannabis sativa

Oliver Berkowitz[1]; Viet Nguyen[1]; Ben Niehaus[2]; Anthony D'Agata[1]; Amelia Pegg[1]; Mathew G. Lewsey[1]; Edhem Čustović[3]; Ricarda Jost[1]; James Whelan[4]

[1] Australian Research Council Research Hub for Medicinal Agriculture, La Trobe Institute of Sustainable Agriculture and Food & Australian Plant Phenomics Network, , La Trobe University, Bundoora, VIC, Australia; [2] SpexAI GmbH, Dresden, Saxony, Germany; [3]

Cannabis sativa L., one of the oldest cultivated crops, has a complex domestication history due to its diverse uses for fibre, seed, oil, and drug production. Its wide geographic distribution together with human selection resulted in phenotypically and genetically highly divergent varieties as a rich resource to study underlying physiological and molecular determinants. Hemp was selected for fibre production and constituted the most wide-spread usage type for millennia. Selection of hemp types favoured late flowering and fast elongation to increase vegetative growth. By contrast, for drug-type Cannabis maximisation of flower production and high drug yield led to narrow selection starting about 1000 years ago. While prohibition of Cannabis cultivation has hampered research, more recently increased medical use of its main specialised metabolites, i.e. the cannabinoids 9-tetrahydrocannabinolic acid (THCA) and cannabidiolic acid (CBDA), has heightened attention of the scientific community and adoption of research outputs in the industry.

While cultivation of Cannabis in Australia is still under strict regulation, we have started to develop phenotyping methodology to monitor Cannabis growth by non-invasive imaging and application of machine learning (ML) approaches. Using multispectral imaging with 15 wavebands in the UV to NIR range within a production facility, we were able to establish a ML multi-modal pipeline based on a customised YOLO and Multi-Axis Vision Transformer (MaxViT) architecture. This allowed to detect flowers within images and classify their maturity as well as to distinguish the three Cannabis chemotypes (THCA-dominant, CBDA-dominant, THCA/CBDA co-accumulating) with about 90% accuracy. In addition, the model was extended to determine cannabinoid tissue concentrations based on ground truth data obtained by liquid chromatography mass spectrometry. With the limited data available encompassing 270 multispectral images across 34 genotypes, model performance was between R^2 0.6 to 0.9 which was restricted by limited generalisation due to dataset imbalances. Nevertheless, the model showed encouraging results in quantifying THCA, CBDA and their precursor CBGA co-occurring in plant tissues. This work provides the spectral imaging approach to distinguish between these chemically highly similar specialised metabolites. Future work will extend this work into an automated, high-throughput platform to monitor Cannabis growth and optimise production.

Poster location: I14

Automated X-ray-Based Spike Analysis for Grain Characterization

Sajid Ullah, Sajid Ullah, Lamis Abdelhakim, Klára Panzarová

PSI (Photon Systems Instruments), spol. s r.o.

Grain yield is a key determinant of cereal crop productivity, with spike morphology playing a crucial role in its assessment. Traditional spike characterization methods are often labor-intensive and time-consuming, limiting their scalability for large-scale breeding programs. To address this challenge, we present an advanced image-based tool leveraging deep learning methodologies for non-invasive, high-throughput spike phenotyping. The system utilizes a U-Net model trained on 200 annotated spike images, incorporating data augmentation techniques such as rotation and scaling to enhance robustness. With the Dice coefficient as the loss function and the Adam optimizer, the model was trained for 60 epochs with early stopping to prevent overfitting. Additionally, adaptive thresholding and the Segment Anything Model (SAM) were evaluated, achieving Dice coefficients of 0.95 and 0.98, respectively, demonstrating the effectiveness of automated spike segmentation. The post-processing of segmented grains extracts key morphological traits, including spike length, grain number, grain width, grain length, and grain area, facilitating precise yield analysis. This innovation enhances the efficiency of crop breeding research by providing an accurate, non-destructive, and scalable solution for spike trait analysis.

Keywords: X-ray imaging, spike phenotyping, deep learning, cereal crops, grain characterization, high-throughput analysis, image segmentation.

Poster location: I15

Breaking Barriers: Overcoming Traditional Bottlenecks in Phenotyping Image Analysis with AI

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Traditional color segmentation poses significant challenges in image-based plant phenotyping, often leading to inaccuracies and inconsistencies. Issues such as the detection of tiny plants, the interference of reflections, or background color can compromise the reliability of results. However, these obstacles are no longer a concern. In this work, we introduce a range of simple yet effective artificial intelligence (AI) models designed for various applications in plant phenotyping. By integrating AI-driven approaches with advanced image analysis, we enhance accuracy and robustness for plant detection, enabling more precise and efficient segmentation and subsequent data evaluation while overcoming the limitations of traditional segmentation methods. Moreover, our AI-powered methodology coupled with image analysis allows for the extraction of a wide range of morphological and physiological traits with high precision and efficiency. This automated approach not only improves phenotyping accuracy but also provides deeper insights into plant growth, development, and stress responses. Moreover, compared to classical methods, our technique significantly increases time efficiency by reducing the need for post-imaging labor-intensive manual analysis while maintaining a high level of accuracy. As a result, our AI-driven workflow offers a more standardized and reproducible procedure, ensuring consistency and reliability in plant phenotyping applications.

Poster location: I16

ESTIMATING DAILY HIGH-RESOLUTION LEAF AREA INDEX (LAI) FOR WHEAT USING PLANETSCOPE DATA

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The emergence of new commercial satellite constellations such as PlanetScope enables the acquisition of high-resolution imagery (3 m spatial resolution, daily revisit), opening up new opportunities for large-scale wheat phenotyping. However, PlanetScope presents notable limitations in terms of spectral coverage and radiometric calibration, which hinder the accurate retrieval of biophysical variables such as the Green Area Index (GAI). This study evaluates the potential of PlanetScope for wheat phenotyping by adapting a generic algorithm initially developed for Sentinel-2 (20m spatial resolution), BV-NNET, for PlanetScope's spectral configuration. In particular, we investigate how integrating crop- and site-specific prior information (e.g., soil reflectance, plant biochemical traits) can mitigate PlanetScope's limitations in spectral and radiometric accuracy. Our dataset spans 10 farmer fields where 4 wheat cultivars were grown under identical conditions within 50×50 m plots to facilitate comparisons between SENTINEL-2 and PLANETSCOPE. To expand the dataset's diversity, we integrated GAI measurements from phenotyping experiments conducted across multiple countries (China, Australia, and Switzerland), encompassing a wide range of genotypes, environmental conditions, and phenological stages.

We explored multiple scenarios from the literature for incorporating prior information, including different statistical distributions (uniform, Gaussian, or data driven distributions) and co-distributions of variables such as soil reflectance and plant biochemistry, used as inputs of the PROSAIL radiative transfer model in the BV-NNET approach. Results demonstrate that when appropriate joint priors are used, the estimation accuracy improves significantly, even if some proposed variable co-distributions do not seem realistic. This highlights the importance of selecting the right priors to optimize biophysical variable retrieval from satellite data.

Poster location: I17

Hybrid Phenological Monitoring from Flowering to Fruitlet: A Low-Input Method for Scalable Field Phenotyping

Herearii Metuarea; Walter Guerra; Pejman Rasti; David Rousseau

Accurate monitoring of phenological stages, such as flowering and early fruit development, is critical for optimizing crop management in both conventional and innovative agricultural systems. Yet, current methods heavily rely on supervised models, which require large, annotated datasets for each stage. Such an approach is often impractical and costly to obtain, especially in terms of the number of phenological stages to annotate and limited expert availability.

In this study, we present a hybrid pipeline that combines supervised detection of all reproductive organs with unsupervised identification of their phenological stages, enabling a scalable and annotation-efficient solution for field phenotyping. In the first step, a supervised object detector is trained to localize visible reproductive structures in RGB images, regardless of their specific developmental stage (e.g., buds, flowers, fruitlets). In the second step, each detected organ is associated with a phenological label by comparing it to a small reference bank via k-nearest neighbor search in a learned embedding space. This space captures fine-grained morphological and color patterns, enabling unsupervised stage recognition.

We applied our approach to apple trees under real field conditions. Results demonstrate that our method can accurately distinguish flowering and fruitlet stages using minimal supervision. Its modular design, low annotation requirements, and robustness to field variability make it particularly suited for phenotyping in innovative agricultural practices, such as low-input management, smart orchard monitoring, and perennial crop observation. Our contribution offers a generic and lightweight alternative to traditional phenotyping pipelines, facilitating phenological monitoring across diverse agricultural contexts.

Poster location: I18

Hybrid Phenological Monitoring from Flowering to Fruitlet: A Low-Input Method for Scalable Field Phenotyping

Herearii Metuarea; Pejman Rasti; Helin Dutagaci; Jérémy Labrosse; David Rousseau[1]

[1] *INRAE*

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Poster location: I20

Seed Phenotyping with Tailored Spectral-Optical Sensors

Andrea Matros[1]; Andreas Backhaus Andrea[1]; Rachel A. Burton[2]; Bettina Berger[2]; Paula Mor Llombart[3]; Lina Maria Cáceres Leal[3]; Mark Tester[3]; Vanessa Melino[4]; Udo Seiffert[1]

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Modern breeding practices, including new sequencing technologies and marker assisted selection, accelerate the breeding of new cultivars. However, selection in niche species (e.g., Salicornia spp.) and for specific metabolic traits (e.g., fructans in cereals, oilseed composition) still requires complex wet lab analyses.

Optical spectroscopy can complement or even replace biochemical analysis of samples in various applications. Such approaches typically involve using mathematical and computational techniques to analyse the recorded spectra and extract information about the samples' properties. Often only a subset of spectral bands is relevant for a given application, allowing for the development of multispectral sensors with improved properties regarding overall energy consumption and final instrument costs without significantly compromising prediction accuracy.

We applied inverted spectroscopy with corresponding calibration models, based on machine learning using the scancor.de/r® platform, to construct application-specific, optimised soft-sensors with individual design of the spectral bands used. Two such examples will be presented here.

(1) In barley (Hordeum vulgare) fructan content, with impact on nutritional quality, was the target trait. To generate a training data set, sugar profiles of 156 accessions were determined by liquid chromatography coupled to high-performance anion-exchange chromatography. From the same accessions, hyperspectral signatures of mature grain were recorded, which could be mapped against the sugar composition by machine learning algorithms. From the data set, spectral signatures indicative for fructan patterns were evaluated and employed for the development of a handheld fructan sensor.

(2) For Salicornia spp., we developed a tailored handheld sensor that can be taken into the field or at the site of seed threshing to rapidly assess seed quality. First, a training data set was generated by biochemical analysis of seed moisture, protein, saponin content (anti-nutritive, bitter-tasting compound), oil content, and fatty acid composition (saturated, monounsaturated, and polyunsaturated fatty acids). For the same genotypes, hyperspectral signatures were recorded and the combined data set was used for the sensor development in the same way as described above. The sensor will support the selection process within the KAUST breeding program and can be used to optimise quality control during harvesting and industrial production.

Poster location: I21

Decentralised and Transparent AI Model Operations for Plant Phenotyping

Andreas Backhaus[1]; Andrea Matros[1]; Udo Seiffert

[1] *COMPOLYTICS GmbH*

Artificial intelligence (AI) models are increasingly shaping crop plant phenotyping - from disease detection to trait evaluation - yet their deployment is often tied to centralised infrastructures. These "black box" systems, controlled by service providers, restrict transparency, complicate validation, and pose risks around reproducibility and model ownership. For plant breeders and researchers, this can compromise confidence: Which model was used? Has it changed? Can it be trusted and independently verified?

We developed a decentralised infrastructure for AI model deployment for a verifiable, token-based alternative. Using blockchain and smart contracts, each model is linked to a unique cryptographic identity via non-fungible tokens (NFTs), while core model parameters are stored on-chain. Larger components are held in the InterPlanetary File System (IPFS), a peer-to-peer data network designed for distributed storage. A neural network-specific model-splitting method can reduce storage requirement by over 90%, significantly lowering gas fees for model deployment directly on-chain.

Smart contracts govern usage rights, model versioning, and provenance, ensuring all updates and transactions are recorded unchangeably and auditable by design. Unlike centralised scoring platforms, model execution can be handled on decentralised, serverless infrastructures (e.g., Internet Computer Protocol), where encrypted models are temporarily retrieved for scoring and never exposed, protecting intellectual property and data integrity.

Despite the complexity of the underlying technologies, these capabilities are fully embedded in the Compolytics sensor firmware and its user interface CICADA, requiring no blockchain knowledge from the user. Users benefit from an easy-to-use system that ensures secure, re-producible, and trustworthy model deployment across sites and seasons.

Importantly, the solution also supports energy-efficient recurring measurements, contributing to the concept of Green Sensing as defined by Compolytics: environmentally conscious sensor technologies with minimal computational and energy overhead. Future extensions include permissionless scoring and integration of zero-knowledge proofs for verifiable results. This decentralised machine learning operations (MLOps) framework offers a robust, future-oriented alternative to current practices fostering openness, reproducibility, and trust in phenotyping AI.

Poster location: I22

Introducing the La Trobe University node of the Australian Plant Phenomics Network

Ricarda Jost PhD[1]; James Whelan[2]; Veronica Borrett[1]; Anthony Bacic[1]; Mathew G Lewsey[3]

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The La Trobe University node of the Australian Plant Phenomics Network (APPN) has been established in 2024. It is funded by the Australian Government's National Collaborative Research Infrastructure Strategy (NCRIS) and specializes in fully automated gantry-mounted imaging systems in controlled environment rooms. Imaging systems include 2D-/3D-RGB, fluorescence, thermal, and hyper spectral VNIR sensors. Rooms accommodate between 10 m2 and 70 m2 of plant growth area, with multi spectral LEDs that can produce between 850 and 1500 µmol m-2 sec-1 maximum light intensity at one meter distance from the light source. Use of five different nutrient stock tanks allows for highly customizable fertigation mixes with automated pH and EC adjustment. Mixes can be delivered to nine separate zones per grow room with each zone serviced by five valve groups. Three plant cultivators manage trials and manual phenotyping records. Data management follows Findable, Accessible, Interoperable and Reusable (FAIR) principles for manual and automated data collection which facilitates downstream data processing and analyses. Study design, data acquisition and analyses are supported by our data management team. The LTU APPN node is supported by analytical 'omics' expertise through the La Trobe Institute for Sustainable Agriculture and Food (LISAF) and the Australian Research Council funded Centre of Excellence in Plants for Space and the Research Hub for Protected Cropping. The facilities are available to researchers and industry partners at subsidized rates. Examples of how these facilities are currently used to optimize plant nutrient use and cultivar performance for protected cropping systems will be presented.

Poster location: I23

AI-based Leaf Image Analysis for Automated Phenotyping of Common Bean Genetic Resources using Citizen Science Experiment (CSE) Data – The EU H2020 INCREASE Project

Evan Musari[1]; Alice Pieri[2]; Valerio Di Vittori[3]; Simone Papalini[2]; Elisa Bellucci[2]; Elena Bitocchi[2]; Emanuele Frontoni[4]; Adriano Mancini[2]; Alessandro Galdelli[5]; Kerstin Neumann[6];

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Artificial Intelligence (AI) and Citizen Science (CS) are being utilised towards automated phenotyping of genetic resources in common bean as part of the INCREASE EU Horizon 2020 Project. The INCREASE Citizen Science Experiment (CSE) involves approximately 1,100 genotyped single-seed descent (SSD) purified accessions of domesticated common bean. The accessions have been phenotyped by over 8,000 volunteer citizens across Europe using a dedicated INCREASE CSA mobile application. This large-scale initiative generated extensive image datasets. A case study using AI-based image analysis using a YOLO (You Only Look Once) model applied to the CSE leaf image data for classifying common bean leaf shapes achieved an overall accuracy of 0.82. Our next step is to extend a similar AI-based approach to additional traits, including flower colour, seed colour and seed shape.

Poster location: I24

Seeing the Similarity: AI-Based phenotyping to select similar varieties in Ornamentals

Sanchari Sircar; Jesper Guijt; Koen van Oostrom; Ronald de Jongh; Michel Ebskamp; Raoul Haegens

Naktuinbouw

At Naktuinbouw (the Netherlands Inspection Service for Horticulture), we conduct DUS testing—assessing the Distinctness, Uniformity, and Stability—to grant Plant Breeders' Rights and/or national listing to plant breeders. For ornamentals like Phalaenopsis, this distinctness testing is performed, among other methods, by comparing photos of candidate varieties to all photos of previous candidate varieties and reference material. Manual comparisons by the DUS experts are often time-consuming with increased risk of human error, potentially leading to missed reference varieties in distinctness testing and resulting in false positive conclusions. Using commercial tools and external service providers creates unnecessary dependencies and security issues. To that end, we have attempted to create an AI-based similarity search system to assist in the selection of similar varieties for DUS examiners.

We have used a Vision Transformer (ViT) model to annotate the images. This output was saved to an FAISS index to enable efficient similarity search across large image datasets. The visual embeddings were further enhanced by using a combination of metadata and morphological descriptions to train the neural network capable of prioritizing specific traits of interest. Other than the ViT model and neural network, additional combinations of models and classifiers were also tested.

A Django web application has been developed where DUS experts can upload candidate images and receive the top-ranked similar images based on visual and trait similarity. This allows quick examination of the candidates against hundreds of images which are there in our reference collection.

Beyond Phalaenopsis, we wish to explore the possibility of applying the current architecture to other ornamental crops. This will be a significant step toward modernizing the DUS examination and management of reference collections by integrating explainable AI tools into regulatory workflows, aiming for greater efficiency, reliability, and scalability.

Poster location: I25

Anatomical comparison of early stages of adventitious and hairy root formation by Magnetic Resonance Imaging (MRI)

Henrik Peuthert[1]; Philipp Rüter[1]; Ljudmilla Borisjuk[2]; Stefan Ortleb[2]; Steffen Wagner[2]; David Wamhoff; Traud Winkelmann[1]

[1] Leibniz Universität Hannover, Institute of Plant Genetics; [2] Leibniz Institute of Plant Genetics and Crop Plant Research (IPK Gatersleben)

The aim of this project is to uncover early cellular and structural distinctions between hairy roots (HR) and adventitious roots (AR) regenerating from rose leaf explants. ARs, being the crucial basis for vegetative propagation via cuttings, typically arise in response to external triggers like wounding, while HRs are initiated through genetic modification by Rhizobium rhizogenes, which inserts root-inducing genes into the host's genome. Ri plants regenerated from HR are of interest in breeding for compactness and drought tolerance.

A set of 106 rose genotypes has previously been characterized for their abilities to form AR (Wamhoff et al. 2024a) and 104 genotypes to form HR (Rüter et al. 2024) in genome-wide association studies. Out of them, three genotypes with contrasting AR and HR formation capacities will be included in the present study: 'Golden Gate' with exceeding AR, 'Ascot' with high HR formation, and 'Herzogin Friederike' with medium AR and HR formation. Leaf explants of these genotypes will be used to induce ARs on petioles in vitro on hormone-free medium, while HRs are generated by R. rhizogenes-mediated transformation. Magnetic resonance imaging (MRI) has demonstrated its potential to non-invasively visualize AR formation on shoots (Wamhoff et al. 2024b) and will be applied to monitor both AR and HR initiation and development over time in intact plant tissues. To confirm HR identity and ensure reliable classification, eYGFPuv fluorescence and PCR will be employed. Complementary histological analyses using the β-glucoronidase (GUS) reporter gene system for HR primordia validation will provide additional detailed anatomical insight into tissue structure and root formation on a cellular level.

A first HR induction experiment of the three rose genotypes with the reporter systems GUS and eYGFPuv confirmed the respective genotypic capacities for HR formation. Explants of 'Golden Gate' did not show HR formation at all while for 'Ascot' the highest HR formation rate could be observed. As expected, explants of 'Herzogin Friederike' showed a medium HR regeneration rate. Additionally, compatibility of the GUS reporter system with histological treatment could be proven with the indigo blue pigment remaining intact throughout fixation, embedding and de-paraffinization. These results pave the way for the next steps, which are first MRI and histological comparisons of AR and HR formation.

Poster location: I26

From Pixels to Phenotypes: Semi-automated Classification of Autumn Reddening and Bud Set Using Hyperspectral Imaging in Scots Pine

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[1] Czech University of Life Sciences Prague, Faculty of Forestry and Wood Sciences; [2] University of Eastern Finland, Faculty of Science, Forestry and Technology

This study investigated key phenological traits, specifically autumn reddening and bud set, in eight European Scots pine (Pinus sylvestris L.) provenances. Autumn leaf reddening (anthocyanin accumulation) and the timing of bud set are responses to environmental stressors such as reduced daylight and cooler temperatures. These traits exhibit substantial genetic variation, influencing species' adaptation to environmental conditions. Our experiment comprised a total of 4366 seedlings in 57 trays. We assigned the provenances to 3 groups corresponding to European regions of similar climatic conditions. All the seedlings were grown in a nursery common garden experiment located in Finland. So far, phenology in forest trees has been assessed via scoring, which can be very subjective and error-prone. Thus, we propose a supervised classification method using hyperspectral images from the VNIR SNAPSCAN camera (imec, Leuven, Belgium). We created a pipeline for the supervised classification using the freeware Spectronon software (Resonon Inc., USA) and Fiji (NIH, USA). The supervised classification method conserves computational power by processing each image (one tray) separately, avoiding the computational burden of appending hyperspectral images together. The supervised classification method establishes a common threshold for classifying individual images by utilizing pixels from all provenances for each class (background, green needles, red needles, dry needles, and buds). We tested the classification results and spectra for provenance group effects using partial least squares discriminant analysis (PLS-DA). The classification results predicted provenance subgroups with 0.95 accuracy (Kappa = 0.92). For comparison, PLS-DA using raw spectra predicted provenance subgroups with 0.82 accuracy (Kappa = 0.73) and first-derivative spectra with 0.93 accuracy (Kappa = 0.89). Although the first-derivative spectra predict the provenance subgroup with comparable accuracy to our classification results, the classification output offers additional insight through graphical visualization of the differences. Moreover, we created a macro counting the terminal buds based on the classification images with high accuracy (F-score = 93%). The proposed high-throughput method allows for time-efficient phenotyping of phenological traits. The new monitoring approach adaptable to any species reveals how population origin shapes tree adaptation and resilience while minimizing observer bias.

Poster location: I27

From hurdles to harmony: FAIR data management for plant phenotyping in EMPHASIS and ELIXIR communities

Farzaneh Kazemipour-Ricci[1]; Isabelle Alic[1]; Cyril Pommier[2]

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The data life cycle comprehension and handling is challenging in research and especially in data-rich domains like plant phenotyping. Plant phenotyping datasets are mostly used only once, due to different reasons such as lack of metadata, documentation compromising meta analysis.

There is a broadening recognition of the value of FAIR and sustainable data practices within the phenotyping community, despite the associated challenges and efforts. That can happen incrementally, supported by appropriate guidance, ensuring a smooth and manageable transition. A key first step offering immediate benefits is designing data workflows with sharing and interoperability in mind, especially through the use of standardized file formats, vocabularies and ontologies, which enable integration across projects and platforms. In addition, many tools and support teams already embed FAIR principles, guiding researchers through best practices, which we will describe in this work.

For that purpose, we will summarize here services and solutions gathered and built by the EMPHASIS and ELIXIR European Research Infrastructures through several of their national nodes including PHENOME-EMPHASIS.fr, according to Open Science policies in Europe.

To begin, data standards have been developed and widely implemented within phenotyping communities (MIAPPE, BrAPI). In addition, data repositories (Zeonodo) and data portals (FAIDARE) are recommended to ensure long term accessibility and findability. To go further, open-source information systems like PHIS are currently used within the community providing FAIR data. PHIS allows to enrich datasets with knowledge and metadata enabling the reuse of data and meta-analyses. It interoperates and integrates data into external resources (e.g. modelling platforms or external databases). In parallel, a set of transversal resources, ranging from guidelines (RDMKit) to training materials and outreach initiatives, supports the broader community.

Importantly, even adopting one or a few well-chosen tools or practices can mark a strong beginning toward data reuse. Starting small, by integrating metadata standards, agreeing on common vocabularies for traits using existing or dedicated ontology, or working with a data steward, can lay the foundation for long-term success. Thanks to these services and tools, several communities such as PHENOME-EMPHASIS have turned FAIR from principles to operational as an accelerator of research efficiency and impact.

Poster location: I28

Unsupervised Contaminant Detection in Pelleted Seeds Using Computed Tomography

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Keywords: Variational Autoencoder, X-ray Computed Tomography, Generative Modelling, Anomaly Detection, Pelleted Seeds, Seed Quality.

Seed pelleting is a widely used technology that enhances seed handling, protection, and germination performance in modern agricultural practices. However, it introduces multiple phytosanitary and biosecurity risks as the pelleting obscures the seed surface, making it difficult to visually inspect for contaminants or perform seed quality control. Thus, X-ray computed tomography was employed to capture the internal and external morphology of pelleted seeds of two species, Beta vulgaris and Cichorium intybus. An end-to-end fully unsupervised pipeline is proposed for non-destructive contaminant detection in pelleted seeds. Our pipeline supports automatic seed extraction and localisation in volumetric images. A 3D beta variational autoencoder (β-VAE) was trained solely on the extracted pure pelleted seeds to learn the underlying representation of the normal class. When abnormal input (contaminant or empty pellet) is fed into the trained model, it produces a high reconstruction error, which is a practical indicator of atypical data and flags anomalous seeds. Our method was evaluated on varying levels of anomalous CT images, showcasing a superior performance over traditional methods, which exemplifies the potential of combining X-ray computed tomography and generative AI modelling for addressing biosecurity and regulatory concerns, without requiring massive datasets or prior annotations.

Poster location: I29

A Deep Learning Approach for Real-Time Detection and Severity Assessment of Apple Scab in Pre- and Postharvest Environments Using YOLOv11

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Agroscope c/o DLZ FI EFD

Apple scab (AS), caused by the fungal pathogen Venturia inaequalis, is one of the most economically significant diseases affecting apple (Malus domestica) production worldwide. Characterized by dark, necrotic lesions on leaves and fruit, AS compromises both yield and marketability, with severe infections leading to premature fruit drop and substantial postharvest losses. Usually methods for assessing AS severity rely on visual scoring, a labor-intensive, time-consuming, and inherently subjective process due to human variability in symptom interpretation. These limitations hinder large-scale phenotyping efforts, particularly in breeding programs aimed at developing resistant cultivars. To address these challenges, this study presents a scalable, deep learning-based framework in object detection and segmentation for automated, real-time identification and quantification of AS symptoms on apple fruit under both pre- and postharvest conditions. The model You Only Look Once version 11 (YOLOv11) was fine tuned in two steps using 840 × 840 pixels images captured under varying illumination, angles, and several apple varieties. First, a detection model was trained to localize individual apples within images, achieving a precision exceeding 90% across diverse orchard and laboratory settings. Subsequently, a segmentation model was fine-tuned to identify and quantify AS lesions on detected fruit, reaching 78% precision in lesion segmentation despite the complexities introduced by natural variability in symptom expression, lighting conditions, and fruit surface topography. Data augmentation techniques including rotation, scaling, and synthetic shadow generation were applied to mitigate biases arising from field conditions such as occlusions, uneven lighting, and heterogeneous lesion patterns. As the YOLOv11-based pipeline supports real-time processing of both static images and video streams, this enables rapid in situ evaluation without the need for specialized hardware. In field trials, the system processed orchard imagery, while postharvest applications facilitated automated grading of stored fruit. This automated solution supports breeding programs for scab-resistant cultivars and provides a scalable tool for precision disease management in commercial orchards. The framework's modular design allows future expansion to other apple diseases, demonstrating the potential of deep learning for agricultural phenotyping applications.

Poster location: I30

de.NBI & ELIXIR-DE - The Infrastructure Powering German Bioinformatics

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The German Network for Bioinformatics Infrastructure (de.NBI), established in 2015 by the Federal Ministry of Education and Research (now Federal Ministry of Research, Technology and Space), serves as Germany's national hub for bioinformatics services, training and cloud computing. It also operates as ELIXIR Germany (ELIXIR-DE), representing the German Node within the European ELIXIR infrastructure. This dual role supports not only data sharing, interoperability, and cross-border collaboration, but also positions German expertise and innovation at the European level.

The network comprises eight Service Centers and a central coordination unit with over 150 active members, making it a key driver of scientific progress. Supported by Forschungszentrum Jülich GmbH since 2022, the network ensures sustainable infrastructure growth through partnerships.

The de.NBI & ELIXIR Germany portfolio includes almost 160 high-quality bioinformatics services covering fields such as human health, plant science and microbial research fields and is available to both academic and industrial users.

Training is another cornerstone of the infrastructure: since 2015, over 500 courses have reached more than 12,000 participants, equipping them with essential bioinformatics skills for data-intensive life science research.

Furthermore, the de.NBI Cloud provides scalable and secure computational power for diverse research needs, supporting more than 4,000 users and over 1,300 projects, enabling big data workflows across diverse research areas.

Lastly, through the de.NBI Industrial Forum, the network strengthens the link between academic research and industrial applications by collaborating with over 45 industry partners to exchange knowledge, foster innovation and translate bioinformatics into practical applications, enhancing research impact beyond academia. For further details on services, training, and collaboration opportunities, please visit http://www.denbi.de .

Poster location: I31

Drone Sampling: A Cost-Effective High-Resolution Approach for Precision Agriculture and Field Phenotyping

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The use of drones in agricultural applications has become increasingly important, particularly for high-throughput phenotyping and precision agriculture. Conventional drone surveys typically rely on orthomosaic generation, which requires substantial image overlap (70–80%) and stable environmental conditions. These requirements significantly increase operational complexity and cost, especially when aiming for millimeter or sub-millimeter resolution necessary to identify specific plant features or diseases. Moreover, sub-mm imaging often necessitates expensive equipment and is sensitive to plant movement, limiting its practical application in dynamic field conditions. To address these challenges, we introduce a novel drone sampling methodology that eliminates the need for orthomosaics by guiding UAVs to specific field locations—such as plot centroids—analyzing individual images and projecting the results with direct georeferencing methods. This approach enables ultra-high-resolution imaging using standard drone equipment, as it allows flights at very low altitudes without the constraints of image stitching. This methodology has been successfully applied in a range of phenotyping and precision agriculture use cases. These include weed detection and classification, flower and wheat head counting, and disease identification. Additionally, the technique has proven valuable in agro-insurance applications, such as assessing drought impact in maize and flood damage in potato fields. These examples demonstrate the method’s versatility and its potential to support both research and commercial agricultural decision-making. In this presentation, we will provide technical insights into the drone sampling workflow, discuss its into the MAPEO drone processing infrastructure, and showcase results from multiple use cases conducted during the 2022–2025 trial seasons. Our findings highlight how this approach can significantly boost the efficiency, resolution, and affordability of drone applications in modern agriculture.

Poster location: I32

High throughput phenotyping of cereal x alfalfa mixed crops

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In agroecology, the combination of cereals and legumes is considered an interesting combination for enriching the soil with carbon and nitrogen while limiting weed growth. However, this practice is tricky to carry out because if alfalfa grows too fast, it can smother the cereal. One way of improvement is the selection of alfalfa genotypes with limited competitive power with the cereal. However, the visual phenotyping of these mixed plots is a complex task to be carried out in the field by simple visual estimation. This is why the development of digital phenotyping methods is a promising way to improve this selection process.

A deep learning model has been developed to automate the multi-class semantic segmentation of images. A total of 6000 images with a dimension of 512x512 pixels were first manually annotated. This dataset was used to train and evaluate the deep learning model. These images include a wide variety of life stages, acquisition systems and agrometeorological conditions, as well as cereal and Fabaceae species.

The model is based on a SegFormer architecture. The predictive performance of the segmentation model was evaluated on 30% of the complete dataset, independent of the training phase. The overall accuracy obtained is 0.91 for the Intersection over Union (IoU). In addition, we combined the output with other already published models to segmentate the fraction of senescence and the fraction of wheat heads.

A mixed crops trial located in Gréoux les Bains (south-east of France) has been conducted by ARVALIS since 2023, in collaboration with INRAE. This trial combines a wheat variety with several alfalfa genotypes. It was phenotyped by an autonomous robot, the PHENOMOBILE, equipped with high-resolution RGB cameras synchronized with a flash. In 2024, 21 measurement dates have been acquired. Each image was analyzed using our segmentation model to estimate the fraction of total land cover by each species, as well as their respective green and senescence fractions. The temporal evolution of these traits shows the main phases of the two crops: the growth and then the senescence of wheat; growth, as well as the regulation phases for alfalfa. Other traits aiming at characterizing the competition between both crops are also proposed, such as the height difference between both crops. They highlight differences in wheat development depending on the associated alfalfa genotype, paving the way for the use of this technique for larger-scale phenotyping,

Poster location: I34

Detection of the grapevine phenological stages using smartphone images

Davide Poggiali[1]; Antonio Carlomagno[2]; Giuseppe Montanaro[2]; Donatella Occorsio[2]; Woula Themistoclakis[3]; Vitale Nuzzo[2]

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In viticulture, many important decisions, such as plant protection, nutrition, and irrigation treatments, are based on the detection of plant phenological stage. Traditionally, phenological stages are established through by visual inspections aided by of descriptive schemes of the grapevine annual cycle (BBCH scale). However, human visual observations are time-consuming, prone to error, and could introduce uncertainty, especially if the observer lacks enough training. In the last decade, several different approaches have been proposed to estimate the phenological stage of grape bunches. The present study aims to combine high-resolution digital images captured with a built-in smartphone camera, segmentation techniques, and Machine Learning models to automatically identify the phenological stage of the bunch in situ at the plant level.

Images of two red grapevine varieties (Aglianico b. and Primitivo b.) were acquired in three different phenological stages: beginning of flowering to fruit set (BBCH 57-71), veraison (BBCH 77), and harvest (BBCH 89). Grapes Reproductive Organs (ROs) were detected and segmented automatically using Deep Learning methods. After the computation of a set of chosen features, a Machine Learning classifier model was trained. The Support Vector Classifiers (SVC) methods had the best overall accuracy among the different classification techniques, reaching an accuracy of 0.89.

This paper expands current knowledge on recognizing grapevine bunch phenological stages automatically. It confirms that a classifier can correctly predict the phenological stage of the grapevine ROs from an image in about nine cases over ten, showing a high per-class accuracy of the model used.

Poster location: I36

Labeling-free plant segmentation for the automatic extraction of plant traits from UAV RGB-imagery

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In plant breeding, plant trait evaluation provides the basis for the selection of plants with the highest performance. The large number of plants requiring screening necessitates the use of High-Throughput Field Phenotyping (HTFP). In crop management, HTFP also has its potential, as it can be used for detection of growth defects and stress across the whole field, supporting precision farming. HTFP systems commonly use remote sensing, where sensors are mounted on platforms to collect data without contact. To extract plant traits from images captured by the sensors, plant outlines must be identified, a process known as segmentation. Supervised deep learning models are popular for this task but often require retraining when field conditions differ from the training data. The training, but especially the annotation of the data is time-consuming and labour-intensive.

Given the variability in the horticulture sector, a more generalized approach is needed. A method was developed for the automatic extraction of plant traits from high-resolution UAV-acquired RGB images that is robust against variations between plants, and fields, without the need for labelling and model training. Segmentation was done using SAM 2.1, in combination with info from the canopy height model, to avoid the segmentation of weeds and soil. The retrieved masks were used to extract plant-level traits.

The method can be used for a variety of plants such as chrysanthemum, azalea, buxus… provided that they do not form a continuous, overlapping canopy, and for the extraction of a variety of traits, such as diameter, height, canopy area, biovolume. For the automatic diameter measurement of around 15.000 chrysanthemums, the average difference with manually measured diameters was less than 2 cm. Furthermore, the method was able to detect subtle changes in plant size between the two data collection dates, demonstrating its sensitivity. Compared to manual field surveys, the method is objective, less labour-intensive, faster and enables full-field coverage.

Poster location: I37

Adjustment of image phenotyping data with respect to developmental heterochrony

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Image phenotyping data consist of time courses of several characteristics measured on plants representing various genotypes subjected to specific treatments. The analysis of such data aimed at comparison of genotypes or treatments is challenging, especially when we want to take into account the shifts in development of plants. The phenomenon of different, possibly genotype-specific, reactions of plants to environmental signals, resulting in entering consecutive developmental stages at different time points, is called a (developmental) heterochrony. Efficient correction for heterochrony is an important step in discovery of traits and their genetic determinants expressed transiently at specific stages.

In order to mitigate the problem, a transformation of time-course data using landmarks is proposed. Transforming data being functional observations is called registration and the transforming function is called warping function. A landmark is defined as an observed feature of objects on which the functional data are observed that is the basis for defining meaningful comparisons. A landmark can be of internal or external type.

We present the estimation of the warping function using principles of functional data analysis. Barley data from high-throughput image analyses conducted under control and drought conditions are used as examples. The first example is based on a single external landmark (the BBCH growth stage) used to register data from spring barley cultivars measured at 32 time points (Mikołajczak et al. 2020). The second example uses data on barley cultivars measured at 44 time points (Chen et al. 2014). In this case, data on reaching a number of leaves were used as landmarks, and registration was done based on multiple landmarks. Next, data on reaching booting and heading will be used as landmarks for the analysis of the later growth stages.

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Poster location: I38

Unified Data Management in the Framework of CZPPN

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The contribution introduces a unified data management and analytical system developed to support the phenomic infrastructures within the emerging Czech Plant Phenotyping Network (CZPPN). The presented data-to-analysis approach primarily serves to streamline and automate data management and analytical processes designed to enhance cross-disciplinary collaboration and align with key trends and best practices in the plant phenomics research discipline, especially those encapsulated in the concept of FAIR and Digital Responsibility Goals (DRGs).

The presentation will highlight the challenges and recommended best practices for managing various aspects of responsible phenotyping data stewardship. These include: describing data with metadata using appropriate ontologies to ensure interoperability across data sources within and beyond CZPPN, implementing robust data security measures to prevent misuse, and addressing the ethical dimensions of data management.

Furthermore, the session will illustrate the data analytical streams being co-developed with the range of data users (e.g. biologists, breeders, agronomists, policy makers). We will present specialised concepts within the computer vision domain with a particular focus on multi-dimensional 3D data analysis (plant scans) and the interconnection of time-series and computer vision models. Consequently, we will describe the agri-system modelling framework that extrapolates and quantifies the effect of plant phenotypes across spatio-temporal scales in order to ascertain the value and impact of the plant phenotypes in a particular environmental (“ExM”) context.

Altogether, we aim to progressively cross-connect the data operations into the pipelines to automate regular tasks required for robust data analytics in support of the CZPPN and how the processes can be used by other networks.

Poster location: I39

Phenotyping From Space: Evaluating High-Resolution Satellite-Based Trait Estimation in Winter Wheat Microplot Trials

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Remote sensing enables non-destructive, high-throughput monitoring of crop physiological traits and has become a key tool in field phenotyping. Over the past decade, sensing technologies and data-driven approaches have been widely adopted in crop improvement programs. Platforms ranging from proximal sensors to UAVs have been developed to enhance the efficiency and objectivity of trait measurements in field trials.

Despite their advantages, proximal and UAV-based phenotyping present several limitations, including high operational costs, time-consuming deployment, and sensitivity to weather conditions—particularly for UAVs, which require low wind speeds and clear skies. Moreover, replicating multi-environment trials remains challenging due to the need for strict protocols and comparable equipment across sites.

To address these limitations, we evaluated the potential of high-resolution satellite imagery for microplot-level phenotyping in a controlled field experiment. Cloud-free satellite images were acquired in April and May of 2022 and 2023 over a winter wheat trial in Mauguio, France, comprising 170 microplots (1.36 × 8 m) with ten varieties, two water treatments, and two sowing dates. The dataset included Sentinel-2 multispectral images (10 bands) super-resolved to 5 m and 1 m using deep learning, and WorldView-2 (WV2) multispectral imagery (8 bands) at 1.6 m, pan-sharpened to 0.4 m. All acquisitions were within five days of in situ biomass sampling and phenomobile measurements. A state-of-the-art neural network (BV-NET) was applied to retrieve Green Area Index (GAI) from each image source, from which mean GAI and vegetation indices were extracted per microplot and date.

This study addresses two key objectives: (1) evaluating the influence of high-resolution image pre-processing (i.e., super-resolution and pan-sharpening) on the retrieval of biophysical variables at the microplot level, and (2) assessing the performance of each sensor and resolution in estimating ground-based phenotyping data and capturing treatment effects.

Preliminary results indicate that WV2 imagery, when pan-sharpened to 0.4 m using suitable methods, effectively captures treatment-induced variability among microplots. These findings support the use of high-resolution satellite imagery as a scalable, consistent, and reliable tool for field phenotyping in multi-environment trials.

Poster location: I40

Close-range monitoring of crop morpho-physiology under AgriPV via robot-mounted 3D-multispectral scanning

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The concept of Agriphotovoltaics (AgriPVs) is rapidly gaining popularity as an innovative and sustainable means for generating energy by mounting solar panels above the crop canopy in agricultural fields. Notably, AgriPV panels influence crop microclimatic factors such as light availability, wind speed, relative humidity, water availability, and temperature, resulting in unique spatio-temporal variations in crop microenvironment under the AgriPV panels. In-depth assessment of crop responses to these changes is essential for optimizing AgriPV operations. While manual measurements of plant growth and assessment of physiological status using handheld instruments may provide some insights, such an approach would be labor-intensive and low-throughput. At the same time, implementing remote sensing approaches is also limited for such farms due to the occlusion of crop canopy under AgriPV panels, in addition to the low resolution of aerial imagery. In such scenarios, close-range 3D-multispectral scanning provides a unique solution by enabling rapid large-scale documentation of crop responses at very high-resolutions. Hence, our study explores the use of a customized field-compatible robot “FieldDeer” equipped with a 3D-multispectral scanning system for documenting and phenotyping morphological and physiological traits of crops under AgriPVs with high precision and high throughput. The trials encompass spinach, soybean, and maize, grown under two types of AgriPV systems. The investigation focuses on assessing long-term crop responses including morphometric features at the plant level, such as canopy cover, height, and volume, as well as short-term responses at the leaf level, such as diurnal changes in leaf angles under dynamic shading conditions. The system also records the reflectance in red, green, blue, and infrared wavebands which provide an insight into the abundance of photosynthetic pigments and overall plant physiological status. Our robot-mounted 3D-multispectral scanning system provides a unique close-range crop monitoring platform for AgriPV systems as it enables high-resolution (individual leaf) and high-throughput (1000–2500 plants/h) data acquisition of the target crops. Furthermore, successful trials of this high-throughput robot-mounted scanning system highlight the potential for its application to alternative cropping systems and field phenotyping.

Poster location: I41

Towards EMPHASIS ERIC: Enabling Integrated Plant Phenotyping for a Sustainable Future

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[1] VIB; [2] Independent Consultant

EMPHASIS is a pan-European research infrastructure that facilitates access to, and drives innovation in, state-of-the-art integrated plant phenotyping infrastructure, tools, data, and expertise across Europe. Its mission transcends national boundaries and empowers research and innovation in Europe and beyond to improve plant-based systems for food, health, bio-based materials, and environmental sustainability.

Currently in the final stages of becoming a legal entity as a European Research Infrastructure Consortium (ERIC) , EMPHASIS builds on a series of European Commission-funded projects and a decade of community engagement. The establishment of EMPHASIS ERIC will mark a major step in operationalising a sustainable constellation of infrastructure installations and enabling services under central governance—offering seamless access and advancing cutting-edge phenotyping practice.

EMPHASIS ERIC's operations are structured around four Functional Units:

- Access – Coordinated transnational access to infrastructure installations via open calls and on-demand schemes;
- Advanced Phenotyping Practices – Community-driven foresighting, development, and pilot implementation of next-generation phenotyping methods;
- Data – Implementation of FAIR data management, standardisation, and interoperability to enhance reproducibility, reuse, and value;
- Education and Training – Capacity-building programmes and knowledge exchange to serve interdisciplinary user communities.

EMPHASIS ERIC is designed not only to advance phenotyping but to unlock its potential across diverse research domains—including plant science, agriculture, agroecology, environmental science, biotechnology, synthetic biology, and more. It supports sustainable agronomic practices essential for food security, bio-based innovation, and ecosystem resilience.

Along with establishment as an ERIC, EMPHASIS's strategic ambition also includes joining the ESFRI Roadmap 2026 under ESFRI Landmark status. ESFRI Landmarks are research infrastructures that have reached an advanced operational phase, provide high-quality services, and serve as key pillars of the European Research Area's excellence and competitiveness. Through these developments EMPHASIS aims to achieve greater sustainability and visibility, and enhance its ability to deliver long-term infrastructure access and enabling services—creating greater value for funders, users, and society.

Poster location: I42

High-throughput phenotyping and identification of african rice accessions via multispectral imaging

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The AfricaRice genebank conserves 20,391 rice accessions, encompassing two cultivated species (Oryza sativa and O. glaberrima) and five African wild species (O. longistaminata, O. barthii, O. punctata, O. brachyantha, and O. eichingeri). O. glaberrima accounts for approximately 17% of the collection. A major challenge in managing O. glaberrima is the high intra-panicle heterogeneity in seed maturity, which leads to variable grain coloration (lemma and palea) within the same seed lot. This variability contributes to misclassification and mislabeling, resulting in errors in genebank curation, management, and utilization.

Additionally, inadvertent mixing of the seeds of the rice accessions during cultivation and post-harvest operations further reduces seed purity and quality. To overcome these challenges, we propose the use of multispectral imaging (MSI) as a rapid, non-destructive, and objective method for rice seed phenotyping and species identification.

In collaboration with Aarhus University and VideometerLab, AfricaRice genebank has developed MSI-based algorithms aligned with standard rice descriptors from Bioversity International, IRRI, and AfricaRice. These tools are now routinely used in the genebank for seed characterization.

In this study, we used a VideometerLab system to capture images of seeds from 25 O. glaberrima accessions (~50 seeds/accession). Feature extraction included both default Videometer features and custom descriptors. Multivariate analysis and machine learning algorithms (LDA, RF, SVM, GLMNET, XGBoost, Naïve Bayes, GBM, and k-NN) were employed to classify seeds by accession. The approach achieved a classification accuracy of 96.8%, demonstrating its effectiveness in discriminating O. glaberrima accessions.

This high-throughput MSI approach offers significant potential to enhance genebank operations by reducing human error and improving the accuracy of rice seed characterization and identification.

Key words: African rice seeds; genebank management; multispectral image analysis; seed phenotype

Poster location: I43

Field Robot for High-Resolution Crop Phenotyping at Organ-Level Scale

Felix Esser; Lasse Klingbeil; Heiner Kuhlmann

University of Bonn

The ongoing progression of climate change requires the support of crop breeding applications and field management to ensure agricultural resilience and food security. These tasks need the determination of phenotypic traits, a labor-intensive process when performed manually. To increase the phenotypic throughput, Unmanned Aerial Vehicles (UAVs) are increasingly used as they can capture images or 3D point clouds of large fields in a short time, which allows the extraction of phenotypic traits efficiently. However, the resolution and precision of the UAV data are often not sufficient for determining characteristics on the scale of individual plants or even plant organs. In this presentation, we present a robotic Unmanned Ground Vehicle (UGV) equipped with multiple laser scanners built to create high-resolution 3D crop reconstructions in agricultural fields at the plant-organ scale. These reconstructions can then be used to determine phenotypic traits such as leaf area, leaf inclination, or leaf length and width. In addition, the centimeter-precise localization of the UGV by fusing RTK-GNSS and inertial sensor data enables the multi-temporal monitoring of phenotypic traits in the vegetation period. We evaluate our robotic UGV in an agricultural field at Campus Klein-Altendorf (Germany) by creating multi-temporal 3D point clouds of sugar beet, potato, soybean, and sugar corn in the growing season 2023. Our high-quality plant reconstructions feature a spatial resolution of 0.5mm and a point accuracy of 0.3mm evaluated using ground truth reference scans.

Poster location: I45

PhenoRob-F: An Autonomous Ground-Based Robot for High-Throughput Phenotyping of Field Crops

Peng Song

Understanding the genetic basis of quantitative traits related to crop growth, yield, and stress response requires the acquisition of large-scale, high-quality phenotypic datasets. High-throughput phenotyping platforms have emerged as effective tools to meet this demand. Among these, autonomous mobile robots have gained prominence due to their ability to carry heavy payloads, their operational flexibility, and their proximity to crops, which allows for higher imaging resolution. In this study, we introduce PhenoRob-F, a cross-row, wheeled robot designed for efficient and automated phenotyping in field conditions. The robot's mobile platform and phenotyping module were engineered to meet the specific demands of field phenotyping, with integrated visual and satellite navigation systems enabling autonomous operation. We validated the robot's performance through a series of experiments involving wheat and rice canopies. Using the YOLOv8m model, we achieved a precision rate of 0.783, a recall rate of 0.822, and a mean Average Precision (mAP) of 0.853 for wheat ear detection. For rice panicle segmentation, the SegFormer_B0 model delivered a mean Intersection over Union (mIOU) of 0.949 and an accuracy rate of 0.987. Additionally, by capturing RGB-D data of maize canopies, we performed 3D reconstructions to calculate plant height, achieving an R^2 of 0.99 when compared to manual measurements. Similar experiments with rapeseed yielded an R^2 of 0.97. Spectral data collected from drought-stressed rice plants enabled the classification of drought severity into five categories, with classification accuracies ranging from 96.7% to 99.14%. Our results demonstrate that PhenoRob-F is an effective tool for high-throughput phenotyping, capable of providing precise data to support phenotypic trait analysis and the selection of superior crop genotypes.

Poster location: I47

Integrating Smart Glasses into Field and Greenhouse Phenotyping pipeline

Kirby De Jode; Maarten Vanderstukken; Sybren Hamers

Iristick NV

Keywords: Assisted Reality, AR, Smart Glasses, digital phenotyping, speech-to-text, voice-directed data collection, harvest assistance, agriculture product development.

Smart glasses are a rapidly emerging mobile data platform that can be operated hands-free via voice commands, a heads-up display, and a suite of embedded sensors and digital features. This allows crop scientist, horticulturalists, and agronomists to consult, and annotate data without disrupting hands-on workflows.

While high-throughput and automated phenotyping platforms have advanced rapidly, many phenotyping activities, particularly in breeding, crop protection and product development, still depend on manual or close-range phenotyping. Smart glasses offer a complementary phenotyping interface for these use cases, enabling real-time data capture and protocol navigation under variable field conditions.

In operational use across crop science organizations, smart glasses have achied up to 55% gains in data capture efficiency and up to 25% reductions in scoring errors, while also supporting real-time remote collaboration during phenotyping and agronomic activities. Their value as a close-range, hands-free digital phenotyping tool, complementary to high-throughput systems, has become evident in contexts were fixed or remote sensing platforms offer limited access or resolution.

This presentation will showcase current platform capabilities and explore both validated and emerging use cases, demonstrating how smart glasses are transforming digital phenotyping workflows and supporting more efficient, accurate, and collaborative data collection in the field and greenhouse.

Poster location: I49

Development of Non-Invasive Imaging Tools to Identify Recombinant Protein Expression in Plant-Based Molecular Farming

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The advancement of plant-based molecular farming relies on rapid, non-destructive methods for quantifying recombinant protein expression. This project aimed to develop and validate a unique 3D hyperspectral imaging platform for the non-invasive detection of food-grade recombinant proteins in Nicotiana benthamiana. This work progressed the technology readiness level (TRL) from 3 to 4/5 by demonstrating the capacity of hyperspectral imaging to identify protein accumulation at both leaf and whole-plant scales.

The study consists of three main parts: (1) collecting hyperspectral data from both individual plants and detached leaves, with protein expression confirmed through wet-lab analysis; (2) developing data processing pipelines and machine learning models to detect protein expression in detached leaves, achieving an accuracy greater than 79%; and (3) translating analytical approaches from leaf-level to canopy-level imaging, confirming the robustness and scalability of the method. The datasets and models generated constitute a valuable resource, which has been structured for future licensing and expansion.

Industry engagement was a core outcome, with international partners expressing interest in commercialisation. The project's non-invasive approach reduces the need for destructive sampling, enables real-time monitoring, and enhances both the scalability and cost-effectiveness of protein quantification in molecular farming. This proof-of-concept data and early-stage intellectual property will be leveraged to expand industry partnerships and validate the technology across a broader range of recombinant proteins. The project's success demonstrates a strong foundation for future development, positioning Australian research at the forefront of plant-based biomanufacturing innovation.

Poster location: I51

Effect of Nitrogen Fertilization on Plant Height in Bread Wheat: Assessment of the Correlations Between Traditional Observations and High-Throughput Phenotyping Approaches

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In this study, the impact of nitrogen fertilization on plant height in bread wheat (Triticum aestivum L.) was evaluated using both conventional phenotypic measurements and high-throughput phenotyping (HTP) approaches. This study was conducted during the 2024–2025 wheat growing season at the experimental fields of Ege University, Department of Field Crops. The experiment followed a randomized complete block design with four replications. Sowing took place on November 29, 2024, with plot dimensions of 1.2 m × 3 m and a 20 cm row spacing. Ten different wheat cultivars were grown under two distinct treatments: low nitrogen (-N: 3 kg/da) and high nitrogen (+N: 9 kg/da). In both treatments, plant height was assessed through manual field observations and estimated using drone-based imaging technologies. A UAV flight was carried out at the beginning of the heading stage using a DJI M350 RTK drone equipped with a MicaSense RedEdge-P multispectral sensor.

Correlations between conventional measurements and drone-derived data were examined to evaluate whether drone-based high-throughput phenotyping could serve as a robust alternative to traditional methods. Moreover, certain cultivars exhibited more pronounced morphological responses under low nitrogen conditions. This study highlights the interaction among genotype, environment, and technology, emphasizing the potential of modern phenotyping tools in agricultural research.

Poster location: I52

From Scan to Growth: a Framework for Modelling Dynamic and Complex Leaf Morphology Using B-splines

Nik Woning; Katarina Smolenova; Cristina Zepeda; Dieke Smit

Wageningen University & Research

Despite the advancement in precise measurements of leaf structure using 3D scanners, leaf shapes used in dynamic 3D simulation models, such as functional-structural plant (FSP) models, remain mostly simplified. Accurate description of leaf structure is crucial in the study of plant-environment interactions, specifically light environment and airflow dynamics. Traditionally, to synthetise leaves for FSP models, the shape of a leaf is combined with monotonous curvature along a single axis. This method fails to capture wrinkly structures, as for example is found in lettuce (Lactuca sativa). On the other hand, 3D scans capture complex shapes and structures but cannot track changes over time since they only provide a static snapshot.

The aim of this study is to devise a method that estimates shape and form over time of leaves with a complex morphology.

In this study, we collected 3D point clouds of lettuce leaves at several growth stages. The 3D point clouds were normalised and sliced along the leaf’s mid-axis, and a non-rational cardinal B-spline was fitted to each slice. The control points of these splines were collected and arranged in a grid. This grid of control points is then used to form a spline surface. By combining the grids of multiple leaves with varying ranks and ages, a distribution space can be formed for each point in this grid, which can be sampled to form synthetic data of leaves of varying ranks and ages. Simulation of growth is accomplished by linear interpolation of two sets of control-point grids that represent two moments in time. The generated B-spline surfaces can be turned into polygonal meshes to be further used in FSP models, as is expected for light simulations. Additionally, synthetic data can be generated to be used in the training of various AI applications. Furthermore, the values of the control points themselves can be used in the analysis of leaf curvature, opening new pathways for advanced phenotyping applications.

Poster location: I54

Plant Phenomics - A young and data-driven discipline about to expand basic concepts of biology

Alexander Bucksch[1]; Chung Yong Suk[2]; Jennifer Clarke[3]; Stefan Gerth[4]; Philipp van Gillhausen[5]; Wei Guo[6]; Jana Kholova[7]; Shree Pariyar[8]; Ethan Pickering[9]; Sindhuja Sankaran[10]; Sahameh Shafiee[11]

[1] University of Arizona; [2] Jeju National University; [3] University of Nebraska Lincoln; [4] Fraunhofer Gesellschaft; [5] International Plant Phenotyping Network e.V.; [6] University of Tokyo; [7] Czech University of Life Sciences; [8] Salk Institute for Biological S

Despite its underrecognition by funders, policymakers, and scientific academies, plant phenomics has emerged as a young and dynamic discipline poised for long-term growth. Plant phenomics already exhibits many of the characteristics of a self-sufficient discipline. However, it faces challenges in developing a conceptual and theoretical framework that effectively bridges the gap between formal and hypothesis-driven sciences in its community.

Over the past ten months, the IPPN working group “The Science of PhenomX” has addressed these conceptual issues as the crucial step toward gaining more recognition. The discussions led to the development of a first cohesive framework that distinguishes plant phenomics from other scientific disciplines. In short, Plant Phenomics employs formal systems, such as sensors, algorithms, and simulations, to aggregate and integrate data on the multiscale dynamics between plants and their environment. In its definition, plant phenomics strongly emphasizes the recognition of all biological and ecological scales equally and distinguishes strictly between observable and measurable quantities. This emphasis defines a space where formal and hypothesis-driven sciences intersect to challenge established concepts, such as the notion that the phenotype encompasses all measurable phenomena or that it is the sum of the genome, environment, and gene-environment interactions.

The presentation highlights examples of phenomicists who identified limitations of existing frameworks. It also invites a broader audience to participate in the initial draft of the framework, fostering a community-driven and inclusive definition of plant phenomics that allows us to grow together.

Poster location: I55

Drone-Based Solar-Induced Fluorescence for Crop Monitoring: Integrating AirFloX with Ground-Based FloX Measurements

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Solar-Induced Fluorescence (SIF) provides a powerful, non-invasive indicator of vegetation health and photosynthetic efficiency. Since plants emit a small fraction of absorbed sunlight as fluorescence during photosynthesis, SIF offers a direct physiological signal that can be used to monitor photosynthetic activity in real time. This makes it highly valuable for modern plant phenotyping, especially under field conditions where environmental variability plays a crucial role.

Recent advances in optical sensor technology have enabled continuous, high-resolution monitoring of SIF across spatial and temporal scales, supporting emerging phenotyping practices in agriculture. However, scaling such measurements from point observations to field or landscape level remains challenging, underscoring the need for large-scale SIF approaches. In this context, drone-based systems provide a promising solution by enabling rapid and spatially extensive measurements under real field conditions.

In this study, we used two complementary SIF measurement systems: FloX, a ground-based spectroradiometer serving as a reference for high-quality, point-specific measurements, and AirFloX, its aerial counterpart mounted on a drone, capturing spatially extensive SIF data across the same plots. FloX acquisition takes longer and requires manual operation, offering detailed but limited coverage, whereas AirFloX enables rapid, large-scale sampling of the entire experiment. The primary aim was to evaluate the accuracy of AirFloX by comparing its measurements with FloX ground-based reference data.

Data acquisition was conducted at the PhenoRob Central Experiment site on the Campus Klein-Altendorf, University of Bonn, situated in the western part of Germany (50°37’N, 6°59’E). This experimental site allowed for detailed assessment of spatio-temporal dynamics in photosynthetic performance under environmental conditions. The trials involved two crop systems: soybean (two varieties: Eiko and Minngold; 4 plots per variety, 8 plots total) and sugar corn (four varieties: Popcorn, Caramelo, Mirza, and Vega; 4 plots per variety, 16 plots total).

This approach highlights the potential of drone-mounted SIF sensors for scalable phenotyping and vegetation stress monitoring, while also providing data to support validation and calibration for the upcoming FLEX satellite mission by the European Space Agency (ESA).

Keywords: Solar Induced Fluorescence (SIF), Photosynthesis, UAV, Crops.

Poster location: I56

RootForce 4.X: a review of the classical image processing pipeline for RSA and growth of cereals via automated X-ray CT

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Cereals such as rice, wheat, and maize have been the most significant source of caloric intake for humans for thousands of years. To understand the basic functionalities of cereals, such as anchoring, nutrient uptake, and storage functions, Root System Architecture (RSA) is a commonly used characterization procedure. RSA requires access to information below ground, which is often obtained through the so-called shovelomics technique. However, applying shovelomics involves invading the root surrounding media, which can consequently alter the non-invaded RSA. Therefore, RSA demands a proper non-invasive 3D imaging technique and suitable algorithms for root trait extraction.

In recent years, X-rays have been one of the most widely used non-invasive imaging techniques, as they penetrate matter without disturbing its inner structure and provide 3D data. However, understanding RSA requires post-processing of X-ray data to derive basic root traits such as root length, minimal and maximal root angle, and packing fraction. To this end, we present in this contribution the results of X-ray data from different root systems using RootForce 4.X, a software for processing and root trait extraction. We outline the fundamental steps within the image processing pipeline to analyze thick and thin roots. Finally, we present features computed on 3D data that also involve root growth.

Poster location: I57

Metadata for non-invasive Field Phenotyping

Lars Grygosch

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Recent advancements in non-invasive sensor systems have transformed field studies in plant phenotyping. Proximal sensing technologies like the Fluorescence box (FLOX) and the light-induced fluorescence transient (LIFT), along with remote sensing methods from satellites (FLEX), aircraft (HyPlant), or UAVs, allow for non-destructive measurements under realistic environmental conditions on different scales. The widespread use of these technologies, combined with the integration of automated systems and machine learning algorithms for data measurement and analysis, has led to a significant increase in both the volume and complexity of data. In response to this data surge, it is crucial to implement sophisticated data management strategies that enhance the findability, accessibility, interoperability, and reusability (FAIR) of data. These strategies are essential not only for enabling access by human researchers, breeders, and other stakeholders but also for improving machine readability and facilitating effective communication among automated systems. To accomplish this goal, we are developing a comprehensive benchmark dataset that showcases typical field phenotypic and remote sensing data. This initiative is supported by advancements in research data management, including templates for data organization. Additionally, we are committed to enhancing FAIRness by creating guidelines to educate researchers and data publishers on effective data documentation, structuring, and licensing practices. By establishing these standards and contributing to FAIRagro, we aim to significantly improve the reproducibility and utility of field phenotyping data for the entire community.

Poster location: I58

Exploring RGB Color Indices as Low-Cost Predictors of Leaf Traits in Cotton

Uğur Çakaloğulları

Ege University

Low-cost and portable imaging methods offer promising alternatives for plant phenotyping, particularly in environments where access to high-throughput platforms is limited. In this study, we evaluated whether color indices derived from RGB images could predict key leaf morphological and physiological traits in cotton.

A standardized imaging protocol was applied using a uniform lighting setup and calibration cards to ensure consistent image quality. Processed RGB images were used to calculate multiple color indices based on RGB and Lab color spaces. These indices were statistically evaluated as predictors for a wide range of leaf traits, including pigment content, surface morphology, stomatal features, and structural characteristics. Second-degree polynomial models were used to assess each index-trait relationship ($n = 80$), with model performance evaluated using adjusted R^2 and normalized RMSE (NRMSE).

Among the evaluated traits, specific leaf area (SLA), chlorophyll content (SPAD), and vein density exhibited the most robust associations with RGB indices. Notably, SLA showed its strongest correlation with the hue angle in Lab space (h_ab; adjusted $R^2 = 0.67$, NRMSE = 19.9%), SPAD with the green channel (G) from RGB (adjusted $R^2 = 0.56$, NRMSE = 9.1%), and vein density with the Triangular Greenness Index (TGI; adjusted $R^2 = 0.61$, NRMSE = 23.9%). In contrast, stomatal traits presented relatively weak associations across all tested indices.

Overall, the results demonstrate the potential of RGB imaging as a low-cost, non-destructive phenotyping tool for assessing leaf traits related to structure and pigment dynamics in cotton. The use of a standardized image acquisition environment combined with calibration cards contributed to the robustness and repeatability of the approach. These findings support the broader adoption of affordable digital imaging workflows for consistent leaf-level phenotyping in both research and practical crop monitoring contexts.

Poster location: I59

NEW APPROACHES IN PLANT BREEDING: HIGH-THROUGHPUT PLANT PHENOTYPING

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Plant breeding improves crop yield, quality, and tolerance levels, ensuring adequate nutrition for a growing population, and enabling stress-tolerant crops to be cultivated based on genotype-environment interactions. Furthermore, plant breeding requires phenotypic selection alongside molecular marker-assisted genomic selection. Therefore, the selection of desired genotypes is based on the comparison of phenotypic and genotypic data. While genotypic observations are not obtained in every generation, phenotypic observations are essential in all breeding processes. The facilitation of phenotypic observations through the use of high-throughput phenotyping (HTP) offers a new perspective on plant breeding. For this purpose, imaging technologies (hyperspectral, thermal, multispectral, LIDAR, etc.) and software are being used in plant breeding, and with technological advancements, many new sensors, cameras, UAVs, and other equipment are being developed. These technologies allow for more accurate analysis of genotype x environment interactions and accelerate the development of high-yielding, stress-tolerant varieties. This poster presents the current use and basic principles of HTP in plant breeding, along with a general overview of the latest technologies used in plant breeding to increase yield and quality.

Key words: Plant breeding, high-throughput phenotyping, phenotypic selection

Poster location: I60

Coupling High-Resolution Lysimetry and Imaging to Decode Ionome–Water Dynamics for Smart Nutrient Management in Tropical Crops

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A plant's ionome, defined by the composition and interaction of 17 essential minerals, plays a crucial role in regulating growth and development. While traditional fertilizer research has focused mainly on yield and biomass, it often overlooks how whole-plant water relations interact with ionomic shifts, an interaction particularly relevant under the high-temperature and high-humidity conditions of tropical regions.

This study investigated how single-mineral alterations, from deficiency to excess, influence the relationship between the ionome and key physiological properties of two Southeast Asian leafy greens, Brassica oleracea (Chinese broccoli) and Amaranthus dubius (Chinese spinach). Plants were grown in a tropical greenhouse using a functional phenotyping platform (PlantArray), integrating high-resolution load-cell lysimeters for continuous monitoring of water relations and an automated robotic imaging system capturing spectral, thermal, and anatomical features.

Eight nutrient solutions were applied, and transpiration, water use efficiency (WUE), mineral use efficiency (NUEcrop), yield, and leaf mineral composition were measured. Fifteen independent experiments generated a large dataset designed for machine learning algorithms aimed at fertigation optimization.

We identified optimum nutrient curves for nitrogen (75% NO_3^-, 25% NH_4^+), potassium, phosphorus, calcium, and magnesium. For nitrogen, 120–160 ppm maximized transpiration, yield, and WUE, whereas NUEcrop declined at 200 ppm, suggesting current grower practices may overapply N. High N reduced leaf concentrations of K^+, P, Ca^{2+}, Mg^{2+}, Fe^{2+}, and Zn^{2+}, but showed strong positive correlations between N and Fe^{2+} (R^2=0.94) and between Ca^{2+} and Mg^{2+} (R^2=0.94).

This integrated lysimetric-imaging approach enables advanced, AI-driven fertilization strategies that improve tropical leafy green yield and quality while reducing mineral waste.

Poster presentations

Session 3:

Phenotyping the hidden half

R01

Phenotyping root anatomical and hydraulics traits in wheat: effects of breeding history and spatial gradients along the root

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Root traits are often overlooked in breeding programs due to the challenges of phenotyping the hidden half. In wheat (Triticum aestivum L.), gaining insights into how root anatomical and functional traits have responded to breeding is essential to understand shifts in water uptake strategies over time. In a previous study, we found a decline in whole root system hydraulic conductance across German winter wheat cultivars released between 1895 and 2002, suggesting that modern breeding may have favored smaller or less conductive root tissues1. However, the underlying drivers of this trend—whether architectural or anatomical—remained unclear.

To address this, here we investigated the variation in root anatomical and hydraulic traits across the same set of cultivars. Crown roots were sampled from a field experiment using shovelomics, and cross-section images at three positions along each root were obtained using a new low-cost, high-throughput imaging system (Rapid Anatomics Tool). The resulting images were used as input for the GRANAR-MECHA pipeline2, to model root hydraulic properties—radial and axial conductance—at the segment level, based on anatomical features for the selected cultivars and along the roots.

We found clear gradients in anatomical and hydraulic traits along the root axis: from base towards the tip, stele and cortex areas and xylem number decreased, while apoplastic barrier development increased, resulting in a systematic increase in radial conductivity and a decrease in axial conductance (by around two- to four-fold). Across cultivars, modern varieties exhibited fewer metaxylem vessels and lower axial conductance compared to historic cultivars, in line with the previously observed decline in whole root system conductance.

Our results indicate that spatial and genotypic variation in root hydraulic properties was associated with changes in xylem and cortex development as well as apoplastic barrier formation. By capturing these relationships, our study demonstrates the potential of a phenotyping pipeline that integrates field sampling, anatomical imaging, and root hydraulic modeling. This approach offers new opportunities to quantify functional root traits and improve our understanding of water uptake dynamics in wheat and other cereal crops.

References

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R02

HYDRAS: Imaging the Hidden Half with Electrical Resistivity Tomography (ERT)

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Changes in precipitation distribution and frequency across Europe related to climate change are a challenge for agriculture. With more intense rainfall and more extended drought periods becoming more likely, agroecosystems need to be made more resilient. Breeding drought-resistant genotypes or adapting agricultural management practices are two aspects to be improved. In this context, soil moisture is a key variable that will help crops bridge periods of drought. Hence, understanding what is happening in the hidden half of the crop, i.e., how soil moisture is being used, is essential to select resilient genotypes and develop suitable management practices. Field-scale studies are needed to fully assess the crop phenotype or the management practice in real soil conditions comparable to production fields. Soil moisture point sensors are useful to monitor soil moisture in the field, but their small volume of observation does not allow high spatial resolution. In this research, we showcase the use of electrical resistivity tomography (ERT) to monitor soil moisture in the root zone in fields of 300 m² over the entire growth period, hence, scaling up information from soil moisture point sensors. As such HYDRAS, the HYdrology, Drones and RAinout Shelter open access international research infrastructure provides both High-Throughput Field Phenotyping (HTFP) both above and below-ground. ERT uses surface electrodes to measure the resistivity of the subsurface, what can be related to soil moisture. The large soil volume investigated by ERT enables the collection of spatial information at a similar scale to that obtained using drone imaging above-ground. By coupling above-ground and below-ground observations it is then possible to obtain a complete representation of the whole crop phenotype throughout the growing season. While the use of ERT to follow soil moisture content is not new, the implementation of ERT within a field phenotyping facility is (Blanchy et al., 2025). Two field experiments will demonstrate how ERT was able to differentiate between soybean varieties and different mulch applications in celery. Derivation of traits useful for crop breeding and to investigate the effects of management will be detailed. Finally, the combination of below-ground and above-ground information in a coupled modelling framework will be discussed.

R03

What are the main characteristics to be considered when describing root architecture in field conditions?

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Root characteristics assessed in field conditions are needed to understand crop resilience to climate changes. Architectural root traits are easily available in controlled conditions but more difficult in field conditions. That’s why, as part of the Horizon Europe project “Root2Res”, we developed a phenotyping toolbox to characterise architectural root traits in field conditions.

The aim of this study is to share, apply and evaluate the main methods used to describe root traits in the field on potato crop. Field experiments were established in Scotland by JHI, Ireland by TEAGASC, France by ARVALIS, Slovenia by KIS and Morocco by ICARDA in 2023 and 2024. Root traits characterization was conducted on most of these sites included shovelomic method, root/soil core extraction and imaging by minirhizotron. We also measured yield components and aboveground traits using sensors to access non-destructive measurements.

First, we investigated correlation between root traits to define a shortlist of “main traits to measure”. The results will highlight the key root traits measured by shovelomic method that we could apply on a higher number of plots to evaluate genetic diversity or variety resilience to drought stress.

Secondly, we investigated the other methods like soil coring or image based on minirhizotron scan. The results will highlight the advantages and disadvantages of each method and how each could answer to a scientific investigation.

Each method will be discussed to improve root growth assessment and modelling under stressed conditions and to characterise more resilient ideotypes/varieties to be used by breeders, agronomists, and farmers.

R04

Brewing Better Roots for the future of coffee - Exploring diversity of root system architecture under contrasting nutrient supply in wild and cultivate coffee species

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Fruit tree crops, such as coffee, are increasingly impacted by climate change, highlighting the need for improved stress resilience. Rootstocks, used in grafting, offer a promising path by rapidly enhancing tolerance to environmental stresses. Given the essential role of roots in nutrient uptake and stability, advancing rootstock breeding and root trait analysis is vital for climate adaptation. Emerging non-invasive imaging technologies now enable high-throughput root monitoring, opening new avenues for sustainable crop improvement.

To investigate differences in coffee root system architecture and its growth dynamics and plasticity, we employed the advanced rhizotron system integrating root and shoot imaging, located in IPK's unique PhenoSphere. Eight coffee genotypes—representing two cultivated (two Arabica types and one Robusta type) and five wild species of Coffea genus—were studied under contrasting nitrogen (N) conditions, with ten replicates per genotype, over a period of three months. The existing deep-learning-based image analysis pipelines were adapted for coffee roots and shoots. Principal component analysis (PCA) of the 54 extracted root traits revealed distinct clustering by species and genotype. Similarly, PCA of the 36 shoot traits showed species- and genotype-specific groupings, although the clustering patterns differed from those observed for roots. N supply had a notable impact on RSA, particularly on root system width (x-parameter): all genotype, except for one, exhibited a significantly reduced width under low-N conditions. In contrast, root system depth was generally unaffected by N supply. Nitrogen availability also influenced shoot traits; shoot dry weight revealed reductions under low-N in all species, except for one species. We are currently analyzing the time-course data to determine the timing and progression of nitrogen effects across the different coffee genotypes. In an earlier test experiment using the large automated phenotyping system with the rhizopot system, roots were sampled for exploring differences in the transcriptome and microbiome with promising first insights. A new experiment is currently conducted on the same system to generate a combined in-depth data set of HTP data, microbiome and transcriptome data that will be used for integration of all data into predictive models that will be used to select resilient genotypes with desirable root traits and NUE.

R05

Root angle variation in the OzBarley population is driven by genetic variation in key expansin genes.

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Roots are essential for water and nutrient uptake, as well as carbon sequestration. Steep root angles enhance access to deep soil water and nitrogen, while shallow angles favour topsoil resource capture. Root angle regulation involves several genes (Kirschner et al., 2024). In barley, ENHANCED GRAVITROPISM1(EGT1) and ENHANCED GRAVITROPISM2 (EGT2) have been linked to root-angle control via cell wall mechanics (Fusi et al., 2022; Kirschner et al., 2021), though their downstream targets remain unknown. To explore this pathway, we used high-throughput phenotyping and genome-wide association studies (GWAS) on 214 diverse OzBarley lines. Haplotype analysis revealed no variants for EGT2 and eight EGT1 variants, which formed four haplotypes; none were significantly associated with the root angle phenotype ($p > 0.1$). However, GWAS identified a significant SNP ($-\log_{10}p = 6.16$) on chromosome 1 within a gene encoding Expansin, a key cell wall-loosening protein (Cosgrove, 2000). Two protein-coding variants for this expansin were found: a missense and a stop-gained mutation. Both alleles were significantly associated with shallow root angles compared to wild type ($p < 0.05$), consistent with haplotype data ($p < 0.05$). The stop-gained allele truncates the C-terminal domain of the Expansin protein, while AlphaFold modelling predicts the missense variant also disrupts protein function. These findings suggest that natural variation in Expansin contributes to root angle variation in the OzBarley panel and support the model in which EGT1 (and EGT2) regulate wall extensibility by modulating enzymes, such as Expansin. Functional validation through CRISPR knockouts and TILLING mutant screens in barley and other species could help validate the functional impact of Expansin

R10

Integrating Root Phenotyping and Performance Proxies into Grapevine Rootstock Breeding

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Hochschule Geisenheim University

Grapevine (Vitis vinifera L.) is a grafted perennial crop cultivated across a wide range of agricultural systems worldwide. The success of modern viticulture in diverse pedoclimatic regions – from Mediterranean and arid to cool and temperate zones – largely stems from the use of rootstocks, which enable growers to manage soil-borne pests and adapt vines to challenging soil conditions.

Today's grape production still relies heavily on rootstock genotypes developed 160 years ago. This enduring reliance highlights both the robustness and efficiency of these plant materials but also raises concerns about a potential performance bottleneck. As global climate change introduces new stressors – such as rising temperatures, erratic precipitation, and extreme weather events – the demand for novel rootstock genotypes capable of mitigating these challenges is growing rapidly.

Given that grapevine breeding cycles, especially for rootstocks, can span several decades, early-stage performance assessment is essential to accelerate breeding progress. As an initial step, we established a rhizobox system to assess early root development in three distinct rootstock genotypes. A combination of software tools was employed to develop a phenotyping pipeline, enabling the characterization of root system architecture via image analysis.

This experimental setup revealed both opportunities and limitations for application in rootstock breeding. The imaging pipeline successfully generated informative data under controlled conditions, allowing the evaluation of key root performance traits. Despite overall strong correlations between above-ground vegetative growth and root parameters, notable variation was observed among replicates within treatments. These findings suggest that the pipeline has strong potential for integration into grapevine rootstock breeding programmes. However, careful data interpretation is required due to inherent scaling limitations.

Future work will include the collection of additional data from the rhizobox trial using hyperspectral imaging and physiological measurements to complement root traits with above-ground indicators of plant performance. These data will support efforts to link rhizobox-derived root parameters with field performance metrics from grafted grapevines across multiple sites. This step is critical to ensure the practical relevance and broader adoption of the phenotyping pipeline in applied breeding contexts.

R11

Unveiling root system variability in lentil core collection through automated high-throughput phenotyping

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Cultivated lentil (Lens culinaris subsp. culinaris) is an annual, self-pollinating diploid legume (2n = 14), playing a crucial role in human diets. In 2023, the global harvested area reached 5.68 million hectares, with a production of 7.01 million tonnes, confirming the crop's relevance worldwide. Climate change is increasingly threatening lentil production, and root system architecture (RSA) traits play a key role in water uptake, significantly influencing yield under drought stress conditions. The objective of this study is to assess the diversity of RSA traits in 64 lentil genotypes obtained through the single seed descent (SSD) method, selecting the lines from a broader core collection established within the framework of the INCREASE H2020 project. Genotypes were chosen based on passport, genotypic, and phenotypic data to maximize genetic diversity. Several root and shoot related traits were investigated, including total and primary root length, root system width, convex hull area, root and shoot biomass. High-throughput phenotyping was conducted using the novel GrowScreen-Rhizo 3 platform at the Forschungszentrum Jülich (Germany). Lentil plants were grown for 26 days in soil filled rhizotrons under controlled conditions, according to a randomized block design with three replicates per genotype. Root and shoot images were captured daily in an automated manner to monitor growth dynamics throughout the experimental period. Statistical analyses revealed significant differences among the genotypes for all evaluated traits. The collected data offer valuable insights for lentil breeding programs, facilitating the identification of genotypes with desirable RSA traits that could enhance water and nutrient uptake efficiency. Particularly, variability in lateral root development and rooting depth may be exploited to select genotypes better adapted to water limited environments. This strategy would support the development of drought resilient lentil varieties with improved yield potential and enhanced nutritional value, contributing to greater sustainability of lentil cultivation under future climate scenarios.

R12

Successful Establishment of a Drought Stress Protocol in Rhizotrons for Phenotyping Root System Architecture in Faba Bean

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Root system architecture (RSA) plays a key role in enhancing drought tolerance in grain legumes. Under controlled conditions, RSA is usually studied using rhizotrons. These are narrow growth boxes with transparent or removable observation windows allowing 2D root imaging. This enables dynamic, non-destructive imaging, and the use of soil rather than sand or gel as a growing medium. However, protocols for non-destructive root phenotyping of crops under water deficit conditions are lacking due to difficulties of rapidly reducing field capacity in rhizotrons. Here, we present a new method of inducing drought stress in rhizotrons, maintaining sufficient colour contrast between the soil substrate and the plant roots for image analysis. The protocol was tested on a set of faba beans containing German and Egyptian cultivars to ensure diversity in RSA. Furthermore, we have optimized a machine learning pipeline for root analysis that is specifically designed for faba bean roots. By using the drought stress protocol and RSA analysis pipeline for faba bean, we aim to take the first steps towards dynamic drought stress root phenotyping of grain legumes under controlled conditions.

R13

3D characterization of crop water use and the rooting system in field agronomic research

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Here we propose and test a new approach to produce 3D characterizations of crop water use and root activity in large field genotype (G) by environment (E) by management (M) experimentation, using electromagnetic induction (EMI) instrument coupled with a quasi-2D inversion algorithm, and crop canopy sensing technologies. A root activity factor (R) was calculated as a function of crop water use, soil water availability, and an indicator of crop demand. We ask i) can this approach provide accurate 3D characterizations of sorghum water use and root activity?, and (ii) does the approach capture complex GxExM dynamics?. This study was conducted based on an on-farm field experiment consisting of the factorial combination of six commercial sorghum genotypes (G), three times of sowing, two levels of irrigation (E), four plant densities (M), and three replications. Two EMI surveys ten days apart were collected using a DUALEM-21S sensor. An artificial neural network (ANN) model was developed to predict 3D soil moisture (θv) using depth-specific true soil electrical conductivity (σ) estimated by the inversion algorithm. Crop water use between surveys was described as the difference of θv. A multispectral index derived from satellite imagery was used as a proxy for crop demand i.e., size of the crop canopy. Results indicate that 3D crop water use could be predicted with high accuracy (LCCC = 0.81). The calculated water use and the value of R were significantly affected by depth, crop growth stage, irrigation treatment, plant density, and their interactions. At flowering, roots were most active at 0–1.3 m under irrigation, and deeper (0.5–1.5 m) under dryland treatment. The highest water use was for three genotypes (i.e., C, E and F) grown under irrigation and high plant densities (i.e., 9 and 12 pl m-2). The smallest water use was observed under dryland treatment, particularly for two genotypes (i.e., B and C) and high plant densities. For the crops at vegetative stages, the values of water use and R were highest in the top 0.5 m of soil depth. We conclude that the approach provides a rapid, and cost-efficient option to phenotype crop root activity i.e., water use, in large field experimentation. We also argue that the improved understanding of the crop water use dynamics can help inform optimum combinations of genotypes and management options i.e., crop designs, across contrasting environments, and help untangle complex GxExM interactions

R14

Monitoring spatial and temporal carbon dynamics in the plant soil system by co-registration of Magnetic Resonance Imaging and Positron Emission Tomography

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The short-lived radioisotope ^{11}C can be applied non-invasively as $^{11}CO_2$ to monitor the transport and allocation of recently fixed carbon (photosynthates) in plants. The combination of this tracer with tomographic imaging technologies like Positron Emission Tomography (PET) and Magnetic Resonance Imaging (MRI) enables the visualization and quantification of carbon transport velocities and allocation patterns within complex 3D structures like root systems and fruits.

Our results show that transport velocities are highly dynamic, varying significantly depending on the plant species, the plant's growth stage, and the specific organ along the transport pathway.

Beyond measuring internal transport dynamics, the combination of these methodologies is crucial for understanding how plants interact with their environment. A substantial amount of photosynthates is transported into the root system and released into the surrounding soil (the rhizosphere) through rhizodeposition, where it serves as a primary food source for the microbiome. Using ^{11}C-PET in combination with MRI, we observed that photosynthates preferentially accumulated in root tips, especially those of young crown roots. This internal pattern was directly reflected in the external carbon distribution in the rhizosphere. Using the stable isotope ^{13}C, it was confirmed that these same root tip areas were "hotspots" of carbon release into the soil. Consequently, this spatial heterogeneity in carbon release directly shapes the structure of the rhizosphere microbial community that consumes these carbon resources.

In conclusion, this work highlights how the combined use of ^{11}C and ^{13}C isotope labeling with PET and MRI provides a powerful tool not only to quantify plant internal carbon transport dynamics, but also to reveal the direct connection between its internal resource allocation strategy and the resulting spatial structure of microbial communities in the rhizosphere. This could be of particular importance for understanding how the root microbiome feeds back on the plant phenotype and vice versa.

R15

Digging Deeper: Automated Analysis of Root System Architecture Using Deep Learning

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Image-based high-throughput root phenotyping has become essential for quantitatively assessing the variation of root system architecture (RSA) among a large set of plant genotypes in response to environmental stimuli. However, automated analysis of large datasets of soil-root images remains challenging due to low image contrast, high levels of structural noise, as well as variability in optical root and soil appearance. To cope with these challenges, we developed two deep learning-based approaches: a U-Net-based model for binary segmentation, and a DeepLabV3+ architecture with a ResNet-50 backbone (DLR50) for multi-class segmentation. These models were trained and validated on large-scale root image datasets captured using high-resolution plant phenotyping systems.

The binary segmentation model was trained on 6,465 maize root images (256×256 pixels) acquired via the IPK large-plant conveyor belt, achieving a mean F1-score of 0.87. For hierarchical RSA segmentation, the DLR50 model was trained on 2,256 barley root images (512×512 pixels) from the automated Rhizotron imaging platform. It achieved F1-scores of 0.83 for axial roots and 0.70 for lateral roots, outperforming an attention-enhanced U-Net baseline (F1-score for lateral roots = 0.66).

Beyond segmentation accuracy, the extracted root traits from the DLR50 predictions showed strong agreement with ground truth annotations, with a coefficient of determination (R^2) of 0.90, compared to 0.85 for the U-Net-based model. In terms of computational efficiency, the pipelines required approximately 80 seconds (binary) and 120 seconds (multi-class) to process a single 6-megapixel cropped root image on a standard workstation (Intel® Xeon® Gold 6130 CPU @ 2.10 GHz).

In summary, deep learning-based image segmentation enables robust and sufficiently accurate processing of complex soil-root images in a fully automated manner, providing plant scientists with powerful and scalable tools for dissecting RSA complexity in high-throughput. As a major drawback, the performance of our present DL framework is naturally tailored to our optical facilities, where ground truth data for model training comes from. However, with the continuously increasing volume of ground truth data from different optical setups and plant species, more general deep learning models for soil-root image segmentation will become feasible.

R16

Investigation of barley root responses to waterlogging

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Barley (Hordeum vulgare L.) is currently the fourth major cereal cultivated worldwide and the most widely produced in Ireland. European countries have recently experienced production losses that could be attributed to extreme weather events, such as waterlogging. Breeding programs have traditionally favoured yield-related traits under optimal conditions, thereby neglecting the selection of abiotic stress resilience in modern cultivars. The proposed research aims at analysing the avility of barley to recover from waterlogging at the root level. This project takes advantage of the European Heritage Barley Collection (ExHIBiT) that was assembled to explore genetic diversity among elite, old cultivars and landraces. From the ExHIBiT core-collection, a representative panel of genotypes with contrasting responses to waterlogging was selected for an in-depth study of barley tolerance. Five barley lines were chosen for each set of tolerant and susceptible candidates, along with two reference lines, in order to perform extensive comparative analysis of waterlogged vs control plants under controlled conditions. Non-destructive image-based phenotyping with the PLANTSCREEN™ ROOT IMAGING SYSTEM (Photon Systems Instruments, PSI) allows accurate and dynamic root monitoring in rhizotrons, providing a window into the rhizosphere under various watering conditions. Roots segments are collected after recovery of waterlogging stress for observation under confocal microscope. To further investigate root plasticity in the representative panel, the focus is currently placed on aerenchyma development and the emergence of adventitious root. Finally, future destructive analysis on plants grown in custom-made rhizoboxes at several time-points are described, such as imaging set up and mean spectra extraction from the hyperspectral VNIR-SWIR cameras of the PLANTSCREEN™ SC IMAGING SYSTEM (PSI), as well as shoot and root ionome profiling which will be performed to gain insight into the modifications in nutrients uptake induced by waterlogging stress.

R17

High-throughput root and shoot phenotyping using the novel platform GrowScreen-Rhizo III at Jülich Plant Phenotyping Centre

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Root phenotyping is a challenging task, mainly because of the hidden nature of the plant organ. One way to make roots accessible is using growth containers with a transparent side. These so called rhizotrons allow non-invasive measurements of roots grown in soil. Manually phenotyping large sets of plants at multiple growth stages and growth conditions is time-consuming and only feasible with the investment of important human resources. Therefore, automated phenotyping platforms for fast and accurate screening of plants are indispensable.

The Jülich Plant Phenotyping Centre (JPPC) is at the forefront of cutting-edge research in promoting the development of novel non-invasive methods for root as well as shoot phenotyping. Recently, we have developed the unique high-throughput phenotyping platform GrowScreen-Rhizo III to simultaneously phenotype root and shoot traits of almost 900 plants growing in soil-filled rhizotrons in an area of around 650 m² greenhouse space. The concept of the platform is a modular plant to sensor approach, where groups of rhizotrons are transported automatically to measurement chambers using automated guided vehicles (AGVs). To be able to image, weigh, and water all plants at least once a day, four measurement chambers are operating in parallel and independently from each other. In the measurement chambers, images of the root system at the transparent plate of the rhizotron and images of the shoot from different view angles are acquired. Our image-based approaches allow us to elucidate the dynamic establishment of root system and shoot development of different crop species, such as wheat, barley, buckwheat, lentil etc. with high temporal and spatial resolution. The platform enables for example screening of whole plant populations and provides the opportunity to identify candidate genotypes with improved plant productivity or resource use efficiency. We have validated the novel platform and will present the broad application and potential of the platform.

R18

Root growth in biopores of spring wheat, faba bean and intercropping system

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Enhancing root systems, particularly through the utilization of biopores, can significantly improve crop access to essential resources, an increasingly critical need as climate change intensifies. In this context, intercropping (also known as mixed cropping) offers a promising strategy to promote deeper root penetration, thereby optimizing water and nutrient uptake and contributing to more resilient agricultural systems. While crop mixtures are known to potentially increase yields compared to monocultures, their effect on root development, especially within biopores, remains insufficiently explored. To address this gap, a field study was conducted to quantify root length density (RLD) and biopore usage in spring wheat and faba bean grown in monocultures and mixtures. The experiment was established at Campus Klein-Altendorf (CKA), one of the University of Bonn's experimental research farms. Root biomass, RLD, root share, and grain yield parameters were measured. Roots were sampled by soil monolith method to a depth of 70 cm. Results showed that the crop mixture had the highest RLD in the topsoil layer (10–20 cm), while in deeper soil layers (40–70 cm), spring wheat exhibited significantly more root growth than faba bean. Within biopores, faba bean demonstrated a higher proportion of root length compared to spring wheat while mixture values were not significantly different from faba bean. Between 50 and 70 cm, absolute RLD in biopores was higher in mixtures than in the average of the sole crops, but the opposite was the case for the share of roots in biopores. Root weight within biopores at 60–70 cm depth was significantly higher in spring wheat as compared to faba bean. The mixture showed intermediate values, with no significant differences compared to the sole crops. No significant differences were found at other depths. These findings suggest that although faba bean utilizes biopores more extensively in terms of root length, spring wheat and mixtures allocate more root biomass to biopores at greater depths. Additionally, Land Equivalent Ratio (LER) values on grain yield were above 1, confirming a yield advantage of intercropping over sole cropping. Overall, the study highlights that while biopore root growth in mixtures was not significantly greater, intercropping contributed to improved yield performance.

R20

Reconstruction of Root System Architecture in 2D+t: benchmarking loss functions in deep learning reconstruction pipelines

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Automatic spatiotemporal reconstruction of root system architecture (RSA) across species and imaging setups remains a phenomics bottleneck. Recent pipelines are divided in two successive stages [Fernandez et al., 2022]: (1) segmenting root pixels (semantic segmentation) in all images and (2) reconstructing the RSA's topology, geometry, and development. Deep learning semantic segmentation methods are trained to minimize pixel-wise losses such as Binary Cross-Entropy (BCE) or overlap losses (e.g. Dice).

These losses are insensitive to root architecture topological features such as organ continuity or branching points. Therefore, this study quantifies the impact of changing loss functions using metrics that capture segmentation accuracy and reconstruction fidelity.

The loss functions are benchmarked using two 2D+t datasets of Arabidopsis and Maize, acquired on different high-throughput platforms, and annotated into 2D+t RSML (Root System Markup Language) graphs.

Three loss functions (BCE, Dice, and clDice [Shit et al., 2021]) were selected to train two models (i.e. Unet and SegFormer), giving 6 segmentation instances. Each segmentation instance is then processed with the RootSystemTracker reconstruction method [Fernandez et al., 2022]. Segmentations and reconstructions are compared considering the following: (i) segmented mask-level accuracy (e.g., accuracy, F1-score, Intersection over Union), (ii) graph-level fidelity (e.g., intercept curve distances), and (iii) trait-level estimates (e.g., length, density, organ count).

Comparative analysis of these indicators enables identification of relations that do not explicitly appear when evaluating segmentation and reconstruction independently in this hierarchical pipeline. The optimized criteria effect may diverge from trait-level extraction needs, which highlights the limitations of single-score reporting and suggests the need for a multi-level evaluation framework aligned with specific phenotyping goals.

R21

Impact of ectomycorrhizal colonization on rooting depth and vertical root density patterns

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Ectomycorrhizal fungi (ECM) form mutualistic associations with tree roots, enhancing nutrient and water uptake and supporting tree resistance to drought stress. ECM act as strong carbon sinks and their association with plants is known to affect root system architecture, for example by increasing root branching and by shortening and thickening roots. However, ECM-derived effects on rooting depth and vertical root density distribution, critical traits under drought stress, remain largely unexplored. In this study, we will investigate how varying degrees of ectomycorrhizal colonization influence root architecture across different soil depths. Using both destructive and non-destructive methods, we will assess root responses in saplings of different tree species grown in forest regeneration sites. Two treatments were applied: ECM inoculation and a non-inoculated control. At the end of the growing season, destructive uprooting will provide precise measurement of rooting depth, vertical root density profiles and degree of mycorrhizal colonization. To complement this, minirhizotron imaging will monitor root and ECM developmental dynamics over time.

During minirhizotron installation, preliminary observations in the top 20 cm of soil collected under sessile oak saplings (Quercus petraea) revealed that saplings with lower mycorrhization rate had a higher density of fine, non-suberized roots while highly mycorrhized saplings were more abundant in thicker, suberized ectomycorrhizal roots. This potentially indicates a differentiation in carbon allocation strategies: prioritizing the development of fine feeder roots in the first case, and towards the formation of ECM associations in the second. Results on potential differences in rooting depth and vertical root density distribution in relation to mycorrhization degree will be available by the time of the conference. As a higher mycorrhization rate appeared to reduce the need for finer root production, we hypothesize that it may also reduce overall rooting depth. This could be potentially due to lower carbon availability for deep root growth and/or a reduced need for deep roots, given the ECM hyphal network's efficient water foraging (especially at shallower depths). Ultimately, our study will improve our understanding on how plant-ECM interactions may shape below ground resource allocation and root morphology, with important implications in the context of tree root adaptations and forest management.

R22

Affordable and Low-Cost Root Phenotyping Methods

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Ege University Faculty of Agriculture

Root phenotyping is an important tool for studying the morphological and physiological characteristics of the below-ground parts of plants. However, traditional methods often require expensive equipment, creating challenges for research groups with limited budgets. Low-cost, open-source methods developed in recent years have made root phenotyping much more accessible. Rhizoboxes (transparent observation boxes) and agar-based systems allow plants to be grown with their roots visible, while shovelomics, a method applied by digging and washing in the field, offers a practical solution. Flatbed scanners, smartphones, and Raspberry Pi cameras can be used for root imaging. These images can be analyzed with free software such as ImageJ, SmartRoot, RootPainter, and DIRT. Furthermore, root development can be monitored over time using the paper roll method and simple minirhizotron systems. These methods can be used in both laboratory and field settings and offer benefits in many areas, including plant breeding, analyzing stress responses, and increasing agricultural productivity. Low-cost root phenotyping solutions provide broad access to scientific studies, increasing research capacity, particularly in developing countries. This poster will present low-cost, accessible and affordable root phenotyping tools.

Key words: Root phenotyping, Low cost, affordable, phenotyping tools

R23

Root and tiller phenotyping to identify new variation for barley breeding

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One major challenge of agriculture is maintaining food security in times of climate change. Generally, different climate models concertedly predict that precipitation events will decrease in quantity while they increase in intensity. This will lead to more extended periods of drought, followed by periods of heavy rainfall. Future plant breeding, therefore, has to account for the genotypes' survival during drought and a good recovery ability after rainfall events. Plants have evolved different strategies to adapt to these threats, for instance through different rooting or tillering strategies. Within two DPPN-ACCESS projects we investigated these two aspects in the wild barley nested association mapping population HEB-25.

By accessing the GrowScreen-Rhizo 3 system (FZ Jülich) we characterized the different root architecture of wild and elite barley. It turned out that elite barley shows a generally wider root system with lots of lateral roots, while wild barley focuses on fast vertical root growth with deeper seminal roots. Based on genome-wide association studies genetic regions involved in controlling root growth could be identified.

The re-tillering behavior of selected barley genotypes was investigated in five different (re-) watering regimes on the APPP-B platform for medium-sized plants (IPK Gatersleben). We were able to show a genotype-dependent (re-) tillering behavior with genotypes maintaining a stable tiller number independent of watering and others with massive additional tillering after re-watering. Notably, this high re-tillering was negatively correlated with harvest index.

Altogether, both experiments highlight the genetic regulation of root and tiller dynamics with valuable genetic variation being available for plant breeding in the wild barley gene pool.

R24

Phenotypic and genetic diversity of root traits in recombinant barley inbred lines

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Root system architecture (RSA) phenotypes have been recognized as a research target in relation to stress tolerance and to their possible beneficial effects on seedlings establishment and yield stability. In recent years, the combination of new phenotyping methods with SNP data and gene expression profiling has provided a path to uncover the key genetic components underlying RSA traits expression. By addressing both the phenotypic and genotypic variance, quantitative trait loci (QTLs) can be identified and mapped using suitable populations. We exploited for our study the HvDRR population, which was created by crossing 23 diverse landraces, cultivars and improved varieties of spring barley with worldwide origin in a double round robin (DRR) design. To this end, we phenotyped over 200 different recombinant inbred lines (RILs) selected from the 45 biparental populations based on phenotypic variation of parental inbreds. A novel non-invasive high-throughput phenotyping platform, GrowScreen Rhizo III, has been applied for screening root growth over time using barley seedlings. Significant differences of RSA traits among the genotypes, including seminal, lateral and total root length, have been observed, and relationships among the traits have been detected. For instance, the total root length differed up to 3.45 times between the 23 parental inbreds three weeks after sowing. Genetic as well as environmental variance and their interaction have been analyzed with mixed-effects models. Through association study with a 50K SNP marker map of the DRR population, new QTLs can be identified and QTL effects on various traits will be analyzed. In future work, we aim at validating candidate QTLs and related candidate genes. Our work will provide novel QTLs and genetic information related to root traits to be exploited in pre-breeding practices of barley and other temperate cereals.

Poster presentations

Session 4:

Phenotyping for improvement of yield and quality

Y46

Autonomous screening for photosynthetic efficiency in common pea breeding lines

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Photosynthesis is fundamental not only for biomass production but also drives symbiotic processes such as nitrogen (N) fixation. In grain legumes, N fixation provides a sustainable protein source, reducing N pollution and the need for synthetic fertilizers. The N fixation acts as an additional physiological sink and can prevent the downregulation of photosynthesis. Furthermore, photosynthetic performance indicates stress tolerance and could serve as an indirect selection trait for high N-fixing and resilient breeding lines. However, given the dynamic nature of photosynthesis under fluctuating field conditions, high-resolution data across diverse genetic resources is required for effective selection.

In a recent project, an autonomous field robot equipped with a light-induced fluorescence transient (LIFT) device was established to measure photosynthetic quantum efficiency (Fq'/Fm'). Over the growing season, the robot autonomously collected over 80,000 measurements across approximately 200 pea breeding lines, capturing genetic variation and environmental interactions. A correlation between yield and photosynthetic response to light intensity was observed. Complementary spectral measurements, thermal and stereo-RGB images will provide additional insights into the relationship between canopy architecture and photosynthesis.

Y47

Multi-sensor phenotyping of yield and yield stability for genotype selection in durum wheat

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Developing climate-resilient wheat varieties requires combining high yield with stability across diverse environments, especially under increasingly variable precipitation and rising temperatures. This study evaluated 64 post-Green Revolution durum wheat cultivars under irrigated and rainfed conditions at two contrasting Mediterranean sites in Spain. To enable genotype selection based on yield and stability, a classification framework was developed. Yield was estimated via linear mixed models, while stability was assessed as the slope of each genotype's yield across environments. Genotypes were grouped into yield and stability categories based on interquartile thresholds, and those with either low yield or low stability were considered undesirable for selection. To support this framework, multi-scale high-throughput phenotyping was performed throughout the season using UAV-based RGB, multispectral, and TIR imaging, along with ground-based RGB and multispectral sensors. The objective was to define seasonal, index-based phenotypes that differentiate desirable genotypes from those with suboptimal performance. RGB and multispectral Vegetation Indices (VIs) and canopy temperature measured at anthesis, grain filling, and their difference (as a senescence proxy) were used to train prediction models for yield and yield stability. 38 candidate indicators were evaluated using cross-validated Random Forests with sequential feature selection, plus environmental covariates (70–30% train-test split). Yield models achieved strong performance ($R^2 > 0.74$, MAPE < 23.64%), while stability prediction, though moderate (R^2 up to 0.44, MAPE ~17%), outperformed similar studies. The 24 selected indices revealed distinct seasonal phenotypes: high-yielding genotypes showed early vigor and rapid decline, while stable ones exhibited more conservative growth and reduced relative greeness. When considering both traits, desirable genotypes were marked by higher early-vigor and lower green retention at grain filling. These findings question that stay-green is desirable for yield improvement, highlighting instead the role of timely senescence at grain filling in promoting yield stability across optimal and stress-prone conditions. The developed approach shifts breeding priorities from yield maximization alone to joint evaluation with stability, promoting resilience and offering a cost-effective, scalable framework to support durum wheat selection under climate variability.

Y48

Stay-green traits captured by spatiotemporal traits of UAV-based canopy spectra from the phenology of different winter varieties and their response to climate

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Stay-green is a heritable trait associated with delayed leaf senescence, crop productivity and quality. As the onset of vegetative growth and progression of senescence reflect plant sensitivity to stresses and climatic conditions, stay-green traits are of particular interest for breeding crop varieties better suited to future climate scenarios. However, knowledge about the seasonal dynamic of wheat stay-green and senescence in response to environmental fluctuations remains limited, despite its importance in the context of climate change. In this study, we investigated the responses of multiple winter wheat varieties to low nitrogen input during the senescence phase and evaluated the potential of unmanned aerial vehicles (UAVs) to quantify stay-green traits at the canopy level. Spanning the years 2021 to 2025, we analyzed the climate response of stay-green traits quantified from UAV spectral data and ground-based sample analysis such as leaf SPAD, chlorophyll and anthocyanin content. Our main hypothesis is that temperature is the primary driver influencing stay-green trend differences between genotypes, which might be reflected in the multitemporal UAV data. Results showed that under low nitrogen conditions, distinct patterns of SPAD and anthocyanin accumulation were observed compared to higher nitrogen treatments. Wheat canopy spectral features showed genotype-specific temporal patterns during the senescence season and were highly variable between nitrogen treatments and varieties. A suite of spectral indices (SIs) calculated from spectra related to absorption signals of chlorophyll and anthocyanin were highly correlated with wheat leaf pigment content. The proposed Spectral indices calculated using reflectance extracted from UAV multispectral were able to track the spatiotemporal variation in wheat stay-green and senescence traits. Our findings demonstrate the plasticity of stay-green responses in winter wheat, highlighting its potential for adapting to reduced nitrogen regimes aimed at environmental sustainability. More importantly, we present a novel approach for assessing stay-green dynamics using canopy spectral responses, offering a scalable remote sensing method for tracking canopy traits temporal responses to climate change. This opens new avenues for high throughput field phenotyping of crop stay-green traits for crop improvement.

Y49

From Subjective to Objective Bud-break Phenology Assessment: CNN-Assisted RGB Imaging in Norway Spruce Seed Orchard

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Climate change poses significant threats to global forest ecosystems, creating an urgent demand for adaptive strategies in forest management and breeding programs. Spring phenological traits, such as bud-burst timing in Norway spruce (Picea abies), are traditionally evaluated through subjective visual scoring methods, typically using scales like the Krutzsch index. These subjective methods are inherently prone to observer bias, as evaluations may differ significantly between individual observers and even vary during the assessment period for the same observer. This variability undermines data consistency, reliability, and ultimately, the precision of genetic trait heritability estimates critical for breeding of resilient genotypes.

Here, we introduce a novel, objective spring phenology assessment method, integrating RGB imaging with a convolutional neural network (CNN) analysis, developed and tested in the Hermanky clonal seed orchard. By utilizing a custom-trained YOLOv7 CNN model, we precisely segmented and quantified the bud-burst phenology by calculating the ratio of bud-burst pixel area to total needle pixel area. The objective CNN-based method demonstrated a strong, yet not perfect, correlation ($r = 0.75$) with traditional subjective scoring. The substantial but incomplete correlation highlights inherent inconsistencies and observer biases within subjective assessments, indicating that observer perception differences significantly affect scoring outcomes. Furthermore, the objective method provided higher broad-sense heritability ($H^2 = 0.55$) compared to subjective methods ($H^2 = 0.45$), underscoring the increased precision and reproducibility of the CNN-assisted approach.

Our findings demonstrate that CNN-assisted RGB imaging significantly enhances the objectivity, accuracy, and reproducibility of phenological assessments. This methodological advancement effectively addresses evaluator biases and provides a scalable, high-throughput alternative for precise trait quantification. Consequently, our approach enables more reliable genetic analyses and optimized genotype selection strategies, thereby contributing to sustainable forestry practices under changing climate conditions.

Y01

Optimized Forage Yield Prediction via Remote Sensing and Machine Learning Techniques

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Forage plants are vital for global livestock and meat production. In Brazil, a leading meat supplier, M. maximus stands out as a highly productive and nutritious species, contributing with U$10.55 billion to the country's revenue in 2023. This study assessed the effectiveness of machine learning (ML) models, trained on drone-acquired RGB and multispectral data, in predicting green mass yield (GMY) and dry matter yield (DMY) of a M. maximus core collection (320 genotypes) population from Embrapa Gado de Corte (Campo Grande, Brazil). High-resolution (0.5cm/pixel) RGB and multispectral orthomosaics, digital surface models (DSMs), and digital terrain models (DTMs) were generated using OpenDroneMap. After removing non-plant pixel, remaining pixels in the RGB images were counted and then six vegetation indices (VARI, TGI, ExGreen, NDVI, NDRE, CCCI), Haralick texture descriptors (derived from gray-level co-occurrence matrices), and canopy height (dCH, from DSM-DTM subtraction) were calculated. These digital features were used to predict GMY and DMY using nine hyperparameter-tuned regression algorithms: linear (LinearRegressor), regularized linear (Ridge, Lasso, ElasticNet), and non-linear (SupportVectorRegressor, RandomForest, AdaBoost, GradientBoosting, KNeighbors). ElasticNet exhibited the best performance (mean Pearson's r of 0.89 and 0.84, and RMSE of 1.37 and 0.332 kg for GMY and DMY, respectively), with Lasso and Ridge showing comparable results. Feature importance analysis highlighted digital canopy height (dCH), plant pixel count, and the triangular greenness index (TGI) as the strongest predictors of both GMY and DMY. Conversely, multispectral indices were the least important, with texture features (correlation and contrast) showing moderate influence. K-fold cross-validation using RMSE and Pearson's correlation validated model performance using an independent holdout dataset. These results underscore the efficacy of drone-based high-throughput phenotyping for accurately predicting GMY and DMY in M. maximus using robust regularized linear models. This approach offers a significant advantage for rapid and non-destructive evaluation of extensive forage germplasm collections, showing potential for accelerating breeding programs and enhancing forage improvement strategies for livestock production.

Y02

Impact of Post-Flowering High Temperatures on Chickpea Seed Size, Colour and Nutrient Density

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Post-flowering high temperatures are becoming increasingly common and significantly influence crop´s yield and seed nutritional value. In this study, the effects of elevated post-flowering temperatures (32º C/25º C, day/night) and two watering regimes (40% and 10% field capacity) on two top-producing Portuguese chickpea genotypes (Elvar and Electra) were evaluated. Results demonstrate that post-flowering temperature is a key determinant of reproductive cycle duration, regardless of both genotype and watering regime. Among the several vegetation indices assessed, ARI (Anthocyanin Reflectance Index), PRI (Photochemical Reflectance Index), and WBI4 (Water Band Index 4) showed genotype-dependent differences. Seed composition was shaped predominantly by environmental conditions, overriding genotypic differences. While yield components were negatively affected, seed nutritional density improved under post-flowering high temperatures, particularly under the 40% watering regime. These changes were mainly due to alterations in the protein-to-starch ratio, which indicates modifications in sink-source relationships, and macronutrients levels. These findings highlight the importance of crop management strategies that balance yield and seed quality under climate change scenarios.

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Y03

Potential for pre-harvest prediction of tuber potato physiological disorders

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Background: Climate change is leading to warmer, drier summers in crop producing regions of the UK and Northern Europe. Periods of drought and water stress during crop growth are associated with potato physiological disorders. The physiological mechanisms behind these stress-induced disorders are not well understood, but sensing techniques show promise in identifying early signs of water stress that may lead to disorders, enabling timely intervention.

Objectives: This study compares two sensing techniques for detecting drought stress with standard physiological methods for measuring water status in potatoes and investigates the relationship between sensing data and drought-induced tuber physiological disorders. The null hypothesis is that there is no significant difference between traditional and sensing-based phenotyping methods in detecting drought stress leading to physiological disorders.

Method: A 2024 polytunnel pot trial was conducted with four varieties demonstrating different levels of susceptibility to drought: Markies (control), Russet Burbank, Challenge (both moderate susceptibility) and Nectar (susceptible) - exposed to 30% of field capacity. The drought stress was applied at tuber initiation for 25 days. Measurements were taken at three different times: 7 days after stress (DAS), 14 DAS, and 21 DAS. Relative leaf water content (RWC), stomatal conductance (SC) were the physiological parameters of crop water status evaluated. Two sensing techniques were employed: thermal imaging to examine leaf temperature, and chlorophyll fluorescence to detect specific fluorescence ratios (Fv/Fm). At the end of the trial, yield parameters were quantified, and physiological disorders were assessed using standard commercial scoring systems.

Results: Preliminary observations show a strong correlation between leaf temperature and both SC and RWC. Among all measured traits, leaf temperature showed the highest predictive power for skin quality (netting and tuber cracking).

Conclusion: These findings highlight the potential of leaf temperature as a non-invasive, high-throughput phenotyping method for assessing drought stress in potatoes, supporting the integration of thermal imaging as a robust and scalable tool for monitoring drought responses and associated skin defect risks in potato breeding and management.

Y04

Multimodal high-throughput phenotyping to link cluster architecture with agronomic and quality traits in Riesling and Pinot noir clones

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Grapevine cluster architecture as the result of cluster weight, length, width, berry number, area and size, is a key determinant of grapevine yield components and wine quality. These traits are important breeding targets that can prevent severe damage caused by Botrytis bunch rot and abiotic stresses such as sunburn. Traditionally, cluster architecture has been scored using low-throughput visual descriptors or with manual measurements using rulers and detaching berries. High-throughput phenotyping (HTP) addresses this limitation using advanced phenotyping methods such as 3D point cloud reconstructions, hyperspectral reflectance signatures and RGB image segmentation to capture cluster architecture phenotypic variability in large grapevine populations. In this study, we studied 221 Riesling clones and 240 Pinot noir clones selected for three cluster compactness types: loose, intermediate and compact. We developed an HTP pipeline consisting of a handheld 3D scanner to collect point clouds, then we used a spectroradiometer to measure hyperspectral reflectance, afterwards berries were manually detached from the clusters to collect RGB images from the berries and rachis and segmented using the Segment Anything Model (SAM) to fully characterize cluster architecture and explore the associations of this integrative trait with agronomic and quality traits. Our results revealed positive significant associations ($p < 0.05$) between cluster weight ($r = 0.53$), volume ($r = 0.52$), length ($r = 0.58$) and width ($r = 0.33$) with vine yield. Similarly, positive associations between berry weight ($r = 0.31$) and number of berries ($r = 0.5$) with yield were also found. On the opposite, a negative significant association ($p < 0.05$) was found between sugar and pH with cluster weight, rachis weight, berry weight, number of berries, berry diameter, cluster volume and cluster length. These results suggest a trade-off between sugar content and cluster yield components, highlighting the impact that cluster architecture has on wine quality. The HTP pipeline used enabled us to evaluate approximately 220 clusters per day and although it was developed for grapevine, its flexible and low-cost design makes it suitable for a broad range of perennial fruit crops. We propose that integrating multimodal datasets generated from multiple HTP platforms into perennial breeding pipelines will facilitate the development of new cultivars with enhanced biotic and abiotic stress resistances.

Y05

Sunlit Insights: Transferring Hyperspectral Imaging from Lab to Field

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Hyperspectral imaging has long been a key tool for non-destructive plant phenotyping. Photon System Instruments (PSI) integrates hyperspectral (HS) cameras into phenotyping pipelines, using them as essential data sources to assess plant health and developmental stages in controlled environments. However, research shows that plant responses to environmental stress can vary significantly between laboratory and field conditions, even in genetically identical plant lines, affecting the accuracy of yield and nutritional predictions. To address this challenge, PSI developed an advanced HS image processing pipeline, tested on a comprehensive dataset of Calendula flowers. This system together with a series of HS image preprocessing steps features a deep learning classifier based on a 1D convolutional neural network, which effectively captures key spectral signatures of each plant pixel despite variations in lighting—an issue that has long hindered the application of field HS imaging for phenotyping. The model achieves high classification accuracy, successfully distinguishing between 10 Calendula lines in field conditions.

This study highlights the advantages of high-speed, high-precision HS imaging, enabling rapid data collection while compensating for environmental variability and noise. Compared to traditional methods like manual sampling, spectrophotometry, or RGB imaging, this approach offers greater reliability, accuracy, and efficiency in field-based plant phenotyping. As a result, this pipeline significantly improves the transition of high-throughput, precise HS phenotyping from laboratory research to real-world field applications.

Y06

An expansion of Australian field phenotyping capacity with the Australian Plant Phenotyping Network

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The Australian Plant Phenotyping Network (APPN) has significantly expanded its field phenotyping capacity, establishing a world leading ecosystem of consistent multimodal sensing platforms across the country to support collaborative research. This ensures that researchers and industry partners throughout Australia can access to the same advanced capabilities, operated by skilled technicians, using standardised protocols and consistent data analysis pipelines.

The same capabilities are deployed at six nodes across the Australian cropping region providing national coverage. The capabilities range from basic RGB multispectral UAVs, UAV mounted high resolution RGB sensors, UAV mounted sensor packages integrating co-aligned RGB, LIDAR and VNIR hyperspectral sensors, and UAV mounted co-aligned VNIR/SWIR hyperspectral sensors. Ground based robotic platforms are equipped with RGB, LIDAR and VNIR hyperspectral sensors. Included in the capabilities are environmental sensors to be deployed at phenotyping sites.

Deploying these capabilities takes considerable expertise and this has hamstrung the phenotyping community in the past. By operating as a coordinated network with shared capabilities and harmonised protocols, the APPN accelerates the deployment and commissioning process. This approach also allows APPN to develop common approaches to the capture, analysis and storage of data, underpinned by FAIR data principles.

The field phenotyping nodes are hosted by The University of Western Australia, Western Australian Department of Primary Industries and Regional Development, The University of Adelaide, Charles Sturt University, The University of Sydney, and The University of Queensland.

The APPN is an initiative which is part of the Australian governments National Collaborative Research Infrastructure Strategy (NCRIS). The APPN provides controlled environment and field phenotyping capabilities to Australian plant researchers and industry. With increasing demand for field phenotyping capabilities across Australia, particularly in grains research, the Grains Research and Development Corporation, an Australian Government R&D corporation has invested in this capacity expansion.

Y07

Wheat plant density estimation by inverting leaf density dynamics retrieved from submillimeter-scale rgb imagery

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Wheat plant density is a fundamental trait for plant breeding. Although many high-throughput phenotyping methods have been proposed in the literature to estimate this trait, most of them have not been tested on independent datasets, indicating a possible lack of generalizability. In this study, we present a novel method that exploits the dynamics of leaf density to estimate plant density.

In the first step, a P2PNET (Song et al., 2021) deep learning leaf tip detection model was trained and validated on 4154 annotated submillimeter-scale RGB images of small-grain cereal plants acquired under passive or active illumination in China and France. This model was then used to count wheat leaves in images acquired at two to four dates before two-leaf stage with PHENOMOBILE or LITERAL phenotyping systems, in five high-throughput field phenotyping experiments. Leaf counts were then converted to leaf densities using the 3D information available, respectively, with LiDAR for PHENOMOBILE, and stereovision for LITERAL. In the second step, wheat plant density was estimated from leaf density dynamics, which is composed of estimated leaf densities and corresponding thermal times after sowing. A wheat leaf dynamic model was used to simulate the evolution of leaf density over thermal time as functions of several variables, including mean time of plant emergence, phyllochron and plant density. This model was then inverted using a lookup table approach to estimate plant density from leaf density dynamics.

The trained leaf tip detection model showed good performance on a test dataset, with a relative root mean square error (rRMSE) of 16%. Plant density estimation was then assessed on PHENOMOBILE and LITERAL independent datasets with manually measured densities, containing, respectively, 130 samples (3 sites) and 66 samples (2 sites). Accurate results were obtained with both PHENOMOBILE (RMSE = 39 plants/m^2, rRMSE = 13%, $R^2 = 0.87$) and LITERAL (RMSE = 22 plants/m^2, rRMSE = 13%, $R^2 = 0.82$) images. Two to three observations performed before the appearance of the second and third leaves were sufficient to get these results. This method not only shows good generalization properties, but also opens up interesting prospects for plant phenotyping, such as phyllochron estimation.

Y08

Model-assisted phenotyping: Is the assimilation of high-throughput field phenotyping data into a crop growth model improve the characterization of wheat varieties?

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The recent development of high-throughput field phenotyping (HTFP) instruments has transformed our ability to characterize crop phenotypes. HTFP platforms now enable frequent, non-destructive measurements of structural traits (e.g. plant surfaces, biomass, yield) in the field, addressing key bottlenecks in breeding programs. These HTFP observations in well-characterized environments paves the way for the use of crop growth models (CGM) to predict structural traits through the estimation of functional traits. These functional traits correspond to varietal input parameters of CGM and are closely linked to the genetic characteristics. This strategy is known as model-assisted phenotyping. This study investigates the contribution of HTFP data in estimating bread wheat functional traits compared to traditional destructive data using an assimilation data framework based on a model-assisted phenotyping process. By assimilating multi-environment, multi-instrument structural trait data, the goal is to improve genotype characterization and enable reliable performance prediction in unknown environments. The study was carried on ten bread wheat varieties cultivated on two experimental platforms in France (16 contrasted environments). The use of a CGM for estimating functional traits requires that model formalisms and interactions of ecophysiological processes are realistic enough. Thus, a mechanistic CGM developed for wheat – SiriusQuality2, providing a detailed and biologically realistic description of the crop ecophysiology was used. The data assimilation framework was designed using the AgMIP calibration protocol. The variety characterization was based on the estimation of 23 parameters with the observation of 11 structural traits – considering phenology, plant surfaces, biomass, yield and their components. The main contribution of HTFP data was evaluated by comparing predictions based on functional traits estimated through assimilation of HTFP data (Green Area Index and fiPAR) with predictions based on functional traits estimated through assimilation of manually acquired data (surfaces from leaves, stems and green fraction, leaves and stem biomass). The findings of this study should support the use of HTFP data over traditional destructive manual measurements for estimating varietal input parameters. Unlike traditional data, which are time-consuming and often less accurate, HTFP data offer high accuracy, are easy to collect, and provide high temporal resolution.

Y09

Trait variations in annual and perennial Hordeum are structured by phylogeny and shaped by life history

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Growing interest in perennial crops for sustainable agriculture is driving research into the genetic, physiological, and morphological traits that distinguish annuals from perennials. While most studies on life history variation have focused on eudicot model species, much less is known about the trait syndromes that differentiate annual and perennial cereal crops. The Hordeum clade, which includes about 33 annual and perennial species, including the annual crop barley, offers a valuable system for investigating these differences in grasses.

We examined 25 functional traits across 48 accessions from 21 Hordeum species in a common garden trial (2021–2023). An updated phylogeny of the genus revealed at least three independent transitions between annual and perennial life histories within the Hordeum clade. Although trait variation was largely shaped by phylogeny, life history (annual vs. perennial) accounted for a significant portion of the variation. Annual accessions exhibited broader trait diversity despite lower overall genetic diversity, largely due to the distinct trait profiles of wild and cultivated barley. Both wild and cultivated barley were characterised by faster growth rates and larger organ sizes than other Hordeum accessions, suggesting that wild barley was already predisposed for domestication.

Annual and perennial Hordeum accessions were consistently differentiated by functional traits, regardless of phylogenetic relationships. Perennials exhibited later flowering, a lower harvest index, and higher carbon-to-nitrogen ratios in both leaves and grains. Environmental factors, particularly temperature at the accession's origin, further explained trait variation: annuals were more common in hotter, drier regions, while perennials were associated with environments characterized by lower daily and seasonal climate variability. Overall, life history transitions in Hordeum involved consistent shifts in development and resource allocation traits that extend beyond the effects of phylogeny and environment. These results now pave the way for the dissection of genetic differences that differentiate annual and perennial Hordeum accessions as the basis for the development of perennial cereal crops.

Y10

AI-supported optimization of the harvest time of Arnica montana

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Arnica montana is an economically important medicinal plant whose extracts, containing the active ingredients helenalin and dihydrohelenalin, are used as raw materials in the pharmaceutical industry due to their various properties. However, the asynchronous flower development of Arnica montana poses a major challenge for determining the optimal harvest time in controlled cultivation, as the active ingredient content and harvestability depend heavily on the phenological stage of the flowers. To solve this problem, a methodological approach was developed that uses image-based monitoring together with a neural network to classify seven defined flower stages in a field-suitable and non-invasive manner. This enables quantitative recording of the stage distribution in the plant population over time. With known concentrations of the target compounds helenalin and dihydrohelenalin for each characteristic stage it is possible to estimate the temporal progression of the potential total active ingredient yield of a crop. The results enable a well-founded determination of the harvest window, taking into account active ingredient accumulation and decreasing harvest efficiency. The presented method has transfer potential to other medicinal plants where morphological characteristics can be used as proxies for ingredient concentrations.

Y11

The Swiss Plant Phenotyping Network (SPPN)

Nathalie Wuyts

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The Swiss Plant Phenotyping Network (SPPN) has recently grown to include members from beyond its two founding institutions, Agroscope and ETH Zurich, encompassing the wider scientific community, industry, and non-profit organisations. The SPPN is set to become recognised as a national node of EMPHASIS, the European infrastructure for plant phenotyping. The SPPN community has expertise in research infrastructure development, phenotyping technology applications, data management and education and training. Our research themes span the broad range from fundamental research in ecology and biology using model plants and crops to applied research in field and orchard crops. Research is conducted at scales ranging from the landscape level to the individual plant and organ level. Current members foresee providing research infrastructure and data services in EMPHASIS, but also wish to contribute to education and training. Come and take a look at the poster to find out more about plant phenotyping in Switzerland.

Y12

High-throughput phenotyping of seed germination, twenty years of experience at GEVES

Didier Demilly; Audrey Dupont; Marie-Hélène Wagner; Sylvie Ducournau

GEVES

Following a proof of concept, high-throughput phenotyping has been developed for seed germination (radicle emergence) under controlled conditions. In-house specifications enabled ESEO (Ecole Supérieure d'Electronique de l'Ouest) to develop an automated image acquisition system using 4 cameras above a Jacobsen table in a climatic chamber. Analysis of the dynamics of seed imbibition showed that the movement of the seed's centre of inertia is reliably linked with germination. Over the years, the duplication and continuous improvement of equipments and methods (like seed deposition, use of pleated paper) have made it possible to work on an increasing number of species (42 species), under broader temperature conditions (from 5 to 30°C), and on an increasing number of seeds (from 800 up to 2400 seed per table). With 5 tables in two climatic chambers, we are able to carry out large experiments. Since 2005, PHENOTIC Platform (PHENOME – research infrastructure) analysed 1.4 million of seeds on 318 000 RGB images for different purposes:

Seed vigour evaluation,

Seed physiology knowledge,

International seed testing development: radicle emergence test,

Genetic resources screening in stress abiotic conditions,

Seed treatment evaluation for priming or biostimulants.

Y13

Development of a pipeline for the determination of wheat head parameters

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To reduce manual effort for breeders, automatic determination of plant parameters is essential for the genotype selection process. For agricultural development, data of different plants and purposes are collected [1, 2]. Overall, small and dense objects in agriculture are challenging to acquire and analyze. Monocular camera data is insufficient due to occlusions in dense scenes. 3D point clouds can address these issues and provide additional parameters about plants. Laser scanners and multi-camera systems are suitable for acquiring point clouds, but laser scanners are limited in phenotyping due to cost, adaptability to deformable objects, resolution, and plant movements, and they do not provide color information [3]. We use Neural Radiance Fields (NeRFs) with a multi-camera setup for colorized 3D reconstruction of point clouds, which are then used for further analysis. Our pipeline contains:

1. Prototype of a multi-camera data collection system specialized for agriculture breeding plots,
2. NeRF-based reconstruction,
3. Clustering-based wheat head identification as baseline approach.

To enhance the quality of the point cloud, an array of 12 full-frame RGB cameras captures the scene in a single shot - synchronized by a high-powered LED flash system using 8 flash heads with a light exposure time less than a millisecond. Localization is further supported by GNSS, IMU, and ultrasonic distance sensors.

To establish a baseline we rely on clustering of the point cloud. Specifically, we use DBSCAN algorithm to identify individual wheat heads, including shape and volume based filtering of leaves and stems.

The results are only first impressions of the current development, partly affected by over-exposed image regions, which impact the 3D reconstruction. A large portion of the wheat heads are sharply visible due to the high-resolution imagery for accurate phenotyping.

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Y14

Stress Matters: Barley's Metabolomic and Phenotypic Responses to Abiotic Challenges

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In natural environments, plants are predominantly exposed to combinations of abiotic stresses rather than single ones. In this study, we investigated leaf metabolomic profiles, phenotypic traits, and yield components of four spring barley genotypes of diverse geographic origin, exposed to drought, salinity, high temperature, and their combination. The aim was to understand genotype-specific responses and identify metabolic pathways and biomarkers linked to stress resilience and yield performance. We found that the Syrian genotype exhibited early metabolic responses, including rapid accumulation of amino acids such as proline, indicating its potential as a donor of adaptive traits in breeding. Combined stress generally induced unique metabolomic changes that differed from single stresses. Some metabolites, such as methionine sulfoxide, consistently accumulated under drought, salinity, and their combination, while others, like leucrose, increased only under drought alone. Metabolite accumulation was significantly affected by genotype, stress type, and their interaction. Several metabolites, including aspartic acid, showed consistent increases across genotypes, suggesting their potential as general stress biomarkers. Combined stresses also induced more pronounced phenotypic changes, often synergistic or additive, compared to individual stresses. Furthermore, significant correlations were observed between specific metabolite levels and phenotypic traits, highlighting the complex interplay between metabolism and morphology under stress. Our findings contribute to a better understanding of stress-response mechanisms in barley and may support the development of more resilient cultivars through integrative phenotyping and metabolomic selection.

Y15

Dissecting Heterotic Potential in Barley (Hordeum vulgare L.) using Pan-Transcriptomics Approaches

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Heterosis, or hybrid vigor, refers to the phenomenon where offspring from two genetically distinct parents outperform both parents in traits such as yield, yield components, and resistance to biotic and abiotic stresses. In crop improvement, heterosis is a key strategy for enhancing global agricultural productivity. Despite its importance, the molecular mechanisms underlying heterosis in crops remain unclear. In this study, we aim to define the molecular mechanisms controlling heterosis in barley by combining phenotypic and pan-transcriptomic data. To define the molecular mechanisms controlling heterosis in barley, we developed 14 F1 hybrids from 15 genetically diverse Ethiopian barley lines by using simple NCII mating design. Both the F1 hybrids and their parental lines were evaluated under field conditions, and six phenotypic traits (days to flowering, plant height, spike length, number of seeds per spike, awn length and thousand seed weight) were collected. Additionally, total RNA was extracted from leaves of both the F1 hybrids and their parental lines at the fourth leaf stage, and mRNA was then isolated from the total RNA and sequenced using Oxford Nanopore Technologies to enable pan-transcriptomic analysis. Phenotypic data analysis revealed significant differences between the F1 hybrids and their parental lines for all traits, except awn length. Estimates of heterosis in F1 hybrids relative to their parents showed both positive and negative mid-parent heterosis across the evaluated traits. The highest mid-parent heterosis was observed in the F1 hybrid 64065a × HB-1307 (35.84%) for number of seeds per spike, while the lowest was recorded in the F1 hybrid 64068a × HB-1307 (-2.62%) for days flowering. Genetic distances among parental lines were estimated using 23,241 SNP-markers. Genetic correlation estimates between parental genetic distances and mid-parent heterosis showed positive and non-significant correlation for plant height, spike length, number of seeds per spike and thousand seed weight, while negative and non-significant correlation for days to flowering. Pan-Transcriptomic analysis of the long-read RNA-seq revealed many differentially expressed genes between the F1 hybrid and their homozygous parental lines. Differential expression analysis identified 421 up-regulated and 986 down-regulated genes in the F1 hybrids as compared with their parental lines. Most of differentially expressed genes were up-regulated in most of F1 hybrids as compared to their homozygous parent. From pan-transcriptomics analysis we also identified more non-additive gene expression patterns than additive in both two and six row barley. The significant phenotypic differences between F1 hybrids and their parents, the lack of significant correlation between parental genetic distance and mid-parent heterosis, and the non-additive nature of differential gene expression, indicate that understanding the connection between heterosis and the pan-transcriptome requires multi-omics data from multiple tissues.

Keywords: heterosis, genetic distance, mid-parent heterosis, pan-transcriptomics, phenotypic traits

Y18

Combining proximal sensing, crop modeling, and ground truth measurements for understanding of crop physiological responses of old and modern wheat cultivars under varying soil nitrogen

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Wheat is the major cereal crop contributing to human food supply all over Europe. Excess use of mineral N fertilizer in crop fields not only increases the production cost but also results in the high N leaching and negative environmental impacts. With "Farm-To-Fork" strategy, the European farmers must reduce around 20-30% of the nitrogen application to crops by 2030. Identifying wheat cultivars that are suitable to lower N applications thus are very important in this context. Old wheat cultivars which were primarily developed under conditions of low nutrient availability, are expected to be better adapted to nutrient-poor soils. Further understandings on how old and modern cultivars respond to varying soil N could be helpful to identify suitable N-related traits and cultivars that support the breeding process. We combine field experiments, crop modeling, statistics, and proximal-sensing (PS) approaches to investigate the responses of agronomic traits and leaf photosynthesis traits and applications of the combined PS and crop modeling in predictions of plant N concentration (Nplant), AGB, and GY for winter wheat. The field trial uses 8 old and modern winter wheat cultivars having different released dates from 1930 to 2017 growing under 4 N application rates (0, 120, 180, and 240 kg N ha-1) with five replications in split-plot design in the Campus Klein-Altendorf, University of Bonn, around 25 km to the south of Bonn. Ground-truth measurement include bi-weekly agronomic traits (Nplant, plant height-PH, leaf area index, length and width, AGB, and yield traits etc.), leaf photosynthesis (maximum carboxylation rate-VCMAX, maximum electron transport rate-JMAX, and stomatal conductance etc.), and below-ground processes (soil water content, mineral N, and root morphology). Proximal sensing products like Nplant, AGB, and PH were quantified on the same sampling dates with UAV flying campaigns, during which high-resolution RGB und multispectral imagery were acquired. The crop model LINTULCC2 is further improved to represent the soil-plant N processes then is integrated with the in-season ground-truth and PS data for data assimilation approach to predict seasonal Nplant and AGB for the selected cultivars. Insights in use of the different ground-truth and PS approaches and combination of the crop model-PS in our small trial will be important for phenotyping of the larger number of wheat cultivars in quantification of Nplant, ABG, and GY under field conditions.

Y19

Exploiting active rgb imagery to estimate leaf chlorophyll content in wheat

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Leaf chlorophyll content (LCC) is closely related to the crop physiological status, hence its estimation is of great interest in high-throughput plant phenotyping. This problem has long been studied in satellite or drone passive remote sensing for the last decades. In general, accurate estimation of LCC heavily depends on our capability to retrieve the actual leaf color, i.e., to convert the optical data to reflectance, which may be difficult under natural light. In this study, we investigate the potential of RGB (Red, Green, Blue) imagery acquired under active illumination with the Phenomobile unmanned ground vehicle, to estimate LCC in wheat.

A three-step, physics-based methodology was introduced to convert Phenomobile images to reflectance. First, differences in incoming flash illumination between R, G and B bands were corrected using calibration images acquired over a reference panel of known reflectance (white balance). Second, a physical model describing the spatial variations of incoming illumination and adjusted with prior calibration, was used to remove the distance-dependent vignetting effect on the images. Third, the reflectance image was computed by dividing the images by the distance-dependent incoming illumination, also derived from calibration. Evaluation on independent datasets showed that reflectance was retrieved with reasonable accuracy, with a relative root mean squared error (RMSE) of about 15%.

This methodology was applied to wheat images acquired at 1.5 m from the canopy and 45° view angle, in three high-throughput field phenotyping experiments in Toulouse and Montpellier (France). Several growth stages were considered in 2024 and 2025, representing 106 microplots and 21 genotypes in total. Concurrently, SPAD measurements were performed on the top three leaves of 20 plants for each microplot in 2024 or only the top leaf in 2025, and converted to LCC based on Cerovic et al (2012). Vegetation pixels were extracted using the SegVeg segmentation model (Serouart et al, 2022), and the average reflectance was computed. Using simply the difference between the red and the blue bands and a logarithm model, LCC was estimated more accurately when using reflectance (RMSE = 4 $\mu g.cm^{-2}$, rRMSE = 11%, $r^2 = 0.82$) instead of white balanced images (RMSE = 9 $\mu g.cm^{-2}$, rRMSE = 22%, $r^2 = 0.41$). This demonstrates the potential of active RGB imagery to estimate LCC and opens up interesting perspectives for the estimation of other biochemical components.

Y20

Modelling plant reponse to salt stress in tomato

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Soil salinity is one of the main abiotic environmental challenges to sustainable agricultural production in major arable regions worldwide. Tomato (Solanum lycopersicum L-Solanaceae family), is one of the most important crops and is widely grown in both open fields and protected environments. Salt stress significantly affects its performance, yield, and quality.

Currently, in Metaponto di Bernalda (MT, Southern Italy) is in progress a trial involving 16 tomato genotypes (S. lycopersicum var. cerasiforme), obtained from previous in-field screening of 48 accessions from a non-redundant reference collection of worldwide genetic resources for salinity tolerance. The experimental trial, realized according a split plot design with 5 repetitions, included three irrigation treatment with normal water (NW, Ece 0,04 DS m-1), irrigation with medium-salinized water (SW2, Ece 10 DS m-1) and with highly-salinized (SW3, Ece 20 DS m-1) water.

Using HTP technology, it is possible to evaluate plant responses by integrating customized physiological, morpho-biometric and biochemical and genetic data.

Plants are being analyzed using, the PHENOLab Plant Phenotyping Platform to assess their status at the time of sampling. PHENOLab features a high-resolution 3D laser scanner (PlantEye F600, Phenospex B.V., Heerlen, The Netherlands) mounted on a high-precision gantry that moves in both x and y directions above the plants. This high-throughput, non-invasive system enables dynamic monitoring of plant growth over time under varying environmental conditions. The platform records detailed morphological traits, including: Digital biomass, Maximum plant height, Projected Leaf Area, Leaf angle and inclination. It also captures physiological parameters, such as: Greenness (Green Leaf Index), Normalized Difference Vegetation Index (NDVI), Plant Senescence Reflectance Index (PSRI), Normalized Pigment Chlorophyll Ratio Index (NPCI).

Results from the trial will be discussed. Also, tissue samples will be collected from genotypes within applied treatments for RNA extraction and RNAseq analysis to model genome-wide expression profiles contributing to salinity tolerance in tomato.

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Y21

PheNo infrastructure - A New Step Forward for Plant Research in Norway

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PheNo – The Norwegian Plant Phenotyping Infrastructure is a new national facility in Norway that will help us better understand how plants develop and respond to their environment. This new plant phenotyping infrastructure uses state-of-the-art technology to observe and measure plant traits in detail. By understanding more about how plants react to the environment, we can support the development of stronger, healthier crops that are better suited for future climatic challenges. This project brings together scientists, companies, farmers, and developers to build a more sustainable future for Norwegian agriculture. Key partners in this infrastructure include NMBU, UiO, UiT, NTNU, and NIBIO — institutions with extensive expertise in plant science, which has been developed through long-term collaboration with major players in the agricultural and horticultural industries. The services are personalised to the needs of national users, with an emphasis on proximity, flexibility, and gradual expansion. By offering state-of-the-art, unique research facilities and data services, PheNo supports research and technological development, laying the foundation for new discoveries and the faster development of new plant varieties and sustainable production systems. PheNo offers services for high-resolution measurements of plants indoors (under controlled growing conditions) and outdoors (in the field), as well as seed phenotyping. The services aim at promoting both research and teaching, covering the entire spectrum from basic plant and molecular biology to practical applications in agriculture, horticulture, and plant breeding. PheNo participates in European collaborations on plant phenotyping and will become a Norwegian node in EMPHASIS once it is established as an official European infrastructure in 2026. Through this collaboration, Norwegian research communities will gain access to many specialized research facilities across Europe, and European researchers, in turn, will benefit from access to phenotyping services under Norway's unique growing conditions. Participation in EMPHASIS is also important for the exchange of knowledge, method development, and collaboration on common data standards. Overall, PheNo aims to strengthen Norway's capacity for a sustainable agriculture, address future climatic challenges, and position Norway as a leader in plant phenotyping research.

Y22

Biological seed priming responses in clover and alfalfa via 3D multispectral imaging

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This study aimed to assess growth dynamics and evaluate the effects of biostimulant seed priming on biomass accumulation and related traits in six legume genotypes using high-resolution multispectral 3D scanning technology. The genotypes included two alfalfa (Medicago sativa) cultivars (Birutė and Milda), two crimson clover (Trifolium incarnatum) cultivars (Kardinal and Redhead), and two zigzag clover (Trifolium medium) genotypes (Melot and breeding line 260z). Five morphological traits—digital biomass, 3D leaf area, average plant height, canopy light penetration depth, and convex hull area—were quantified alongside three spectral indices: Green Leaf Index (GLI), Normalized Difference Vegetation Index (NDVI), and Normalized Pigment Chlorophyll Index (NPCI). Phenotyping was conducted biweekly, resulting in nine scans for alfalfa and crimson clover and six for zigzag clover. Manual plant height measurements and shoot fresh/dry weights were recorded at the end of the experiment. Results indicated that alfalfa and crimson clover accumulated biomass and height more rapidly than zigzag clover. However, zigzag clover, particularly genotype 260z, exhibited the most pronounced positive response to treatment, including increased biomass and higher NDVI values, suggesting improved physiological performance. Positive biostimulant effects were assessed in Melot, Redhead, and Birute, as reflected in increased biomass accumulation. ANOVA revealed strong species effects ($p < 0.001$) but weak overall treatment effects and no significant species × treatment interactions. A significant reduction in NPCI ($p = 0.0047$) across several genotypes following treatment suggests potential stress mitigation through improved pigment balance or antioxidant activity. Correlation analyses confirmed strong relationships between digital, dry, and fresh biomass, respectively $r = 0.68, 0.73, 0.93$ ($p < 0.001$), and between digital and manual height measurements ($r = 0.95$, $p < 0.001$) validating the accuracy of 3D phenotyping. These findings underscore the value of genotype-specific screening for biostimulant applications and support multispectral 3D scanning as a reliable, non-destructive phenotyping tool.

Y23

MIAPPE: its evolution, current state and the landscape of implementations

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The Minimum Information About Plant Phenotyping Experiments (MIAPPE) standard is a community-driven project aimed at provision of recommendations on harmonization of data obtained in plant research. MIAPPE contains a specification of metadata required to adequately describe entities occurring in the experiments and their properties. Ten years after the publication of the first version in [1], which was followed by significant improvements in version 1.1 [2], we present the latest modifications of the standard leading to version 1.2. Some new metadata fields and properties have been added. Among others, the identification of "Biological Material" source was improved and “Trait” description was extended following ongoing developments in information systems. Spreadsheet templates have been constructed to facilitate the acquisition of data sets in accordance with MIAPPE. Links to information about MIAPPE 1.2 are given at www.miappe.org.

In addition to the description of the current state, we present information on the impact of MIAPPE on the community and on its presence in projects containing plant data management aspects.

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Y24

Time-series multispectral UAV imaging and N-sensor measurements reveal dynamic N-responses and breeding gains for N-uptake and protein yield in Norwegian spring barley

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ProteinBar is a collaborative project along the grain value chain in Norway to ensure a better utilization of domestically produced barley for animal feed. Through adaptation of sensor technologies, split fertilization strategies and breeding of new barley varieties we aim to increase the protein content of barley. We make use of various sensor technologies to gain insight into the nitrogen (N) uptake and remobilization in the barley plants during the field season and build-up of grain yield and protein content. In the present research, we investigated a historical set of ten 2-row and ten 6-row varieties representing approximately 40 years of barley breeding. These were tested in a split plot yield trial with 90 kg N/ha and 140 kg N/ha fertilization levels. The trial was phenotyped weekly with multispectral UAV imaging, and in addition, Yara N sensor measurements from the tillering stage to anthesis. Flag leaf samples were collected at anthesis and analysed for macro and micronutrients, including N. NDVI was derived from the time-series multispectral data and dynamic phenotypes were calculated as genotype means for each of the two N fertilization treatments.

The results revealed a consistent trend with increased N uptake and grain yield in the modern versus older varieties. This trend was apparent for both 2-row and 6-row barley. Conversely, there was a negative trend for protein content, likely due to a dilution effect from the higher yield levels of the modern varieties. PCA and correlation analyses showed that under the lower fertilization treatment (90 kg N/ha) the protein yield (calculated from the grain yield and grain protein content) could be explained by the N content in the flag leaf and Yara N sensor measurements during stem elongation. While grain yield was mainly associated with thousand kernel weight and days to maturity. Similar associations among traits were identified for the higher fertilization treatment (140 kg N/ha) with strong associations between grain protein deviation, the first N-sensor measurement and N content in the flag leaf. NDVI dynamics showed that the higher fertilization level resulted in a higher leaf canopy N content over the growing season for all varieties, indicating that a higher N availability in the soil resulted in higher N uptake. Also, different genotypes responded differently to different fertilization treatment, highlighting potential “high responsive” genotypes.

Y25

Improving UAS-Based Hyperspectral Reflectance Calibration for Field Phenotyping: Quantifying Atmospheric Correction Impacts on Vegetation Indices and Nitrogen Response

Wuhua Wang; Anirudh Belwalkar; Ying Yuan; Xiaoxin Song; Kang Yu

With the advancement of unmanned aerial systems (UAS) and remote sensing technologies, UAS-based hyperspectral imaging has emerged as a powerful tool for remote sensing and crop phenotyping. However, the propagation of atmospheric correction bias into the resulting hyperspectral reflectance imagery remains an understudied area. We used hyperspectral imagery acquired by two UAS-mounted sensors covering the VNIR (400–1000 nm) and SWIR (900–1700 nm) ranges. We evaluated the surface reflectance derived using three atmospheric correction approaches: (1) a physics-based approach using LibRadtran radiative transfer modeling, (2) empirical calibration using a ground-based single white calibration panel, and (3) empirical calibration using ground-based double-panel (gray and white). Vegetation indices using the NIR and SWIR bands, such as NDVI, NDWI, LWVI2, and NRI, were calculated based on these correction methods, and their responses to nitrogen fertilization treatments were assessed using ANOVA. Field measurements of top-of-canopy (TOC) spectral reflectance were carried out utilising the ASD FieldSpec 4 spectrometer to validate reflectance derived from UAS. Spectral angle mapper (SAM) and root mean square error (RMSE) metrics were used to further assess spectral correction accuracy. Results indicate that the double panel-based correction method yielded the lowest RMSE and the most accurate reflectance values compared to in situ measurements. While the physically-based modeling approach exhibited slightly high error, it produced spectral curves that were highly consistent in shape with reference spectra, as evidenced by comparable SAM values demonstrating its robustness in spectral pattern reconstruction. All vegetation indices responded significantly to nitrogen treatments ($p < 0.001$), with NDVI showing the strongest overall response. SWIR-based indices such as NRI850_1510 also exhibited notable sensitivity, particularly to temporal variations, highlighting their potential for capturing dynamic nitrogen effects across growth stages. By quantifying error propagation from correction models to downstream indices, this study bridges theoretical radiometric modeling with practical UAS calibration, providing critical insights for robust hyperspectral data preprocessing in precision agriculture.

Y26

Employing UAV Imaging and Spectral Indices to Advance Ryegrass Breeding: A Norwegian Field Study

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Perennial ryegrass (Lolium perenne L.) is a key forage species valued for its biomass yield, digestibility, and adaptability. In the face of climate change and drought, scalable, non-destructive phenotyping tools are essential to accelerate breeding. This study uses UAV-based multispectral and structural imaging to predict fresh biomass (FM), dry biomass (DM), and dry matter content (DMC) in ryegrass over three years and multiple harvests, comparing two field layouts: single, unreplicated rows and replicated plots.

UAV data included five-band multispectral reflectance and 3D canopy features, combined with local weather data aggregated over multiple time windows. Random forest models were trained and cross-validated within and across years to assess prediction accuracy, genetic heritability, and genotype ranking consistency.

Results showed high prediction accuracy for FM and DM ($R^2 = 0.70–0.80$), with lower accuracy for DMC. Prediction accuracy was similar across row and plot layouts, but plots exhibited lower error and higher trait heritability (up to 0.85) compared to rows (up to 0.70), indicating better genetic signal due to environmental noise buffering. Incorporating weather data improved model performance, especially during early and stress-affected harvests, by capturing environmental influences not directly visible in UAV imagery.

Temporal trends revealed highest accuracy and genetic consistency in the first annual cut, with declines under summer stress. Rank correlations between layouts were high initially (>0.85) but decreased under stress, supporting the use of plots for advanced selection and rows for early screening.

This study highlights UAV phenotyping's potential to support forage breeding by enabling repeated, non-destructive biomass estimation. It underscores the importance of experimental design, integration of environmental data, and timing in optimizing prediction quality and genetic resolution. Future work should explore hyperspectral data, temporal modeling, and multi-environment validation to further enhance predictive capacity and support genomic selection in climate-resilient ryegrass breeding.

Y27

Field-based high-throughput phenotyping for early growth of single common bean plants using UAV-based 3D point clouds

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The common bean (Phaseolus vulgaris L.) is a major global food legume and a sustainable source of protein for direct human consumption. In Europe, grain legume production for direct human consumption is low, relying heavily on overseas imports. For farmers to adopt common bean cultivation in Europe, the crop must be suitable for large-scale production. In these production systems, weed competition during crop establishment is crucial, especially given Europe's limited herbicide use. Therefore, breeding for rapid, uniform germination and canopy development is essential for large-scale production. However, identifying underlying genetic loci of traits of interest requires precise, early-stage phenotyping. These measurements are subjective, less detailed, and costly when done manually, and impractical for large-scale, multitemporal measurements. Thus, high-throughput phenotyping over time, along with improved automated pipelines for parameter extraction, are needed.

We cultivated 224 accessions of common beans, mostly from the INCREASE project collection, as single plants across two years and two locations. We used a UAV to capture RGB images from five camera angles on multiple dates. 3D point clouds were constructed using the structure-from-motion (SfM) technique. For plant parameter extraction, we developed an automated pipeline using the ExGR index for plant-soil separation. Following that, the DBSCAN algorithm was used to cluster the vegetation point cloud into single plants. The parameters of interest, such as plant height, volume, projected area, and surface area, were automatically calculated for each plant on multiple dates in each location and year. The mean of the four biological replicates per field and date was calculated, showing that distinct differences in the extracted parameters between genotypes could already be detected 21 days after sowing. These datasets can be used for downstream analysis, such as genotype-phenotype associations, and provide a foundation for phenotyping plants in diverse environments and across multiple growing seasons.

Y28

DeepCollar: a precise and reliable high throughput, method for phenotyping maize stem elongation, collar appearance, leaf azimuth and individual collar height from temporal series of multi-view images

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High throughput image-based plant phenotyping platforms allow following the dynamics of development of thousands of individuals plants, and the understanding of the control of growth as a function of genotypic and environmental cues. We propose DeepCollar, a method for quantifying maize stem growth together with dynamics of appearance and positioning of individual collars (leaf insertion points). First, we used a deep-learning detection model (YOLOv4) to detect collars on a time series of multi-view maize plant images. The detector was trained to distinguish between collars bearing a leaf pointing to the right or to the left of the image. Stem length dynamics was estimated as the highest collar height at a given date. Kinetics of individual collar positions and ranks were calculated first using a peak-detection algorithm on time-density plot of collar heights, where peaks correspond to 'plateau' reached by stabilized collars. Left/Right labeling of collars belonging to a plateau was then used together with viewing angle to estimate leaf azimuths. An automatic clustering algorithm enables the association of detected collars with the plateau they reach. Finally, collar emergence dates were estimated as the date at which the stem first reached a plateau. To evaluate the method, we developed a dedicated annotation tool that selects the best control images and allows the user to easily check and remove false positive detected plateaus. This tool can be used not only for checking, but also to obtain verified and reliable data from the automated pipeline. This check was performed on 1,000 plants imaged 40 days from 12 directions. Results showed that 98 % of collars were detected. For 75 % of plants, the algorithm detected 100% of the plateaus without errors. Additionally, 20 % of the plants exhibited false-positive plateaus, which were easily removed by the users. Only 3 to 5 % of plants displayed too many errors and were tagged as 'unsolved' by the annotator. The annotation process took around 15 s per plant, which is acceptable to get 97 % of the plants checked and precisely measured without errors. Overall, this study demonstrated that maize stem growth and individual collar height is measurable with a very high reliability on a phenotyping platform, at the cost of a few hours of human annotation posterior to a robust automated detection.

Y29

Hyperspectral data-based growth state estimation of rice plants cultivated in closed plant factories with artificial lighting

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In producing components for useful human applications, e.g., cytokine and vaccine, using bioreactors, genetically-modified (GM) plants have an advantage over conventional bacteria and animal cells from the view point of safety and preservation. Considering the possible environmantal impact of GM plants, it is required that plant-made pharmaceutical (PMP) proteins are cultivated in closed Plant Factories with Artificial Lighting (PFAL). Our project "Scientific Research toward the realization of a plant factory with artificial lighting that contributes to food security" aims to develope a multi-use closed PFAL system that is optimized for effectively producing multiple PMPs by cultivationg GM rice plants. The project is consisted of three sub-projects, i.e., (1) development of precision control of environmental parameters of PFAL, (2) development of high-level expression technology of useful components by genome editing and (3) development of PFAL system for rice plant. This study belongs to the first whose objective is to control environmental parameters of PFAL, developed by the sub-project (3), for maximizing the useful contents in rice grains by referring to growth states of the rice plants, developed by the subproject (2). In addition to standard environmental parameters, e.g., temperature and photoperiod, parameters related to UV-a and high Electrical Conductivity (EC) nutrient solution as beneficial stresses are controlled to enhance production of the useful components. In this study, we demonstrate nondestructive plant growth state estimations based on hyperspectral data, including hyperspectral image acquisition of rice plants cultivated under various conditions in PFAL, machine-learning-based estimation of protein contents in rice grains as useful components, machine learning-based estimation of anthocyanin contents in rice leaves as response to applied beneficial stresses, deep learning-based rice ear detection for automation of rice grain analysis, and sterile rate estimation of rice ears based on hyperspectral segmentation.

Y30

High-throughput multispectral phenotyping of anise under variable nitrogen and irrigation regimes

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Multispectral remote sensing has emerged as a powerful high-throughput phenotyping approach for noninvasive monitoring of crop performance by capturing reflectance across multiple regions of the electromagnetic spectrum, including blue, green, red, red-edge and near-infrared bands. In this study, we evaluated the potential of multispectral imaging to assess key agronomic traits of anise (Pimpinella anisum L.) under contrasting nitrogen and water regimes. Two field trials were established: one implementing six nitrogen fertilization levels (0, 20, 40, 60, 80 and 100 kg N ha^{-1}) under broadcasting sowing, and the other combining three irrigation treatments (drip, sprinkler and rainfed) with four sowing patterns (20, 40 and 60 cm row spacing, plus broadcasting). Multispectral images were acquired at three critical growth stages, and a suite of established spectral vegetation indices sensitive to nitrogen status (e.g., NDVI, GNDVI) and water stress (e.g., NDWI, PRI) were computed. Index values varied systematically with applied nitrogen and irrigation levels, demonstrating strong correlations with conventional agronomic measurements of biomass and chlorophyll content. These findings confirm that multispectral remote sensing constitutes a robust, high-throughput tool for quantifying treatment effects on anise, facilitating precision nutrient and water management in aromatic crop production systems.

Y31

A computational pipeline for identifying genotype-specific responses to planting density in wheat using high throughput phenotyping

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Planting density is a critical factor in plant studies, as plant-plant interactions driven by different densities shape the canopy development and architecture, influencing light interception, growth and yield. However, the knowledge about the plasticity of canopy architecture in respond to planting density remains limited. We hypothesize that genotypic variations in architecture plasticity contribute to genotype-specific responses to planting density. Using 200 winter wheat cultivars grown under three planting densities (30, 89, and 270 plants m^{-2}) at the high-throughput phenotyping (HTP) platform Phenoarch, we captured images of 2,400 plants daily and processed with a computational pipeline. This pipeline combined a deep learning algorithm for image binarizations, a space carving algorithm to reconstruct 3D architectures of each pot and a simulation workflow that constructs 3D architectures of virtual canopy and estimate light interception at plant and canopy levels. Preliminary results showed the ability of our pipeline to estimate light interception efficiency (LIE) and to derive the light extinction coefficient (k). LIE explains 51% of shoot dry matter and showed an asymptotic relationship with shoot fresh weight, depending on planting density. This pipeline opens several avenues for further research: 1) analyzing the vertical distribution of canopy volume to understand its impact on light interception and genotypic variation; 2) comparing LIE between actual canopy and synthetic canopy constructed from identical plants architectures to assess genotypic competitiveness or cooperativeness; 3) estimating pot-specific light radiation use efficiency by integrating simulated light interception and daily dry matter accumulation. Overall, this study demonstrated the capability and potentials of the HTP combined with computational pipeline to investigate genotypic diversity in canopy architecture and its response to planting density.

Y32

Effects of Different Soil Nitrogen Levels on UAV-Derived Canopy Indices in Bread Wheat (Triticum aestivum)

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Canopy indices derived from multispectral imagery are valuable tools in crop monitoring, as some are strongly correlated with grain yield. This study was conducted during the 2024–2025 wheat growing season at the experimental fields of Ege University, Department of Field Crops. Ten widely grown commercial bread wheat (Triticum aestivum) cultivars were used as plant material. The experiment followed a randomized complete block design with four replications. Sowing took place on November 29, 2024, with plot dimensions of 1.2 m × 3 m and a 20 cm row spacing.

Two nitrogen regimes were applied at sowing: low nitrogen (-N: 3 kg/da) and high nitrogen (+N: 9 kg/da). A UAV flight was carried out at the beginning of the heading stage using a DJI M350 RTK drone equipped with a MicaSense RedEdge-P multispectral sensor. Orthomosaics were generated using Agisoft Metashape, and canopy indices were calculated for each plot using QGIS software. The evaluated indices included the Normalized Difference Vegetation Index (NDVI), Green Normalized Difference Vegetation Index (GNDVI) and Red Edge Normalized Difference Vegetation Index (RENDVI)

Results indicated that soil nitrogen levels had a significant effect on the canopy indices. Many of the indices exhibited high heritability, highlighting their potential utility in selection processes within plant breeding programs.

Y33

Device and methodology for high-through-put measurement of leaf and canopy photosynthesis and transpiration provides genetic tools for adjusting plant water-use characteristics

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Research focused on boosting crop yields by improving photosynthesis and reducing the accompanying water loss are among the key tasks of plant biology and breeding. For such tasks, rapid measurement of in situ leaf gas exchange traits is needed. Despite remarkable progress, a device designed for rapid snapshot measurements of net CO2 assimilation rate (Anet) and stomatal conductance for water vapour (gsw) of many leaves in the field is still missing.

We present here the methodology and the device Karal, which enables fast measurements of Anet, transpiration (E) and gsw of many leaves using the principle “several leaves – one measurement”. This simple device involves two-side laminar air flow leaf chamber using reference gas from closed buffer and methodology that summarises short standardised individual measurements of different leaves into one measurement.

Parallel measurements with Li-Cor devices provided a good correlation, however data acquisition was several-fold faster with Karal and it was based on a considerably higher number of leaves. As such, the true power of Karal is in phenotyping numerous leaves of many genotypes in the field to collect canopy level snapshot values of Anet and gs in situ. This information is sorely needed for determining genotypic differences of yield potential.

We also demonstrate our recent advances utilizing guard cell CO2-singaling based on protein kinases MPK12 and HT1 to improve tomato water-use efficiency and whole plant stomatal conductance at different CO2 concentrations. We show how MPK12:HT1-based guard cell CO2-sensing mechanism can be used as a rheostat to adjust plant transpiration at different CO2 concentrations. As such this mechanism provides a tool to design crops with water-use characteristics suited to different agricultural practices.

Y34

Plant Height Measurement in Spring Wheat Using UAV-Based RGB and LiDAR Data

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Efficient phenotyping of key traits like plant height (PH) is crucial for accelerating genetic gains in wheat breeding. PH influences yield through effects on lodging resistance, harvest index, and resource-use efficiency. Traditional manual methods are labor-intensive and less suited to early-generation trials typically arranged in small plots. Unmanned aerial vehicles (UAVs) offer a high-throughput, non-destructive alternative. RGB sensors are cost-effective but may lack accuracy, while LiDAR systems provide detailed 3D canopy data with better ground separation. This study compares PH measurements obtained manually with those derived from UAV-based RGB and LiDAR sensors to assess their accuracy and suitability for wheat phenotyping. The aim was to identify the most effective aerial sensing approach for estimating plant height. Field trials were conducted at the Stende Research Centre of the Institute of Agricultural Resources and Economics in northwest Latvia during the 2025 growing season, using 24 spring wheat genotypes. Sowing was done with a cassette-type seeder in 1-meter-long plots (three rows, 0.25 m spacing). Two sowing densities were included: 500 seeds/m^2 (standard) and 260 seeds/m^2 (reduced). Each genotype was planted in one row and replicated three times across different field zones to account for spatial variation. Manual plant height data were collected at the flowering growth stage (GS65) from five randomly selected plants per row. Simultaneously, high-resolution UAV imagery was captured using a DJI Matrice 300 RTK equipped with a Sentera AGX710 multispectral sensor (including RGB) and a Zenmuse L2 sensor (LiDAR scanner with integrated RGB camera). The multispectral sensor flew at 15 m (0.4 m/s, 4.3 mm/pixel, 75% overlap), and the LiDAR at 12 m (0.5 m/s, 3.2 mm/pixel, 85% overlap). Plant height was estimated as the difference between the digital surface model (DSM) and the digital terrain model (DTM), producing a canopy surface model (CSM). A total of 180 measurements were used to evaluate the relationship between ground-measured PH and UAV-derived height (HCSM). Our research established a strong and significant relationship between manually measured plant height and the height estimated using the Zenmuse L2 aerial platform. Using this sensor, we found that the LiDAR scanner outperformed the RGB camera when compared to ground reference measurements. UAV-derived height was generally lower than the manually measured height for both sensors.

Y35

AN IMAGE ANALYSIS OF RAINFED SAFFLOWER (Carthamus tinctorius L.) GENOTYPES AT FLOWERING TIME

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Safflower is an important oil crop, known for its ability to tolerate marginal conditions, but its production is still minimal. More research is needed to develop commercial safflower genotypes with productivity and quality traits that will satisfy the producer, to increase safflower production. High-throughput plant phenotyping enables quick and effective selection between genotypes. This experiment was conducted in Izmir/Bornova (38.453326, 27.219803) during the winter safflower production season of 2024–25 under Mediterranean climate conditions. The objective of this experiment was to use high-throughput phenotyping tools to determine the flowering and plant height characteristics of local safflower genotypes sown as winter crops and growing under natural rainfall. In this study, 16 local safflower genotypes and five registered varieties, which were collected from different parts of Turkey, were used as seed material. The experiment was set up using a randomised complete block design with four replications. Sowing was carried out using a parcel sowing machine in plots consisting of four rows, each 4 metres long, with a row spacing of 20 cm.

A UAV flight was carried out at the flowering stage using a DJI M350 RTK drone equipped with a MicaSense RedEdge-P multispectral sensor. Orthomosaics were generated using Agisoft Metashape, and canopy indices were calculated for each plot using QGIS software. The evaluated indices included the Normalised Difference Vegetation Index (NDVI), Green Normalised Difference Vegetation Index (GNDVI), and Red Edge Normalised Difference Vegetation Index (RENDVI). The flowering trait was determined using NDVI data, and the genotypes were categorised by flowering class, growth pattern, and predicted yield.

It was concluded that using high-throughput phenotyping tools to determine important agronomic traits in safflower plants is an effective and applicable method in plant breeding programmes.

Keywords: safflower, high-throughput phenotyping, rainfed, NDVI

Y36

Drone-based field phenotyping for nitrogen use efficiency across wheat varieties

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Drone remote sensing technology has been increasingly used for field phenotyping studies, enabling the acquisition of a diversity of traits. Yet, what phenotyping traits play a relatively important role in explaining the variations in nitrogen use efficiency (NUE) between different varieties is not well understood. Here, we investigated a drone remote sensing multispectral data-driven method for crop nitrogen response phenotyping and for the estimation of NUE based on a four-year field trial testing the responses of 18 winter wheat varieties to three N rates. The main objective was to understand the effectiveness of drone-sensed traits in identifying N deficiency and explaining the variations in NUE across wheat varieties. The spectral features and texture features as well as their time series were extracted from the multispectral images and were employed in machine learning models for classifying nitrogen deficiency responses and for predicting NUE. Our preliminary results show that low nitrogen rates caused significant shifts in canopy spectral reflectance characteristics, specifically through the red-edge spectral indices derived from multispectral images. Slightly contrasting to published work, our results showed that texture features failed to deliver consistently accurate predictions of N responses between varieties. Spectral proxies of the canopy structure and time series metrics were also found to be related to NUE, which, however, requires further evaluations based on ground truth data. Finally, this study demonstrates promise in indirectly predicting NUE using drone data and machine learning models, highlighting the effectiveness of specific image-based features in explaining varietal differences in NUE. This study establishes a drone remote sensing data-driven workflow for high-throughput field phenotyping of NUE-critical traits, demonstrating the potential of drone remote sensing data for generating data-driven insights and for identifying high NUE phenotypes for improved NUE in breeding. It also underscores the importance of feature selection as a part of the modelling method and validating findings under different environments.

Y37

UAV-Based Estimation of Nitrogen Balance Index at Different Leaf Positions in Maize Under Varying Nitrogen Treatments

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Nitrogen(N) is an essential nutrient for maize growth and development, directly influencing the plant's photosynthetic capacity and overall growth status. Nitrogen balance index (NBI) measured by the Dualex sensor reading is accepted as an indicator of estimation of N nutrient status in crops, and the spatio-temporal variation of Nitrogen balance index is an important crop phenotypic trait of great significance for evaluating crop productivity.

The objective of this study is to develop a method that integrates UAV-based multispectral data with a bell-shaped function to accurately predict the NBI at different leaf positions in maize. Based on a one-year field experiment, we measured maize leaf Dualex values at different growth stages, and UAV-based multispectral images were captured. Considering that N content in maize leaves typically follows a bell-shaped distribution along the vertical canopy profile, we combined UAV spectral data with a bell-shaped function model to predict NBI across different leaf positions. The results demonstrated that integrating UAV multispectral data with a bell-shaped distribution model can accurately predict the spatio-temporal dynamics of NBI. Moreover, N application levels significantly affected NBI in maize leaves. This study provides a practical approach for rapid prediction of nitrogen balance between maize leaf layers, offering a valuable nondestructive approach for understanding nitrogen allocation and for improving nitrogen management.

Y38

Exploiting cereal biodiversity in nutrient use and biological interactions in crop resilience breeding (CerealBio)

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European cereal production faces growing pressure to reduce agrochemical inputs while maintaining high productivity and resilience amid climate change. The CerealBio project aims to address these challenges by harnessing biodiversity and ecosystem interactions to design new resilient ideotypes of wheats and oat. These ideotypes integrate traditional yield-focused traits with novel, underutilized traits related to root architecture, nutrient use efficiency, microbiome interactions, and disease resistance, thereby contributing to sustainable intensification and climate change mitigation. At its core is the ambition to explore and exploit genetic variation governing plant-environment interactions, particularly under nutrient-limited and biologically managed conditions. The project targets enhanced nitrogen use through improved uptake and utilization, emphasizing the genetic control of root traits and genotype-by-nitrogen interactions. Simultaneously, the emerging concept of neighbour-modulated susceptibility (NMS) is investigated, wherein disease resistance is shaped by intraspecific interactions, with implications for varietal mixture design. Phenotyping is central to CerealBio, enabling dissection of complex traits across diverse conditions:

- High-throughput phenotyping at IPK to assess root system architecture, shoot development, and photosynthesis under contrasting nitrogen levels.
- Aeroponic phenotyping via RootPhAir at UCL enabling time-resolved tracking of lateral root responses to nitrogen shifts, revealing root plasticity in uptake strategies.
- Multisensory stress phenotyping (PlantArray) at JKI measures transpiration, biomass, and water use efficiency under nitrate vs. ammonium nutrition and variable drought stress.
- Assessment of NMS using imaging platforms at IPK (BlueVision) and SLU. A probe genotype is co-grown with test genotypes, then challenged with pathogens to score NMS effects.
- UAV based phenotyping of field trials (CREA, UCD, UNIBO, JKI) at different European latitudes discloses the performance of the new wheat and oat ideotypes under farming conditions

Together, these integrated phenotyping strategies provide a multidimensional view of genotype performance, allowing the identification of key traits and genotypes for breeding resilient cereals. Outputs include novel alleles, phenotyping protocols, and marker-trait associations to support breeders and agronomists in designing climate-resilient, low-input cereal systems.

Y39

Implementation of medium throughput proxies for photosynthetic capacity in wheat pre-breeding

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Conceptual models of wheat yield describe it as a function of source (photosynthetic capacity) and sink strength (the plant’s ability to utilize assimilates for grain production). Understanding the status of source strength in breeding material—and the potential for its enhancement—is needed to achieve further genetic gains in yield. A retrospective analysis of top-performing lines from CIMMYT’s elite spring wheat nursery identified radiation use efficiency (RUE) as a key driver of genetic yield improvement over a 14-year period (2003-2016). However, restricted genetic variability for RUE within elite germplasm, coupled with the high cost, labor-intensive nature of RUE phenotyping, continues to constrain the use of this trait in breeding. In this context, the use of models to predict RUE based on ground based hyperspectral data offer a promising solution to overcome the limitations of low throughput and destructive sampling associated with traditional RUE estimation methods. Leveraging existing hyperspectral and growth analysis data collected across diverse panels and environments—including optimal conditions, heat, and drought stress—we pursued the following objectives: (1) evaluate existing models based on vegetation indices across more diverse germplasm and environmental conditions; (2) explore the use of raw hyperspectral data to develop new models using genomic best linear unbiased prediction (GBLUP) and deep learning approaches; (3) assess the impact of environmental covariates; (4) investigate temporal and spatial considerations in collecting ground-based hyperspectral data; and (5) test the utility of these models within a pre-breeding pilot program for RUE. Preliminary results are presented and discussed in this study.

Y40

Correlation of RGB Image-Based Metrics with Chlorophyll Content and Feed-Quality Parameters in Hydroponically Grown Barley Fodder

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Climate related risks in livestock production and rising feed prices have promoted hydroponically grown barley fodder as a sustainable, nutrient-rich alternative that minimizes land and water use. Rapid assessment of fodder quality may be feasible through RGB image analysis. This study investigated the relationship between RGB (red, green, blue) image-derived metrics and chlorophyll content as well as feed quality traits—acid detergent fibre (ADF), neutral detergent fibre (NDF) and crude protein—in barley fodder (Hordeum vulgare L.) grown for eight days in a controlled environment. Plants were cultured under five irrigation levels and two temperature regimes. On days 7 and 8, 40 samples per day (80 total) were photographed. Mean R, G and B values and several colour indices (e.g., green channel intensity, G/R ratio, excess green) were extracted via image processing in Photoshop. Leaf chlorophyll was quantified in the laboratory protocol, while ADF, NDF and crude protein were measured by near-infrared (NIR) spectroscopy. Statistical analyses revealed significant correlations between image-based variables and laboratory measurements. Consequently, RGB imaging represents a rapid, low-cost and non-destructive tool for predicting chlorophyll concentration and key feed-quality constituents in barley fodder. Integrating this approach into batch-scale quality monitoring of closed production systems could optimise irrigation and temperature management, delivering tangible benefits for sustainable feed production and animal performance.

Y41

From Pixels to Polymorphisms: Linking Phenomics and Genomics in Modern Plant Breeding

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Molecular markers are increasingly being used in plant genetic analyses for purposes such as revealing individual variations in DNA sequences, determining genetic distances, identifying varieties, and improving qualitative and quantitative traits. Molecular markers are particularly useful tools in plants for marker-assisted selection (MAS), genome-wide association studies (GWAS), and the identification of QTLs affecting complex heritable traits. As genomic tools for plant breeding develop and our understanding of plant genomes expands, rapid and high-throughput phenotyping methods continue to be discussed as important improvements in plant breeding programs. GWAS find gene regions associated with phenotypes through the analysis of correlations between genetic variation (specifically SNPs) and phenotypic variation. However, typical GWAS studies often rely on one-time, manual phenotyping of data, which reduces resolution and accuracy. High-throughput phenotyping (HTP) overcomes these limitations by collecting phenotypes from large numbers of individuals in a rapid, accurate, and time-series format. HTP-enhanced GWAS significantly increases the strength of genetic association by working with higher-resolution, environmentally neutral, and time-varying phenotype data. Leveraging robotics, artificial intelligence, and precise environmental control imaging technologies, these powerful technologies, compared to traditional phenotyping techniques, assess plant growth, performance, and phenotypic responses to stressors in both field and greenhouse environments. Similar to molecular and genomic technologies, these research areas are expected to further develop in the coming years and be incorporated into contemporary plant breeding.

Y43

Screening of Mentha breeding material for drought stress tolerance using High-throughput Phenotyping (HTP) platform

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Drought stress poses a major constraint to Mentha productivity and biomass quality. The genus Mentha spp (mint) comprises economically important aromatic and medicinal plants cultivated worldwide for their essential oils, flavor, and pharmaceutical properties. This study aimed to identify drought-tolerant genotypes in a Mentha breeding program using a high-throughput phenotyping (HTP) platform at APPP-A platform at IPK through the framework of "DPPN-ACCESS". Sixty-nine Mentha accessions representing multiple species were grown under controlled environmental conditions and subjected to either well-watered or drought-stress treatments. Phenotypic traits were acquired through visible and fluorescence imaging using LemnaTec Scanalyzer3D over a 27-day period. Eighteen digital traits were extracted, encompassing morphometric, colorimetric, and physiological parameters. Principal component analysis and drought tolerance indices were used to evaluate genotype responses. Biovolume was selected as the primary trait for stress response. Drought-tolerant genotypes (e.g., ME009, ME027) showed stable performance across multiple indices and fluorescence efficiency (Fv/Fm), while sensitive genotypes (e.g., ME002, ME077) showed significant biomass loss and reduced photosynthetic efficiency. These results provide valuable insights for breeding drought-resilient Mentha cultivars.

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Keywords:

Mentha, drought stress, high-throughput phenotyping, HTP, biovolume, fluorescence imaging, drought tolerance indices, LemnaTec, Fv/Fm, digital traits, medicinal plants, biomass quality, plant stress physiology, phenomics

Y44

Growth Dynamics Phenotyping in Cassava Breeding Trials: Challenges and Opportunities of Aerial Information

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Cassava is a vital staple crop for food security in Sub-Saharan Africa, providing a primary source of calories for millions of people. Despite its importance, yields remain low due to environmental stressors such as poor soils and erratic rainfall. The CASS (Cassava Source-Sink) project, a multidisciplinary research consortium, addresses this gap by re-engineering cassava's internal physiology to favor increased carbohydrate flow toward the roots. Demonstrating the effectiveness of these genetic innovations under real field conditions is critical to guide breeding decisions.

UAV-based phenotyping is being applied to capture key indicators of above-ground growth in cassava field trials. Using drone-acquired time-series data, traits like plant height, canopy volume, and seasonal relative growth rates are quantified. This enables a dynamic view of growth that goes beyond classical fixed-point measurements. These UAV-derived indicators are integrated with final harvest outcomes to support identification of modified genotypes that shift growth strategies in line with improved source-sink relations.

While UAV time series provide a powerful, non-destructive way to monitor growth, interpreting above-ground signals as reliable proxies for source-sink dynamics remains challenging. For instance: (i) canopy expansion may suggest vigorous growth, but without corresponding root data, it's unclear whether this reflects productive allocation to sinks or inefficient shoot biomass investment; (ii) environmental fluctuations (e.g., rainfall anomalies or nutrient limitations) can mask genotype-specific responses, complicating efforts to isolate true source-sink effects; and (iii) beyond ~100 days after planting, dense canopy cover reduces visibility of individual plants, making accurate volume estimation difficult.

Despite these challenges, the growing availability of high-resolution aerial data and improved analytical tools is enabling new strategies to strengthen cassava phenotyping. E.g., integrating aerial and ground-based imagery can improve canopy volume estimates, especially in later stages when canopy closure reduces accuracy. Meanwhile, high-temporal UAV time series support algorithmic tools that enhance trait resolution at the plant level. These advances make it increasingly feasible to extract precise growth indicators under complex field conditions.