



Integrated functional plant phenotyping IPAP4 conference in Brno

Zintegrowane fenotypowanie funkcjonalne roślin
Konferencja IPAP4 w Brnie

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This article presents the achievements and prospects of plant functional phenotyping discussed at the IPAP4 conference in Brno. Topics included high-throughput phenotyping systems such as RGB, thermal, multispectral, and hyperspectral imaging; chlorophyll fluorescence; 3D methods; and UAV-based phenotyping. Many presentations focused on plant responses to abiotic stresses, integrating phenotypic data with genomic and environmental data and applying machine learning to image analysis and agronomic trait prediction. The presentations also covered methods for root system phenotyping, research on algae and cyanobacteria, and approaches to data organization and reuse. The work presented showed that phenotyping is increasingly moving beyond describing plant traits to become a tool for predicting plant responses under natural conditions and supporting breeding decisions.

Keywords: environmental stress, field trials, machine learning, phenomics, phenotyping, spectral imaging, UAV

Artykuł przedstawia osiągnięcia i perspektywy fenotypowania funkcjonalnego roślin omawiane podczas konferencji IPAP4 w Brnie. Obejmowały one systemy wysokoprzepustowego fenotypowania: obrazowanie RGB, termiczne, multispektralne i hiperspektralne, fluorescencję chlorofilu, metody 3D oraz fenotypowanie z wykorzystaniem bezzałogowych statków powietrznych (BSP, ang. unmanned aerial vehicle, UAV). Dużą część prezentacji poświęcono reakcji roślin na stresy abiotyczne, łączeniu danych fenotypowych z danymi genomowymi i środowiskowymi oraz zastosowaniu uczenia maszynowego w analizie obrazów i przewidywaniu cech agronomicznych. Omówiono także metody fenotypowania systemu korzeniowego, badania alg i cyanobakterii oraz sposoby organizacji i ponownego wykorzystania danych. Przedstawione prace wskazały, że fenotypowanie coraz częściej wykracza poza opis cech roślin i staje się narzędziem do przewidywania ich reakcji w warunkach naturalnych oraz do wspierania decyzji hodowlanych.

Słowa kluczowe: BSP, doświadczenia polowe, fenomika, fenotypowanie, obrazowanie spektralne, stres środowiskowy, uczenie maszynowe

Introduction

Functional plant phenotyping quantitatively characterizes physiological, morphological, and developmental traits that describe how plants function under specific environmental conditions. These include water-use efficiency, transpiration rate, photosynthetic performance, growth dynamics, and shoot and root system structure. From this perspective, the phenotype, which results from genotype–environment interactions, changes with the developmental stage and the course of stress exposure. As genotyping and omics approaches have advanced, accurately describing the phenotype has become a principal challenge for interpreting genetic variation biologically and applying that knowledge in breeding (Rybka & Nita, 2014; Sytar et al., 2018).

Traditional measurements, generally taken at individual time points and for a limited number of traits, are increasingly being replaced by non-destructive, repeated measurements over time. Hi-

gh-throughput phenotyping platforms, including unmanned aerial vehicles (UAVs), enable RGB, thermal, multispectral, and hyperspectral imaging; chlorophyll fluorescence measurements; 3D scanning; and automated environmental monitoring. These methods allow researchers to track the dynamics of plant responses rather than record them at a single point in time.

The growing number of sensors and increasing measurement frequency mean that data acquisition itself is no longer the main limitation. Instead, integrating, standardizing, and automatically analyzing data, and linking them to genomic, environmental, and agronomic information, are becoming increasingly important. This has driven the rapid development of machine learning, image analysis, predictive modeling, and standards that enable data reuse. The central theme of IPAP4 (4th Integrated Plant and Algal Phenomics Meeting, Brno, 2026; <http://psi.cz/ipap/>) was combining new measure-

ment technologies with data analysis and biological interpretation.

The conference was organized by Photon Systems Instruments (PSI, Drásov, Czech Republic). Consequently, a substantial part of the program presented studies conducted by teams using the company’s platforms in controlled-environment and field research.

Opening session

The conference began with a working-group meeting on data management, held at Photon Systems Instruments (PSI) premises. Two lectures opened the official program and set out its main perspectives: developing research infrastructure and applying phenotyping results in agriculture and the food economy.

Martin Trtílek, CEO of Photon Systems Instruments, presented recent developments in automation, imaging, and sensor integration, including the AlgaeScreen platform, new environmental monitoring systems, and hyperspectral solutions. His lecture outlined a direction in instrumentation development that integrates imaging, physiological, and environmental measurements into a single automated research system.

Antony Bačić of La Trobe University, Australia, offered a broader perspective. He emphasized that

phenomics is not limited to measuring plant traits more accurately and rapidly. Its value depends primarily on whether the resulting data enable identifying and exploiting traits that improve productivity, stress tolerance, yield quality, and sustainable production. Phenotyping should therefore connect plant physiology knowledge with breeding objectives, agricultural practice, consumer expectations, and agricultural and food-policy goals. Phenomics matters not for the amount of data it generates, but for the tangible benefits it delivers throughout the agri-food chain.

Together, the two lectures defined the conference’s principal directions: advances in phenotyping technologies and the application of the resulting knowledge in biological research and agricultural practice.

The scientific program comprised four thematic sessions: integrated functional phenotyping for plant performance and stress resilience; innovative phenotyping technologies for agriculture under a changing climate; algal biotechnology and phenotyping; and AI-assisted imaging and sensor technologies in plant phenotyping. The lectures were followed by two parallel workshops: a Data Management Working Group roundtable and a hybrid workshop on Controlled Environment Plant Phenotyping (CePPG).

Table 1
Tabela 1

An overview of the latest developments in phenotyping, as presented in oral presentations at IPAP4 in Brno
Przegląd najnowszych osiągnięć w zakresie fenotypowania zaprezentowanych w wystąpieniach ustnych na IPAP4 w Brnie

Author/title of the presentation Autor/tytuł wystąpienia	Material and phenotyping method Materiał i sposób fenotypowania	Conclusions Wnioski	Bibliography, examples Bibliografia, przykłady
Session 1. Integrated Functional Phenotyping for Plant Performance and Stress Resilience Sesja 1. Zintegrowane fenotypowanie funkcjonalne pod kątem wydajności roślin i odporności na stres			
Thomas Altman et al.: the IPK Gatersleben team and partner institutions from Germany and Italy <i>Plants – Dynamic Genetic Systems in Dynamic Environments: Assessment of (Growth) Performance through Automated Non-invasive Phenotyping</i>	Maize, oilseed rape, <i>Arabidopsis</i> , and other species. Automated imaging of above-ground parts and roots, chlorophyll <i>a</i> fluorescence, and the integration of phenotyping with GWAS and omics analyses. At the IPK PhenoSphere, the development of 11 maize lines was compared under dynamically simulated climatic conditions, as well as in greenhouse and field experiments.	Conditions simulating a field environment allowed for a better reproduction of the natural dynamics of plant growth and development than standard greenhouse conditions.	Heuermann et al., 2023 Knoch et al., 2024 Shi et al., 2026
Carl-Otto Ottosen et al.: Aarhus University and University of Copenhagen, Denmark. <i>Plant Responses to Co-occurring Heat and Water Deficit Stress – Are the Modern Wheat Genotypes More Resilient?</i>	Older and modern wheat genotypes were subjected to water deficit combined with heat stress (31 °C and 37 °C) during the stem elongation and flowering stages. Photosynthesis, stomatal conductance, leaf temperature, and chlorophyll content were evaluated using the PlantScreen and PhenoLab systems.	Modern genotypes were less susceptible to the combined effects of water deficit and elevated temperature than older genotypes. They maintained more stable rates of photosynthesis, stomatal conductance, and leaf cooling, and exhibited higher chlorophyll content during the flowering stage. The mechanism regulating photosynthesis depended on the developmental phase.	Ibrahimova et al., 2025 Jahangirlou et al., 2026 Jensen et al., 2024 Liu et al., 2026 Mendanha et al., 2020 Sharma et al., 2015 Sørensen et al., 2026

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Marek Živčák et al.: Slovak University of Agriculture (SUA), Slovakia. <i>A High-Throughput Phenotyping Approach to Screen for Genotypic Variation in Wheat Tolerance to Nocturnal Warming</i>	Wheat genotypes; nighttime temperature elevated by 3–4 °C under constant daytime conditions; observations from emergence to grain maturity. PlantScreen platform (PSI); RGB imaging, chlorophyll fluorescence, and VNIR/SWIR hyperspectral imaging, supplemented by photosynthesis measurements.	Elevated nighttime temperatures accelerated leaf area development, the attainment of maximum photosynthetic efficiency, and the subsequent senescence of the plants. The response to nighttime warming was clearly genotype-dependent, which points to the possibility of selecting varieties with greater tolerance to this stress.	Barboricova et al., 2022 Brestic et al., 2018 Chovancek et al., 2019 Shomali et al., 2025
Muhammad Ahmad et al.: Austrian Research Center for Forests (BFW), Austria <i>From pixels to pathways in trees: multi-scale phenotyping of drought response in seedlings of a widespread Oak</i>	Pedunculate oak (<i>Quercus robur</i> L.) seedlings; 17 families from a seed orchard; 38-day drought and recovery cycle. Chlorophyll fluorescence and thermal imaging were performed using the PHENOPlant platform, equipped with the PlantScreen Modular System (PSI). For 12 families exhibiting diverse responses, time-resolved transcriptomic and metabolomic analyses were conducted on pooled leaf and shoot samples.	The families differed in their physiological response to drought. The accumulation of sugars, associated with the activation of starch degradation pathways, was potentially linked to drought tolerance and requires validation.	
Éva Darkó, István Molnár et al.: HUN-REN Agricultural Institute, Martonvásár, Hungary <i>Utilisation of high-throughput phenotyping platform in Martonvásár (Hungary)</i>	Cereals—primarily wheat, barley, and maize—are evaluated for their responses to abiotic stresses and for various agronomic traits. The PlantScreen (PSI) platform, installed at HUN-REN in 2023, comprises two independently controlled growth chambers equipped with an automated irrigation system. Measurements include chlorophyll and fluorochrome fluorescence, RGB and thermal imaging, 3D laser scanning, and hyperspectral imaging across the VNIR and SWIR ranges (380–1700 nm).	The platform enables the selection of genotypes with increased tolerance to abiotic stresses and favorable agronomic traits. The platform is also made available to external users.	Kruppa et al., 2024 Türkösi et al., 2025
James Whelan et al.: Zhejiang University, China <i>Plant Phenomics for Discovery</i>	Rice, soybean, and <i>Arabidopsis</i> . Quantitative 2D and 3D imaging using the PlantScreen Phenotyping System (PSI), involving the automated detection of trays and pots, segmentation of rosettes and leaves, and extraction of morphological traits. Image analysis—including the assessment of image complexity based on entropy—was integrated with ionomics and other „omics” analyses.	Phenotyping can reveal gene functions and cellular processes that are not apparent from omics data alone, and it can generate hypotheses for functional studies. The examples presented highlighted, among other things, the role of mitochondria in plant growth and yield.	He et al., 2026 Lozano-Claros et al., 2020 Nguyen et al., 2022 Sarić et al., 2025
Jana Kholová and team, CATRIN / IPK / PSI, Czech Republic. <i>Genetic determination of physiological responses to drought stress in barley (<i>Hordeum vulgare</i> L.) landraces</i>	121 local landraces of spring barley originating from Europe, Asia, and Africa; control and drought conditions; two independent experiments. PlantScreen platform; RGB and thermal imaging, chlorophyll fluorescence, and manual assessment of agronomic traits. Data were filtered based on developmental stage, stress intensity, number of observations, heritability ($H^2 > 0.7$), and coefficient of variation ($CV < 21\%$); subsequently, a GWAS was conducted using 18,629 SNP markers.	A total of 434 marker–trait associations were identified, spanning 265 unique loci. Some of these loci were linked to photosynthesis and the regulation of stomatal apparatus—notably on chromosomes 1H, 2H, and 6H—pointing to new sources of variation useful for breeding drought-resistant barley.	Kholova et al., 2022 Kosová et al., 2014 Varshney et al., 2021
Huma Majeed et al.: IPK Gatersleben and NPZ Innovation, Germany <i>STRESS-STOPP: Increasing drought stress adaptation in oilseed rape – yield stability and stress tolerance as selection targets for optimization via physiological phenotyping</i>	Winter oilseed rape; 80 lines across three Container/PhenoCrane experiments, including 20 lines also evaluated under control conditions; two supplementary rhizotron experiments. Daily RGB imaging and 3D laser scanning; twice-weekly hyperspectral imaging and chlorophyll fluorescence; measurements of SPAD, osmolarity, stomatal conductance, transpiration rate, and leaf-to-air vapor pressure deficit. A total of 56 root traits and over 30 shoot traits were extracted.	The traits examined made it possible to differentiate genotypes based on their response to drought, with their utility depending on the developmental stage and the nature of the stress. Promising indicators included osmolarity, chlorophyll content, stomatal conductance, transpiration rate, shoot traits derived from 3D imaging, and root architecture. Ongoing analyses are aimed at integrating these indicators into genomic-phenotypic selection models.	Majeed et al., 2024
Session 2: Innovative phenotyping technologies for agriculture in a changing climate Sesja 2: Innowacyjne technologie fenotypowania na rzecz rolnictwa w zmieniającym się klimacie			
Astrid Junker et al.: AJ Consulting (Halle) and IPK Gatersleben, Germany <i>From Sensors to Decisions: Translating Plant Phenotyping Innovation into Breeding and Agronomic Value</i>	A cross-section of examples illustrating the use of phenotyping in research, breeding, and agronomy—ranging from platforms operating in controlled environments to field-based sensors, UAVs, and remote sensing. The entire process is covered, including experimental design, sensor selection and calibration, feature extraction, data analysis, uncertainty assessment, and interoperability, as well as the FAIR principles and data harmonization.	Sensors alone do not create value. Phenotyping only becomes useful once data has been transformed into reliable and interpretable information, delivered in a timeframe that allows it to be used for specific breeding and agronomic decisions.	Arend et al., 2016 Junker et al., 2015 Ugochukwu i Phillips, 2022

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Kerstin Neumann et al.: IPK Gatersleben, Germany <i>High-Throughput Phenotyping Reveals Genetic Diversity for Climate Adaptation in Chickpea</i>	200 chickpea lines from the INCREASE T-Core panel, sourced from gene bank material, were studied. During the vegetative phase, the plants were subjected to drought or a combination of drought and high temperature, followed by rewatering. Under controlled conditions, the study evaluated growth dynamics, biomass accumulation, changes in plant coloration, and chlorophyll fluorescence parameters—specifically QY, Fv/Fm, and NPQ. The phenotypic data were then integrated with the results of whole-genome sequencing.	The genotypes differed significantly in their response to drought and co-occurring stresses (drought and temperature), as well as in their capacity for recovery. This made it possible to identify traits and candidate genes that could be useful in breeding chickpea varieties better adapted to drought and high temperatures.	Gadilil et al., 2025 Lauterberg et al., 2023 Lauterberg et al., 2024 Sahu et al., 2025 Schüler et al., 2025 Soleimani et al., 2026 Wonneberger et al., 2025
Tim van Daalen et al.: international IPPN working group and the Netherlands Plant Eco-phenotyping Centre (NPEC), the Netherlands <i>Describing High-Throughput Plant Phenotyping experiments</i>	Data from high-throughput plant phenotyping, including images, environmental measurements, and traits recorded over time. The scope of information required to describe experimental design, platform configuration, environmental conditions, sensor settings, measurement protocols, and trait extraction was analyzed. The starting point for this work was the MIAPPE (Minimum Information About Plant Phenotyping Experiments) standard and the FAIR principles.	Data from high-throughput phenotyping are rarely reused because, without a full description, they lose the context necessary for their interpretation. The team has proposed an extension called MIAPPE-HTP, which includes metadata regarding platforms and experimental workflows, along with the automation of data recording. This is intended to facilitate the integration of experiments, meta-analyses, and the use of data for training AI models.	Papoutsoglou et al., 2020 https://www.miappe.org/
Marie Blomme et al.: Ghent University, Belgium <i>Hyperspectral imaging as a non-destructive phenomics tool to guide the discovery of novel metabolites during tomato–Serendipita interactions</i>	Tomato (<i>Solanum lycopersicum</i> cv. ‘Money-maker’) and lines with impaired salicylic acid- and jasmonic acid-dependent signaling, colonized by the endophytic fungus <i>Serendipita</i> . Two experimental setups were used: whole plants and hairy root cultures. Multispectral and hyperspectral imaging were combined with the assessment of fungal growth and root colonization.	Multispectral and hyperspectral imaging detected subtle spectral changes associated with the interaction between the tomato plant and <i>Serendipita</i> . These findings are intended to serve as a basis for transcriptomic and metabolomic analyses aimed at identifying unknown metabolites and gaining insight into the chemical communication between the plant and the endophyte.	Tran Minh et al., 2025 http://hdl.handle.net/1854/LU-01KEVB-WYND7PCFQN-HB598QPJQN
Iñigo Saiz-Fernández et al.: CATRIN, CARC, NEIKER, Czech Republic and Spain <i>LOCOPOTS: a Low-Cost high-throughput screening platform for in vitro POTatoes under abiotic Stress</i>	30 potato varieties were cultivated in vitro under controlled conditions, as well as under nutrient deficiency and salinity stress. The LOCOPOTS platform integrates individual plant cultivation, low-cost RGB imaging, and automated image segmentation using a U-Net neural network. Growth, coloration, vegetation indices, and chlorophyll fluorescence were evaluated, and the results were complemented by metabolomic profiling.	Growth traits, color indices, and chlorophyll fluorescence differentiated the varieties in terms of their response to nutrient deficiency and salinity. Metabolomic analyses revealed genotype-dependent alterations in carbon and nitrogen metabolism and identified potential chemical markers of stress. LOCOPOTS enables low-cost, reproducible, and space-efficient preliminary selection of potato germplasm.	Saiz-Fernández et al., 2026
Peter Pietrzyk et al.: Fraunhofer Institute for Integrated Circuits IIS, Germany <i>Opportunities and Challenges of 3D Root and Shoot Phenotyping in Controlled Environments</i>	Sugar beet, maize, and young citrus trees serve as examples for the phenotyping of underground organs, above-ground parts, and individual leaves. Optical 3D imaging was combined with X-ray computed tomography, enabling the non-destructive assessment of shoot and root architecture as well as the monitoring of their growth over time. The studies were conducted under controlled environmental conditions at the Fraunhofer IIS/EZRT facility.	3D phenotyping provides information on the spatial structure of shoots, leaves, roots, and storage organs—data that cannot be obtained from 2D images. However, it requires longer acquisition times, careful calibration, the processing of large datasets, and reliable segmentation. Proper preparation of the measurement process is more effective at limiting errors than attempting to correct them later during image processing.	Pietrzyk et al., 2026a Pietrzyk et al., 2026b
Alexey Shapiguzov et al.: University of Helsinki, Finland <i>Exploring flash-induced chlorophyll fluorometry: from mitochondrial mutants to tomato production</i>	OJIP chlorophyll fluorescence kinetics were recorded following short light pulses, using both point-measurement and imaging systems. The study examined <i>Arabidopsis</i> mutants with increased mitochondrial respiration, as well as plants treated with methyl viologen under varying oxygen availability. Measurements taken in a light-adapted state were calibrated using mutants with disrupted metabolic processes and analyzed via machine learning methods. The approach was also tested across different seasons in a commercial tomato greenhouse.	The I-P phase of OJIP kinetics may reflect oxygen availability in tissues and the intensity of mitochondrial respiration. In a light-adapted state, the signal is more challenging to interpret in mechanistic terms; however, its diurnal and seasonal variability can be used for the ongoing assessment of a plant’s physiological status and to assist in the management of greenhouse conditions.	Baral & Brosché, 2026 Punkkinen et al., 2026 Punkkinen et al., 2024 Selinski et al., 2024 Shapiguzov & Kangasjärvi, 2022 Shapiguzov et al., 2020 Vainonen et al., 2023

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Phanchita Vejchasarn: Ministry of Agriculture, Thailand. <i>Toward Climate-Resilient Rice: Integrative Genomic Approaches for Candidate Gene Discovery Under Drought-prone Environments</i>	Diverse rice genotypes were cultivated under conditions of limited water availability. Assessments were made of yield and root architecture traits, including root growth angle, metaxylem vessel size, and lateral root density. The genetic basis of these traits was analyzed using GWAS and quantitative trait locus (QTL) mapping, employing high-density genomic markers.	Higher yields during drought were associated with a steeper root growth angle, larger metaxylem vessels, and a lower density of lateral roots. This architecture may facilitate water uptake from deeper soil layers and enhance water transport capacity. Genomic analyses identified a DRO1-type region, as well as candidate genes involved in regulating the root growth angle and the development of vascular tissues.	Klinsawang et al., 2024 Siangliw et al., 2022
Session 4. AI-assisted imaging and sensor technologies in plant phenotyping Sesja 4. Obrazowanie wspomagane sztuczną inteligencją i technologie czujnikowe w fenotypowaniu roślin			
Sónia Negrão et al.: School of Biology and Environmental Science, University College Dublin, Ireland <i>The Road to Precision: Spectral Imaging for Abiotic Stress Responses – Are We There Yet?</i>	Traditional cultivars and local landraces of barley were evaluated for their tolerance to abiotic stresses under both controlled conditions – encompassing both root and shoot systems – and in the field. A deep learning network was developed for the segmentation of hyperspectral images, and feature importance was assessed using machine learning methods. Phenotypic data were integrated with genome-wide association studies (GWAS) and an analysis of temporal changes.	Neural networks enabled the prediction of tolerance and the ranking of genotypes under field conditions, while the utility of individual vegetation indices varied between the early and late stress phases and the recovery phase. The developed tool, 3DQTL-Vis, facilitated the identification of genomic regions associated with the response of barley to waterlogging.	Al-Tamimi et al., 2022 Bernád et al., 2026 Bucksch et al., 2026 Chang et al., 2026
Anshu Rastogi et al.: Poznań University of Life Sciences, Poland <i>Integration of Hyperspectral Reflectance and Sun-Induced Fluorescence for Stable Estimates of Gross Primary Productivity in Peatlands.</i>	A peatland in Poland, featuring plant communities that include <i>Sphagnum</i> mosses, dwarf shrubs, and other vascular plants. Warming and reduced precipitation were simulated using infrared heaters, open-top chambers, and rain shelters. Measurements included hyperspectral reflectance spectra, solar-induced chlorophyll fluorescence (SIF), community-level gross primary productivity (GPP), and leaf-level chlorophyll fluorescence.	Short-term warming and reduced precipitation altered the composition of plant communities and their physiological functioning, with the response varying by species. Far-red SIF and full-spectrum integrated SIF showed a strong correlation with GPP ($R^2 > 0.85$) across all vegetation types and climatic conditions. This indicates the utility of SIF for monitoring the carbon balance of peatlands.	Bandopadhyay et al., 2020 Rastogi et al., 2022
Krystyna Rybka et al.: Plant Breeding and Acclimatization Institute – National Research Institute, Poland <i>Monitoring Yield-Related Spectral Responses of Spring Cereals under Contrasting Hydrothermal Conditions Using UAV-Based Phenotyping.</i>	Spring wheat, spring barley, and oats were studied in field trials conducted in Strzelce during 2024–2025. The 2024 season was characterized by a prolonged drought, while 2025 was cooler and wetter. Five drone flights were performed using a DJI Phantom 4 Multispectral, and the following vegetation indices were calculated: NDVI, GNDVI, NDRE, LCI, OSAVI, and EVI. Weather conditions were characterized using the SPI and HTC indices, and the spectral indices were correlated with crop yield.	During the drought season, the correlations between spectral indices and crop yield were stronger than in a year with more favorable water conditions. The most stable relationships were observed for indices sensitive to the red-edge spectral range and chlorophyll content—specifically, NDRE and LCI. However, the utility of these indices varied depending on the crop species, the timing of phenotyping, and weather conditions; therefore, yield assessment requires a multi-index approach that accounts for the specific progression of the growing season.	Góral et al., 2026 Góral & Rybka, 2026
Lamis Abdelhakim et al.: Photon Systems Instruments (PSI), Czech Republic <i>Root-to-Shoot Stress Response Dynamics: A Case Study of Barley Drought Resilience.</i>	Ten barley genotypes were evaluated during early developmental stages in rhizoboxes under conditions of moderate drought. The PlantScreen Root system allowed for the control of substrate moisture, as well as simultaneous, non-destructive imaging of both roots and above-ground plant parts. Morphological traits were determined based on RGB images, while multispectral and near-infrared imaging were used to assess physiological traits, including root water content. Image segmentation and feature extraction were performed automatically. The results were compared with field evaluations conducted as part of the BarleyMicroBreed project.	The genotypes differed in the growth dynamics of their roots and above-ground parts, as well as in their response to drought. A combined analysis of both plant components makes it possible to identify traits—manifesting as early as the seedling stage—that may be linked to the plant's subsequent performance and yield stability under drought conditions.	Bandopadhyay et al., 2020 Kurtz-Sohn et al., 2026 Neuwirthová et al., 2026 Tietze et al., 2025

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Nuria De Diego et al.; CATRIN, VSB—Technical University of Ostrava, PSI, Czech University of Life Sciences Prague, Czech Republic <i>AI-Powered Digital Biomarkers for Stress Resilience and Genotype Classification</i>	Four methods for analyzing phenotypic data are presented. AMULET was used to detect <i>Pseudomonas syringae</i> infections in <i>Arabidopsis</i> , while SPROUT was employed to track seedling emergence based on sequences of RGB images. The MARIGOLD project combined field-based hyperspectral and RGB imaging with machine learning to classify marigold genotypes. Complex data from multifactorial experiments were also analyzed using topological data analysis and contrastive learning methods.	AMULET detected infections before the appearance of visible symptoms, while SPROUT automatically reconstructed the germination process and determined associated traits. In an experiment involving marigolds, the models classified genotypes and identified stable spectral traits linked to the absorption of carotenoids and chlorophyll. Topological methods made it possible to discern relationships between genotype, experimental variant, and time—connections that were not readily apparent through traditional analyses.	Klimeš et al., 2026 Panáček et al., 2026 Saiz-Fernández et al., 2026 Zdražil et al., 2025 Zdražil et al., 2026
Katarzyna Retzer et al.: Institute of Forest Ecology, BOKU University, Austria <i>Affordable Infrared DIY Microscopy for Non-Invasive Root Phenotyping</i>	Roots of various plant species growing in mini-rhizoboxes filled with soil. The low-cost, modular system is built with OpenFlexure microscope components, infrared illumination and 3D printed parts. Time-lapse imaging at a magnification of up to 10× enabled the observation of epidermal cells and root hairs, and at a magnification of approximately 2× it was possible to track gravitropism and the direction of root growth. The results were compared with shovelomics assessment of root architecture in five locations on two continents.	Infrared illumination enables long-term observation of roots in the dark without disrupting their natural growth through visible light. This affordable and scalable system combines detailed assessment of cells and root hairs with an analysis of the dynamics of the entire root system; furthermore, comparisons with field measurements allow for the evaluation of the significance of the observed traits under natural conditions.	Pree et al., 2024
Zhibo Cai et al.: Wageningen University & Research (WUR), Netherlands <i>SP3D: A Benchmark for Systematic Comparison of Image-Based 3D Reconstruction Methods of Cucumber Plants</i>	36 greenhouse cucumber plants were imaged at six time points over a seven-week growth period, ranging from the 2-leaf stage to approximately 27 true leaves. The SP3D dataset includes multi-view images with plant masks, reference data obtained from a structured-light scanner, and destructive leaf area measurements. Three 3D reconstruction methods were compared: multi-view stereo (MVS), neural radiance fields (NeRF), and 3D Gaussian splatting (3DGS).	MVS provided the most accurate reconstruction of plant geometry and leaf surface area, achieving an F1 score of 91.7%, with leaf area estimation errors of 14.0% at the individual leaf level and 5.9% at the whole-plant level. The accuracy of all methods decreased as the plants grew and leaves began to overlap. NeRF and 3DGS consistently overestimated leaf surface area, a result of creating double layers in the reconstructed surfaces.	Poorter et al., 2010 Poorter et al., 2022 Yuan et al., 2025
Rijad Sarić et al.; La Trobe University, PSI, Scientific Instruments Australia and Zhejiang University—Australia, Czech Republic, China <i>Linking Rosettes to Leaves: An AI-Driven RGB Imaging Pipeline for Arabidopsis thaliana Phenotyping</i>	<i>Arabidopsis thaliana</i> ecotypes were imaged using RGB cameras under controlled conditions. The developed pipeline included the segmentation of the entire rosette, the identification of individual leaves, and the tracking of these leaves over successive time points—even in cases where leaf blades partially overlapped. Growth, morphological, and color-related traits were automatically extracted, and the similarity in the development of rosettes and leaves was analyzed using clustering methods.	Identifying and tracking individual leaves over successive time points enables the analysis of their growth and physiological changes—details that are not revealed when assessing the rosette as a whole. Morphological traits made it possible to group ecotypes based on similarities in their development. The next stage will involve developing a leaf-tracking model applicable to various species.	Sarić et al., 2025
Tim van Daalen, Sebastian Seitner et al.: Netherlands Plant Eco-phenotyping Center (NPEC), Wageningen University & Research (WUR), The Netherlands. Plant Sciences Facility, Vienna and BioCenter Core Facilities GmbH (VBCF), Austria <i>Enabling Reproducible Phenotyping: An Open-Source Python PlantScreen and Fytotron APIs.</i>	Programming interfaces for the PlantScreen phenotyping system and the Fytotron environmental control system. Based on the API documentation, OpenAPI specifications were developed, from which Python client packages—along with their corresponding documentation—are automatically generated. Following any changes to the specifications, the packages are regenerated and tested.	Shared, open, and tested software packages replace disparate—and often incompatible—solutions developed by individual research centers. They facilitate the direct integration of data from PlantScreen and Fytotron into automated analysis workflows, enable the use of consistent procedures across different laboratories, and allow for the creation of comparable datasets containing both measurement results and instrument metadata. This enhances research reproducibility and fosters collaboration between institutions.	

Algal biotechnology and phenotyping

Analyzing relationships among environmental conditions, photosynthetic function, and observed phenotype can help identify strains resistant to adverse conditions and select organisms useful for biomass production, wastewater treatment, and ma-

nufacturing valuable products. The session also highlighted algal biomass as a source of compounds used in agriculture, including biostimulants, whose effects on crop productivity can be assessed using phenotyping methods. Prof. Allahverdiyeva-Rinne of the University of Turku, Finland, presented work from her research group (Borhan et al., 2026; Cho-

vancek et al., 2025; Huokko et al., 2026; Mustila et al., 2025).

The AlgaeScreen platform exemplifies advances in high-throughput phenotyping of photosynthetic microorganisms by enabling automated strain cultivation, monitoring, and selection. The system combines colony-growth assessment with measurements of absorption and emission spectra in the VIS–NIR range, protein fluorescence imaging, variable chlorophyll fluorescence measurements, and analysis of macromolecular composition using Raman spectroscopy (Masuda et al., 2026; Rana et al., 2026; López-Adams et al., 2026). An extension of this approach is distributed phenotyping, in which data from multiple bioreactors are transferred to a common infrastructure, integrated in the cloud, and analyzed using predictive models. This enables not only the characterization of culture physiology but also real-time optimization of cultivation conditions (Zavřel et al., 2019; Zavřel et al., 2026).

Studies of photoprotective mechanisms in diatoms also demonstrated the importance of high-throughput phenotyping. Analysis of *Phaeodactylum tricornutum* mutants showed that Lhcx proteins make additive contributions to the rapid component of nonphotochemical chlorophyll fluorescence quenching (qE). However, individual mutations often had subtle, environmentally dependent effects, complicating analysis with conventional physiological methods and underscoring the need to phenotype large numbers of lines in parallel (Buck et al., 2019; Lepetit et al., 2017).

Phenotyping was also applied directly to optimize cyanobacterial cultivation as “cell factories.” In ethylene-producing strains, the study investigated how growth rate, culture density, and light availability affected production efficiency. Maximum growth and maximum productivity did not occur under the same conditions: high volumetric productivity was associated with high cell density and pronounced self-shading. The research also included modifications of carbon and energy fluxes involved in growth, photoprotection, electron transport, and ethylene synthesis (Zavřel et al., 2019).

This part of the conference was complemented by studies that expanded phenotyping’s analytical capabilities. Functionalizing membrane inlet mass spectrometry (MIMS) probes with immobilized enzymes enabled indirect detection of compounds that cannot permeate the membrane. Using glucose oxidase as a model enzyme demonstrated the potential for selective metabolite determination in complex samples without prior separation (Zlámál et al., 2026).

Parallel workshop sessions

One parallel workshop addressed data management in high-throughput phenotyping, particularly data description, integration of data from multiple sources, and reuse in accordance with the FAIR principles. The second workshop focused on phenotyping plants under controlled conditions and the potential to predict yield-related traits from changes observed at successive developmental stages.

Poster session

The posters presented a range of phenotyping applications, from physiological analysis of individual organs to automated processing of field-trial data. Studies of plant responses to environmental stresses combined root and shoot assessment with RGB, multispectral, and hyperspectral imaging at multiple time points.

The studies addressed, among other topics, the effects of biostimulants under water deficit, mitigation of chilling injury in maize, the role of the DHN3 gene in wheat responses to drought, and the role of GABA metabolism in responses to pathogens. Ogrodowicz et al. (2025) showed that barley tolerance to combined drought and *Fusarium* infection was associated with heading date, cuticular wax composition, and preserved chloroplast integrity.

Field studies used UAV imaging of maize at multiple time points to assess plant height, canopy cover, vegetation indices, and growth dynamics as yield predictors (Adak et al., 2021; Kovačević et al., 2024). Thermal imaging of 196 spring wheat genotypes showed that genotype discrimination depended on measurement time, developmental stage, and water availability. Under water stress, the greatest differentiation was observed at approximately 2:00 p.m.

Deep learning models segmented UAV-acquired hyperspectral images, transferring an algorithm developed under controlled conditions to field data with only a slight reduction in segmentation quality. Meanwhile, combining X-ray microtomography with deep learning enabled nondestructive three-dimensional characterization of fruit internal structure and automated extraction of phenotypic traits.

A separate group of posters focused on organizing and analyzing phenotypic data in accordance with the FAIR principles and the MIAPPE and BrAPI standards. The tools presented included ISA Wizard, which facilitates preparing standardized meta-data, and an interactive dashboard for analyzing and visualizing multidimensional phenotypic data.

Visit to PSI

The conference concluded with a visit to the Photon Systems Instruments headquarters in Drásov near Brno, featuring practical demonstrations of platforms used for high-throughput phenotyping of plants and algae. The program included four stations: the robotic AlgaeScreen™ system for automated cultivation and analysis of microalgal colonies; the modular PlantScreen™ platform for shoot phenotyping; a system for simultaneous imaging of roots and shoots in rhizoboxes; and the mobile PlantScreen™ Field platform designed for field measurements.

The Polish participants were particularly interested in the new PlantScreen™ Modular system being prepared for the Plant Breeding and Acclimatization Institute – National Research Institute in Radzików. The platform combines an automated plant conveyor with a chamber for RGB imaging, chlorophyll fluorescence, thermal imaging, VNIR/SWIR hyperspectral imaging, and 3D scanning, providing an integrated system for investigating growth, physiology, and stress responses.

Conclusions

The studies presented at IPAP4 showed that plant phenotyping is increasingly moving away from single-time-point measurements toward repeated observations of changes during growth, development, and stress responses. Researchers increasingly combine imaging, physiological, environmental, and genomic data, and their analyses use conventional statistical methods as well as machine learning and predictive modeling.

Particularly notable were advances in methods that enable simultaneous assessment of multiple traits and organs, transfer phenotyping from controlled environments to the field, and automate the analysis of large datasets. In the studies presented, the value of a measured trait, its dynamics, developmental stage, and measurement timing were important. This expands opportunities to identify traits associated with stress tolerance and productivity but also requires careful experimental standardization and retention of complete data-acquisition information.

Phenomics is therefore increasingly moving from describing phenotypes to interpreting and predicting subsequent plant performance. The usefulness of new technologies will be determined not by the number of parameters recorded but by their ability to be transformed into information useful for biological research, plant breeding, and agricultural practice.

Wykaz skrótów:

2D, 3D: two- and three-dimensional imaging;
 3DGS, MVS, NeRF: 3D reconstruction methods;
 AI: artificial intelligence;
 API, BrAPI: application programming interfaces, including for breeding data;
 BSP, UAV: unmanned aerial vehicles;
 CV: coefficient of variation;
 EVI, GNDVI, LCI, NDRE, NDVI, OSAVI: spectral vegetation indices;
 FAIR: Findable, Accessible, Interoperable, Reusable;
 GABA: γ -aminobutyric acid;
 GPP: gross primary productivity;
 GWAS: genome-wide association studies;
 SPI, HTC: precipitation and hydrothermal indices;
 ISA: Investigation–Study–Assay;
 MIAPPE, MIAPPE-HTP: plant phenotyping metadata standard and its high-throughput extension;
 MIMS: membrane inlet mass spectrometry;
 QTL: quantitative trait loci;
 RGB: red, green, blue;
 SNP: single-nucleotide polymorphism;
 SPAD: relative chlorophyll index;
 SWIR, VIS–NIR, VNIR: spectral regions used in imaging;
 Fv/Fm, OJIP, I–P, NPQ, qE, qY, SIF: chlorophyll fluorescence-related notation;
 F₁, H², R²: statistical measures;
 DHN3, DRO1: gene designations;
 Lhcx: protein family involved in photoprotection.

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