First Conference of CRC1644

PhenPlasPlants 2025

International Conference
on
Phenotypic Plasticity in Plants

Collaborative Research Center 1644
(CRC1644)

WIS – Wissenschaftsetage im
Bildungsforum Potsdam

Funded by
DFG Deutsche Forschungsgemeinschaft
German Research Foundation

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Funded by DFG Deutsche Forschungsgemeinschaft
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1.) Program – Day 1

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Technical University of Munich, DE

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University Orléans INRAE, P2e laboratory, Orléans, FR

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European Molecular Biology Laboratory (EMBL), Heidelberg, DE

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1.) Program – Day 2

10th of October

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Keynote 1

9th October 2025, from 9:30 to 10:15

Phenotypic plasticity and adaptive evolution in Mediterranean gypsum endemics: insights into climate change response

Silvia Matesanz García

Rey Juan Carlos University, Madrid, Spain

Keywords
phenotypic plasticity, adaptive differentiation, population, Mediterranean plants, climate change

Abstract

Climate change is a major threat to plant populations, especially in the Mediterranean. For gypsophiles—species restricted to gypsum soils—migration is a limited response due to specific edaphic needs, low dispersal, and fragmented distributions. Consequently, in situ processes like adaptive evolution and phenotypic plasticity are essential for their persistence. Future adaptive responses to climate change depend not only on historical evolutionary dynamics but also on the strength of selection and the evolutionary potential of functional traits and their plasticity. Our research investigates: i) the evolutionary potential of key functional traits and their plasticity; ii) whether past selection has shaped population phenotypes and plasticity patterns; and iii) the ability of gypsophiles to express adaptive transgenerational plasticity to drought. Using a quantitative genetics approach, our research shows that gypsophiles exhibit adaptive phenotypic plasticity to drought, sometimes aligned with selection patterns. High genetic variation for plasticity within populations supports their capacity to further evolve adaptive plasticity in response to climate change. This plasticity may have contributed to maintaining high genetic variation, enabling adaptation to contrasting climatic conditions. Populations of several Iberian gypsophiles display similar drought responses, likely shaped by natural selection in heterogeneous environments, and suggesting independent evolution of functional traits and their plasticity. Furthermore, gypsophiles express adaptive transgenerational plasticity to drought, though its extent varies among species. Our findings emphasize that, together, phenotypic plasticity and adaptive evolution (both past and future) play a key role in shaping population responses to changing conditions, particularly in stressful and spatially constrained habitats like gypsum outcrops.

Session 1: Vasculature & Metabolomics

9th October 2025, from 10:45 to 12:15

10:45 – 11:15

Root Cortical Plasticity for Improved Crop Performance

Hannah Schneider

Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany

Keywords

Root, Anatomy, Plasticity, Drought

Abstract

In Poaceae (grasses), the root cortex exhibits plasticity, developing several anatomical tissues from cortical parenchyma, including root cortical aerenchyma, sclerenchyma, and root cortical senescence. These root tissues are not static; instead, their dynamic formation, influenced by the environment, significantly impacts soil resource acquisition by influencing root placement in resource-rich soil domains, enhancing metabolic efficiency during soil exploration, altering rhizosphere microbiota composition, and modifying radial and axial resource transport. We aimed to identify combinations of cortical tissues that enhance plant growth and stress tolerance. Through a phenotypic screen of wheat root anatomy across a developmental gradient, we observed significant phenotypic variation and plasticity in the formation of both multiseriate cortical sclerenchyma (formed by lignin deposition in cell walls) and root cortical senescence (resulting from programmed cell death of cortical cells). The benefit of multiseriate cortical sclerenchyma for drought tolerance was contingent upon the successive formation of root cortical senescence. This highlights how different tissues in the root cortex, and their plastic responses, can interact to influence stress tolerance and overall plant performance. While promising, integrating these complex and interacting plastic traits into breeding programs presents significant challenges due to their plasticity and complex interactions. Root anatomical tissues and their plasticity present a promising yet underexploited avenue to deliver substantial improvements in crop yield and climate resilience by optimizing water and nutrient uptake.

11:15 – 11:30

Plasticity of Secondary Cell Walls to Water Limitation in the Vasculature of Arabidopsis

Ulrike Lehmann [1], Felix Ruhnow [2], René Schneider [1]

[1] University of Potsdam, Institute of Biochemistry and Biology, Plant Physiology, Potsdam, Germany

[2] Centre of Genomic Regulation, Department of Quantitative Cell Biology, Barcelona, Spain

Keywords
xylem plasticity, Arabidopsis accessions, water limitation, automated phenotyping, high-throughput phenotyping

Abstract

Water scarcity is a major cause of crop losses, yet plants can adapt by modifying their xylem architecture to enhance water transport. A key aspect of this adaptation is the development of specialized xylem cell walls, which must withstand the mechanical stress associated with high transpiration rates. Interestingly, different Arabidopsis thaliana accessions show variation in their growth performance and xylem architecture under water limitation, but the molecular mechanisms underlying these plastic responses remain poorly understood. To address this gap, we aim to characterize how Arabidopsis accessions differ in root and xylem phenotypes under water limitation through automated, high-throughput morphological and anatomical analyses, quantify the relationship between root growth dynamics and xylem architecture, and identify the genetic and molecular factors underlying xylem plasticity. Our findings will provide critical insights into the genetic and physiological basis of xylem cell wall plasticity, paving the way for strategies to enhance drought resilience in crops.

11:30 – 11:45

The role of AGO10 in developmental plasticity

Liese Schnurbusch [1], Sebastian Wolf [1]

[1] Centre for Plant Molecular Biology, University Tübingen, Tübingen, Germany

Keywords
Vasculature, Root meristem, hormone signalling

Abstract

As sessile organisms, plants need to integrate external inputs and internal signals, balancing plasticity and robustness, for appropriate development according to their environmental context. In the Arabidopsis root, ARGONAUTE10 (AGO10) is required for vascular patterning and phenotypic robustness by protecting HD-ZIP III transcription factor transcripts from miRNA165/66-mediated degradation. The absence of AGO10 leads to release of cytokinin (CK) buffering, increased vascular cell number and ectopic xylem strands. Under carbon stress conditions, ago10 mutant populations split into two phenotypic classes, distinguishable by root length, vascular cell number, as well as by degree of xylem differentiation. We found that these two classes show markedly divergent transcriptional patterns, with almost half of the differentially expressed genes assumed to be regulated by HD-ZIP IIIs. Notably, genes associated with jasmonic acid (JA) biosynthesis, response, and signalling are strongly upregulated in one of the phenotypic classes and appear repressed in the other class. Additionally, investigation of CK signalling revealed discrete transcriptional CK responses in each phenotypic class, further corroborated by reporter analysis. Compellingly, JA signalling deficiency prevents the separation into distinct phenotypic groups. This alludes to a role of both CK and JA signalling in controlling developmental plasticity of the root vasculature. By further investigation using genetic tools and metabolomic analysis, we aim to uncover possible crosstalk between these phytohormones and to elucidate the link between the AGO10/HD-ZIP III module and hormonal signalling in maintaining robust patterning.

11:45 – 12:00

Phenotypic plasticity of cambial secondary growth in *Arabidopsis thaliana* in response to temperature

Buddhika G. Pathirana [1]; Michael Lenhard [1]; René Schneider [2]; Dongbo Shi [3]

[1] University of Potsdam, Institute for Biochemistry and Biology, Genetics Research Group, Potsdam, Germany

[2] University of Potsdam, Institute of Biochemistry and Biology, Plant Physiology, Potsdam, Germany

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Keywords
Arabidopsis thaliana, secondary growth, cambium stem cells, phenotypic plasticity, temperature response, reaction norms

Abstract

Secondary growth, driven by vascular cambium stem cells (CSCs), supports plant development by generating secondary vasculature for efficient transport and by increasing radial thickness to enhance mechanical support. While cambial activity is known to respond to environmental cues, the reaction norms of CSC proliferation and differentiation as well as the genetic and molecular basis of CSC plasticity in response to temperature remain poorly understood. In this study, we used the hypocotyls of Arabidopsis thaliana seedlings as a model system to investigate the phenotypic plasticity of cambium-derived secondary growth under varying temperature conditions. We cultivated 10-day-old seedlings from 24 natural A. thaliana accessions at five controlled temperatures (12 °C, 17 °C, 22 °C, 27 °C, and 32 °C) for a period of seven days. Secondary growth was quantified by measuring the increase in the cross-sectional area of the vascular cylinder during this interval. Our results revealed accession-specific reaction norms, with various curve shapes and peak responses occurring at different temperatures. Most accessions exhibited reduced cambial activity at lower temperatures, followed by increased growth as temperature rose, with peaks commonly observed at intermediate to higher temperatures. The degree of plasticity varied considerably among accessions, some displayed strong temperature-dependent responses, while others maintained relatively stable growth across conditions. This study provides a foundational dataset for investigating the genetic and molecular mechanisms underlying temperature-induced plasticity in secondary growth and lays the groundwork for future genome-wide association studies aimed at identifying key regulators of vascular development.

12:00 – 12:15

Phenotypic plasticity of the diurnal pattern of starch metabolism in response to a fluctuating environment in *Arabidopsis thaliana*

Dhanush S. Srikanthan [1], Joerg Fettke [1]

[1] University of Potsdam, Institute of Biochemistry and Biology, Biopolymer Analytics, Potsdam, Germany

Keywords
Starch metabolism, Phenotypic plasticity, Arabidopsis thaliana, Photoperiod and nitrogen response, Metabolic flux modeling

Abstract

Molecular mechanisms in starch metabolism, is being highly regulated during the night to match carbon supply and demand under changing environmental conditions. Arabidopsis thaliana with its broad geographical distribution and adaptation to diverse environments, can be used in our research to investigate how Arabidopsis thaliana accessions display phenotypic plasticity of starch metabolism to variable nitrogen levels and photoperiods. Using an integrated approach of combining high throughput phenotyping of starch granule parameters (number per chloroplast, size, and morphology), biochemical characterization of degradation pathways, and kinetic modelling of metabolic fluxes, we aim to identify the genetic and molecular basis of variation in starch metabolism. Preliminary data reveal the differences in starch degradation rates among accessions exposed to varying photoperiod and nitrogen levels, with some accessions showing minimal response while others exhibit higher alterations in starch degradation. Our research aims to contribute to the substantial understanding of the molecular mechanisms underlying phenotypic plasticity in plant starch metabolism, potentially identifying key genes, enzymes, isozymes, and metabolites that regulate starch metabolism.

Session 2: Development & Morphogenesis

9th October 2025, from 13:15 to 14:45

13:15 – 13:45

Cell cycle-driven growth reprogramming encodes plant age into leaf morphogenesis

Xin-Min Li

Institute of Botany, Chinese Academy of Sciences (CAS), Beijing, China

Keywords
leaf morphogenesis, heteroblasty, fate-mapping, growth-reprogramming, cell cycle control

Abstract

How is time encoded into organ growth and morphogenesis? We address this question by investigating heteroblasty, where leaf development and form are modified with progressing plant age. Combining fate mapping through live-imaging, computational analyses, and genetics, we identify age-dependent changes in cell cycle-associated growth and histogenesis that underpin leaf heteroblasty. In juvenile leaves, cell proliferation competence is rapidly released in a “proliferation burst” coupled with fast growth, whereas, in adult leaves, proliferative growth is sustained for longer, at a slower rate, by the SPL9 transcription factor. SPL9 directly activates CYCD3 genes to maintain cell proliferation and tissue morphogenetic potential in response to inputs from both shoot age and individual leaf maturation along the proximodistal axis. SPL9 also enables the species-specific action of homeobox genes in complex leaf shape evolution. We validate these findings by rational reprogramming of leaf growth and form through targeted expression of SPL9.

13:45 – 14:00

Plasticity of leaf epidermal cell shape complexity in *Arabidopsis thaliana* under temperature variation

Prabal Das [1], Adeleh Dehghani Nazhvani [2], Jacqueline Nowak [2,3], Arun Sampathkumar [1]

[1] Max Planck Institute of Molecular Plant Physiology, Plant Cell Biology and Morphodynamics, Potsdam, Germany

[2] University of Potsdam, Institute of Biochemistry and Biology, Bioinformatics, Potsdam, Germany

[3] Max Planck Institute of Molecular Plant Physiology, Systems Biology and Mathematical Modelling, Potsdam, Germany

Keywords

Cellular Plasticity, Temperature Adaptation, Epidermal Cell Morphology, Arabidopsis thaliana, Genetic Variation

Abstract

Plants undergo morphological and developmental changes as adaptive responses to temperature fluctuations, enabling them to maintain growth and function under varying temperature conditions. While progress has been made on several fronts, a complete understanding of cellular and genetic mechanisms underlying these responses is lacking. In particular, the morphology of leaf epidermal pavement cells, which are critical for maintaining cell structural integrity as cells enlarge, is largely unknown. Here, we investigate the genetic architecture and molecular mechanisms governing the plasticity of leaf epidermal cell shape complexity in Arabidopsis thaliana across different temperature conditions. Using a combination of natural variation among Arabidopsis accessions, imaging, molecular perturbations, and quantitative morphometric analysis, we characterize temperature-dependent changes in cell shape, cell packing, microtubule, and cell wall organization. Preliminary results reveal substantial natural variation in the plasticity of epidermal cell morphology including traits such as cell lobing, aspect ratio, and packing density responding to temperature changes, suggesting that genetic background influences the extent of these responses. By linking cell-level architectural plasticity with tissue-scale growth responses, we aim to advance our understanding of how cellular morphology contributes to temperature adaptation in plants.

14:00 – 14:15

Flower size plasticity in *Arabidopsis thaliana* in response to temperature change

Amna Sarmad [1], Jan Hoffmann [1], Airi Lamminmäki [1], Roosa Laitinen [1]

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Keywords
phenotypic plasticity, MADS AFFECTING FLOWERING LOCUS 2-5 (MAF2-5), alternative splicing

Abstract

Plants exhibit phenotypic plasticity, allowing them to rapidly adjust to environmental fluctuations such as temperature variations. The genetic mechanisms underlying plasticity responses, particularly temperature-dependent flower size plasticity which directly influences reproductive success and adaptation, are not fully understood. Taking advantage of natural variation and mutants in Arabidopsis thaliana, our previous work identified the MADS AFFECTING FLOWERING LOCUS 2-5 (MAF2-5) gene cluster as significantly involved in temperature-mediated flower size plasticity. Alternative splicing of MAF2 and MAF3 is known to control vernalization-dependent flowering time at low temperatures, led us to investigate whether temperature-dependent flowering time genes beyond MAF2-5 are linked to flower size plasticity. We grew ten flowering time-related mutants at 17°C and 25°C with and without vernalization and measured them for flowering time and flower size. We found that vernalization reduced temperature-mediated flower size plasticity. In addition, all non-vernalized mutants showed significantly smaller flowers at 17°C compared to WT resulting in reduced flower size plasticity. However, no connection between temperature-mediated flower size plasticity and flowering time was observed. We are currently further detailing flower size plasticity in flowering-related mutants, investigating the influence of flower size on outcrossing, and exploring the role of alternative splicing within the MAF2-5 gene cluster in driving temperature-mediated flower size plasticity. We are also characterizing the role of hormones in mediating temperature-dependent flower size plasticity. This research provides knowledge of plant responses to climate change, thereby improving our understanding of plant resilience.

14:15 – 14:30

A quest for temperature sensors: what can we learn from Capsella?

Pauline Gutsche [1], Saket Namdeo Nikose [1], Katja E. Jaeger [1], Philip A. Wigge [1]

[1] Leibniz Institute of Vegetable and Ornamental Crops (IGZ) e.V., ADAPT 1, Großbeeren, Germany

Keywords
prion-like domains, temperature sensing, Capsella

Abstract

Rising temperatures pose a significant threat to global food security. To develop climate-resilient crops, it is essential to identify genetic factors that enable plants to withstand heat stress. While several signalling pathways regulating thermomorphogenesis have been described, the molecular mechanisms underlying temperature sensing remain poorly understood. Recent findings suggest that intrinsically disordered protein domains, such as prion-like domains (PLDs), can potentially function as molecular thermosensors by undergoing phase separation in response to elevated temperatures (Jung et al., 2020). While some examples of temperature-responsive PLD proteins have been described in Arabidopsis thaliana, it is not known if this is a common mechanism in other species. Here, we investigate the molecular behaviour of PLD containing proteins in the closely related genus Capsella under variable temperatures. We identified PLDs as key mediators of thermomorphogenesis, confirming that this mechanism is also conserved in Capsella. PLDs are often enriched in repetitive sequences, most prominently repetitive polyglutamine sequences, which we found to be significantly longer in Capsella than in Arabidopsis. Furthermore, we found that transcription factors are enriched in PLDs, and that these domains are crucial for protein phase separation at low temperatures and under heat stress. Accordingly, these proteins are potential regulators of gene regulatory networks in response to changing temperatures. We are testing the possible physiological relevance of our candidates in temperature sensing using CRISPR-Cas9 mutagenesis. By identifying PLD-driven phase separation as a conserved thermosensory mechanism, our work lays the foundation for future strategies to enhance thermotolerance in crops. Deciphering the amino acid code that drives temperature responsiveness in PLDs will provide valuable insights into plant stress adaptation mechanisms.

14:30 – 14:45

GET pathway facilitates light-mediated flower size plasticity in *Arabidopsis thaliana*

Jan Hoffmann [1] *, Kimmo Kivivirta [1] *, Gregory Andreou-Huotari [1], Roosa Laitinen [1]

[1] Organismal and Evolutionary Research Programme, Faculty of Biological and Environmental Sciences, Viikki Plant Science Centre, University of Helsinki, Helsinki, Finland

* These authors contributed equally

Keywords
flowers, plasticity, light, GET, Arabidopsis

Abstract

In sessile plants, phenotypic plasticity allows rapid adaptation to changing environmental conditions. Amongst these conditions, light is a key factor that varies both spatially and temporally. As primary energy source in photosynthesis light is essential for plant growth, development and reproductive success. Another key trait associated with reproductive success is flower size. However, the effects of light on plastic responses in flower size remain poorly understood. We therefore investigated the effect of changing light on flower size plasticity making use of natural variation in 290 A. thaliana accessions grown under normal (110 µmol/m2/s) and low (58 µmol/m2/s) light. All accessions exhibited varying degrees of flower size plasticity, with flowers being, on average, 19.6% smaller in low light conditions. A total of 16.8% of variation in flower size across light conditions could be attributed to genotype by environment interaction, indicating a genetic basis for light-mediated flower size plasticity. Genome wide association analysis revealed one significant association on chromosome 1 linked to light-mediated flower size plasticity. Using 20 candidate T-DNA lines we identified that two genes of the Guided Entry of Tail-anchored proteins (GET) pathway, namely G1IP-like (GET2-like) and G1IP (GET2), facilitate light-mediated flower size plasticity. While loss of function in G1IP is known to cause root hair growth defects, the gene is highly expressed in flowers. However, the role of G1IP and the flower-specific G1IP-like in flowers remain unknown. We are therefore currently investigating by which mechanisms the GET pathway regulates light-mediated flower size plasticity in A. thaliana.

Keynote 2

10th October 2025, from 9:15 to 10:00

Tipping the Balance: Brassinosteroids, Epigenetics, and the Growth–Survival Dilemma

Brigitte Poppenberger

Technical University Munich, Biotechnology of Horticultural Crops, Munich, Germany

Keywords
Brassinosteroids, bHLH proteins, DNA methylation, trade-offs

Abstract

In favorable environmental conditions, plant growth is guided by genetically encoded developmental programs that are modulated by environmental inputs to ensure adaptive plasticity. Under abiotic or biotic stress, however, plants must prioritize stress protective reactions over growth, as their activation is energy-demanding. This entails a dynamic reallocation of resources, often requiring active growth repression to ensure survival. The underlying regulatory modes are governed by phytohormones, including the brassinosteroids (BRs), steroids that act as key integrators of growth and stress signaling. Our research investigates the mechanistic basis of growth trade-offs, with a focus on BR-mediated signaling hubs that serve as integration points with stress response pathways. Specifically, we explore how BR signaling modulates thermotolerance and immunity, two stress contexts that inherently limit growth. Particular emphasis is placed on BR-regulated transcription factors, which not only influence gene expression through direct promoter binding but also modulate epigenetic landscapes that govern transcriptional regulation via alternative means. In this talk, I will present recent results on these distinct modes of transcription factor activity and their roles in stress responses in Arabidopsis thaliana.

Session 3: Epigenetics & Reproduction

10th October 2025, from 11:30 to 13:00

11:30 – 12:00

Epigenetic and phenotypic plasticity in poplar trees: forward, reverse epigenetic to populations and predictive models using deep learning

Stéphane Maury

University Orléans INRAE, P2e laboratory, Orléans, France

Keywords
tree, epigenetic, water stress, multi-omics, epitype, deep learning

Abstract

Epigenetic regulation, particularly DNA methylation, plays a pivotal role in tree phenotypic plasticity and adaptive potential under climate change. Using a reaction norm approach, we demonstrated that DNA methylation modulates key genes involved in developmental plasticity, hormonal signaling, and responses to water availability, temperature. We also observed epigenetic memory between embryonic and post-embryonic stages as well as short-term and interannual stress memory in trees. Reverse genetic analyses using RNAi lines revealed that altered methylation profiles compromise plasticity, drought tolerance and symbiotic interactions (ANR EpiMYc 2024-2028), indicating a potential priming mechanism and suggesting a trade-off between plasticity and genome integrity. To explore the evolutionary relevance of these findings, we conducted population epigenomic studies across natural populations of black poplar and oak, uncovering substantial methylation variation linked to geographic origin and gene expression (EPITREE 2018-2023). To further dissect the role of epigenetic variation in complex trait regulation, we analyzed 200 Populus nigra genotypes from Western Europe grown in common gardens in France and Italy. Multi-omics integration—including SNPs, transcriptomics, DNA methylation polymorphisms (SMPs), and spectral data—enabled the development of predictive models using statistical learning approaches. These models improve trait prediction and provide insight into the interactions among genomic, epigenomic, and transcriptomic layers (ADAAPT 2025-2030). Overall, our work highlights the functional and evolutionary significance of DNA methylation in shaping tree plasticity, stress memory, and adaptation. These findings offer valuable perspectives for forest breeding and management strategies in the context of rapid environmental change.

12:00 – 12:15

Unravelling the Influence of Temperature on Apomictic Endosperm Development through Phenotypic Plasticity

Sinah Tabea Ehlert [1], Chi-Ying Hsueh [1], Duarte D. Figueiredo [1]

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Keywords
Autonomous seed development, Temperature, Arabidopsis thaliana, Boechera sp.

Abstract

Reproduction via seeds can occur sexually or asexually. In either case, plants produce seeds consisting of an embryo, the nourishing endosperm and the protective seed coat. The asexual pathway is called apomixis, a process of reproduction (almost) independent of sperm cells. This pathway can be separated into the following steps: (1) apomeiosis, the suppression of meiosis leading to diploid ovules, (2) parthenogenesis, the formation of an embryo without fertilization and (3) the formation of an endosperm either via pseudogamy (pollen are required) or autonomous endosperm (AE) formation. When drawing attention to the habitat of asexually reproducing species (animals as well as plants), it was observed that apomicts tend to colonize colder and more northern environments than their sexual relatives. Thereby, I aim to test a possible role of (cold) temperature as a switch from sexual to apomictic AE formation by making use of phenotypic plasticity of AE formation under different temperatures. I thereby aim to identify (epi-) genetic temperature-dependent determinants of AE formation in a variety of geographically distinct Arabidopsis thaliana ecotypes. Moreover, I will test the influence of temperature on the mode of reproduction on a natural apomict, Boechera sp., which is a close relative of Arabidopsis thaliana. With this, we aim to study how sexual and asexual endosperms respond to changes in temperatures, and whether these responses can be adaptive.

12:15 – 12:30

Spatial transcriptomics reveals developmental patterns in the reproductive and vegetative shoot primordia of Norway spruce

Sami Saarenpää [1], Nathan Zivi [2], Yuvarani Masarapu [1], Sybil Herrera Foessel [1], Alina Orozco[1], Marie Englund [3], Jens Sundström [2], Stefania Giacomello [1]

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Keywords
Spatial Transcriptomics, organ development, reproduction, conifers, atlas

Abstract

In the gymnosperm seed plant lineage, such as conifers, reproductive structures emerge from distinct shoot meristems, resulting in pollen or seed cones, differing from angiosperms. Despite this, genetic mechanisms regulating female organ identity have been primarily studied through evolutionary and developmental research using known angiosperm genes. To address this gap, we utilize Spatial Transcriptomics to investigate the development of female reproductive structures in Norway spruce (Picea abies). We utilize the Visium platform to compare spatial gene expression in female seed cones and vegetative shoot primordia during early development, highlighting pivotal pathways involved in female reproduction. Uniquely, we include the acrocona mutant, which produces both seed cone and vegetative lateral organs, to analyze developmental plasticity and identify candidate genes important for seed cone development. We establish 14 tissue clusters across the 88 processed tissue sections, identifying novel markers for distinct tissue domains while illustrating spatial regulatory cascades of transcription factors that influence lateral organ development. For example, we emphasize the evolutionary significance of the YABBY gene family in conifers and study its spatial gene expression patterns. Overall, our spatiotemporal atlas identifies genes, pathways and evolutionary relationships related to lateral organ development. It provides a valuable resource for researchers to study gymnosperm developmental processes.

12:30 – 12:45

Floral phenotypic plasticity in response to light quality and temperature changes

Sofya Koblova [1], Zhaohui He [1], Kerstin Kaufmann [1]

[1] Humboldt University, Institute for Biology, Plant Cell and Molecular Biology, Berlin, Germany

Keywords
Flower development, shade avoidance, thermomorphogenesis

Abstract

Arabidopsis thaliana produces systemic responses to neighbor cues and shade—collectively referred to as shade avoidance—which mechanistically overlap with its responses to non-stressful temperature changes, known as thermomorphogenesis. Key regulators of shade response include phytochromes, in particular phyB [1], which suppresses shade and darkness response upon photoactivation by red light and suppression of a group of bHLH transcription factors called PIFs [2], and the E3 ubiquitin ligase complex COP1/SPA [3]. phyB is also subject to heat inactivation, and several PIFs, namely PIF4 [4] and PIF7 [5] have been demonstrated to regulate thermomorphogenesis. Shading and heat affects leaf shape and senescence, stem and petiole elongation, seed dormancy, flowering time and branching pattern [6]. However, those responses have not been systemically described for flowers, which we aim to achieve in our study. We have conducted a phenotypic plasticity screen of 17 A. thaliana ecotypes in 4 conditions: 22 and 27ºC in white light and light with addition of far-red. For each sample, flowers of stage 14 were collected and measured to track the responses in organ length. The accessions varied in sensitivity to the cues and the direction of the response, indicating a strong genetic component in the plasticity. For one accession, Bur-0, cell shape data were collected to infer the source of length change. Selected lines with contrasting response were subjected to bulkRNA seq to analyze the general and ecotype-specific transcriptional responses to the studied cues, and GxE at transcriptome level was detected.

12:45 – 13:00

Phenotypic Plasticity Across Aridity Gradients: Lessons from a Mediterranean Annual Grass

Ruchi Tiwari [1], Johannes Metz [1]

[1] Plant Ecology & Nature Conservation Group, Institute of Biology & Chemistry, University of Hildesheim, Hildesheim, Germany

Keywords

Abstract

Phenotypic plasticity enables plants to cope with variable environments and is a key mechanism for persistence under climate change. However, its distribution along environmental gradients remains poorly understood. We investigated plasticity in Brachypodium hybridum, a widespread Mediterranean annual grass, across 14 Israeli populations spanning arid to mesic conditions. Seeds were advanced to the F2 generation and grown in a greenhouse under six treatments combining three irrigation levels (drought to high water) with the presence or absence of competition from common grassland species. Plasticity was assessed in relation to both precipitation variability at the populations' origins and the degree of drought adaptation of the maternal plants. Plasticity, quantified as the coefficient of variation across treatments, differed among traits: highest for fitness- and growth-related traits, lowest for phenology. Contrary to the expectation that environmental heterogeneity promotes plasticity, populations from arid, variable-rainfall sites showed reduced plasticity in flowering time, leaf number at flowering, and height traits, while plasticity in maximum height and vegetative biomass remained stable along the gradient. Within-population variation was high but largely independent of ancestral drought adaptation, indicating considerable within-generation flexibility. Leaf economic traits displayed strong context-dependent plasticity. Drought induced conservative strategies, with lower specific leaf area (SLA) and higher leaf dry matter content (LDMC), whereas competition promoted acquisitive strategies, with higher SLA and lower LDMC. Overall, results suggest that in mesic, competitive environments plasticity enhances resource capture, whereas in arid habitats selection favors specialized, less plastic phenotypes, potentially constraining resilience under future climate change.

Session 4: Methods & Tools

10th October 2025, from 14:00 to 15:30

14:00 – 14:30

PlantSeg 2.0 and GoNuclear: Accessible 3D Segmentation of Cells and Nuclei in Microscopy Data

Qin Yu

European Molecular Biology Laboratory (EMBL), Heidelberg, Germany

Keywords
Computer Vision; Deep Learning; Instance Segmentation; Morphodynamics; Bioimage Analysis

Abstract

PlantSeg is a widely adopted software for 3D cell segmentation in dense plant tissues, with nearly 300 citations to date. In this talk, I will present recent developments in PlantSeg 2.0, which significantly enhance usability and performance. Key updates include a user-friendly Napari interface, multi-channel image support, integrated proofreading tools, training capabilities, and a one-click pipeline for instance segmentation. Additionally, PlantSeg now supports seamless nuclear segmentation through a newly integrated workflow. I will also introduce GoNuclear, a complementary package offering deep learning models for accurate 3D nuclear segmentation in both plant and animal tissues—even under weak or noisy imaging conditions. Together, these tools provide robust, accessible pipelines for high-quality image analysis across a range of biological systems.

14:30 – 14:45

GPxLMM: Gaussian Process-Augmented Linear Mixed Models for Genotype-by-Environment Interaction Analysis

Bibiana M. Horn [1], Zoran Nikoloski [2,3], Christoph Lippert [1]

[1] Hasso-Plattner-Institute for Digital Engineering, Digital Health and Machine Learning, Potsdam, Germany

[2] University of Potsdam, Institute of Biochemistry and Biology, Bioinformatics, Potsdam, Germany

[3] Max Planck Institute of Molecular Plant Physiology, Systems Biology and Mathematical Modelling, Potsdam, Germany

Keywords
Statistical Genetics, Genotype-by-Environment Interaction, Multivariate Linear Mixed Models, Gaussian Processes, Covariance Learning

Abstract

Genome-wide association studies of complex traits become particularly challenging when investigating genotype-by-environment interactions (GxE), especially when analyzing multiple correlated traits simultaneously. Traditionally, modeling the intricate trait relationships that arise in GxE analyses has required sophisticated analytical gradient calculations and simplifying assumptions about the covariance structure. Instead of manually specifying these relationships, our method employs GPyTorch to learn them directly from the data. We introduce GPxLMM, a framework that integrates Gaussian process-based covariance modeling with downstream linear mixed model (LMM) inference for fixed effect estimation. GPxLMM combines the flexibility of Gaussian processes for modeling complex inter-trait covariances with the comprehensive hypothesis testing capabilities of multivariate LMMs. Furthermore, its full implementation in PyTorch allows for GPU acceleration during both covariance training and downstream analysis. We validate GPxLMM's ability to detect heterogeneous GxE effects through comprehensive phenotype simulations using real genetic architectures from Saccharomyces cerevisiae and Arabidopsis thaliana, demonstrating the method's power to identify environment-specific genetic signals.

14:45 – 15:00

Single-plant omics: Profiling individual plants in a field to identify processes affecting yield

Michael van de Voorde [1,2], Sam de Meyer [1,2], Daniel Felipe Cruz [1,2]; Stijn Hawinkel [1,2], Tom de Swaef [3], Peter Lootens [3], Jolien de Block [1,2], Tom van Hautegem [1,2], Dirk Inzé [1,2], Hilde Nelissen [1,2], Isabel Roladán-Ruiz [3], Steven Maere [1,2]

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Keywords
single-plant, multiomics, lab-field gap, plant development

Abstract

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

15:00 – 15:15

Unraveling Genetic and Environmental Interactions in *Arabidopsis thaliana* Using a Multi-Scale Life Cycle Model

Alejandro León-Ramírez [1], Juliette de Meaux [1], Nadine Töpfer [1]

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Keywords
Life Cycle Model, Phenological Plasticity, In-Silico Analysis, Metabolic Model

Abstract

Understanding how genetic variation drives phenotypic differences remains a major challenge in biology, particularly for complex traits like phenology. Phenological plasticity often arises from the integration of multiple environmental cues, which poses challenges in dissecting the interplay between plant genotypes and their environments. In this project, we address these challenges by developing and employing in silico analyzes of a multi-scale life cycle model to study the adaptive potential and ecological performance of A. thaliana. Our framework integrates (1) a germination model that accounts for dormancy levels, soil temperature, and moisture; (2) a phenological model that predicts life cycle duration based on core flowering-regulating genes; and (3) a whole plant model composed of root, leaf and stem encompassing 861 metabolites and 891 biochemical reactions per tissue, which examines key biochemical processes affecting growth in response to resources such as light and nitrogen. To complement our computational approach, we incorporate experimental data from the “TRR 341 Plant Ecological Genetics”, providing empirical validation and deeper insights into the life cycle strategies of urban A. thaliana populations. Our findings demonstrate how plants adapt to varying levels of soil macronutrients and contrasting warm and cold environments. Traits such as the leaf-to-root biomass ratio, germination timing, and growth strategies respond dynamically to these conditions. In warmer climates, plants often complete their life cycle within a single year, adjusting their phenology to avoid excessive heat. In colder environments, some cohorts delay germination for several years to evade harsh winter conditions, resulting in diverse growth trajectories. These results underscore the critical role of environmental factors in shaping plant life history strategies.

15:15 – 15:30

The effect of trait interactions on the plant global form and function space

Milad Rahimi-Majd [1,2], Zoran Nikoloski [1,2]

[1] University of Potsdam, Bioinformatics Department, Institute of Biochemistry and Biology, Potsdam, Germany

[2] Max Planck Institute of Molecular Plant Physiology, Systems Biology and Mathematical Modeling Group, Potsdam, Germany

Keywords
plant economics, plant trade-off strategies, covariate analysis, mutual information

Abstract

The integration of plant growth, survival, and functionality trait space has been studied using either a single axis of variation, given by the Leaf Economics Spectrum (LES), or through more extended multidimensional frameworks. The extended models, in addition to the LES, incorporate other orthogonal axes of variation, including whole-plant and organ-level size dimension as well as a bi-dimensional root economics space. These theories are mainly based on the direct correlations of traits, using methods rooted in Principal Component Analysis (PCA), without controlling for covariates in pairwise trait relationships. In this study, we highlight the crucial role of interaction effects in uncovering the true relationships of the plant functional traits. Importantly, we demonstrate significant deviations form well-stablished patterns of trade-off strategies along the root fast-slow and the plant above-ground size dimensions when considering the trait interactions on the pairwise relationships. Based on these findings, we discuss the essential need for considering the interaction effects in studies of trait integration. This approach is particularly crucial for capturing robust patterns in the plasticity of plant functional and morphological traits resulting from genetic and environmental factors.

3.) Poster program

Poster session 1

9th October 2025, from 16:30 to 19:00

1 **Boyana Kozhuharova** *University of Potsdam, DE*

Toward Automated Phenotyping of Root Hair Plasticity in *Arabidopsis thaliana* under Varying Nitrogen Availability

2 **Yasin Kaya** *Max-Planck Institute for Plant Breeding Research, Cologne, Germany*

Evolutionary Genomics of Structural Variations and Rapidly Evolved Gene Families in East African *Arabis alpina* and *Arabidopsis thaliana*

3 **Subash Sitaula** *University of Potsdam, DE*

Genomic and functional underpinning of reaction norms of the leaf-economic spectrum across Nitrogen gradients

4 **Thi Chi Tran** *University of Potsdam, DE*

Phenotypic plasticity of leaf form and function in response to temperature in *Capsella bursa-pastoris*

5 **Chi-Ying Hsueh** *Max Planck Institute of Molecular Plant Physiology, Potsdam, DE*

Brassinosteroid-mediated environmental plasticity of seed development

6 **Emilian Paulitz** *University of Potsdam, DE*

Interrogating the genetic basis of phenotypic plasticity to nitrogen availability using pan-genome-scale metabolic models of *Arabidopsis thaliana*

7 **Jan-Niklas Weder** *University of Cologne, DE*

From Starch to Sugars: A kinetic model for starch degradation in *Arabidopsis thaliana* accounting for phenotypic plasticity in response to day lengths and nitrogen changes

8 **Sayantani Chanda** *Banaras Hindu University, Varanasi & ICAR-National Institute for Plant Biotechnology, New Delhi, IN*

Phenotypic and Biochemical Plasticity in *Brassica juncea*: Unlocking Genetic Resistance to Powdery Mildew

9 **Richard Gossens** *University of Helsinki, FN*

Transcriptional co-regulator RCD1 influences RNA splicing through interaction with the pre-spliceosome

10 **Xufeng Chen &**
Ashwin Ananthanarayanan *Max Planck Institute of Molecular Plant Physiology, Potsdam, DE &*
University of Potsdam, DE

Plasticity of lipid metabolism in *Arabidopsis thaliana* exposed to different temperature regimes

Poster session 2

10th October 2025, from 10:00 to 11:30

11 **Vera Hesen** *University of Potsdam, DE*

Intraspecific variation and plasticity in the Leaf Economics Spectrum of *Arabidopsis thaliana* in response to nitrogen-availability

12 **Liam Lumley** *University of Potsdam, DE*

Plasticity in thermal acclimation in selfing vs. outcrossing Capsella species

13 **Salma Tariq** *University of Potsdam, DE*

Estimating Accession-Specific Kinetic Parameters to Understand Photosynthetic Variation in *Arabidopsis thaliana*

14 **David Hobby** *University of Potsdam, DE*

Integrating Dynamic Mode Decomposition with Genomic Prediction to Predict Plant Development

15 **Micaela Milani &** *University of Potsdam, DE &*
Viviane Heise *University of Potsdam, DE*

Phenotypic plasticity of thermotolerance in *Capsella rubella*

16 **Saket Nikose** *Leibniz Institute of Vegetable and Ornamental Crops (IGZ), Großbeeren, DE*

Analysis of thermomorphogenic responses in Capsella: Overlap with Arabidopsis and genetic basis of hypocotyl plasticity

17 **Adeleh Dehghani Nazhvani** *University of Potsdam, DE*

Plasticity of cell, leaf and rosette shape in *Arabidopsis thaliana* in response to temperature

18 **Kaijing Zhang &** *Leibniz Institute of Vegetable and Ornamental Crops (IGZ), Großbeeren, DE &*
Xinkai Zhou *Humboldt University, Berlin, DE*

A comparative cellular atlas of environmental plasticity in leaves

19 **Patience Bwanu Iliya** *University of Potsdam, DE*

High-dimensional Bayesian Optimization Methods for Estimating Kinetic Parameters of the Calvin-Benson Cycle

20 **Gregory Andreou-Huotari** *University of Helsinki, FN*

Spliceosomal factor SmF modulates temperature-mediated flowering and leaf size plasticity in *Arabidopsis thaliana*

Poster session 1

9th October 2025, from 16:30 to 19:00

Poster #1

Toward Automated Phenotyping of Root Hair Plasticity in *Arabidopsis thaliana* under Varying Nitrogen Availability

Boyana Kozhuharova [1,2], Jacqueline Nowak [1], Michael Sauer [2]

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[2] University of Potsdam, Institute of Biochemistry and Biology, Plant Physiology, Potsdam, Germany

Keywords
Arabidopsis thaliana, root hairs, phenotyping, segmentation, nitrogen

Abstract

Root hairs are specialized epidermal outgrowths essential for water and nutrient uptake, anchorage, and interactions with the soil microbiome. Their pronounced phenotypic plasticity in response to environmental stimuli, such as nitrogen availability, makes them ideal candidates for developing automated phenotyping frameworks. This project focuses on establishing a robust, high-throughput pipeline for automated segmentation and trait analysis of root hairs across diverse genetic backgrounds and nitrogen gradients in Arabidopsis thaliana. Our project leverages the EPSINOID2 (ID2) regulatory network, known to negatively regulate root hair formation, to uncover genetic modulators of root hair plasticity under different nitrogen conditions. Furthermore, we are screening 24 genetically diverse Arabidopsis thaliana accessions for variations in root hair development, aiming to identify genotype-specific responses. Given the extensive microscopy image dataset, current annotation processes pose a significant limitation. To overcome this, we are exploring semi-supervised and iterative deep-learning strategies designed to dramatically speed up image annotation and segmentation workflows. Ultimately, our goal is to deliver a broadly applicable, automated phenotyping approach, enabling rapid and comprehensive analyses of root hair traits to facilitate genetic and environmental studies on plant adaptive responses.

Poster #2

Evolutionary Genomics of Structural Variations and Rapidly Evolved Gene Families in East African *Arabis alpina* and *Arabidopsis thaliana*

Yasin Kaya[1]; Sileshi Nemomissa[1]; Angela Hancock[1]

[1] Max-Planck Institute for Plant Breeding Research, Cologne, Germany

Keywords
structural variations, gene family evolution, local adaptation

Abstract

High-elevation “sky islands” in tropical East Africa represent extreme environments that provide unique selective pressures that often drive genomic changes. Under these challenging conditions, morphological and physiological divergences frequently emerge—ranging from stress-tolerant perennial growth forms (Arabis alpina) to ruderal annual strategies (Arabidopsis thaliana)—to maintain metabolic stability and preserve genetic integrity. Here, we investigate genomic rearrangements and gene family expansions/contractions in East African A. alpina and A. thaliana, comparing them to their respective references, A. alpina (Pajares) and A. thaliana. By leveraging high-quality genome assemblies of multiple accessions, we identify widespread inversions, translocations, and chromosomal shifts through synteny analysis, highlighting extensive genome plasticity that likely underpins local adaptation. Focusing on gene family evolution, we identified several expansions in repeat-like genes across multiple East African genomes over the last two thousand years. These expansions likely enable quick responses to environmental stressors and are accompanied by enrichment in defense-related, stress-response, and reproductive-development genes, underscoring the essential role of structural variation in shaping adaptive potential. Notably, certain accessions exhibit a high proportion of rapidly expanded gene families, indicating accelerated evolutionary processes driven by both biotic and abiotic pressures. A selection scan on rapidly evolving genes reveals that many defense-related families are under purifying selection, suggesting functional constraints and highlighting their importance for survival in harsh Afroalpine conditions. Overall, our findings illustrate how structural variation and lineage-specific gene family expansions contribute to the remarkable adaptability of Afroalpine crucifers. By illuminating the interplay between genome architecture and selective pressures in tropical alpine ecosystems, this study advances our understanding of how pronounced environmental gradients can foster rapid evolutionary change.

Poster #3

Genomic and functional underpinning of reaction norms of the leaf-economic spectrum across Nitrogen gradients

Subash Sitaula [1]; Vera Hesen [2]; Michael Lenhard [1]; Anja Linstädter [2]

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[2] University of Potsdam, Institute for Biochemistry and Biology, Biodiversity Research / Systematic Botany, Potsdam, Germany

Keywords
Nitrogen gradients, Leaf Economic Spectrum (LES) traits, Plasticity, GWAS

Abstract

Phenotypic plasticity enables plants to modify their traits in response to changing environmental conditions. Leaves, which are the primary organs for photosynthesis and resource acquisition, demonstrate this plasticity by altering various traits in response to different environments. The Leaf Economic Spectrum (LES) framework describes the coordinated variation of key leaf traits, such as leaf area, specific leaf area (SLA), and leaf dry matter content (LDMC), spanning from resource-conservative to resource-acquisitive strategies. While LES traits capture the intraspecific variation that occurs in response to environmental cues, the genetic basis of plasticity under different nutrient conditions, like nitrogen availability, remains unclear. To address this gap, we calculated several plasticity indices for LES traits, including stomatal density, in Arabidopsis thaliana plants grown under three nitrogen levels (12, 100, and 200 mg/L) and used them as inputs for genome-wide association studies (GWAS). Our results reveal distinct candidate loci linked to different leaf traits and highlight the varying sensitivity of plasticity indices in GWAS analyzes for detecting candidate loci. These findings underscore the complex genetic architecture underlying leaf trait plasticity in response to changes in nitrogen availability. Future research will focus on validating these candidate genomic regions to clarify their roles in controlling plastic responses. Overall, this study offers valuable insights into the genetics of plant adaptation to fluctuations in nutrient availability.

Poster #4

Phenotypic plasticity of leaf form and function in response to temperature in *Capsella bursa-pastoris*

Thi Chi Tran [1], Neeltje Schilling [1], Pascal Finger [1], Christian Kappel [1], Soraya Soleymanifar [1], Michael Lenhard [1]

[1] University of Potsdam, Institute of Biochemistry and Biology, Genetics, Potsdam, Germany

Keywords

Phenotypic plasticity, capsella bursa pastoris, ambient temperature, reaction norm, leaf shape, stomata density, QTL mapping

Abstract

Leaf morphology exhibits substantial interspecific variation and phenotypic plasticity, often reflecting environmental temperature. In many plant species, including the genus *Capsella*, leaf thickness, stomatal density, and the extent of leaf-margin dissection decrease with increasing ambient temperature. We investigated natural variation in temperature-responsive leaf traits among multiple accessions of *Capsella bursa-pastoris* and found strong genotype-by-environment interactions. Across accessions, lower growth temperatures promoted more dissected leaves, higher stomatal density, increased leaf length, and greater dry mass. The magnitude of these responses varied significantly among accessions, indicating underlying genetic diversity in plasticity. Genetic analyses suggest that multiple alleles contribute to the observed variation in temperature-dependent leaf dissection, with *REDUCED COMPLEXITY A* (RCO-A) emerging as a candidate gene. These findings highlight both the complexity and the evolutionary potential of temperature-mediated leaf trait plasticity in *C. bursa-pastoris*, and provide a foundation for future work to identify causal genes and elucidate their functional roles.

Poster #5

Brassinosteroid-mediated environmental plasticity of seed development

Chi-Ying Hsueh [1], Sinah Ehlert [1], Yuki Hamamura [2], Duarte Figueiredo [1]

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Keywords
Seed development, brassinosteroids, temperature

Abstract

Plants are sessile organisms that have developed strategies to cope with various environmental challenges throughout their life cycle. In most natural accessions of Arabidopsis thaliana, temperature changes have been observed to influence seed traits, such as endosperm proliferation and seed size. However, it remains unclear of how seeds perceive temperature cues and regulate the temperature responses. Brassinosteroids (BRs), a class of plant hormones, are promising candidates in this process since we observed that seeds of BR mutants show attenuation in temperature responses when compared to wild-type seeds. Therefore, my PhD thesis aims to investigating the role of BR in regulating the developmental plasticity of seeds in response to temperature. Firstly, I will characterize the genetic importance of BRs in regulating thermomorphogenesis in seed development. To further understand the BR-signaling networks, I will focus on the study of the key BR effector transcription factor, BRASSINAZOLE-RESISTANT 1 (BZR1). We aim to carry out CUT&RUN profiling and transcriptomic analysis to identify genetic determinants regulated by BZR1 during temperature changes. Moreover, since we have shown that BRs promote seed expansion in a manner dependent on the composition of the cell wall, I aim to understand whether seed coat cell wall compositions are modulated by different temperatures. This study will enhance our understanding on developmental plasticity of seeds in response to temperature, thereby facilitating crop engineering to adapt diverse environmental conditions.

Poster #6

Interrogating the genetic basis of phenotypic plasticity to nitrogen availability using pan-genome-scale metabolic models of *Arabidopsis thaliana*

Emilian Paulitz [1,2]; Fayaz Soleymani Babadi[1,2]; Sandra Correa Córdoba[1,2]; Zoran Nikoloski[1,2]

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[2] Max Planck Institute of Molecular Plant Physiology, Systems Biology and Mathematical Modelling, Potsdam, Germany

Keywords
Metabolism; Nitrogen availability; Computational prediction; Pan-genomics; Arabidopsis

Abstract

The combinatorial explosion of abiotic stresses and genotypes is often prohibitive for experimental studies of the genetic basis of phenotypic plasticity. We address this issue by employing pan-genome-scale metabolic models of Arabidopsis thaliana. Genome-scale metabolic models are collections of biochemical reactions and biophysical constraints. These models have been used to predict how nutrient uptake and intracellular metabolic fluxes shape plant phenotypes, including gas exchange and growth. Our contribution comprises the manually curated pan-genome-scale metabolic model of A. thaliana that can be readily adapted to accessions of interest, thus posing a valuable resource for the community. The pan-genome-scale metabolic model was constructed using whole-genome assemblies of 162 Arabidopsis accessions. Their annotation yielded that 9% of enzymes are variably present in accessions, resulting in variability in the corresponding accession-specific metabolic networks. The compartmentalization of the models is rendered accession-specific by predicting and integrating transporter activities and the subcellular localization of enzymatic reactions. Here, we observed a modest variability, with 25% of enzyme localization and 19% of transporter activity exhibiting variation in at least one accession. Using these data alongside the publicly available transcriptomics data, we devised accession- and leaf-specific models for 102 accessions. The resulting accession-specific models were used to simulate different levels of nitrogen availability, thereby predicting reaction norms for the accessions. Quantitative proteomics and metabolomics data collected from a subset of the accessions will be used to validate predictions and enhance the accession-specific and union models in an iterative process. In this way, our study aims to gain insight into the genetic basis of phenotypic plasticity to nitrogen availability and growth in Arabidopsis.

Poster #7

From Starch to Sugars: A kinetic model for starch degradation in *Arabidopsis thaliana* accounting for phenotypic plasticity in response to day lengths and nitrogen changes

Jan-Niklas Weder [1]; Nadine Töpfer [1]

[1] University of Cologne, Institute for Plant Sciences, Center for Data and Simulation Science, Köln, Germany

Keywords
kinetic modeling, starch degradation, metabolic modeling

Abstract

Transient starch is a fundamental component of all plants. It serves as an intermediate carbon storage, which is synthesized in the plastids of photosynthetically active tissues and subsequently degraded at night. Mutants that cannot form or break down transient starch show a reduction in growth compared to the wild type. Furthermore, patterns of starch degradation show phenotypic plasticity in response to changes in day length or nitrate levels. A kinetic model of starch degradation can provide insights into the mechanisms underlying these observations and identify interconnections between phenotypic plasticity, metabolism, and starch granule properties. While individual enzymes involved in severe degradation, as well as their interdependence, have been described, detailed models incorporating their kinetic properties remain scarce. The most comprehensive models encompass only a subset of the reactions involved and lack some of the enzymes involved in the transition from granular to soluble starch. Existing models are also generic without any organism-specific considerations. Here, we develop a comprehensive kinetic model of the starch degradation pathways in Arabidopsis thaliana. In our model, we include the enzymes necessary for the initial transition from an insoluble to a soluble state. Accession-specificity of the model is achieved by incorporating accession-specific estimated and measured enzyme kinetic properties, as well as experimentally determined starch granule properties and time-resolved metabolomics data for different day lengths and nitrogen levels. With our model, we aim to provide insights into the mechanisms that control degradation rates at night and which enable phenotypic plasticity with respect to nitrogen and light.

Poster #8

Phenotypic and Biochemical Plasticity in *Brassica juncea*: Unlocking Genetic Resistance to Powdery Mildew

Sayantani Chanda [1,2], Surendra Kumar Gond [1], Ashish Kumar Gupta [2]

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[2] ICAR-National Institute for Plant Biotechnology, New Delhi, India

Keywords
Powdery Mildew, Brassica juncea, Phenotypic Plasticity, Disease Resistance, Antioxidant Enzymes

Abstract

Phenotypic plasticity expresses the ability towards altering its observable traits of a given genotype in response to environmental conditions, a significant factor in a rapidly changing climate. Environmental factors like humidity, temperature, air circulation, and light significantly influence plant-pathogen interactions, particularly the spread of powdery mildew (PM), a fungal disease caused by Erysiphe cruciferarum that affects Brassica crops. This study assessed the plastic responses of Brassica juncea genotypes against PM under natural field conditions at Pusa, New Delhi,India, during the 2023–2025 rabi seasons. A diverse panel comprising 172 re-synthesized B. juncea (RBJ) lines, 192 introgressed lines (ERJ), and 50 additional Brassica accessions were assessed at 90 and 110 days after sowing (DAS) for visible disease symptoms for quantifying phenotypic plasticity, including leaf spotting, wilting, and mildew coverage. Biochemical analyses were also conducted to measure antioxidant enzyme activities (catalase, superoxide dismutase, and peroxidase) associated with defense responses. Results revealed significant genotypic variation in resistance expression, with six ERJ lines, two RBJ lines, and 27 other accessions showing moderate resistance (10–30% disease severity), while ten accessions exhibited high resistance (5–10% severity). Resistant genotypes consistently demonstrated elevated antioxidant enzyme activity, indicating a strong plastic biochemical defense mechanism, whereas susceptible lines had lower activity and more severe symptoms. These findings underscore the importance of phenotypic and biochemical plasticity in disease resistance and provide a foundation for breeding climate-resilient Brassica cultivars. Identifying and utilizing genotypes with robust defense responses is significant for sustaining mustard production under biotic stresses.

Poster #9

Transcriptional co-regulator RCD1 influences RNA splicing through interaction with the pre-spliceosome

Richard Gossens [1], Julia Vainonen [1], Garima Bhatia [2], Paul Torben [3], Lennart Wirthmueller [3], Barry Pogson [2], Saijaliisa Kangasjärvi[1], Jaakko Kangasjärvi[1], Alexey Shapiguzov[1,4]

[1] University of Helsinki, Finland

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[4] Natural Resources Institute Finland (LUKE), Piikkiö, Finland

Keywords
Stress signalling, RNA splicing, RNA sequencing, co-immunoprecipitation, mass spectrometry, cell biology

Abstract

Plants face constant fluctuations in environmental conditions and various stress signalling pathways aid plants in coping with these fluctuations through influencing the expression of nuclear genes. The nuclear protein RCD1 integrates multiple stress signalling pathways by interacting with over 30 transcription factors (TFs), yet its role as transcriptional co-regulator has remained unclear. Our study reveals that the rcd1 mutant exhibits genome-wide defects in alternative splicing, indicating that the mechanism by which RCD1 regulates gene expression is more complex than was previously thought. We show that RCD1 physically interacts with spliceosomal machinery, to be precise mainly components of the the pre-spliceosome. Moreover, the size and abundance of RCD1 nuclear bodies changes upon pharmacologically inhibiting the pre-spliceosome but not upon inhibition of the precatalytic spliceosome. Domain analysis indicates that RCD1's TF-binding domain is not required for interaction with spliceosomal components. These findings suggest that RCD1 regulates gene expression, not only by modifying transcription, but also by engaging in RNA splicing. We hypothesize that RCD1 regulates co-transcriptional splicing by recruiting splicing factors to active chromatin through its interaction with DNA-bound TFs on one hand and interactions with splicing apparatus on the other.

Poster #10

Plasticity of lipid metabolism in *Arabidopsis thaliana* exposed to different temperature regimes

Xufeng Chen [1]; Ashwin Ananthanarayanan [1,2]; Mustafa Bulut [3]; Sandra Marcela Correa Cordoba [1,2]; Alisdair Robert Fernie [1]

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Keywords
Plasticity, Lipid Metabolism, Constraint Based Modeling, Lipidomics, Temperature

Abstract

Being sessile organisms, plants must continuously adapt to fluctuating environmental conditions. Phenotypic plasticity, defined as the capacity of a genotype to produce variable phenotypes in response to environmental cues, enables plants to adapt and thrive under aging conditions such as temperature, light, water availability and/or nutrients. Particularly, changes in temperature profoundly affect plant physiology, processes such as growth, metabolism, flowering, reproduction and stress responses. At the metabolic level, plants respond to temperature fluctuations through well-characterized mechanisms such as lipid remodeling, wherein the composition and structural properties of membrane lipids are modified. Notably, the extent of lipidomic changes in response to temperature varies considerably among different Arabidopsis thaliana accessions, indicating substantial genotype-by-environment variation. Despite this, the genetic basis of lipidome plasticity remains largely unknown. Through our project, we aim to elucidate the genetic basis of lipid composition adjustments to temperature using an integrative approach that combines constraint-based modeling (CBM) with lipidomic profiling. The novelty in our approach lies in using reaction rates derived from condition- and accession-specific metabolic models, rather than directly using lipid abundance data as phenotypic traits, to construct reaction norms. By characterizing these reaction norms, we will obtain plasticity indexes that serve as traits for a genome-wide association study (GWAS), ultimately uncovering genes that govern lipidome plasticity.

Poster session 2

10th October 2025, from 10:00 to 11:30

Poster #11

Intraspecific variation and plasticity in the Leaf Economics Spectrum of *Arabidopsis thaliana* in response to nitrogen-availability

Vera Hesen [1]; Hiba El Hijabi [1]; Subash Sitaula [2]; Michael Lenhard [2]; Anja Linstädter [1]

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Keywords
Arabidopsis thaliana, Leaf Economics Spectrum, Phenotypic plasticity, nitrogen-availability, intraspecific variation

Abstract

Leaf morphology and function are plastic in response to many environmental cues. A powerful method to describe leaf phenotypes is the Leaf Economics Spectrum (LES), that assumes plants have trade-offs in their resource allocation to leaves. LES combines multiple leaf traits (eg leaf area and weight) into a single axis of variation, which reflects resource-acquisitive versus resource-conservative strategies of plants. While the concept LES is well-established, little is known about the plasticity of the individual and composite LES traits. In our study, we investigate the variation in the plasticity of LES traits across A. thaliana accessions in response to changes in nitrogen availability. We aim to (1) demonstrate the level of plasticity of LES traits across a panel of global A. thaliana accessions, (2) study whether variation in plasticity of LES traits is associated with environmental parameters at the accession's site of origin and (3) explore how accession's plasticity patterns are related to their ecological strategies. We conducted a large greenhouse experiment where we grew a global panel of 200 A. thaliana accessions on three different nitrogen-availability levels. We measured LES traits on the 7th leaf and in addition determined fitness proxies. We assessed the magnitude of plasticity and associated this with various ecological and environmental factors. Combining the well-established plant-ecological concept of the Leaf Economics Spectrum with the plethora of resources of model-species A. thaliana has to offer will allow us to better understand eco-evolutionary trade-offs and plasticity in LES strategies.

Poster #12

Plasticity in thermal acclimation in selfing vs. outcrossing Capsella species

Liam Lumley [1], Ralph Tiedemann [1]

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Keywords

Thermotolerance, Gene regulatory network or GRN, Capsella grandiflora, self-compatibility

Abstract

Plants respond to heat stress via several genetic and molecular mechanisms which ultimately act to increase the tolerance of plants to heat stress, a phenomenon referred to as thermotolerance. Different thermotolerance types have been characterized on the basis of the heat stress regime. Acquired thermotolerance (aTT) refers to the phenomenon of plants to survive a typically lethal heat stress, granted the plants had prior exposure to recent sub-lethal heat stress, however, the extent of this response varies between individual plants. This project focusses on elucidating the genetic basis and evolution of physiological plasticity as expressed in acquired thermotolerance (aTT), using three Capsella species with different aTT and reproductive mode (selfing vs. outcrossing). Using C. grandiflora, a combination of phenotypic and transcriptomic data is collected during an artificially induced aTT response in order to perform a GWAS analysis to identify genetic polymorphisms associated with aTT plasticity. Additionally, using a targeted expression association study, this project aims at inferring the heat-inducible gene-regulatory network in C. grandiflora and which of its genes harbor natural genetic variation. Furthermore, this project will assess how the evolution of self-compatibility in C. rubella and C. orientalis impact aTT plasticity and its intraspecific variation.

Poster #13

Estimating Accession-Specific Kinetic Parameters to Understand Photosynthetic Variation in *Arabidopsis thaliana*

Salma Tariq [1], Anika Küken [1]

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Keywords
accession-specific parameters, Bayesian parameter estimation, metabolic modeling, genotype-phenotype link, environmental adaptation, growth plasticity

Abstract

Photosynthetic activity in Arabidopsis thaliana accessions varies across different environments due to differences in their genetic makeup. However, the underlying genetic and molecular basis of the variation in photosynthetic traits, such as metabolite concentrations and enzyme activity, remains unclear. Kinetic models that relate enzyme activity with metabolite concentration based on kinetic parameters can help to understand functional differences across A. thaliana accessions. Hence, we estimate accession-specific kinetic parameters in a large-scale kinetic model of photosynthesis[1] by fitting experimental data on metabolite concentrations measured in a panel of A. thaliana accessions from diverse geographical origins, all grown under identical environmental conditions. To analyze accession-specific differences across estimated kinetic parameters considering also uncertainty in parameter estimation we employ Bayesian parameter inference. The results show clear differences in kinetic profiles, indicating variation in the efficiency and enzymatic properties of photosynthetic processes. These differences may be linked to genetic variation and to adaptation to the environmental conditions of the regions where the accessions originated. Overall, this work shows how kinetic modeling and Bayesian inference can be used together to better understand the factors that drive differences in photosynthetic activity in A. thaliana.

Poster #14

Integrating Dynamic Mode Decomposition with Genomic Prediction to predict plant development

David Hobby

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Keywords
genomic prediction; time-series data; developmental dynamics; forecasting; high-throughput phenotyping

Abstract

Abstract We present a new methodology, termed dynamicGP, which merges Dynamic Mode Decomposition (DMD) with Genomic Prediction (GP) to address this challenge. DMD is used to analyze time-series data by extracting temporal patterns and identifying dynamic structures in time-resolved data. We applied this method to time-resolved phenomena, comprising diverse growth-related traits from a maize MAGIC population. DMD revealed temporal relationships underlying various growth traits. Using genomic data, we investigated heritability and predictability of key components of the DMD algorithm, including the operator encapsulating the system's dynamics. This operator can be used to forecast the plant phenome in future time-points using the state of the phenome in a preceding time point. We predict the operator from genomic marker data by directly predicting the intermediate components of the DMD algorithm. We used two approaches to assess accuracy of the dynamics obtained from the the predicted operator: (1) recursive, beginning with the initial state of the phenome at the first time point, the subsequent phenomes are obtained using predicted phenomes at each intermediate time point; and (2) iterative, using the measured phenome values at each time point to predict the phenome in the following time point. We showed that dynamicGP outperformed rrBLUP baseline predictions. We further introduce an extension to dynamicGP which integrates environmental variables to further increase prediction accuracy.

Poster #15

Phenotypic plasticity of thermotolerance in *Capsella rubella*

Micaela Milani [1], Viviane Heise [1], Isabel Bäurle [1]

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Keywords
Acquired thermotolerance, heat stress, Capsella rubella and Intraspecific variation

Abstract

Climate change threatens agricultural productivity and biodiversity through presenting considerable challenges to plant survival, mostly through the increased frequency and intensity of abiotic stresses like heat stress. Plants, being sessile, have evolved molecular mechanisms that allow them to grow and reproduce even in such stressful environmental conditions. There are three types of thermotolerance, basal thermotolerance (bTT), which is the ability to withstand severe heat stress without prior acclimation. Additionally, a plant can withstand heat stress after prior exposure to an environment with moderate heat stress (priming), called acquired thermotolerance (aTT). This priming environment induces a more heat-resistant physiological state as a plastic response through changes in gene expression and metabolic pathways. This response can also be actively maintained by the plant (memory of acquired thermotolerance, maTT).

Preliminary data shows that the Capsella genus displays variation in response to acquired thermotolerance. Based on this, in our project, we address several aims. (1) the identification of intraspecific variation in responses to heat in the thermotolerant species Capsella rubella. (2) the understanding of molecular mechanisms that underpins this response to aTT and (3) the determination whether this difference observed can be applied to real-life field conditions using near-isogenic lines.

We screened 47 Capsella rubella accessions and identified candidate accessions, that showed a varied response to the tested heat treatments, thus confirming intraspecific variation does exist. We, therefore, aim to characterize the particular accessions further and investigate the molecular and genetic basis of the variation in thermotolerance.

With the knowledge of the genetic basis that underpins these phenotypic responses, we may have a route to how we could modify crops in the future to withstand rising temperatures.

Poster #16

Analysis of thermomorphogenic responses in Capsella: Overlap with Arabidopsis and genetic basis of hypocotyl plasticity

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Keywords
Thermomorphogenesis, Capsella, Temperature sensation, Phenotypic plastic

Abstract

Plants respond to different external environmental cues, which include conditions such as temperature, light, pH, humidity, etc. and resources such as water, nutrients, space, etc. Out of these cues, the response to the temperature is quite peculiar. Plants show phenotypic plasticity when grown under various temperature conditions. The ability of the plants to show growth and developmental response in response to warm temperatures is termed thermomorphogenesis. Genotype-specific variation in thermomorphogenesis is key to the plant's adaptation to a changing climate. Understanding how plants adapt to different climates in the face of the upcoming challenges of global warming and crop production is crucial. Here, we proposed the plant species from the genus Capsella, such as C. rubella and C. grandiflora, as an excellent evolutionary system to understand the questions of phenotypic plasticity in temperature response behaviour. As the species Capsella is very closely related to Arabidopsis, the recent advances in the study of Arabidopsis thaliana will help to understand the changes in regulators of thermomorphogenesis in Capsella. The main goals of this project are to 1) determine the suite of thermomorphogenic responses in Capsella. and 2) Identify the genetic basis of variation in plasticity in Capsella. Supporting the idea that molecular mechanisms may generate plasticity in natural populations.

Poster #17

Plasticity of cell, leaf and rosette shape in *Arabidopsis thaliana* in response to temperature

Adeleh Dehghani Nazhvani [1], Prabal Das [2], Jacqueline Nowak [1,3], Arun Sampathkumar [2]

[1] University of Potsdam, Institute of Biochemistry and Biology, Bioinformatics, Potsdam, Germany

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Keywords

Morphological plasticity, Phenotypic variation, Leaf morphology, Pavement cells, Rosette architecture

Abstract

Understanding how plants respond to environmental conditions, particularly temperature, is crucial for uncovering adaptive mechanisms in plant morphology. Morphological plasticity allows plants to optimize growth and development in response to their environment, and exploring this variation can reveal genotype-specific strategies for adaptation. In this study, we investigated 24 accessions of Arabidopsis thaliana germinated and grown at 17, 22 and 27°C, focusing on natural variations in shape plasticity on different levels, from the whole rosette to single leaves and down to individual leaf epidermal cells. We quantified several shape-related traits across all accessions and levels, such as area and circularity. In addition, we implemented level-specific traits. At the rosette level, we calculated the total leaf number, as well as two customized traits which assess the distribution of leaf growth across different radial zones and rosette symmetry. At the leaf level, we examined leaf elongation and narrowing, while at the cellular level, we characterized the shape complexity of pavement cells in the upper epidermis using GraVis, a graph-based image analysis tool We examined correlations between different morphological traits across scales to better understand how they may be interrelated. Our multi-scale quantitative approach highlights significant diversity in morphological traits across A. thaliana accessions under a constant growth temperature. These findings provide insight into natural variation and potential adaptive strategies in response to moderately growth conditions.

Poster #18

A comparative cellular atlas of environmental plasticity in leaves

Kaijing Zhang [1], Xinkai Zhou [2]

[1] Leibniz Institute of Vegetable and Ornamental Crops (IGZ) eV, Großbeeren, Germany

[2] Humboldt University, Institute for Biology, Plant Cell and Molecular Biology, Berlin, Germany

Keywords
Temperature, nitrogen, leaves, single nuclei sequencing, tissue-specific

Abstract

Leaves are important environmental sensory organs that exhibit phenotypic plasticity in response to fluctuating environmental conditions, such as temperature, light, humidity, and nitrogen. Growth of the leaf blade and petiole is highly plastic responding to ambient temperature; as major organs of photosynthesis leaves are also sensitive to changes in nutrient supply like nitrogen, N status affects leaf size and epidermis traits. Gene expression regulatory networks play a critical role in shaping plants' plasticity, these networks are cell-type specific and gated by the circadian clock. Capsella bursa-pastoris and Arabidopsis thaliana are close relative species with a broad eco-geographical distribution. In this study, we will use A. thaliana and C. bursa-pastoris as comparative models to understand the tissue-level gene expression induced by multifactorial environmental molecular perturbations, and to address the question to what extent mechanisms underlying plastic responses to environmental factors are conserved across species. The main goals of this project are: 1) to dissect the transcriptional landscape responding to temperature and nitrogen in leaves. 2) to reveal the chromatin and cis-regulatory code underlying tissue-specific responses. 3) to understand conserved features of gene regulatory networks between A. thaliana and C. bursa-pastoris.

Poster #19

High-dimensional Bayesian Optimization Methods for Estimating Kinetic Parameters of the Calvin-Benson Cycle

Patience Bwanu Iliya

University of Potsdam, Bioinformatics Department, Potsdam, Germany

Keywords
Bayesian optimization, Kinetic parameters, Calvin-Benson cycle, A/Ci curves, Chi-square

Abstract

Kinetic models of the Calvin–Benson cycle, parameterized with species- or condition-specific rate constants, offer a mechanistic foundation for understanding how photosynthetic metabolism responds and adapts to environmental variation. Such models are essential for predicting carbon assimilation under fluctuating nitrogen, light and CO_2 conditions. However, accurate parameter estimation remains a major bottleneck, particularly in large-scale models with highly nonlinear relationships and often underdetermined parameters given the available data. We benchmark three state-of-the-art high-dimensional Bayesian optimization (HDBO) methods for their ability to estimate kinetic parameters from photosynthetic CO_2 response (A/Ci) curves. These curves characterize the dependency of the net CO_2 assimilation rate (A) on the intercellular CO_2 concentration (Ci) and are widely used to infer photosynthetic capacities and limitations in vivo. We simulate synthetic A/Ci datasets using a mass-action kinetic model of the Calvin–Benson cycle in Arabidopsis thaliana, comprising 112 parameters. Each HDBO method is tasked with recovering the original parameter set by minimizing a chi-square cost function between simulated and target A/Ci curve. All three methods exploit the inherent structure of biochemical networks—where topological and kinetic dependencies constrain the effective degrees of freedom—to accelerate convergence. Across 10,000 iterations per method, we observe that each method demonstrates its capability to adaptively focus the search within the relevant subspaces, achieving reasonable fits. These results highlight the effectiveness of HDBO techniques in biochemical model calibration. Our findings demonstrate that HDBO is a promising tool to significantly improve the precision and computational efficiency of kinetic parameter estimation in large-scale photosynthetic models.

Poster #20

Spliceosomal factor SmF modulates temperature-mediated flowering and leaf size plasticity in *Arabidopsis thaliana*

Gregory M. Andreou-Huotari [1], Mikael Broche [1], Jan Hoffmann [1], Zoran Nikoloski [2,3], Roosa Laitinen [1]

[1] Organismal and Evolutionary Biology Research Program, Viikki Plant Science Center, University of Helsinki, Helsinki, Finland.

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[3] Bioinformatics Department, Institute of Biochemistry and Biology, University of Potsdam, 14476 Potsdam, Germany.

Keywords
Temperature, plasticity, alternative splicing

Abstract

Plants, as seemingly static organisms, must sense and adapt to changes in their environment. We have previously shown that flower size plasticity to temperature in Arabidopsis thaliana mainly follows additive inheritance (Andreou et al., 2023), and we have also shown that temperature-mediated flower size plasticity in A. thaliana is controlled by the alternatively spliced known flowering-time gene cluster MAF2-5 (Wiszniewski et al., 2022). Since alternative splicing is regulated by the spliceosome, we reasoned that mutations in spliceosomal factor genes may influence the degree of size plasticity. In this project, we investigated mutants for 12 spliceosome-associated genes for their temperature-mediated growth size plasticity, in flowers and leaves, from 17 to 25 °C. Compared to wild type, we saw significantly reduced flower size plasticity to temperature in a line carrying a mutation in the SmF gene, which encodes one of seven Sm proteins present in four of the major spliceosomal small nuclear ribonucleoproteins (U1, U2, U4 and U5 snRNPs). The reduced flower size plasticity in the SmF mutant was associated with reduced plasticity in petal conical cell area and number. In addition, the SmF mutant lost dominance of MAF2 and MAF3 variant 1 splice isoform at the colder temperature. This mutant also showed impaired leaf growth at 17 °C, which resulted in increased expression of disease resistance genes and reduced fitness. Interestingly, this mutant showed high ozone tolerance, despite more open stomata suggested by water loss experiments. Our study highlights the role of SmF in independently controlling leaf and flower size plasticities to temperature.

References

Andreou G et al., 2023. Quantitative Plant Biology 4:e4.
Wiszniewski et al., 2022. iScience 25:11.

5.) Directions

Our conference takes place at the **WIS | Wissenschaftsetage im Bildungsforum (Am Kanal 47, 14467 Potsdam, Telephone: (0331) 977 4599)**

If you arrive at the central station in Potsdam (Hauptbahnhof), you can either walk 15 minutes to the venue or take the following public transport options:

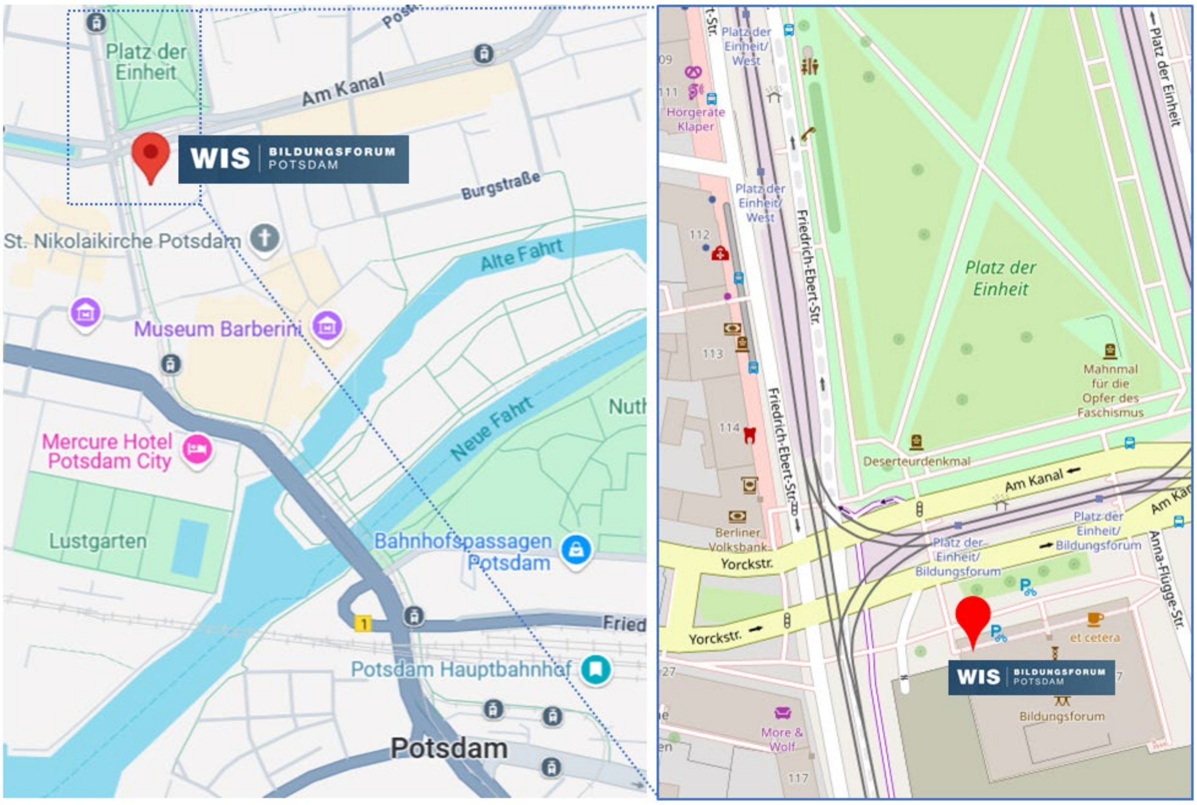
Tram 96, direction **Potsdam, Campus Jungfernsee**: Potsdam Hbf → Alter Markt/ Landtag

OR

Bus 695, direction **Potsdam, Science Park West**: Potsdam Hbf → Potsdam, Platz der Einheit/ West

OR

Bus 605, direction to **Potsdam, Science Park West**: Potsdam Hbf → Alter Markt/ Landtag



Potsdam Hauptbahnhof = Potsdam central station

6.) Additional information

Internet access

There will be WiFi available on-site via eduroam or provided password

Public transport information

Information on public transport schedules can be accessed via the local public transport websites.

www.vbb.de

www.bahn.de

Emergency numbers

Fire brigade & ambulance	112
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7.) Attendee list

Ordered alphabetically (according to first name):

Adeleh Dehghani Nazhvani

Alejandro Leon Ramirez

Amna Sarmad

Anika Küken

Anita Henze

Anja Linstädter

Annika Saß

Aparna Sekar

Arsalan Khan

Arun Sampathkumar

Ashwin Ananthanarayanan

Bibiana Horn

Boyana Kozhuharova

Brigitte Poppenberger

Buddhika G. Pathirana

Chibueze Ene

Chi-Ying Hsueh

Christoph Lippert

David Hobby

Dhanush Srikanth Srikanthan

Dongbo Shi

Duarte Figueiredo

7.) Attendee list

Eirini Kaiserli

Emilian Paulitz

Florian Müller

Gregory Michael Andreou-Huotari

Hannah Schneider

Hui Cao

Isabel Bäurle

Jacqueline Nowak

Jan Hoffmann

Jan-Niklas Weder

Joerg Fettke

Johannes Metz

Kaijing Zhang

Karun Wilson

Keya Akter

Khalil Said

Laitinen Roosa

Liam Lumley

Liese Schnurbusch

Mathias Tupinier

Micaela Milani

Michael Lenhard

Michael Sauer

7.) Attendee list

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Milad Rahimi Majd

Mody Tejasvinee

Nadine Töpfer

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Nina Freimuth

Patience Bwanu Iliya

Pauline Gutsche

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Qin Yu

Rajadurga Rajenderan

Ralph Tiedemann

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Tahir Mujtaba

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