VISCEA
Vienna International Science
Conferences and Events Association

International Conference

Plant Hormones & Growth Regulators

Programme & Abstracts

Vienna, Austria
February 17-18 , 2020

International Conference

Plant Development & Other Growth Regulators

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Vienna, Austria

February 17 – 18, 2020

Organizing Committee

Local Organizing Committee	International Organizing Committee
Alisher Touraev (Local Organizer, Austria) Klaus Palme (Conference Co-Chair, Germany)	Zhi-Yong Wang (USA) Ana Caño Delgado (Spain) Ana Margarida Fortes (Portugal) Jerry Cohen (USA) Salim Albabili (Saudi Arabia) Alicja Banasiak (Poland) Dominique Van Der Straeten (Belgium) Maria Samsonova (Russia) Carolin Delker (Germany) Minsung Kim (United Kingdom)

Welcome to the International Conference on "Plant Hormones & Other Growth Regulators"!

Plant growth regulators (also called plant hormones) are numerous chemical substances that profoundly influence the growth and differentiation of plant cells, tissues and organs. Plant growth regulators function as chemical messengers for intercellular communication. There are currently five recognized groups of plant hormones: auxins, gibberellins, cytokinins, abscisic acid (ABA) and ethylene. They work together coordinating the growth and development of cells. Ethylene is mainly involved in abscission and flower secscence in plants and is rarely used in plant tissue culture. In addition to the five principal growth regulators, two other groups sometimes appear to be active in regulating plant growth, the brassinosteroids and polyamines.

As agriculture becomes more mechanized and science increases the possibilities for using inputs to enhance production, the role of PGRs becomes more vital.

Through discussions of the "classical five" phytohormones–gibberellins, cytokinins, ethylene, abscisic acid, and auxins–and the growing number of nontraditional PGRs such as oligosaccharins and brassinosteroids, the International conference "Plant Hormones and Other Growth Regulators" discuss the past and present uses of PGRs in managing crop yield and offers some speculation on future directions.

This two-days event will provide leading academy and industry scientists a platform to communicate recent advances in **"Plant Hormones & Other Growth Regulators",** and an opportunity to establish multilateral collaboration.

The **International Conference on "Plant Hormones & Other Growth Regulators"** will cover the following research topics:

- ***Hormone Metabolism and Transport***
- ***Hormone Perception & Signaling***
- ***Hormone Biosynthesis & Metabolism***
- ***Hormone Interactions***
- ***Hormones in Cell Differentiation and Morphogenesis***
- ***Hormone Evolution***
- ***Hormone Imaging***

Approximately 150 participants are expected to attend this exciting scientific forum including almost 30 lectures delivered by worldwide known invited speakers and young, talented speakers selected from submitted abstracts. The program combines plenary lectures, poster sessions, a unique Conference Dinner Party and sightseeing tours of Vienna.

Prof. Alisher Touraev (VISCEA, Austria, Local Organizer)

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International Conference on "Plant Hormones & Other Growth Regulators" (February 17 - 18)

February 17 (Monday)

08.00 - 17.00	***Registration***
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09.20 - 10.30	**Keynote Lecture:** **Zhi-Yong Wang (USA):** Plant Growth Regulation by Integration of Hormonal, Nutritional, and Environmental Signals
10.30 - 11.00	***Coffee break***
11.00 - 12.30:	**Session I: Hormone Metabolism & Transport**
Chairs	*Ana Caño Delgado (Spain) & Ana Margarida Fortes (Portugal)*
11.00 - 11.30 (+5)	**Ana Caño Delgado (Spain):** Brassinosteroid Signaling in Plant Development and Adaptation to Stress
11.35 - 12.05 (+5)	**Ana Margarida Fortes (Portugal):** Reprogramming of Hormonal Metabolism in Susceptible and Resistant Grape Cultivars upon Infection with Botrytis cinerea
12.10 - 12.25 (+5)	**Debora Gasperini (Germany):** Jasmonates on the Move: How Hormone Pool Redistribution govern Plant Acclimation Responses
12.30 - 14.00	***Lunch + Poster Session + Conference Photo***
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14.30 - 14.50 (+5)	**Václav Motyka (Czech Republic):** Cytokinin N-Glucosides and their Parts in Evolution and Biology of the Family of Cytokinins
14.55 - 15.10 (+5)	**Amirbahram Moradi (Germany):** Development of a Genotype-Independent high-throughput System for Accelerated Breeding Innovations in Sugar Beet
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16.35 - 17.05 (+5)	**Salim Albabili (Saudi Arabia):** Anchorene and Zaxinone, Two Novel Carotenoid-Derived Growth Regulators

17.10 - 17.30 (+5)	**Alicja Banasiak (Poland):** SAM Organogenic Activity and Vascular System Development in the pin1 mutant of Arabidopsis are determined by ontogenetic Changes in Auxin Biosynthesis and Transport Pathway
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09.35 - 10.05 (+5)	**Maria Samsonova (Russia):** Model Based Crop Improvement
10.10 - 10.30 (+5)	**Eline Saenen (Belgium):** Exposure to Ionizing Radiation disturbs the Hormonal Balance in Arabidopsis thaliana Plants
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Chairs	*Carolin Delker (Germany) & Klaus Palme (Germany)*
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11.35 - 12.05 (+5)	**Carolin Delker (Germany):** Tissue-Specificity in Hormonal Regulation of Plant Thermomorphogenesis
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Abstracts of Oral Presentations

Plant Growth Regulation by Integration of Hormonal, Nutritional, and Environmental Signals

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Growth and development in plants are controlled by multiple hormones, a wide range of environmental signals, and nutrients. How these hormonal, environmental and metabolic signals are integrated into coherent growth decisions is a central question in plant biology. Using the Arabidopsis hypocotyl elongation as model system, we have dissected the molecular circuitry that integrates diverse signals to control cell elongation. At the center of this regulatory circuit is a module of interacting transcription factors, including the BR-activated BZR1 family transcription factors, the auxin response factor 6 (ARF6), the phytochrome-interacting factors (PIFs), and the GA-sensitive DELLA proteins. BZR, ARF, and PIF factors act cooperatively to promote cell elongation, while their DNA-binding activities are inhibited by the DELLA proteins. We named this transcriptional integrator BAP/D module, for the synergy among BZR1, ARF6, and PIFs and their antagonism by DELLA. The BAP/D module effectively explains how cell elongation is controlled by a wide range of signals: BR, auxin, and shade/darkness promote cell elongation by activating BZR1, ARF6, and PIFs, respectively, while GA does so by inducing degradation of DELLAs. Each input pathway feedback inhibits its own signal, but tends to cross-activate other hormone signals, to potentially optimize output responses. Additional signals impinge on one or more components of BAP/D to modulate growth. For example, sugar signaling through Target Of Rapamycin (TOR) stabilizes BZR1, warm temperature increase cell elongation by activating PIF4, the circadian clock controls PIF activity through both transcriptional regulation and direct protein-protein interaction with clock component TOC1, and the UV receptor UVR8 binds and inhibits BZR1. Further, all the hormone-responsive components of BAP/D are posttranslationally modified by sugars (O-GlcNAc and O-fucose). As such, the BAP/D module acts as a central molecular circuit that integrates nutritional, hormonal, and environmental signals in plant growth regulation.

Brassinosteroid Signaling in Plant Development and Adaptation to Stress

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Brassinosteroids (BRs) are plant steroid hormones essential for plant growth and development. They play key roles in cell division, elongation and differentiation of different cell types and different organs along the plant life cycle. Such understanding is gained from recent studies using mainly Arabidopsis primary root as a model system. The plant dwarfism associated to BR deficiency led to the identification of BR signaling components controlling plant growth. In growing cells, the membrane steroid receptor BRI1 binding to the ligand triggers a signal cascade in the cytoplasm that will let the transcription of BR-responsive genes in the nuclei driving major cellular responses in the plant. In special cells, such as stem cells and the vascular tissues, BRI1-like receptors BRL1 and BRL3 confer cell-specificity to the BR pathway. Our lab has just started to elucidate how the BRL3 signaling contribute to plant adaptation to drought. At the conference, I will summarize our recent advances in the area of spatiotemporal control of BR action in in plant growth and development and in plant adaptation to drought stress.

Reprogramming of hormonal metabolism in susceptible and resistant grape cultivars upon infection with Botrytis cinerea

Diana Pimentel (1), Marilia Almeida-Trapp (2), João Coelho (1), Alexander Erban (3), Flávio Soares (1), Pedro Reis (4), Cecília Rego (4), Joachim Kopka (3), Axel Mithöfer (2), **Ana Margarida Fortes** (1)
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Hormones, fatty acids and phenylpropanoids play pivotal roles in plant–microbe interactions. Infection of grapes with the necrotrophic pathogen Botrytis cinerea leads to significant economic losses worldwide. In this work, changes in hormonal, primary and secondary metabolisms in grapevine (Vitis vinifera) were compared between a susceptible (Trincadeira) and a resistant (Syrah) variety during grape ripening and upon infection with Botrytis cinerea. Peppercorn-sized fruits were infected in the field and mock-treated and infected berries were collected at green, veraison and harvest stages for hormone analysis, metabolomics and targeted qPCR analysis. Results indicate a substantial reprogramming of metabolism in response to fungal attack. High basal levels of salicylic acid (SA), jasmonates and IAA at an early stage of ripening, together with activated SA, jasmonates and IAA signaling, likely regulate a fast defense response leading to grape resistance/ tolerance towards B. cinerea. The balance among the different phytohormones seems to depend on the ripening stage and on the intra-specific genetic background and may be fundamental in providing resistance or susceptibility. On the other hand, hexacosanoic acid, epigallocatechin, and trans-4-hydroxycinnamic acid were among the compounds present in higher level in Syrah infected and non-infected berries comparing to Trincadeira and may be involved in structural and/ or biochemical defense mechanisms. Altogether, this study underlines the importance of constitutive defenses against necrotrophic pathogens and provides insights into possible strategies for conventional breeding and/or gene editing aiming at improving grape resistance against Botrytis cinerea.

Jasmonates on the move: how hormone pool redistribution govern plant acclimation responses

Adina Schulze, Marlene Zimmer, Stefan Mielke, Hagen Stellmach, Charles W. Melnyk, Bettina Hause, **Debora Gasperini**
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Multicellular organisms rely on the movement of signaling molecules across cells, tissues, and organs to communicate among distal sites. In plants, localized leaf damage activates jasmonic acid (JA)-dependent transcriptional reprogramming in both harmed and unharmed tissues, but the mechanisms and mediators involved in the transmission of such long-distance signals are not fully understood. Here, we found that following shoot wounding, the relocation of endogenous jasmonates through the phloem is essential to initiate JA signaling and stunt growth in unharmed roots of Arabidopsis thaliana. By employing grafting experiments and hormone profiling, we uncovered that the hormone precursor cis-12-oxo-phytodienoic acid (OPDA) and its derivatives, but not the bioactive JA-Ile conjugate, translocate from wounded shoots into undamaged roots. Upon root relocation, the mobile precursors cooperatively regulated JA responses through their conversion into JA-Ile and JA signaling activation. Collectively, our findings demonstrate the existence of long-distance translocation of endogenous OPDA and its derivatives, which serve as mobile molecules to coordinate shoot-to-root responses, and highlight the importance of a controlled hormone pool redistribution among organs during plant stress acclimation.

ROS but not natural auxin regulate Brefeldin A induced PIN1 internalization in root cells

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Multiple abiotic and biotic factors regulate the endocytotic activity that affects the abundance and distribution of receptors and transporters on plasma membranes. Experiments using the synthetic auxin 1-NAA have shown that endocytosis of the PIN family of auxin transporters can be inhibited by auxinic compounds. However, the most important natural auxin, IAA, showed little inhibitory activity in the absence of a supplementary antioxidant. We asked whether the low activity of IAA was related to IAA stability in the incubation solution or whether IAA interacts with antioxidants to inhibit of endocytosis. We monitored IAA stability in the incubation solution, using a DR5 reporter to estimate the loss of auxin activity over time, finding that IAA is both stable and active. We were therefore unable to explain the low ability of IAA to inhibit endocytosis by IAA degradation. Furthermore, when applied in the absence of auxin, antioxidant butylated hydroxytoluene (BHT) caused an increase in the internalization rates of both PIN1 and PIN2; this increase was unaffected by the simultaneous application of IAA, further indicating that endocytosis is not inhibited by the natural auxin IAA under physiologically relevant conditions. Analysis of BHT activity shown that PIN1 circulation is regulated by ROS.

Cytokinin N-glucosides and their parts in evolution and biology of the family of cytokinins

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Since their discovery over forty years ago, cytokinin (CK) N-glucosides have been mostly overlooked as irreversibly inactive members of the family of CKs. Our findings, however, argue against their general image as irreversible CK forms lacking biological activities. We have found (1) a widespread distribution of CK N7- and N9-glucosides across the plant kingdom with distinct representation in the total CK pool increasing from lower (evolutionary older) to higher (evolutionary younger) plants, (2) their changing levels as well as expression of CK-N-glucosyltransferase UGT76C1 and UGT76C2 genes during Arabidopsis ontogenesis, (3) obvious physiological activities when exogenously applied to some model plants and (4) noticeable metabolic conversions in plant tissues differing between N7- and N9-glucosides and depending on the particular parent compounds. Based on these findings, CK N-glucosides seem to be more prevalent and more relevant to CK biology being involved in CK evolution and having some unique function(s) in plants. The involvement of CK N-glucosides in evolution and biology of CKs suggests that these long-ignored compounds merit further investigation and will be discussed at the conference. [Funded by Czech Science Foundation (19-12262S)].

Development of a genotype-independent high-throughput system for accelerated breeding innovations in sugar beet

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Sugar beet is one of the most important industrial crops in terms of sugar production in Europe. The application of new breeding technologies requires efficient in vitro protocols to regenerate sugar beet plants from isolated guard cell protoplasts. However, in sugar beet this is strongly genotype-dependent and results in low regeneration frequency in a number of cultivars. We have developed a high-throughput screening system which allows to quantify proliferation rates of immobilized guard cell protoplasts. Our method enables high-throughput screening of different media components resulting in the identification of regulators triggering proliferation reprogramming. Several chemicals were identified overcoming recalcitrance and inducing proliferation of non-responsive sugar beet genotypes. The success of this strategy opens up applications for other recalcitrant crops with high agronomical value.

JAR1-mediated drought tolerance mechanisms during different developmental stages in Arabidopsis thaliana

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Jasmonic acid (JA) and its receptor-active derivatives (bioactive JAs) regulate a range of biological processes including defense against biotic and abiotic stresses. The most biologically active form is JA-isoleucine conjugate (JA-Ile), which is formed from (+)-7-iso-JA by JAR1 (Jasmonate Resistant 1). While the biotic stimulation of JA signaling has been quite well described, experimental data on the regulation of JAR1 during development and/or abiotic stresses such as water deficiency are lacking. We thus performed studies in wild type Arabidopsis, a loss of functions mutant (jar1) and a gain of function JAR1-OE line (35S::JAR1) under control and drought stress conditions in the reproductive and vegetative stages. We analyzed hormonal contents, gene expression through RNA-seq and corresponding phenotypic traits including stomata regulation by cytosol specific redox and Ca2+ signaling using ratiometric biosensors. JAR1-OE lines showed a stunted growth of the shoot compared to wild type whereas jar1 showed narrow but longer leaf sizes and early flowering. Upon drought stress, JAR1-OE plants displayed a higher leaf water content, smaller stomatal aperture and enhanced tolerance under drought stress conditions than the wild type plants. In contrast, jar1 mutants were hypersensitive to drought. Under these conditions, the levels of JA-Ile were significantly higher in both wild type and JAR1-OE lines, while jar1, as expected, was unable to increase JA-Ile content. Interestingly, we also observed an increase of general bioactive JA content in the bolting stage (flower bud initiation) compared to vegetative stages in the wild type plants independent on stress conditions. qPCR analysis showed that JA signaling genes, JAR1 and VSP1, were also up-regulated during the reproductive stage as well as under drought stress conditions but more detailed data will be obtained from the RNA-seq analyses. Form these findings, we conclude that JAR1 plays a central role in the drought tolerance mechanism by increasing JA-Ile content in the bolting stage of the plant.

Modern chemical approaches to understanding indole-3-acetic acid biosynthesis

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Recent advances in analytical instrumentation have opened up new avenues for very rapid and comprehensive analysis of the flow of stable isotopic labels from early intermediates (anthranilate, indole, serine, tryptophan) throughout the indole metabolome. We utilize a simple yet powerful liquid chromatography–high resolution-mass spectrometry (LC-HR–MS) based method for the facile characterization of the small indolic metabolite profiles of plants. The method uses the well-known quinolinium ion (m/z 130.0651) and its isotopomers generated in the MS processes as a signature with high mass accuracy that can be used to screen plant extracts for indolic metabolite allowing short (30 second) as well as longer tracing times. Rapid analysis, coupled with a large and expanding chemical library of inhibitors of tryptophan synthase, TAA, and YUCCA as well as environmental manipulations now allows the flow of carbon through these pathways to be measured and compared.

Anchorene and Zaxinone, Two Novel Carotenoid-Derived Growth Regulators

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Mutant analysis and application of chemical inhibitors of carotenoid biosynthesis suggest the presence of yet unidentified carotenoid-derived regulatory metabolites, apart from the known hormones abscisic acid and strigolactones. This presentation describes the discovery of two novel carotenoid-derived growth regulators and their role in different aspects of plant's life. The first one, anchorene, is a short chain isoprenoid-dialdehyde that acts as a specific signal required for the outgrowth of anchor roots, the less investigated root type in Arabidopsis. We identified anchorene by testing the effect of known and presumed carotenoid cleavage products on Arabidopsis root growth/architecture, and confirmed its presence as a natural metabolite. Furthermore, we showed that the formation of anchor roots is a carotenoid-dependent process which can be triggered by exogenous anchorene application to carotenoid-deficient mutants. Using auxin-reporter lines and RNAseq studies, we demonstrated that anchorene promotes the formation of anchor roots by modulating auxin homeostasis. The second one is zaxinone, a carotenoid metabolite that is formed in rice by a specific clade of the plant carotenoid cleavage dioxygenases represented by the zaxinone synthase (ZAS). A rice loss-of-function mutant (zas) shows growth retardation, low-tillering phenotype and contains higher levels of strigolactones. Exogenous application of zaxinone rescued mutant's phenotypes and increased root growth in wild-type seedlings, indicating the role of zaxinone as an important regulatory metabolite that affects hormone homeostasis and is required for normal rice growth.

SAM organogenic activity and vascular system development in the pin1 mutant of Arabidopsis are determined by ontogenetic changes in auxin biosynthesis and transport pathway

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The shoot apical meristem (SAM) activity is responsible for two interrelated processes: organogenesis and vascular differentiation. Research has shown that both processes are regulated by PIN1-dependent polar auxin transport (PAT). The fact that none of these two processes is completely blocked by the inhibition of PAT, by the mutation in the PIN1 gene nor by chemical inhibitors treatment, prompted us to search for alternative mechanisms that participate in their regulation. Our research proved that pin1 mutants of Arabidopsis use additional sources of auxin to drive organogenesis and vascularization: acropetal auxin transport in vascular strands and local biosynthesis of auxin in the organogenic zone of the SAM. Interestingly, we also revealed that the way, in which vascularization proceeds depend on the auxin source and transport pathway.
Funding: National Science Centre, grant No. 2014/15/B/NZ3/00858

A tale of two hormones: ethylene and auxin in plant growth

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The gaseous hormone ethylene plays a key role in plant growth and development, and is a major regulator of stress responses. It inhibits vegetative growth by restricting cell elongation, mainly through crosstalk with auxins. However, it remains unknown whether ethylene controls growth throughout all plant tissues or whether its signaling is confined to specific cell types. We employed a targeted expression approach to map the tissue site(s) of ethylene growth regulation. The SCF-EBF E3 ubiquitin ligases EBF1 and EBF2 target the degradation of EIN3, the master transcription factor in ethylene signaling. We coupled EBF1 and EBF2 to a number of cell type-specific promoters. Using phenotypic assays for ethylene response and mutant complementation, we revealed that the epidermis is the main site of ethylene action controlling plant growth in both roots and shoots. Suppression of ethylene signaling in the epidermis of the constitutive ethylene signaling mutant ctr1-1 was sufficient to rescue the mutant phenotype pointing to the epidermis as a key cell type required for ethylene-mediated growth inhibition. Cross-talk with the auxin pathway, forming a reciprocal loop, will be discussed.

Model based crop improvement

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Recent advances in crop genomics, breeding, and phenotyping open an opportunity for application of an integrated model-based approach to dissect crop phenotypes to their underlying genetic basis, enumerate beneficial alleles segregating in populations and to understand how initial domestication and subsequent diversification happen. Here I will present two case studies featuring how such an approach can be used for chickpea improvement.

Exposure to ionizing radiation disturbs the hormonal balance in Arabidopsis thaliana plants

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The Chernobyl and Fukushima nuclear accidents released a large amount of radionuclides, leading to large-scale radioactive contamination. Field studies in both areas showed that ionising radiation (IR) induced morphological abnormalities in pine trees which seem to resemble loss of apical dominance. Exposing Arabidopsis thaliana plants to IR in lab conditions also resulted in morphological abnormalities with multiple flowering stems and signs of fasciation. The mechanisms behind those abnormalities in plants have not been elucidated. Therefore, A. thaliana plants were exposed during 2 weeks to different dose rates of IR after which a transcriptomic profiling was carried out using RNAsequencing. A general observation was the enrichment of GO terms related to the metabolism of hormones such as jasmonic acid, auxins and cytokinins. To get more insight into the mechanisms, the levels of phytohormones were quantified. Results indicate significant changes in the levels of auxins, cytokinins and jasmonates after irradiation. The possible influence of those changes on plant development will be further investigated.

Role of the ER in Controlling Nuclear Auxin Uptake and Function

Alistair M. Middleton[1], Cristina Dal Bosco[2], Phillip Chlap[3], Robert Bensch[3], Ken-ichiro Hayashi, Rainer Uhl, Olaf Ronneberger[3], Christian Fleck[7], Alexander Dovzhenko[2], **Klaus Palme**[1,2,5,7]
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Auxin acts as a master regulator of developmental processes and environmental responses by mediating signal transduction into transcriptional programs and triggering the degradation of Aux/IAA transcriptional repressor proteins in the nucleus. However, the question whether and how auxin movement between the nucleus and the surrounding compartments is regulated remain elusive. We were able to show that diffusion of a fluorescent auxin analog into the nucleus is restricted. We then applied an innovative pipeline consisting of advanced microscope prototypes, image segmentation and artificial intelligence driven computation pipeline to analyze the behavior of thousands of single cells in response to auxin. By combining mathematical modeling with time course assays on auxin-mediated nuclear signaling and quantitative phenotyping in single plant cell systems, we showed that ER-to-nucleus auxin flux represents a major subcellular pathway to directly control nuclear auxin levels. Our findings propose that the homeostatically regulated auxin pool in the ER and ER-to-nucleus auxin fluxes underpin auxin-mediated downstream responses in plant cells.

Tissue-specificity in hormonal regulation of plant thermomorphogenesis

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Plant hormones are essential coordinators of phenotypic plasticity in response to environmental and endogenous signals. Elevated ambient temperatures have been shown o profoundly affect various aspects of plant growth and development. An early response to warm temperature can be observed in young seedlings which respond with increased elongation of petioles, hypocotyls and roots.
On the molecular level, shoot thermomorphogenesis has been shown to involve numerous light signaling components that trigger a successive action of auxin and brassinosteroids which show differential tissue-specificity in their mode of action. Furthermore, root thermomorphogenesis seem to be governed by signaling components that are partially distinct from shoot temperature signaling.

High-content screening for improved understanding of growth regulators for plant cell proliferation and embryogenesis

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Plant growth regulators influence the growth and differentiation of plant cells. These chemicals are capable of reprogramming the cellular fate. Tracking the effects at single-cell level is more informative over the analysis at population, tissue or organ levels. Single-cell studies can provide mechanistic insights and functional changes incurred by the chemicals. In this regard, we have established a high-content screening pipeline suitable for various plant cells (protoplasts; microspores) in different plant species. We present data on high-content screening to identify new regulators to break the recalcitrance or to enhance the proliferation frequency. We tested various plant hormones and validate the efficacy of 2,4-D (an auxin) in promoting the microcalli formation. We present the data on redox-active reagents that promote cell proliferation and are sufficient to induce microcalli formation even in the absence of 2,4-D. These systematic screens at single-cell resolution provide deep insights into the mechanisms involved in determining cellular dedifferentiation.

Insights into the PIN protein complex

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The regulation of cellular auxin efflux controls the rate, direction and localization of plant growth. Although auxin efflux transporters can be found in diverse protein families, the PINs have been most regularly associated with the establishment and maintenance of instructive auxin maxima. PINs are regularly observed in polar plasma membrane domains, but little is known about the local protein environments of active PIN proteins in the plasma membrane, or the protein-protein interactions which direct them there. We have used a range of biochemical techniques to show that PINs are found in 350KDa protein complexes which contain a PIN hetero- or homodimer at their core. This central unit, the PIN core complex, is the smallest unit which retains the capacity for cellular auxin efflux. Heterologous expression of PIN proteins in mammalian cells is not sufficient for stable dimer assembly, but dimers are recovered after treatment with flavonols, natural auxin efflux inhibitors, or NPA, their synthetic anolog. The ability of NPA to inhibit lateral root formation is lost when plants expressing antibody fragments which inhibit PIN dimer assembly are treated with the chemical. This has led to the hypothesis that dimerization equilibria favour PIN proteins being held in an inactive state. Proteins with diverse functions and localizations also interact with the PIN complex. A series of knock-out plants which lack these proteins have been constructed, and display partially overlapping phenotypes. These phenotypes will be introduced, and the role played by the respective genes in polar PIN trafficking discussed.

The Role of Auxin in the Pattern Formation of the Asteraceae Flower Head (Capitulum)

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Natureoften creates complex structures by rearranging pre-existing units. One such example is the flower head (capitulum) in daisies, where a group of flowers (florets) and phyllaries (modified bracts) are arranged to superficially mimic a single flower. The capitulum is a key taxonomical innovation that defines the daisy family (Asteraceae), the largest flowering plant group. However, patterning mechanisms underlying its structure remain elusive. Here, we show that auxin, a plant hormone, provides a developmental patterning cue for the capitulum. During capitulum development, a temporal auxin gradient occurs, regulating the successive and centripetal formation of distinct florets and phyllaries. Disruption of the endogenous auxin gradient led to homeotic conversions of florets and phyllaries in the capitulum. Furthermore, auxin regulates floral meristem identity genes, such as Matricaria inodora RAY2 and M. inodora LEAFY, which determine floret and phyllary identity. This study reveals the mechanism of capitulum patterning and highlights how common developmental tools, such as hormone gradients, have independently evolved in plants and animals.

Iodosalicylates, iodobenzoates and plant-derived thyroid hormone analogs in lettuce plants

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According to the literature on plant hormones and regulators little is known on the potential synthesis and role of iodosalicylates (ISA), iodobenzoates (IBeA) and plant-derived thyroid hormone analogs (PDTHA) in plants. The results of our study demonstrated the presence of various iodobenzoic (IBeA) and iodosalicylic acids (ISA) such as: 5-iodosalicylic acid (5-ISA), 3,5-diiodosalicylic acid (3,5-diISA), 2-iodobenzoic acid, 4-iodobenzoic acid, 2,3,5-triiodobenzoic acid in lettuce plants. The presence of iodotyrosine (I-Tyr) and PDTHAs: triiodothyronine (T3) and thyroxine (T4) was also confirmed. PDTHAs are probably synthesized mainly in the roots and are further transported to the leaves. Benzoic and salicylic acids are the likely precursors for the synthesis of all analyzed ISAs and IBeAs. 5-ISA is converted to 3,5-diISA, which together with I-Tyr forms T3, T4 or other PDTHAs. It has been found that exogenous 5-ISA and 3,5-diISA as well as inorganic KIO3 can stimulate PDTHA synthesis in lettuce plants. it should be mentioned that in agricultural practice, biofortification of plants in iodine increases the content of organic iodine compounds in plants. This can have a positive effect on the consumer's organism.
This research was financed by the NCN, Poland (grant UMO-2017/25/B/NZ9/00312).

Effect of abscisic acid on global redox proteome of Arabidopsis thaliana

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Abiotic stress perception in plants is closely linked to the production of reactive oxygen species (ROS), which act as important signal molecules. These reactive species interact with cysteine containing amino acids and modify protein thiols which play important roles in regulation of diverse protein functions, including their enzymatic activities, stability and protein-protein interactions. Identification of the protein targets of redox modification is crucial to understanding their role in plant stress responses. We have utilized recent technical advances in detection of redox modifications coupled with MS-based proteomics platforms to analyze global changes in redox status of proteins in response to abscisic acid (ABA) as a proxy for abiotic stress response in Arabidopsis thaliana. ABA caused massive changes in the redox status of more than 900 proteins in Arabidopsis. Proteins involved in both primary and secondary metabolism, proteins stability, photosynthesis and cell wall synthesis showed significant changes in their oxidation status in response to ABA. Similarly, proteins involved in signaling, hormone biosynthesis and lipid signaling and metabolism also exhibited significant changes in their ABA-dependent redox status. Interestingly, for many of these proteins, the transcript levels of their corresponding genes or the overall protein abundance did not change in response to ABA, suggesting that changes in their oxidation status is important for their role in response to abiotic stress. Analysis of the redox sensitive proteins related to photosynthesis suggests the role of energy rebalancing mechanisms in plant stress responses.

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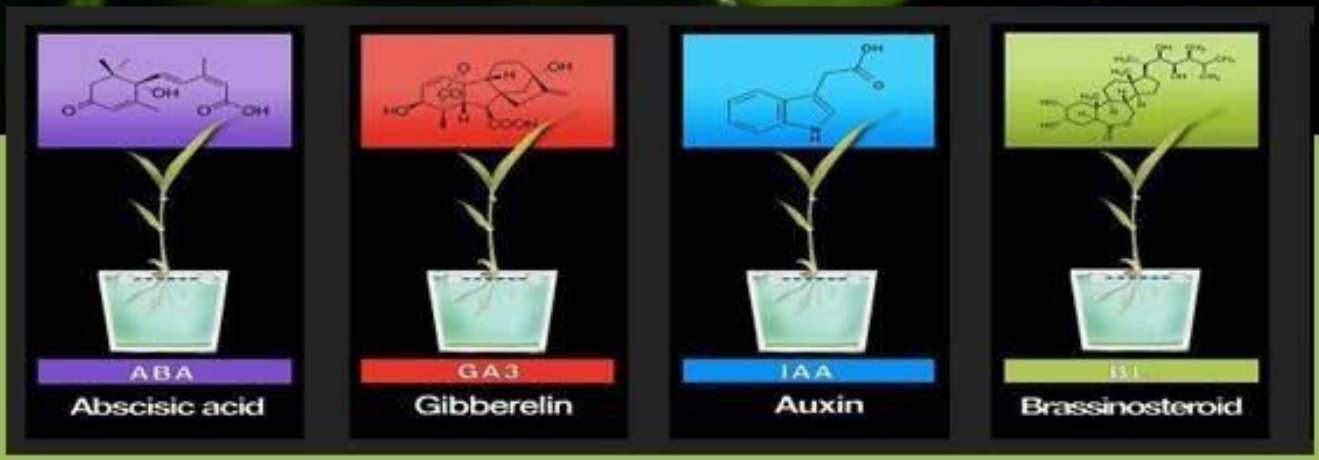

Poster №1:

In vivo and Ex vivo Magnetic Resonance Spectroscopy (MRS) for the measurment of GABA and Glutamate functions in the root system

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For their survival, plants depend on a growth pattern that is adaptive to their surroundings and is regulated by various growth hormones. Under the ground, this growth pattern is manifested in a plastic response of the root system. Together with the well-known growth hormones (Auxin and Cytokinin), other secondary metabolites (e.g., Ethylene and Abscisic acid) act Eo ipso as growth hormones. Together, they form an intricate regulation network that controls the plant growth pattern. Interestingly, most of the known classical neurotransmitters, i.e., molecules that operate for the advancement of plastic response mechanisms in animals' central nervous system, also operate as part of this intricate growth regulation network. Recently, we initiate a project to utilize magnetic resonance spectroscopy (MRS), a measurement technique that is key to biomedical research but is rarely used in plant research, to study the function and interaction pattern of native plant neurotransmitter molecules. We concentrate on the root system characterization of GABA and Glutamate, the most abundant neurotransmitters of animals. For the study, we are developing an MRS receiver coils for in vivo and ex vivo measurements using the most advanced MR scanners that are used in chemistry and biomedicine. Our research will pave the way to understanding the functions of these molecules in the root system, and on a broader level, for the understanding of general plasticity principles across biological kingdoms.

Poster №2:

Effects of aminophenol on photosynthesis and chlorophyll fluorescence of lettuce

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The effect of different doses of aminophenol (0, 5 µM, 50 µM, 500 µM, 5 mM) in the acute (1x application) and chronic (regular application) variants on the photosynthesis rate (Pn) and chlorophyll fluorescence of lettuce was studied in a greenhouse experiment over the course of 40 days. The obtained results show that with increasing concentration of aminophenol in both application variants the Pn and chlorophyll fluorescence decreases in comparison with control plants. In the event of an acute paracetamol effect, the Pn is reduced by the control (6.03 µmol CO2/m2/s) and 5 mM (4.89 µmol CO2/m2/s). In chronic effects of medicines on the Pn, depending on the variant. The Pn in the control plants was 6.02 µmol CO2/m2/s and at the highest concentration of aminophenol was 4.91 µmol CO2/m2/s. Also, the chlorophyll fluorescence, as determined by Fv/Fm, decreased after treatment with aminophenol. In lettuce plants growing in acute medicines treatment, fluorescence was in control plants 0.827 and at the highest medicines concentration 0.758 In chronic aminophenol treatment, the Fv/Fm interval was from 0.827 (control) to 0.736 (5 mM).

Poster №3:

Strigolactone- and nitric oxide-mediated changes in root architecture of Arabidopsis thaliana

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Both nitric oxide (NO) and strigolactone (SL) are growth regulating plant signals.
Beyond the wild-type (WT) Arabidopsis thaliana, S-nitrosoglutathione reductase (GSNOR) deficient gsnor1-3, GSNOR overproducer 35S:FLAG-GSNOR1, SL deficient max1, max2-1 and max2-2 mutants were examined. We compared root growth parameters and reactive nitrogen species levels were also detected, moreover the expressions of NO-associated (NIA1, NIA2, GSNOR1, GLB1, GLB2) as well as SL-associated (CCD7, CCD8, MAX1, MAX2, D14) genes were analysed. We found differences in NO and SNO levels of the mutant lines and were able to partly explain these changes by differences in expressions of NO- and SL-associated genes. For instance, in max2 mutants enhanced endogenous NO/SNO levels were accompanied by down-regulation of NIA and GLB genes and low GSNOR1 protein amount compared to the WT. The results indicate signal interplay between NO and SL in the regulatory network of Arabidopsis root development. This work was supported by National Research, Development and Innovation Fund (NKFI-6, K120383) and UNKP-19-3 New National Excellence Program of Human Capacities.

Aminooxyacetic acid (AOA) suppresses SI -induced programmed cell death (PCD) in self-incompatible Petunia hybrida L. pollen tubes

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Petunia hybrida L. is characterized by a Solanaceae type SI in which self pollen is rejected by S-RNAse being expressed by pistil as result of its cytotoxic function. Despite numerous attempts to understand the mechanism of S-RNAse-based SI it remains just incompletely studied. The involvement of the hormonal regulation in SI mechanism is the finding observed by us for the first time (Kovaleva and Zakharova 2003) and allowed to conclude that ethylene is the factor required for pollen tube growth. Recently we have demonstrated the presence of PCD markers, such as DNA fragmentation, in growing in vivo self-incompatible pollen tubes during the passage of the SI mechanism as well as possible involvement of hormonal regulation in the its action (Kovaleva et al. 2019). Preliminary treatment of stigmas with AOA, inhibitor of ACC synthesis, led to stimulation of pollen tubes growth when the latter did not exhibit any hallmarks of PCD. These data argue in favor of assumption that ethylene controls the passage of PCD in incompatible pollen tubes in the course SI functioning.

The content of phytohormones in the mesophyll and the leaf conducting system, depending on its age and ontogenesis phase of Solanum tuberosum

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We studied the distribution of endogenous phytohormones, namely zeatin, IAA and ABA in different parts of the leaf, depending on their age and phase of plant ontogenesis. The hormone content was determined by enzyme immunoassay. The analysis of the localization of hormones in different leaf tissues revealed the specifics of their distribution. The zeatin content in the leaf mesophyll was much higher compared to the central vein and petiole. With increasing leaf age, the content of zeatin decreased, while the decrease in the leaf mesophyll was more significant than in its conducting system. In contrast cytokinins, the number of IAA in the central vein+petiole system significantly exceeded the IAA content in leaf mesophyll. In younger leaves, both mesophyll and the central vein with a petiole contained more IAA compared to the leaves of the lower tier. The distribution of ABA in different parts of the leaf is opposite to zeatin and similar to IAA. In contrast phytohormone-stimulants, the content of ABA increased with increasing calendar age of the leaves. In the process of plant ontogenesis, the content of zeatin (3 times) and, especially, IAA (10 times) in the leaf mesophyll decreased significantly compared to its conducting system, respectively, of cytokinins - 2 times, and auxins - 4 times. Features of the mapping of hormones within the leaf are discussed in connection with the transport of assimilates.

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