



International Conference

Plant Development: Systems Approach

Programme and Abstracts

Vienna, Austria

June 28 – 29, 2019

Organizing Committee

Local Organizing Committee	International Organizing Committee
Alisher Touraev (Austria, VISCEA) Klaus Palme (Germany)	Klaus Palme (Co – Chair of the Conference) Jan Traas Hiroyuki Nonogaki Stephan Wenkel Pascal Ratet Keith Lindsey Ji-Young Lee Annette Becker Stefan de Folter Benoit Menand Philippe Gallusci

SPONSORS AND EXHIBITORS OF THE CONFERENCE



PhytoTech
LABS



BERTHOLD

REGENT INSTRUMENTS INC.



Our company is committed to deliver high performance image analysis systems with advanced technology for researchers and specialists who study trees and plants.

Each system performs precise measurements and analyses of a specific part of plant (e.g. roots, leaves, seeds, tree rings or wood cells)

or a specific application (e.g. Arabidopsis seedlings or forest canopy). A system includes a dedicated software program and a high quality scanner or digital camera that can produce well contrasted images. Analyses are done easily by the software due to its specialized built-in knowledge. For instance, root overlap at forks and tips are taken into account to provide accurate measurement of root length and area by WinRHIZO™ software.

Software programs come in different versions to meet users' needs. With clients in over 91 countries, our software programs are improved and updated regularly to comply with different needs and new trends in plant science all over the world. Lower versions can be upgraded at anytime.

Scanners are calibrated permanently using extremely precise standards. The calibration is automatically used by our software to produce accurate measurements and analyses. Some systems come with accessories that make scanning faster and easier especially with washed roots. An additional lighting system is used to eliminate shadows around thick samples such as needles, seeds and roots.

Installation requires a PC computer with operating system Windows Vista, Windows 7, Windows 8 or Windows 10.

www.regentinstruments.com for more details on plant morphological measurements, and tree-ring and forest canopy analysis. Various applications using color analysis, such as insect and disease damage quantification, are also presented. **sales@regentinstruments.com** for questions and orders.

Welcome to the 2nd International Conference on “Plant Development: Systems Approach”!

Plant development is the process by which structures originate and mature as a plant grows. Over the past couple of decades, the plant developmental biology has primarily focused on the nano scale, with the goal of identifying the molecular players underlying the core processes of development. Now the field is moving on to understanding the properties of the dynamic systems driven by these molecular players.

The **International Conference on “Plant Development: Systems Approach”** to be held on June **28-29**, 2019, in Vienna, Austria will discuss the application of molecular approaches, the role of meristem-derived signals in patterning developing organs, cellular mechanisms of development in flowering plants etc.

Vienna is located in the heart of Europe on the banks of the Danube River, and considered as one of the most important economic, cultural and touristic large cities of central Europe. Apart from providing top science lectures, the Conference will capture the spirit of the city, thanks to the central location of the venue offering a multitude of cultural events.

This **two-day** event will provide the leading academy and industry scientists with a platform to communicate recent advances in **“Plant Development”**, and an opportunity to establish multilateral collaboration.

The **2nd International Conference on “Plant Development: Systems Approach”** will cover the following research topics:

- ***Seed Development, Dormancy and Germination***
- ***Plant Organ Development (Shoot, Root, Leaf)***
- ***Making Plant Flower***
- ***Modeling and Systems Biology of Plant Development***
- ***Plant Male and Female Gametophyte Development***
- ***Plant Zygotic and Somatic Embryogenesis and Regeneration***
- ***Hormones and Plant Development***
- ***Signaling in Plant Development***
- ***Plant Cell Fate, Totipotency, Lineage and Polarity***
- ***Epigenetics and Plant Development***

Approximately 150 participants are expected to attend this exciting scientific forum including almost 40 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)
Prof. Klaus Palme (Chair of the Conference Scientific Program)

Table of Contents

Scientific Programme	6
Abstracts of Oral Presentations	9
Abstracts of Poster Presentations	24
List of Poster Presentations	32
List of Participants	33

SCIENTIFIC PROGRAMME

International Conference “Plant Development: Systems Approach” (June 28-29, 2019)

June 28 (Friday)

08.00 - 17.00	Registration
	Opening
09.00 - 09.20	Welcome address by Alisher Touraev (Local Organizer, Austria) Welcome address by Klaus Palme (Conference Co-Chair, Germany)
	Keynote Lecture:
09.20 - 10.30	Jan Traas (France): Leaf Morphogenesis: from Morphodynamics to Morphomechanics
10.30 - 11.00	Coffee break
11.00 - 12.30:	<u>Session I: Seed Development, Dormancy & Germination</u>
<i>Chairs</i>	<i>Hiroyuki Nonogaki (USA) & Jan Traas (France)</i>
11.00 - 11.25 (+5)	Hiroyuki Nonogaki (USA): Seed Germination and Dormancy: Novel Mechanisms and Evolutionary Questions
11.30 - 11.45 (+5)	Wojciech Glinkowski (Poland): Characterization of Transport-Related Genes in Developing Pods and Seeds of Yellow Lupine (<i>Lupinus luteus</i>) Based on the RNA-Seq Analysis
11.50 - 12.05 (+5)	Modesto Berbel Cascales (Spain): NAM Genes are Involved in the Control of the Fusion and Number of Stamens in Papaveraceae Juss
12.10 - 12.25 (+5)	Mariapina Rocco (Italy): Modern Wheat Variety vs Ancient One: Germination and Development, a Focus on Gibberellin Expression
12.30 - 14.00	Lunch + Poster Session (all numbers)
14.00 - 15.30	<u>Session II: Leaf Development</u>
<i>Chairs</i>	<i>Stephan Wenkel (Denmark) & Pascal Ratet (France)</i>
14.00 - 14.20 (+5)	Stephan Wenkel (Denmark): The Shady Side of Leaf Development: The Role of the REVOLUTA/KANADI1 Module in Leaf Patterning and Auxin-Mediated Growth Promotion
14.25 - 14.45 (+5)	Pascal Ratet (France): Lotus Japonicus NOOT-BOP-COCH-LIKE1 is Essential for Nodule, Nectary, Leaf and Flower Development.
14.50 - 15.05 (+5)	Xiangnan Li (China): Induction of Cold Tolerance by Priming and Stress Memory in Crops
15.10 - 15.25 (+5)	Ismael Mazuecos Aguilera (Spain): Molecular and Functional Characterization of INAPERTURATE POLLEN1 in the Basal Eudicot <i>Eschscholzia Californica</i>
15.30 - 16.00	Coffee break
16.00 - 17.30	<u>Session III: Root Development</u>

Chairs	<i>Keith Lindsey (UK) & Ji-Young Lee (South Korea)</i>
16.00 - 16.20 (+5)	Keith Lindsey (United Kingdom): Control of Root Development in Arabidopsis
16.25 - 16.45 (+5)	Ji-Young Lee (South Korea): Systems Approach to Identify Gene Modules that Regulate Storage Root Growth and Yields
16.50 - 17.05 (+5)	Kseniia Kuznetcova (Russia): Role of CLE Peptides in Storage Root Development in Raphanus, Brassica and Beta species
17.10 - 17.25 (+5)	John Schiefelbein (USA): Single-Cell RNA Sequencing of Arabidopsis Roots
17.30 - 19.00	Welcome Reception + Poster Session (all numbers)
	Conference Dinner Party
19.00 - 22.00	Traditional Austrian food and wine, located in one of Vienna's famous 'Heurigen' Cost: 50,- EUR

June 29 (Saturday)

08.00 - 17.00	Registration
09.00 - 10.30	Session IV: Flower Development
<i>Chairs</i>	<i>Annette Becker (Germany) & Kasper van Gelderen (Netherlands)</i>
09.00 - 09.20 (+5)	Annette Becker (Germany): CRABS CLAW Acts as a Bifunctional Transcription Factor in Flower Development
09.25 - 09.45 (+5)	Kasper van Gelderen (Netherlands): Light Signaling, Root Development, and Plasticity
09.50 - 10.05 (+5)	Martina Cerise (Italy): OsFD4 Promotes Flowering in Rice by Interacting with the Florigens
10.10 - 10.25 (+5)	Milena Kulasek (Poland): Auxin Spacio-Temporal Distribution in Lupinus Luteus Pistils and Stamens during Floral Development and Abscission
10.30 - 11.00	Coffee break
11.00 - 12.30	Session V: Hormones in Plant Development
<i>Chairs</i>	<i>Klaus Palme (Germany) & Stefan de Folter (Mexico)</i>
11.00 - 11.20 (+5)	Klaus Palme (Germany): Data driven modeling reveals crucial roles of intra- and extracellular auxin flux in regulation of diverse developmental functions
11.25 - 11.45 (+5)	Stefan de Folter (Mexico): The Integration of Transcription Factor and Hormone Signaling Functions during Gynoecium Development
11.50 - 12.05 (+5)	Václav Motyka (Czech Republic): Cytokinin N-Glucosides and their Role in Control of Plant Development
12.10 - 12.25 (+5)	Natalia Tikhenko (Germany): Hormonal Stress during in Vitro Culture Stops the Postzygotic Barriers and Leads to Changes of the Program of Embryo Development in Intergeneric Hybrids of Cereals
12.30 - 14.00	Lunch + Poster Session (all numbers)
14.00 - 15.30	Session VI: Signaling & Epigenetics During Plant Development

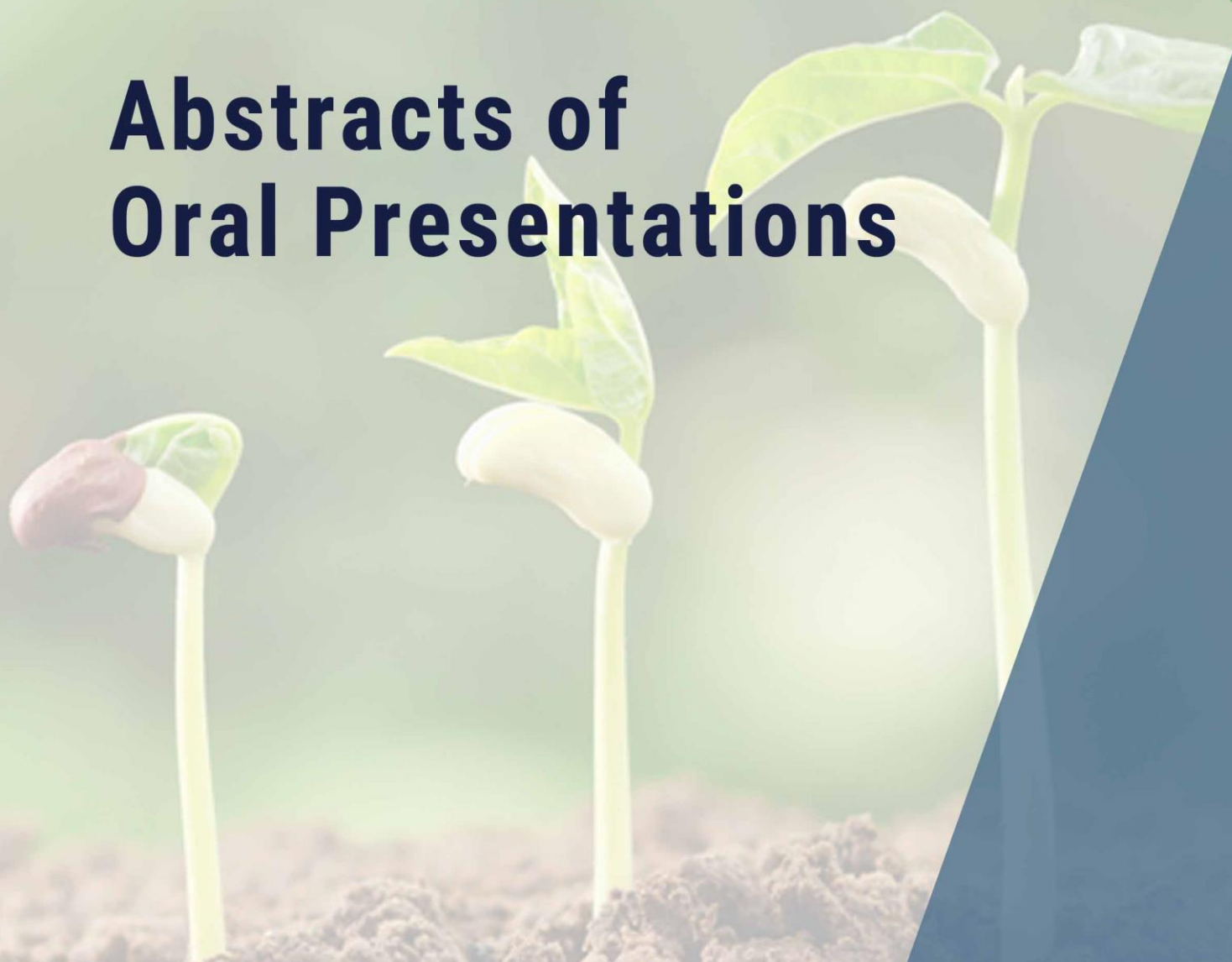
<i>Chairs</i>	<i>Benoit Menand (France) & Philippe Gallusci (France)</i>
14.00 - 14.30 (+5)	Benoit Menand (France): A Pharmacogenetic Approach to Decipher the Role of the TOR Signaling Pathway in Plant Growth and Development
14.35 - 15.05 (+5)	Philippe Gallusci (France): DNA methylation in plant development: a focus on fleshy fruits
15.10 - 15.30	<i>Closing Ceremony & Conference Photo</i>



VISCEA

Vienna International Science
Conferences and Events Association

Abstracts of Oral Presentations



www.viscea.org

Leaf morphogenesis: from Morphodynamics to Morphomechanics

Jan Traas

RDP, ENS-Lyon, 46 Allée d'Italie, Lyon, France. Correspondence to: Jan.Traas@ens-lyon.fr

Many plant species have thin leaf blades and axisymmetric elongating organs, such as stems and roots. We provide evidence that a single mechanism can account for these fundamentally different organ shapes. We show that the three-dimensional geometry of leaves is governed by microtubule alignment along predicted mechanical stress patterns along internal walls. Depending on the primary shape of the primordium, this process has the potential to amplify an initial degree of flatness, or to promote the formation of nearly axisymmetric, mostly elongating organs. This mechanism may explain leaf evolution from branches, which is alternative to Zimmermann's influential, but widely questioned, telome theory.

Seed Germination and Dormancy: Novel mechanisms and evolutionary questions

Hiroyuki Nonogaki

4017 ALS Bldg, Department of Horticulture, Oregon State University, Corvallis, USA, OR 97331. Correspondence to: hiro.nonogaki@oregonstate.edu

A series of discoveries has been made in seed germination and dormancy research. Some of them revitalized the classic story of endosperm weakening through the modification of the secondary cell walls, which is the core mechanism of seed germination in a number of species. Now, the role of primary cell wall synthesis and degradation in seed germination control, which remained elusive in the past research, is well explained by new evidence. Dormancy research has brought a breakthrough in our understanding of the hormonal regulation of germination. A unique ABA signaling pathway in seeds has been discovered and started to reveal the core mechanisms of seed dormancy. While the identification of more factors associated with seed germination and dormancy advances our understanding about seeds, it also raises questions about the evolution of seed programs, such as reserve accumulation, desiccation tolerance and dormancy. Evolutionary aspects of seed programs will also be discussed in this talk.

Characterization of transport-related genes in developing pods and seeds of yellow lupine (*Lupinus luteus*) based on the RNA-Seq analysis

Wojciech Glinkowski*, Milena Kulasek, Krzysztof Jaworski, Paulina Glazińska

1. Nicolaus Copernicus University, Faculty of Biology and Environmental Science, Torun
 2. Nicolaus Copernicus University, Center for Modern Interdisciplinary Technologies, Torun
- *Correspondence to: wglin@doktorant.umk.pl;

Yellow lupine has a great economic and agricultural importance, alongside other legume plants such as soybean or chickpea. Seeds of *Lupinus luteus* have a relatively high protein and lipid content, coupled with good amino acid profile, which makes them a valuable nutrient source. The RNA-Seq transcriptome analysis of pod walls and seeds revealed many differentially expressed genes involved in the transport of carbohydrates and amino acids. Genes responsible for accumulation of oils and proteins were also differentially expressed across different stages of development. Moreover, many sequences responsible for phytohormone and nitrate trafficking were also identified, which might suggest a crosstalk between hormone homeostasis and seed filling. These preliminary results might shine a new light into regulation of both pod and seed development from a perspective of nutrient availability, transport and storage.

This study was financed by NCN grant Sonata nr 2015/19/D/NZ9/03601.

NAM genes are involved in the control of the fusion and number of stamens in *Papaveraceae* Juss

Berbel Cascales, M., Romero García A.T., Becker, A., Mazuecos Aguilera, I., Dommès, A.B.2., Ben-Menni Schuler, S., Fernández Fernández, M.C., Suárez Santiago, V.N.

Department of Botany, University of Granada. Institute of Botany, Justus-Liebig University Giessen. Department of Cell Biology, University of Granada. Correspondence to: mberbel@ugr.es

Papaveraceae show very different configurations of androecium. *Papaveroideae* androecium has numerous free stamens, while in *Fumarioideae* it is formed by six stamens arranged into two bundles of three fused stamens. We conducted a comparative functional study by Virus-Induced Gene Silencing (VIGS) of the NO APICAL MERISTEM (NAM) genes, belonging to the NAC transcription factors in *Eschscholzia californica* (*Papaveroideae*) and *Cysticapnos vesicaria* (*Fumarioideae*). 47% of the analyzed flowers in *C. vesicaria* showed unfused or partially unfused stamens, and often stamens were fused to gynoecium, and gynoecium malformation were observed. This suggests a function of NAM genes in stamen fusion of *C. vesicaria*. In contrast, stamen number but not fusion was affected when the two NAM paralogs were silenced in *E. californica* indicating functional divergence of NAM genes in *Papaveroideae* and *Fumarioideae*. In addition, we will present our latest results on phylogeny, expression, and function of NAM genes in *C. vesicaria* and *E. californica* to understand their role in stamen organization.

Modern wheat variety vs ancient one: germination and development, a focus on gibberellin expression

Mariapina Rocco*, Marco Racioppi, Giuseppe D'Antona, Mauro Marra

1. University of Sannio, Science and Technology Department, Benevento, Italy
2. Department of Biology, University of Tor Vergata, Rome, Italy. Correspondence to: rocco@unisannio.it

Ancient wheat species have been suggested to have health benefits when compared with modern cultivars of bread and durum wheat. It is known that the modern wheat has a higher productivity but it is less healthy for human nutrition and respond worse to stress compared with ancient one. Moreover, in unfavorable conditions the ancient varieties of wheat have shown a greater germinal power. Germination and development involves the coordinated regulation of several genes and the control of hormone levels. In aleurone cells, a set of genes show increased expression at the RNA and transcriptional level in response to gibberellic acid. Bioactive gibberellins (GAs) are diterpene phytohormones that modulate seeds germination and growth of the plant. In this work, we decided to carry out a differential analysis of an ancient wheat cultivars and the modern variety during the early stages of germination and development. A comparison of the corresponding germination performances, hormone level variations, protein changes representation, was performed. In particular, we focused on genes expression involved in the biosynthetic pathway of GAs to valuate which kind of genes are more up or down regulated.

The shady side of leaf development: the role of the REVOLUTA/KANADI1 module in leaf patterning and auxin-mediated growth promotion.

Stephan Wenkel

University of Copenhagen, Denmark. Correspondence to: wenkel@plen.ku.dk

Leaves are present in all land plants and are specialized organs for light harvesting. They arise at the flanks of the shoot apical meristem (SAM), and develop into lamina structures that exhibit adaxial/abaxial (upper/lower side of the leaf) polarity. At the molecular level, an intricate regulatory network determines ad-/abaxial polarity in *Arabidopsis thaliana* leaves, where the Class III Homeodomain Leucine Zipper (HD-ZIPIII) and KANADI (KAN) proteins are key mediators. The HD-ZIPIII REVOLUTA (REV) is expressed in the adaxial domain of lateral organs, whereas KAN1 is involved in abaxial differentiation. The REV/KAN1 module directly and antagonistically regulates the expression of several genes involved in shade-induced growth and auxin biosynthetic enzymes.

Lotus Japonicus NOOT-BOP-COCH-LIKE1 is Essential for Nodule, Nectary, Leaf and Flower Development.

Pascal Ratet

Institut des Sciences des Plantes de Paris Saclay, France, IPS2, BATIMENT 630 PLATEAU DU MOULON, RUE NOETZLIN, CS 80004, 91192 GIF SUR YVETTE cedex. Correspondence to: pascal.ratet@cnrs.fr

The NOOT-BOP-COCH-LIKE (NBCL) plant genes are orthologs to the Arabidopsis thaliana BLADE-ON-PETIOLE1/2. NBCLs are key developmental regulators essential for plant shaping mainly throughout the regulation of organ boundaries, the promotion of lateral organ differentiation and the organ identity acquisition.

We have studied in details the role of the LjNBCL1 gene in *L. japonicus* development. Our study unveiled exciting and original new findings concerning the roles of this gene in *L. japonicus* vegetative and reproductive development (Magne et al., *Plant J.* 94(5): 880-894 2018).

The LjNBCL1 gene is involved in the determinate symbiotic nodule identity and plays a major role in *L. japonicus* secondary inflorescence meristem initiation and development and thus in the promotion of the floral meristem fate determinacy. In the Ljnbcl1 mutants, 13% of the leaves had an additional leaflet relative to *L. japonicus* GIFU, suggesting that LjNBCL1 contributes to leaf patterning. The Ljnbcl1 mutant is also drastically impaired in flower formation leading to severe sterility and one astonishing structure formed instead of flowers is a single fused trumpet-like organ replacing the 21 Lotus floral organs. This work proves in addition the evolutionary ontology existing between stipule and nectary glands since nectary gland development is abolished in the Ljnbcl1 mutant.

Control of root growth in Arabidopsis

Keith Lindsey

Department of Biosciences, Durham University, UK, Durham , DH1 3LE. Correspondence to: keith.lindsey@durham.ac.uk

Plant development contrasts with animal development by exhibiting a high degree of flexibility (plasticity), in which final form is unpredictable. This plasticity represents a mechanism for responding to environmental change, such as variations in availability of water, nutrients, light, or attack by herbivores. While animals respond to such environmental challenges through behavioural change, plants use plasticity in development to adapt and survive, and this is mediated to a significant extent through the activity of meristems and control of cell elongation. In this talk I will present some of our work on the genetic and signalling mechanisms, and in particular the crosstalk between ethylene, auxin and cytokinin, that control meristem activity and cell elongation and regulate growth during root development in Arabidopsis. I will describe a proposed molecular mechanism by which the POLARIS peptide regulates ethylene receptor function in the Arabidopsis root, and the use of mathematical modelling to predict signalling-gene interactions.

Induction of cold tolerance by priming and stress memory in crops

Xiangnan Li

Northeast Institute of Geography and Agroecology, Chinese Academy of Sciences, Shengbei RD 4888, Changchun, China. Correspondence to: lixiangnan@iga.ac.cn

Cold is one of the major environmental factors limiting plant growth and development. The increased climatic variability and more frequent episodes of extreme conditions also result in plants being exposed to not only one single cold event but also multiple abiotic stresses at different periods. Although the abiotic stresses occurring at different stages result in a higher risk of injury, earlier stress events may prime the plant to protect it against later stresses. A large body of evidence has shown that a previous exposure to different types of stress can affect the subsequent responses and eventually prepare the plants to more quickly or actively respond to future stresses. Cold stress tolerance in plants involves diverse and multiple physiological and molecular mechanisms. Priming and stress memory are key processes, by which plant may increase the tolerance to subsequent drought events. Stress memory involves multiple modifications at physiological, proteomic, transcriptional levels and epigenetic mechanisms. We summarized recent advancements in physiological, biochemical, and molecular studies related to drought priming and its effect on drought tolerance in plants. The mechanisms of drought stress memory and the possible priming induced cross-tolerance to other abiotic stresses are discussed. As one of main focuses in plant-abiotic stress research, studies on plant drought priming and stress memory is still rare. To date, most of results on plant drought priming were obtained in controlled lab experiments, which might be different from the natural conditions. Thus, in future studies, a combination of experiments from controlled lab evaluations with observations and simulation under field conditions should be performed. Collectively, to further understanding the processes and mechanisms of priming effects, eco-physiologists and molecular biologists should work together to reveal the complete regulation network at different levels and scales, such that management strategies could be developed to sustain crop prod.

Molecular and functional characterization of INAPERTURATE POLLEN1 in the basal Eudicot *Eschscholzia californica*

Mazuecos-Aguilera, I., Berbel-Cascales, M., Ben-Menni Schuler, S., Fernández-Fernández, M.C.1, Romero-García, A.T., & Suárez-Santiago, V.N.

Department of Botany. University of Granada. Correspondence to: ismaag@ugr.es

The apertures of the pollen grain perform a significant role in pollen survival and successful reproduction. The main diversity of the angiosperm pollen grain is associated with variations in the apertural pattern. Nevertheless, little is known about the genetic determinism of the apertural system.

INAPERTURATE POLLEN1 (INP1) gene is involved in the formation and location of the aperture areas in the *Arabidopsis thaliana* pollen grains. We conducted a molecular analysis and a functional study of INP1 in the basal eudicot *Eschscholzia californica* (Papaveraceae, Ranunculales). We characterized two variants of INP1 differing in 4 amino acid residues. INP1 is expressed in all plant organs, although the highest levels of expression have been found in the stamens. During the pollen development phases, INP1 start its expression before the formation of the pollen stem cells, reaching a maximum expression at the tetrad phase. After that, expression levels are highly reduced till the mature pollen phase. INP1 silencing has resulted in inaperturate pollen grains, which validates its function in *E. californica*. This fact suggests that INP1 function is conserved in basal Eudicot lineages.

Systems Approach to Identify Gene Modules that Regulate Storage Root Growth and Yields

Goh Choe1*, **Yi Zheng2***, **Nam V. Hoang1***, **Cecilia Aliaga Fandiño1§**, **Jaeryung Hur1§**, **Zhangjun Fei2** and **Ji-Young Lee1****

1. School of Biological Sciences, Seoul National University, Seoul, Republic of Korea

2. Boyce Thompson Institute, Ithaca NY USA

*§ These authors contributed equally.

Correspondence to: jl924@snu.ac.kr

Root crops serve as very important food sources for various nutrients. Despite of their importance, very little is known about how their root growth and yield are regulated. Radish, *Raphanus sativus* L., is a major root crop closely related to *Arabidopsis*. We recently reported that the growth of radish storage tap roots is led by cell proliferation in the cambium. To understand its underlying molecular basis, we generated a compendium of tissue-specific transcriptome data using laser capture microdissection (LCM) of radish tap roots in three growth stages of two inbred lines, which display contrasting root growth and yields. From these data, we confirmed the evolutionary conservation of expression of many key factors involved in vascular cell proliferation and patterning. Furthermore, we identified cohorts of growth and stimuli responsive genes that show opposing expression dynamics between inbred lines. Interestingly, the expression of these stimuli responsive genes was conserved in *Arabidopsis* roots, prompting us to investigate their role in the cambial activity. A series of perturbation analyses in *Arabidopsis* revealed the network highly inter-wired between stimuli-responsive transcription factors and already-defined cambial regulators. Our study provides a foundation for engineering schemes of root crops with sustainable yields.

Role of CLE peptides in storage root development in Raphanus, Brassica and Beta species

Kseniia A. Kuznetcova^{*}, Irina E. Dodueva, Maria S. Gancheva and Ludmila A. Lutova

Saint Petersburg State University, Department of Genetics and Biotechnology, Universitetskaya embankment, 7/9, Saint Petersburg, 199034, Russia. ^{*}Correspondence to: kskuz95@mail.ru

This work is focused on investigation of CLE peptides role in storage root formation among agricultural plants. The objects of this study are species and varieties of Brassica, Raphanus and Beta genera contrasting in the ability to form storage roots. Histological analysis showed that an increased activity of the cambium meristem leading to an increase in the number of cambial cells and xylem elements is a main difference between varieties with a storage root and without it. According to our data, the major role in storage root formation is played by CLE19 and CLE41 genes; their expression is confined to specific root tissues and increases during the growth of storage root. Overexpression of CLE41 in wild plant species which do not form storage roots (e.g. *Raphanus raphanistrum*) led to the appearance of certain characteristics of cultivated varieties: an increase in the root diameter due to elevated cambium activity, an increase of xylem mass and also a decrease of lignified xylem elements number. We speculate that selection of plant forms which demonstrate high CLE41 expression level could play a role in the domestication of crop-root cultures with soft edible storage root and contribute to the selection of productive varieties. The work was supported by RSCF 16-16-10011 and RFBR 18-04-01017 grants.

Single-Cell RNA Sequencing of Arabidopsis Roots

Hui Ryu, Ling Huang, Hyun Min Kang and John Schiefelbein

Department of Molecular, Cellular, and Developmental Biology, University of Michigan, Ann Arbor, MI USA. Correspondence to: schiefel@umich.edu

Single-cell RNA sequencing (scRNA-seq) has been used extensively to study gene expression from individual animal cells, but it has not been widely applied to plants. Here, we describe the use of a droplet-based microfluidics platform for high-throughput scRNA-seq to obtain single-cell transcriptomes from protoplasts from more than 10,000 *Arabidopsis* root cells (<https://doi.org/10.1104/pp.18.01482>). We find that all major tissues and developmental stages are represented in this single-cell transcriptome population. Further, distinct sub-populations and rare cell types were identified, including putative quiescent center (QC) cells. A focused analysis of root epidermal cell transcriptomes defined developmental trajectories for individual cells progressing through root-hair and non-hair cell differentiation. In addition, single-cell transcriptomes were obtained from root epidermis mutants, enabling a comparative analysis of gene expression at single-cell resolution and providing an unprecedented view of the impact of the mutated genes. Overall, this study demonstrates the feasibility and utility of high-throughput scRNA-seq in plants and provides a first-generation gene expression map of the *Arabidopsis* root at single-cell resolution.

CRABS CLAW Acts as a Bifunctional Transcription Factor in Flower Development

Annette Becker

Germany. Correspondence to: annette.becker@bot1.bio.uni-giessen.de

The gynoecium of lowering plants (angiosperms) is the most important morphological character that unites all angiosperms and it is of major economic importance, as most of our food is, at least indirectly, derived from angiosperm gynoecia. CRABS CLAW (CRC) is a major regulator of gynoecium development in angiosperms. Plants deficient in CRC function show shorter and wider gynoecia that sometimes fail to fuse at their apices indicating that CRC is important for regulating growth along the horizontal and longitudinal axis as well as carpel fusion. The genetic interactions of CRC have been studied in detail and it is from those that we know about its role in adaxial-abaxial polarity regulation of the gynoecium and regulation of auxin biosynthesis and homeostasis for floral meristem termination. However, it remains unclear how CRC exerts its role as transcription factor. Here, we show that CRC activates some and represses other transcription factors regulating different developmental processes in the gynoecium. We propose a framework for its transcriptional regulation and identify some of CRC's target genes important for adaxial/abaxial polarity in the gynoecium.

OsFD4 promotes flowering in rice by interacting with the florigens

M. Cerise¹, F. Giaume¹, M. Galli³, V. Brambilla², A. Gallavotti³, F. Fornara¹

1. Department of Biosciences, University of Milan, Italy
2. Department of Agricultural and Environmental Sciences, University of Milan, Italy
3. Waksman Institute of Microbiology, Rutgers, New Jersey, USA. Correspondence to: martina.cerise@unimi.it

In rice, the transition between the vegetative and reproductive phase occurs at the shoot apical meristem in response to external cues. The Florigen Activation Complex, FAC, has a predominant role during this process. It is composed by two florigen molecules, the bZIP transcription factor OsFD1, and Gf14c which bridges the interaction between them. The FAC controls the expression of genes important for the floral transition, but only few FAC targets are known yet.

We report the isolation and functional characterization of OsFD4, a bZIP transcription factor homologous to OsFD1. The *osfd4* mutants show delayed flowering compared to the wild type suggesting that OsFD4 promotes the floral transition in rice. Here we demonstrate that OsFD4 can form a FAC itself and redundancy with OsFD1 is being tested. Finally, using DNA Affinity Purification sequencing we found direct OsFD4 targets. We found that OsFD4 has affinity for specific consensus sequences and that they are partially shared with OsFD1. New direct targets of OsFD4 and OsFD1 will help to understand how the florigens control the early stages of floral transition.

Auxin spacio-temporal distribution in *Lupinus luteus* pistils and stamens during floral development and abscission

Milena Kulasek [1,*], Wojciech Glinkowski [1], Jacek Kęsy [1], Paulina Glazińska [1,2]

[1] Department of Biology and Environmental Protection, Nicolaus Copernicus University, Lwowska 1, 87-100 Torun, Poland.

[2] Centre for Modern Interdisciplinary Technologies, Nicolaus Copernicus University, Wilenska 4, 87-100 Torun, Poland.

* Correspondence to: milena.kulasek@gmail.com

Auxin is a hormone that orchestrates many developmental processes in plants, including these concerning fertility. It displays dynamic concentration changes in stamens and pistils during flower development and maturation. Unfertilized flowers usually undergo abscission. In yellow lupine abscission zone (AZ) forms around the time of anthesis, which indicates, that flower fate is determined before fertilization.

In this study we aim to verify hypothesis that there are differences in auxin concentration in lupine flowers depending on their fate. We performed whole-mount auxin immunolocalization of stamens and pistils isolated from flowers at various developmental stages and formed at extreme sites of inflorescence axis, which determines probability of their abscission.

The results showed that auxin concentration patterning in yellow lupine flowers plays a role in proper development of this organ.

Funded by NSC PRELUDIUM grant no. 2017/25/N/NZ3/00524

Data driven modeling reveals crucial roles of intra- and extracellular auxin flux in regulation of diverse developmental functions

Palme, Klaus

Institute of Biology II / Molecular Plant Physiology, BIOSS Centre for Biological Signalling, Studies, Center for Systems Biology, Albert-Ludwigs-Universität Freiburg, Schänzlestr. 1

79104 Freiburg. * Correspondence to: klaus.palme@biologie.uni-freiburg.de

The phytohormone auxin acts as a master regulator of developmental processes and environmental responses. The best characterized process in the auxin regulatory network occurs at the subcellular scale, wherein auxin mediates signal transduction into transcriptional programs by triggering the degradation of Aux/IAA transcriptional repressor proteins in the nucleus. However, whether and how auxin movement between the nucleus and the surrounding compartments is regulated remain elusive. By combining mathematical modeling with time course assays on auxin-mediated nuclear signaling and quantitative phenotyping in single plant cell systems, we show that ER-to-nucleus auxin flux represents a major subcellular pathway to directly control nuclear auxin levels. Homeostatically regulated auxin pool in the ER and ER-to-nucleus auxin fluxes underpin auxin-mediated downstream responses in plant cells. We further characterized the relative importance of local auxin biosynthesis, auxin transport and mechanical constraints during leaf development. Our data suggest that the site-specific accumulation of auxin, regulated by the balanced action of cellular auxin efflux and local auxin biosynthesis, is crucial for leaf vein formation.

The integration of transcription factor and hormone signalling functions during gynoecium development

Stefan de Folter

Mexico. Correspondence to: stefan.defolter@cinvestav.mx

Most angiosperms produce flowers with a pistil or so-called gynoecium in their center, which is the female reproductive part of the flower. The initiation of the gynoecium lays the foundation for correct fruit development very early on. Transcription factors that promote meristematic activity have important roles in these early events. Furthermore, also hormonal signaling pathways, like cytokinin and auxin, are crucial for correct early development.

In Arabidopsis, in the young gynoecium, high cytokinin signalling is present in the medial domain, in contrast to the lateral domain. We found that cytokinin signalling, that can provide meristematic properties required for Carpel Margin Meristem (CMM) activity and growth, is enabled by the transcription factor SPATULA (SPT) in the medial domain. Meanwhile, cytokinin signalling is confined to the medial domain by the cytokinin response repressor AHP6, and perhaps by ARR16 (a type-A ARR) as well, both present in the lateral domains (presumptive valves) of the developing gynoecia. Moreover, SPT and cytokinin, probably together, promote the expression of the auxin biosynthetic gene TAA1 and the gene encoding the auxin efflux transporter PIN3, likely creating auxin drainage important for gynoecium growth. The integration of these findings gives the first gene regulatory network acting during early gynoecium development.

However, it is reasonable to think that more regulatory networks are necessary for correct gynoecium development, which is the challenge for the near future to unravel.

Cytokinin N-glucosides and their role in control of plant development

Eva Pokorná, Lucie Doležalková, Tomáš Hluska, Roberta Filepová, Petre I. Dobrev, Václav Motyka*

Institute of Experimental Botany of the Czech Academy of Sciences, Prague, Czech Republic.

Correspondence to: *vmotyka@ueb.cas.cz

Cytokinins (CKs) are a class of phytohormones affecting many aspects of plant growth and development. In the complex process of CK homeostasis in plants, N-glucosylation represents one of important metabolic pathways although its products, CK N7- and N9-glucosides, are considered to lack any relevant physiological impact. In spite of a widespread image of CK N-glucosides as irreversible and inactive CKs, we demonstrated antisenescent activities of CK N9-glucosides in oat leaves in dark and their more pronounced inhibitory effects on maize primary root growth in comparison to corresponding N7-glucosides. Additionally we revealed substantial variations in distribution of particular CK N7- and N9-glucosides during ontogenesis in Arabidopsis leaves and roots and their influence on expression patterns of CK responsive genes in maize. Our findings argue against generally accepted view of CK N-glucosides, at least those glucosylated at N9-position, as CK stable deactivation products and will be discussed with respect to their potential involvement in plant development and physiological significance in plants. [Funded by Czech Science Foundation (19-12262S)].

Hormonal stress during in vitro culture stops the postzygotic barriers and leads to changes of the program of embryo development in intergeneric hybrids of cereals.

Tikhenko N1-2*, Rutten T1, Senula A1, Rubtsova M1, Boerner A1

1. Leibniz Institute of Plant Genetics and Crop Plant Research, Corrensstr. 3, D-06466, Gatersleben, Germany, 2SPb Branch Vavilov Institute of General Genetics, RAS, 199034, St. Petersburg, Russia.

In intergeneric crosses between hexaploid wheat (*Triticum aestivum* L.) and rye (*Secale cereale* L.), postzygotic barriers may occur at different stages of hybrid development. One of these barriers is embryo lethality, which is genetically determined by the interaction and expression of two incompatible loci in wheat (Eml-A1) and rye (Eml-R1). Using in vitro culture methods as stressors, this hybrid lethality can be overcome. The high regenerative capacity of the abnormal embryos suggests that the reproductive barrier in these hybrids may have an epigenetic origin that can be easily overcome by culturing immature embryos via callus induction. The key roles of double fertilization and stress factors in the implementation of the apical meristem formation program in embryos from incompatible intergeneric crosses between hexaploid wheat and rye during in vitro culture are discussed. We propose a hypothetical model for a wheat–rye lethality system involving differential expression of incompatible wheat Eml-A1 and rye Eml-R1b alleles in an identical genetic background.

A Pharmacogenetic Approach to Decipher the Role of the TOR Signaling Pathway in Plant Growth and Development

Adam Barrada, Shaista Ahmed, Manon Brenière, Meriem Djendli, Julie Nardini, Mélanie Soula, Marie-Hélène Montané, **Benoît Menand**.

Aix Marseille Université, CEA, CNRS, BIAM, Marseille, France F-13009. Correspondence to:

benoit.menand@univ-amu.fr

Target of Rapamycin (TOR) protein is the central component of the TOR signaling pathway which regulates cell growth and metabolism in response to environmental cues in eukaryotes. TOR has been the subject of many studies in yeast and animals due to its implication in diseases but the exploration of this pathway is less advanced in plants. In order to find new components of the plant TOR signaling pathway, we have performed a screen of *Arabidopsis thaliana* ethyl methanesulfonate (EMS) mutants having different sensitivity to ATP-competitive TOR inhibitors. We will present recent advances on the use of this screen to discover new members of the plant TOR pathway, such as the DYRK kinase YAK1 (Barrada et al 2019 Development: dev.171298), and to help understand how the TOR pathway regulates plant growth and development.

DNA methylation in plant development: a focus on fleshy fruits

Philippe GALLUSCI

UMR EGFV, Bordeaux University, INRA, Bordeaux Science Agro, Villenave d'Ornon, France

Correspondence to: philippe.gallusci@inra.fr

Epigenetic refers to heritable changes in chromatin organization, which may lead to modifications in gene expression but the underlying genomic DNA sequence remains unchanged. DNA methylation which occurs on the 5th carbon of cytosine (5mC) is major epigenetic marks controlling fleshy fruit development and ripening.

Initial evidence of the importance of DNA methylation in the control of fruit development was provided in tomato. We have now generated tomato lines that are impaired in DNA methylation homeostasis. Metabolomics and RNA seq analysis were performed on fruits of hypermethylated lines indicating that several aspects of fruit ripening are inhibited. Inhibition of fruit ripening is due to the hypermethylation and repression of the expression of genes encoding ripening transcription factors and rate-limiting enzymes of important metabolic pathway. The results are consistent with DNA demethylation being critically important to tomato fruit ripening control and suggest crosstalks with other fruit developmental factors. Current work aims at determining the network of genes and related processes under direct methylation control in tomato fruits. Similar work aiming at analyzing whether similar mechanisms also exist in other fleshy fruits such as grape will be discussed.



Berthold Technologies Bioanalytic is a business unit of the Berthold Technologies Group, a global technology leader in life sciences, process control and radiation protection with more than 350 employees. We have based ourselves in Bad Wildbad, located in the beautiful Black Forest in Southwest Germany. This area of Germany is known as the land of inventors and craftsman, a tradition which has been engraved into our DNA.

The Bioanalytic division is renowned for its microplate readers, luminometers, radio HPLC detection systems, gamma counters and in vivo imaging solutions, which have been trusted by scientists across the globe for almost 70 years.

By acquiring Titertek-Berthold in January 2017, we have complemented our product portfolio with microvolume spectrometers, microplate washers and microplate workstations, supporting our mission to solve even the most complex bioanalytical challenges.

We can be reached at bio@berthold.com

<https://www.berthold.com/>



VISCEA

Vienna International Science
Conferences and Events Association

Abstracts of Poster Presentations



www.viscea.org

Poster № 1: Evolution of the INAPERTURATE POLLEN1 gene conforms to the Angiosperm systematics but not to its diversity of apertural systems

Suárez-Santiago, V.N.1, Mazuecos-Aguilera, I.1, Berbel-Cascales, M.1, Ben-Menni Schuler, S.1, Fernández-Fernández, M.C.1, Romero-García, A.T.1

Department of Botany. University of Granada. Correspondence to: vsuarez@ugr.es

The apertural system of the pollen grains is defined by the number, shape and position of the apertures. Angiosperms possess enormous variation in apertural systems. Only two genes involved in the formation of the apertures are known, INAPERTURATE POLLEN1 (INP1) and D6 PROTEIN KINASE LIKE3. However, nothing is known about how these genes have evolved in Angiosperms and about the relationship between their diversification and the diversification of the apertural systems. We conducted a phylogenetic analysis of the INP1 gene in Angiosperms. Our gene tree reflects very well the Angiosperm systematics. The great diversity of apertural systems does not seem to be associated with gene duplications. Only one event of gene duplication was detected at the base of the Core Eudicots. The absence of duplications and the lack of resolution in the relationships between the main clades suggest that an ancestral copy of INP1 was distributed among the main clades when the initial Angiosperm radiation occurred. The lack of correlation between INP1 diversification and diversity of apertural systems supports that INP1 is not the main responsible for the diversity of apertural systems.

Poster № 2: Identification and expression of miR390/TAS3/tasiARF module during flower development and abscission in yellow lupine

Paulina Glazińska*1,2, Milena Kulasek1, Wojciech Glinkowski1, Waldemar Wojciechowski1,2

1. Department of Biology and Environmental Science, Nicolaus Copernicus Univ., Torun, Poland,

2. Centre for Modern Interdisciplinary Technologies, Nicolaus Copernicus Univ., Torun, Poland

Correspondence to: paulina.glazinska@umk.pl

Recent studies have shown that sRNA influence the localization of the hormone response pathway, e.g. the expression of auxin response factors ARF2, 3 and 4 is under direct control of ta-siARFs created via miR390-directed cleavage of TAS3 transcript.

Our study aimed at identifying the small ncRNAs in *Lupinus luteus* by NGS of sRNA libraries generated from flowers and flower pedicels. Their target genes were identified using transcriptome and degradome sequencing.

Among identified sRNAs, there were members of MIR390 family. Identified transcripts of ARF2, 3 and 4 are possibly down-regulated by two LI-siARFs originate from TAS3 transcript containing two binding sites for miR390. LI-miR390 and, surprisingly, LI-siR240, guide cleavage of another TAS3 mRNA. This is the first report on TAS3 processing regulated by siRNA.

The presence of the whole miR390/TAS3/tasiARF module suggests its vivid role in lupine flower development and abscission.

Funded by NSC grant No. 2015/19/D/NZ9/03601 and by the Program Supported by RM-111-222-15 in association with the IPG, PAS.

Proteomic approach to the Orobanchaceae question

Juraj Kleman, Katarina Klubicova, Maksym Danchenko, Terezia Salaj, Radoslava Matusova

Correspondence to: Radka.Matusova@savba.sk

Plant Science and Biodiversity Center SAS, Institute of Plant Genetics and Biotechnology, Akademicka 2, P.O. Box 39A, 950 07 Nitra, Slovakia.

Some Orobanchaceae family genera, like *Striga*, *Phelipanche* and *Orobanche*, are known for their parasitic life strategies. Their seeds can lay dormant in soil for years, awaiting optimal conditions. One of which is the presence of an appropriate host in the near vicinity, which they detect by reacting to host root exuded germination stimulants (e.g. strigolactones). These root parasites can cause field infestations, leading to huge yield losses. Several genomic studies have been performed already, but the process of reacting to the germination stimulants remains unclear. We approach this topic on a proteomic level. Thanks to dynamic nature of proteomes, this strategy could give additional information on the changes occurring during the plant development processes in parasitic plants.

Work was supported by Scientific Grant Agency VEGA (VEGA 2/0138/17).

Interspecific Gene Flow in Hybrid Swarm of *Pinus sylvestris* and *Pinus mugo*

Miroslav Klobucnik^{1,2} Martin Galgoci^{1,3} Andrej Kormutak¹

1. Plant Science and Biodiversity Center SAS, Institute of Plant Genetics and Biotechnology, Akademicka 2, 950 07 Nitra, Slovakia

2. Comenius University in Bratislava, Faculty of Natural Sciences, Ilkovicova 6, 842 15 Bratislava 4, Slovakia

3. Constantine the Philosopher University in Nitra, Faculty of Natural Sciences, A. Hlinku 1, 949 74 Nitra, Slovakia

Introgressive hybridization is defined as a backcrossing of spontaneous interspecific hybrids with one or both parental species. The offspring generated in this way should have higher heterozygosity and adaptability compared to the parents. We have followed gene flow between the species *P. sylvestris* and *P. mugo* in their putative hybrid swarm near Zuberec in Slovakia. Using the species-specific cpDNA marker, the restriction profiles were analyzed in open pollination progenies of 10 maternal trees, of which 8 individuals exhibited *P. sylvestris* haplotype (S) and produced 29.1 percent of embryos possessing *P. mugo* haplotype (M). Likewise, 2 trees of the haplotype M produced 2.25 percent of embryos of the haplotype S. Considering the paternal inheritance of cpDNA in conifers, the results indicate preferential pollination of the hybrids with pollen of the trees with the identical haplotype and also some gene exchange between trees with different haplotypes.

This work was supported by grant VEGA No. 2/0063/17.

Dynamics of phytohormones in stolons *Solanum tuberosum* in connection with tuberization

T.I.Puzina, I.Yu.Makeeva

Orel State University, 95 Komsomolskaya str., Orel, 302026, Russia. Correspondence to: tipuzina@gmail.com

In the regulation of tuberization initiation and assimilate transport into forming tubers, the dynamics of phytohormones in the process of ontogeny of potato plants are of great importance. The content of 4 groups of phytohormones was determined by enzyme immunoassay. We found that the maximum amount of zeatin, IAA and, above all, GA3 fell on the initial stage of stolon development. At the beginning of budding, the content of ABA increased 2.6 times and exceeded the number of GA3, which was accompanied by a stolon growth retardation and tuberization initiation. At the same time, the level of zeatin did not change, and the amount of IAA decreased. In the flowering phase, the content of phytohormones in stolons depended on the size of the formed tubers. The stolons of large tubers contained less zeatin and ABA, but significantly more IAA and GA3. Against this hormonal background, the diameter of the xylem vessels increased by 30% and the thickness of the outer phloem increased by 25%. At the end of the growing season, the level of ABA in stolons sharply increased. Thus, the analysis of the hormonal situation showed that the ontogenesis of the stolon could be divided into 3 stages: before budding, the ratio of phytohormones with a positive sign of action to ABA was 2.8 (growth of the stolon), at the beginning of budding - 0.7 (initiation of tuberization), after flowering - 0.5 (growth of young tubers).

Endosperm in angiosperm plants and genome imprinting

Kordyum E.L.

Institute of Botany, National Academy of Sciences of Ukraine, Kyiv, Ukraine

Correspondence to: cellbiol@ukr.net

The modern ideas about a role of epigenetic systems in the regulation of gene expression allowed to approach to understanding the mechanisms of such phenomenon in plant vital activity as genome imprinting (Henderson, Jacobsen, 2007). This phenomenon concerns to the epigenetic modification of alleles inheritable on the maternal or paternal line, that leads to their different expression depending on parents' origin. Thus, maternal and paternal genomes are not functionally equivalent in consequence of genome imprinting (Grossniklaus, 2005). The regulation of genome imprinting in plants includes DNA methylation and chromatin modification playing an important role in the imprinting regulation in mammals also. It is very interesting that genome imprinting is known in the present time, in the first place, for the endosperm, that is a highly specialized tissue. Endosperm not only provides an embryo with necessary nutrients but perform the particular biological role in the formation of a seed and a fruit. Available data on genome imprinting in the endosperm have been only obtained in the investigations of triploid endosperm developing after double fertilization in an embryo sack of the Polygonum-type that is the most distributed among angiosperm plants. Therefore, it is considered the necessity and timeliness of further research of genome imprinting in endosperm of other ploidy, which develops in embryo sacks of different types – from diploid (Oenothera-type) till pentaploid (Plumbago-type) and nineploid (Peperomia-type), as well as in endosperm of three types – nuclear, cellular and helobial. Undoubtedly, the investigations of these directions will extend our knowledge on the site of genome imprinting in plant ontogenesis, its epigenetic regulation, and a role of endosperm development and functioning in the seed and fruit formation.

Henderson J.R., Jacobsen S.E. Epigenetic inheritance in plants. *Nature*, 2007, 447, P. 418-424.

Grossniklaus U. Genomic imprinting in plants: a predominantly maternal affair. In: *Plant Epigenetics*. Blackwell Publishing; Sheffield: 2005. P. 174-200.



PhytoTechnology Laboratories

P.O Box 12205
Shawnee Mission, KS 66282-2205

Tel: 888-749-8682, 913-341-5343
Fax: 888-449-8682, 913-341-5442

E-Mail: info@phytotechlab.com
Web: www.phytotechlab.com

PhytoTechnology Laboratories™' goal from inception has been to do one thing and do it right. That is why you will not find us manufacturing products for mammalian or insect cell culture; we solely focus on serving the plant science and plant biotech markets. PhytoTechnology Laboratories™ success over the past few years has been due to our loyal customers.

Each member of our staff is committed to bringing you the highest quality product available. In addition to quality products, we make every effort to provide the best possible service in the industry. Most orders are shipped within 24 to 48 hours of receipt. New technical information is continuously being developed to help customers use our products. In addition to our in-house staff, PhytoTechnology Laboratories™ has a network of outside consultants and advisors that counsel us on the strategies for the development of the company, and the planning required to maintain a healthy business community.

To meet our vision, our new catalogue contains over 800 products, including media, biochemicals, and equipment and supplies developed and tested specifically for the plant sciences. This includes over 150 new products that have been added since our last catalogue. **Thinking Green:** In an effort to help support our recycling and environmental management efforts and as a responsible corporate community member, this catalogue is being provided in an electronic format to reduce the number of trees required to print the catalogue and reduce the petroleum based products required for printing and cost associated with distributing the catalogue.

PhytoTechnology Laboratories™ not only offers quality media and biochemicals, but also provides custom media manufacturing and packaging.

Manufacturing: PhytoTechnology Laboratories™ can manufacture proprietary media formulations to meet your requirements for specific plant cell lines. Our capability gives plant researchers the opportunity to have proprietary custom media manufactured in batch sizes ranging from 100 L to 50,000 L. This Our confidentiality agreement assures you that all records pertaining to custom media manufacturing will be held in the strictest confidence.

Packaging: We can package a standard medium formulation or your proprietary media in any package size that best meets your media preparation requirements. Simply let us know the standard batch size that you prepare and we can package your media in that package size. With custom packaging, your products will be available in ready-to-use quantities, saving your technicians time and improving their efficiency.

List of Poster Presentations

Poster number. Author and title	Page in Abstract book
Poster № 1. Suárez-Santiago, V.N. Evolution of the INAPERTURATE POLLEN1 gene conforms to the Angiosperm systematics but not to its diversity of apertural systems	24
Poster № 2. Paulina Glazińska. Identification and expression of miR390/TAS3/tasiARF module during flower development and abscission in yellow lupine	24

List of Participants

Becker Annette

Justus-Liebig University Giessen Germany
annette.becker@bot1.bio.uni-giessen.de

Berbel Modesto

University of Granada, Granada Spain
mberbel@ugr.es

Bilynska Olena

Harkov Ukraine

Cerise Martina

University of Milan, Milan Italy
martina.cerise@unimi.it

Wenkel Stephan

University of Copenhagen, Frederiksberg C,
Denmark wenkel@plen.ku.dk

van Gelderen Kasper

Utrecht University, Utrecht
Netherlands k.vangelderer@uu.nl

De Folter Stefan Centro de Investigación y
de Estudios Avanzados del Instituto Politécnico
Nacional (CINVESTAV-IPN) Irapuato Mexico
stefan.defolter@cinvestav.mx

Elashmouny Amany
Cotton Research Institute Egypt, Egypt
amanyash@hotmail.com

Fedoreyeva Larisa
All_Russia Research Institute of
Agricultural Biotechnology, Moscow,
Russian Federation iab@iab.ac.ru

Gallusci Philippe

University Of Bordeaux, Bordeaux, France
philippe.gallusci@inra.fr

GlazinskaPaulina

Nicolaus Copernicus University Torun, Poland
pglaz.pg@gmail.com

Glinkowski Wojciech

Nicolaus Copernicus University,
Toruń Polan
wglin@doktorant.umk.pl

He Xingyuan

Northeast Institute of Geography &
Agroecology, Chinese Academy of Sciences
Changchun, China hexingyuan@iga.ac.cn

Kleman Juraj

Slovak University of Agriculture/Slovak
Academy of Sciences Nitra, Slovakia
juraj.kleman@savba.sk

Klobucnik Miroslav

Plant Science and Biodiversity Center SAS,
Nitra, Slovakia
miroslav.klobucnik@savba.sk

Kordyum Elizabeth

Institute of Botany, Kyiv, Ukraine
cellbiol@ukr.net

Kudryashov Andrey

Saint Petersburg State University, Saint
Petersburg, Russian Federation
a23.10.2012@yandex.ru

Kulasek Milena Nicolaus Copernicus
University in Torun, Torun, Poland
milena.kulasek@gmail.com

Kuznetcova Kseniia

Saint Petersburg State University, Saint-
Petersburg, Russian Federation
kskuz95@mail.ru

Lee Ji-Young

Seoul National University, Seoul,
South Korea
jl924@snu.ac.kr

Li Xiangnan

Northeast Institute of Geography &
Agroecology, Chinese Academy of Sciences
Changchun, China lixiangnan@iga.ac.cn

Lindsey Keith

Durham University, Durham, United Kingdom
keith.lindsey@durham.ac.uk

Mazuecos-Aguilera Ismael

University of Granada, Granada,
Spain ismaag@ugr.es

Menand Benoit

Aix-Marseille Université, CEA, CNRS,
Marseille, France
benoit.menand@univ-amu.fr

Motyka Václav

Institute of Experimental Botany of the Czech
Academy of Sciences, Prague, Czech Republic
vmotyka@ueb.cas.cz

Nonogaki Mariko

Oregon State University, Corvallis
United States mnonogak@hotmail.com

Nowack Bryan

University of Potsdam, Berlin,
Germany
bryan.nowack@t-online.de

Oomen Ronald

Vilmorin-Mikado LEDENON, France
ronald.oomen@vilmorin.com

Osterburg Jenny

Strube Research GmbH & Co. KG, Söllingen,
Germany j.osterburg@strube-research.net

Palme Klaus

University Of Freiburg, Freiburg,
Germany
klaus.palme@biologie.uni-freiburg.de

Potsenkovskaya Elina

Saint-Petersburg State University, Saint-
Petersburg, Russian Federation
epots556@gmail.com

Puzina Tamara

Orel State University Named After I.s.
Turgenev, Orel Russian Federation
tipuzina@gmail.com

Ratet Pascal

CNRS Gif Sur Yvette, France
pascal.ratet@cnr.fr

Rocco Mariapina

Università degli Studi del Sannio,
Benevento, Italy
rocco@unisannio.it

Schiefelbein John

University of Michigan, Ann Arbor
United States schiefel@umich.edu

Song Fengbin

Northeast Institute of Geography &
Agroecology, Chinese Academy of Sciences
Changchun, China songfb@iga.ac.cn

Suárez-Santiago Víctor
University of Granada, Granada, Spain
vsuarez@ugr.es

Traas Jan
INRA - ENS-Lyon Lyon Cedex 07, France
Jan.Traas@ens-lyon.fr

Suffert Frédéric
Institut National des Enculeurs de Mouches,
Thiverval Grignon, France
suffert@versailles.inra.fr

Tvorogova Varvara
Saint Petersburg State University, Saint
Petersburg Russian Federation
krubaza@mail.ru

Tikhenko Natalia
Leibniz Institute of Plant Genetics and Crop
Plant Research, (IPK) Gatersleben,
Germany tikhenko@ipk-gatersleben.de