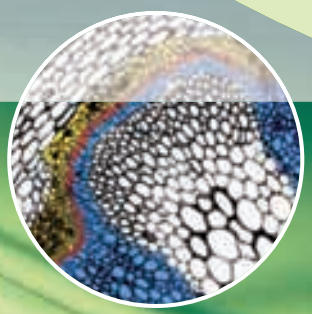
annual report 13

GREGOR MENDEL INSTITUTE OF MOLECULAR PLANT BIOLOGY

GMI



annual report 13

GMI



Published by:
Gregor Mendel Institute
of Molecular Plant Biology GmbH
Dr. Bohr-Gasse 3
1030 Vienna, Austria
E: office@gmi.oeaw.ac.at

Editor: Thomas Friese
Photographers: Herbert Blazejovsky,
Ruben Gutzat, Oliver Zehner
GMI logo: Lo Breier
Graphic design: Atelier Blazejovsky
Printing house: Riedel Druck GmbH, 2214 Auersthal
© Gregor Mendel Institute of Molecular Plant Biology 2014

The GMI is a basic research institute of the
Austrian Academy of Sciences

Contents

4 Directors' Statement
6 Introducing the GMI

RESEARCH GROUPS
8 Busch Group
12 Djamei Group
16 Greb Group
20 Jonak Group
24 Mittelsten Scheid Group
28 Nodine Group
32 Nordborg Group
36 Riha Group
40 Tamaru Group

GENERAL
44 GMI Key Facts
44 Publications
50 Grants
52 PhD Program
54 Seminars
56 Professional Training & Personal Development
57 Alumni
58 Events
60 Management
61 Administration & Services
62 Scientific Advisory Board
63 The Austrian Academy of Sciences
63 The City of Vienna
64 Location & Travel Directions

Dr Magnus Nordborg
Scientific Director

Dr Markus Kiess
Business Director

Directors' statement

The GMI continues to improve, and we are convinced that it is now one of the very best places worldwide to carry out basic research on plants. During 2013, the institute was — for the first time in its history — subject to a 5-year evaluation by an external review board in addition to its regular yearly review by its Scientific Advisory Board. Both reviews were extremely positive, noting that the GMI is on a fantastic upward trajectory and that the institute's scientific reputation continues to grow. During the last year, 27 papers were published, including several in the very top journals. The GMI entered a phase of change; Armin Djamei (from the Max Planck Institute in Marburg, Germany) and Frederic Berger (from the Temasek Life Sciences Laboratory in Singapore) joined as new group leaders to begin to replace the four Junior Group Leaders who will leave during the next two years: Karel Riha, Thomas Greb, and Hisashi Tamaru are departing in 2014, and Claudia Jonak in 2015. Managing these changes will be challenging, but we are convinced that it can be done.

We are proud to be one of a relatively small number of institutions world-wide focusing on basic research in plant biology, a field we are convinced will play an increasingly important role in coming years in light of the challenges posted by securing sustainable sources of food and energy.

In conclusion, we want to thank the Austrian Academy of Sciences for its continued support, without which the GMI would not exist; the Federal Ministry of Science, and the City of Vienna for their general support of the VBC; and everyone, especially those at the GMI, for making this an amazing place to work.

Magnus Nordborg *Markus Kiess*

Introducing the Gregor Mendel Institute

Profile

The Gregor Mendel Institute of Molecular Plant Biology (GMI) was founded by the Austrian Academy of Sciences (ÖAW) in 2000 to promote research excellence in molecular plant biology. It is one of the few institutes worldwide that focuses on basic research using plants. The GMI is located in the purpose-built ÖAW Life Sciences Center, completed in January 2006, in the heart of Vienna's most important life sciences research complex, the Vienna Biocenter Campus (VBC). The Vienna Biocenter Campus encompasses independent and academic research institutes as well as biotechnology companies, thus providing an environment of powerful research synergies for the GMI. Neighbours include important institutes like IMP, IMBA, and MFPL.

Research

Research at the GMI covers many aspects of molecular plant genetics, including basic mechanisms of epigenetics, population genetics, chromosome biology, developmental biology, stress signal transduction, and biotrophy. During the last 20 years, the model plant *Arabidopsis thaliana* has emerged as the primary experimental system for molecular biology and is thus also the model organism used at the GMI, although other organisms are also studied. Research is carried out by ten independent research groups, led by either senior group leaders with contracts of unlimited duration, or junior group leaders with limited appointments. The focus is on scientific excellence and publication in high impact journals. Notably, GMI researchers have one of the highest publications rates in journals such as *Nature* and *Science* in Austria.

The GMI's research activities are supported by an efficient administration and a world-class scientific infrastructure consisting of the GMI's own services, including state-of-the-art plant growth facilities and a new supercomputing center, and joint services with the IMP and

IMBA. Block funding is received from the Austrian Academy of Sciences with additional resources provided by a variety of national, European, and other international funding agencies.

Importance of experimental plant research

Plants are the primary producers of the world's ecosystem and thus essential for all life on earth, a basic fact receiving new attention with rising food prices, diminishing fossil fuel reserves, and a changing climate. Major innovations will be required to guarantee sustainable food and energy production in the 21st century, and some of them can only come from basic plant research, such as that carried out at the GMI.

But research on plants can also lead to fundamental scientific breakthroughs beyond plant biology. Gregor Mendel's discovery of the basic principles of genetics, Barbara McClintock's discovery of transposons, and the recent work on epigenetics and RNA silencing are only a few of the dozens of examples. What critical discoveries will plant research bring in the future?

These are exciting times, for there is still much to learn, from the biology of roots, via basic gene regulation (in particular through epigenetics, a GMI strength), to the genetic architecture of adaptive variation. The possibility of fundamental discoveries in these and other areas seems high, and everyone at the GMI is excited to be part of this endeavor.

Education

The GMI offers PhD positions within the framework of the prestigious Vienna Biocenter (VBC) International PhD Program, and is also involved in several externally funded doctoral programs. In the summer months, GMI research groups host students from the VBC Summer School. Additionally, GMI staff members present lectures and organize journal clubs and laboratory courses at the University of Vienna. The GMI is also committed to participating in outreach activities to promote the importance of plant science for the general public.

Working at the GMI

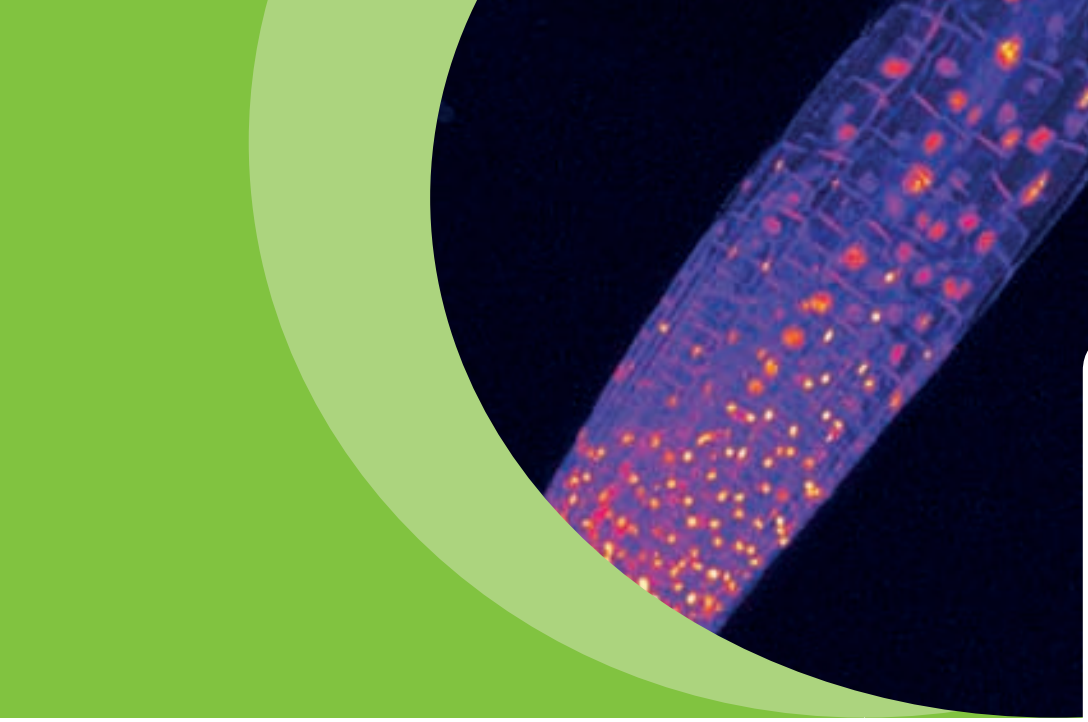
The GMI provides a lively, international working environment with some 100 staff from over 20 countries. The working language is English. Research is complemented by scientific events, such as a flourishing seminar series, an annual scientific retreat and GMI-organized conferences, and social events such as ski trips to the nearby Alps, sports events and festivities.

Regulation of root development in *Arabidopsis*

Although the roots of plants are hidden from view, they are of utmost importance for plants and for the broad colonization of the earth with plants. Roots anchor the plants in the ground, explore the soil, and gather all essential nutrients for plants. Regulating the continuous and highly plastic development of the root is therefore essential to any plant. During the past decade the root has been successfully used as a model for studying organ development. Applying quantitative genetics tools coupled with novel tools for automated image acquisition and analyses, we use the natural variation present in hundreds of *Arabidopsis* accessions to uncover novel classes of regulators and regulatory networks that tune root growth. We use genetics and systems biology tools to dissect the functions of these novel regulators and regulatory networks.

Plants have been highly successful in colonizing the vast majority of the earth's land surfaces. Intriguingly, this was achieved without the presence of fast chemo-electrical information processing systems, such as a central nervous system, or significant motility. A key to this success was presumably the evolution of organismal development towards an unmatched plasticity. Most of the development in plants happens post-embryonically after a short and stereotypical embryogenesis. In almost all vascular plants this development includes the periodic formation of new organs, above and below ground, and the growth of these initiated organs. Organ initiation and growth is highly influenced by environmental conditions. The orchestration of growth and development within and between tissues and organs is realized using a highly complex system of intercellular communication that relies on chemical signaling such as hormones, receptor/ligand based signaling and moving proteins.

To understand the molecular basis of growth and development and how environmental information is integrated into it, the root of *Arabidopsis thaliana* has proven to be an excellent model. Much of the progress in this field was facilitated by the discrete arrangement of tissues and developmental zones in the *Arabidopsis* root, which made it possible to determine the stage of development and the tissue identity of a cell simply by its position in the root (Fig 1). Using this simple model, remarkable progress



WOLFGANG BUSCH

wolfgang.busch@gmi.oeaw ac.at

Joined GMI in Jan 2011

PhD: Max Planck Institute for Developmental Biology/Eberhard-Karls-Universität, Tübingen, Germany

Previously

– Postdoctoral Fellow, IGSP Center for Systems Biology, Duke University, USA, 2008. Laboratory of Philip Benfey

has been made in understanding regulatory processes that underlie plant development. However, it is still largely unclear how those networks and pathways interact to regulate root growth and development in a coordinated manner, and how they quantitatively modulate growth.

A promising avenue for comprehending developmental regulation at a quantitative level is quantitative genetics. Such an approach is not only inherently quantitative, it also promises to discover genes not easily found with traditional mutageneses, potentially allows for detecting non-additive genetic interactions (epistasis), and provides a 'toolbox' of lines and alleles that can be exploited for the functional characterization of the gene and a quantitative assessment of genotype to phenotype relations.

The main research interests of our lab are to identify and characterize regulatory genes and networks that control root growth and development in a quantitative manner. For this we assess trait variation present in natural and artificial populations of *Arabidopsis thaliana*, use quantitative genetics to map this variation to the genome, identify and validate the causal genes and gene networks, and characterize their molecular functions.

KURZ UND KLEIN – A NOVEL F-BOX GENE THAT QUANTITATIVELY REGULATES ROOT GROWTH AND DEVELOPMENT

Growth and development are ultimately regulated at the cell level. Thus, finding the genes that determine where and when cell divisions occur and when and how cells differentiate is fundamental to comprehending organ growth. Using automated confocal microscopy to generate 3D images of the roots, we were able to capture the cellular architecture of the roots of more than 1600 individual plants from 200 natural *Arabidopsis* accessions originating in different regions of the world. We could then identify genomic regions associated with variations in cellular architecture such as the size of the cells or of the root apical meristem (the zone

Group members:

Postdoctoral Fellows

Takehiko Ogura
Daniela Ristova
Santosh Satbhai

Technicians

Aaron Appleyard*
Bettina Zierfuss
Marietta Zinner
Bonnie Wolhrab

PhD Student

Radka Slovak

Programmer

Christian Göschl

Visiting Scientists

Huang Xianzhoug*
Sun Li*
Yan Gong (Summer School)*

(*left the lab in 2013)

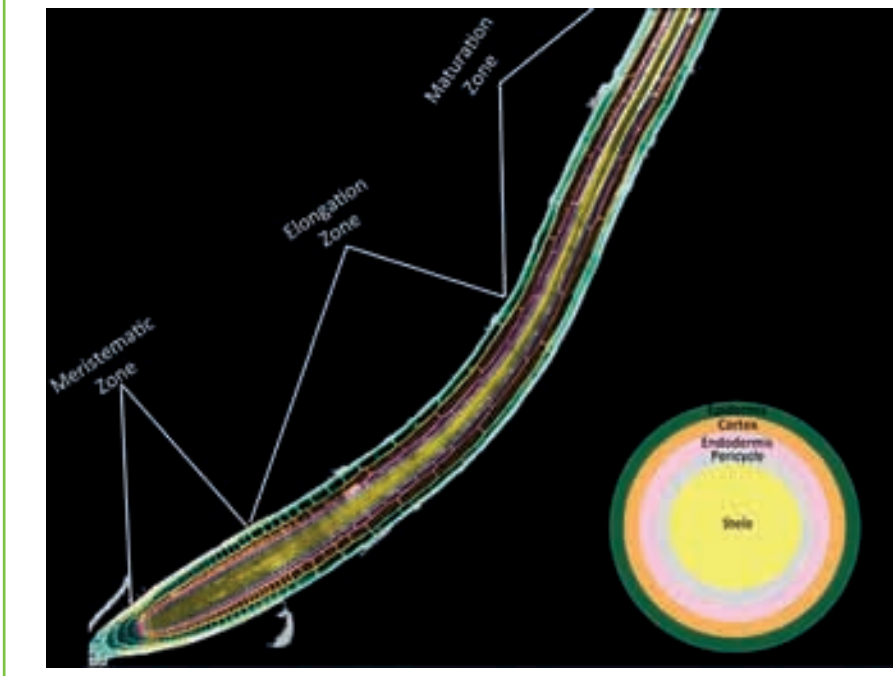


Fig. 1.

Tissue architecture and progression of development in Arabidopsis roots. Lower right: Schematic cross-section of a mature region of the Arabidopsis root (not in-scale). Upper left: Medial longitudinal section of an Arabidopsis root. Developmental zones are indicated. Different cell types/tissues are shaded with different colors (colors as in scheme at the lower right).

in which cells divide; Fig. 1). The most significant genome region was located in the coding region of an uncharacterized F-box gene. Using mutant lines in which the F-Box gene was down-regulated compared to wild type, both the length of the meristem and the length of mature cells were significantly decreased (Fig. 2). Overexpression of the gene resulted in a longer meristem and longer cells (Fig. 2). Not unexpectedly, the growth rate of the mutant was lower and that of the overexpressor was higher than that of wild type (Fig. 2), suggesting that this gene is a regulator of root growth. In correspondence to the mutant phenotype, we named the gene *KURZ UND KLEIN (KUK)*. Using a transgenic approach we could also show that polymorphisms in the coding region account for the major component of *KUK* allele-dependent variation of meristem and cell lengths. The KUK protein is present in all cell types from the distal meristem transition zone all the way through the elongation zone to the point where the cells enter the maturation zone. This expression pattern is consistent with a function of *KUK* in regulating proliferation and differentiation. Interestingly, *KUK* protein is not always present. The discovery of *KURZ UND KLEIN* opens up a number of very interesting questions that we will try to answer in the next years. For instance, how do the changes in the KUK protein sequence lead to smaller or larger cells and meristems and subsequently cause different root lengths? Which genes and molecular pathways are targeted by *KUK* to determine cell and meristem lengths? And what are the implications of the transient expression of the KUK protein?

QUANTITATIVE REGULATION OF ROOT GROWTH DIRECTION

Root growth variation affects numerous root traits differently, and it has been shown that many root architecture traits are controlled independently and in a quantitative manner. This includes traits controlled by the plant hormone auxin such as root gravitropism, root growth rate, and lateral root formation. This poses the question how the auxin signaling system can be modulated for the tuning of only one specific process, without affecting the plethora of other processes governed by auxin. To elucidate this question, we used a chemical genomics approach, utilizing different sensitivities of natural accessions towards a low concentration of the auxin transport inhibitor 1-N-Naphtylphthalamic acid (NPA). We observed the most striking natural variation in traits related to the root growth direction. Genome wide association mapping revealed two significantly associated SNPs. Strikingly, these were located in the coding regions of genes closely tied to the cellular membrane transport involved in auxin transport, root gravitropism and consequently control of root growth direction. We are characterizing the molecular functions of these genes and their alleles.

TUNING GROWTH RATE TO ENVIRONMENTAL CONDITIONS

Plant growth is exquisitely coordinated with environmental conditions. In particular, root architecture is highly dependent on soil conditions and local mineral contents. Root architecture is the outcome of local developmental decisions, like lateral root outgrowth and growth rate modulations of primary and lateral roots. However, little is known about how these quantitative regulations are achieved. Using our large-scale phenotyping pipeline we have phenotyped hundreds of *A. thaliana* accessions for root growth traits. We determined large variations in root development under Sulfur (-S), Iron (-Fe), and Phosphorus (-Pi) depleted conditions, as well as low and high temperature (10ºC, 29ºC) and low pH conditions. Most interestingly, most accessions show distinct root growth profiles (Fig. 3), indicating that accessions respond to different environmental cues in a specific manner. Using this variation for genome wide association mapping and in conjunction with advanced data mining of transcriptome and interactome data, we uncover the genes, their alleles and the gene networks that mediate the observed specificity in tuning growth responses.

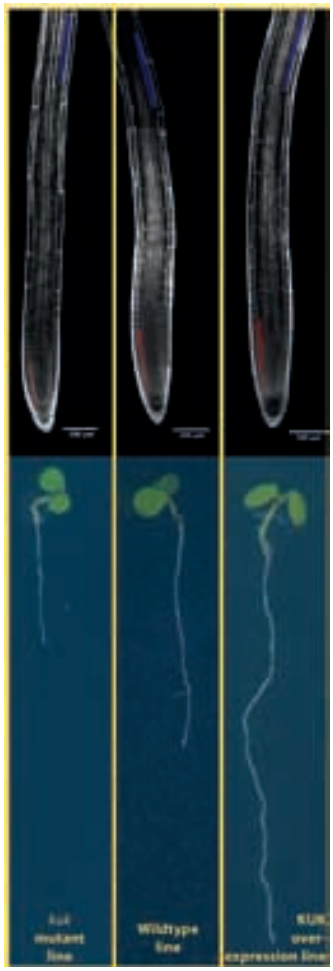


Fig. 2.

The role of KUK. Meristem length (upper panel; highlighted in red), mature cell length (upper panel; highlighted in blue) and root length (lower panel) in representative plants of kuk-1 mutant, Col-0 wild type and 35S::KUK overexpression lines.

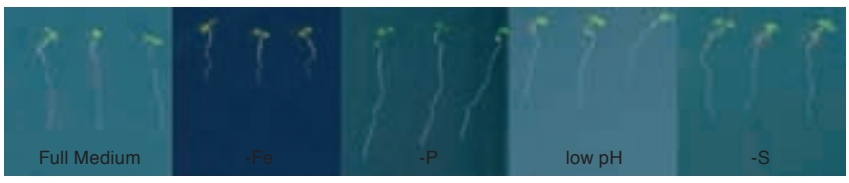


Fig. 3.

Root growth response of an Arabidopsis accession to different growth conditions. Plants 5 days after germination; –Fe: Iron deficient medium; -P: Phosphorus deficient medium; low pH: medium adjusted to pH 4.6; -S: Sulfur deficient medium.

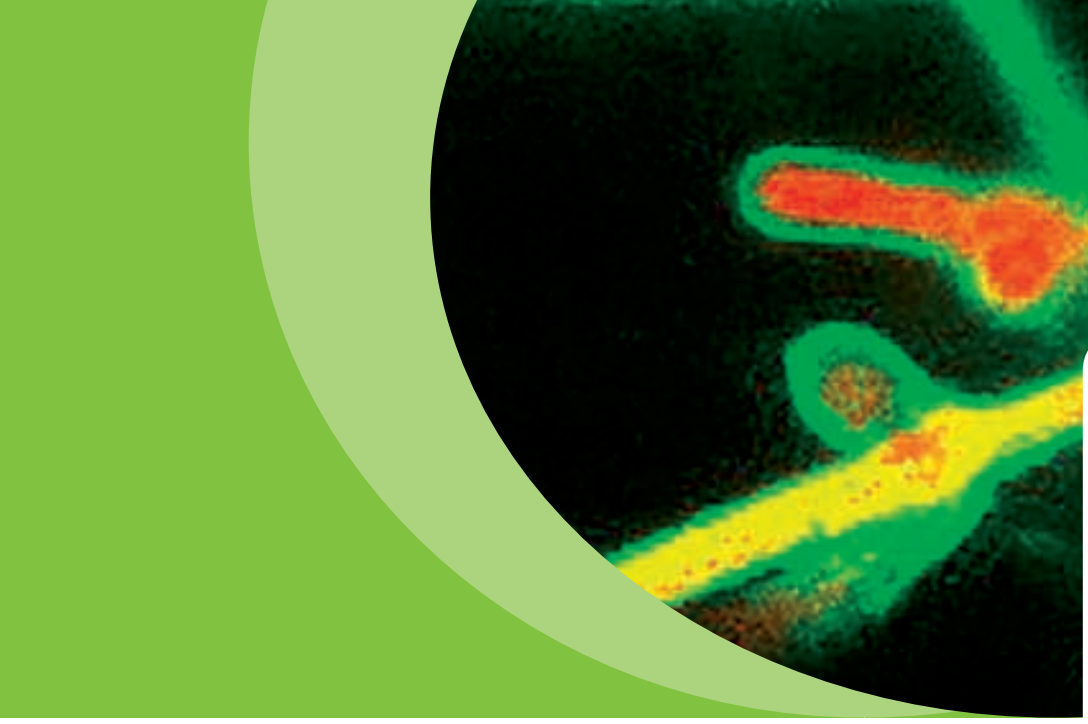
Effectomics – exploring the toolbox of biotrophic plant pathogens

Biotrophic pathogens (disease-causing parasites which feed on a host plant without killing it) colonize the tissues of living hosts and are therefore masters in manipulating the immune defense responses, metabolism and development of their host plants. The focus of our research is to reveal the underlying molecular mechanisms of biotrophy in the model pathosystems *Ustilago maydis* - Maize and *Ustilago bromivora* - *Brachypodium*. In an integrative approach we functionally explore the effectome (pathogen-derived secreted manipulative molecules) to gain insights into the metabolic processes of the targeted hosts and to understand the critical needs of the pathogens.

Successful plant biotrophic pathogens require a constant sensing and adapted molecular manipulation of the host metabolism to balance the interaction and keep the host alive. To suppress the highly evolved plant defence system and divert the host metabolism, plant pathogenic biotrophs coevolved fascinating strategies [1]. The molecular basis for the host plant manipulation is encoded in a versatile secreted effector repertoire found in biotrophic pathogens [1, 2]. Effectors are secreted manipulative molecules employed by the pathogen to create favourable conditions for its reproductive success inside the living host. A functional characterization of effectors is challenging as they are mostly proteins without known motifs relating them to a putative function. Nevertheless, characterisation of these effectors and their host target sites give fundamental insights into the requirements of the pathogen and point to the targeted key-nodes in the host metabolic network. Effector studies may thus have rewarding implications in pest control and plant breeding in the field.

USTILAGO MAYDIS - MAIZE, THE CURRENT MODEL SYSTEM

In this scenario, the *Ustilago maydis* - *Zea mays* pathosystem has emerged as a versatile model for studying biotrophic grass - fungal pathogen interactions [3, 4]. The corn smut fungus *U. maydis* belongs to the group *Ustilaginales* (Phylum: *Basidiomycota;* Class: *Teliomycetes*).



ARMIN DJAMEI

armin.djamei@gmi.oeaw ac.at

Joined GMI in Sep 2013
PhD: University of Vienna

Previously

- Project Group Leader, Department of Organismic Interactions, Max Planck Institute for Terrestrial Microbiology, Marburg, Germany, 2012-2013
- Postdoctoral Fellow, MPI for Terrestrial Microbiology, Marburg, Germany, 2007-2012
- Postdoctoral Fellow, Vienna Biocenter, Vienna, Austria, 2007

Group members:

Postdoctoral Fellow
Tilo Guse

Trainee
Barbara Cania

PhD Students
Franziska Rabe
Alexandra Stirnberg
Simon Uhse

Besides its importance as a prominent pest of maize/corn (*Zea mays*), the corn smut fungus has become a model smut for several other reasons including its small genome size (20.5Mb), ease of symptom recognition (forms local tumours within a week of infection), and amenability to molecular genetic manipulation [5, 6] (Fig.1: disease symptoms on maize).

The fact that most effector proteins are novel and of unknown function motivated our group to follow a systematic approach whereby we clone all ~300 putative effector genes of *U. maydis* in a gateway compatible library to perform various screens.

These screens will provide insights into:

1. The localisation and place of action of the putative effectors
2. Interaction partners on the host side
3. Functional aspects / pathways the effector might interfere with

The integration of results of several screens will be the basis for distinct individual functional studies. Unfortunately, the *U. maydis* host plant maize is less suitable for both-sided molecular functional studies due to its long generation time, space requirements, and cross pollination nature. Therefore, we are currently exploring an alternative grass-pathosystem with special emphasis on the plant side.

USTILAGO BROMIVORA - BRACHYPODIUM, THE FUTURE MODEL SYSTEM

In a recent report, the smut *Ustilago bromivora* was identified to infect *Brachypodium distachyon* [7]. This model grass has a short generation time of 6-8 weeks, and stable transformations take only a few months [8]. Spores of *U. bromivora* were kindly provided by Dr Thierry Marcel (Grignon, France). In our laboratory we are currently establishing the

Fig. 1.

Scheme of fungal hyphae penetrating and secreting effector proteins into the host cell.

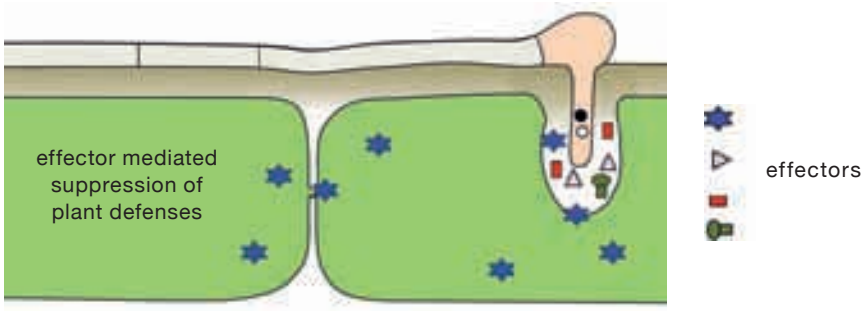
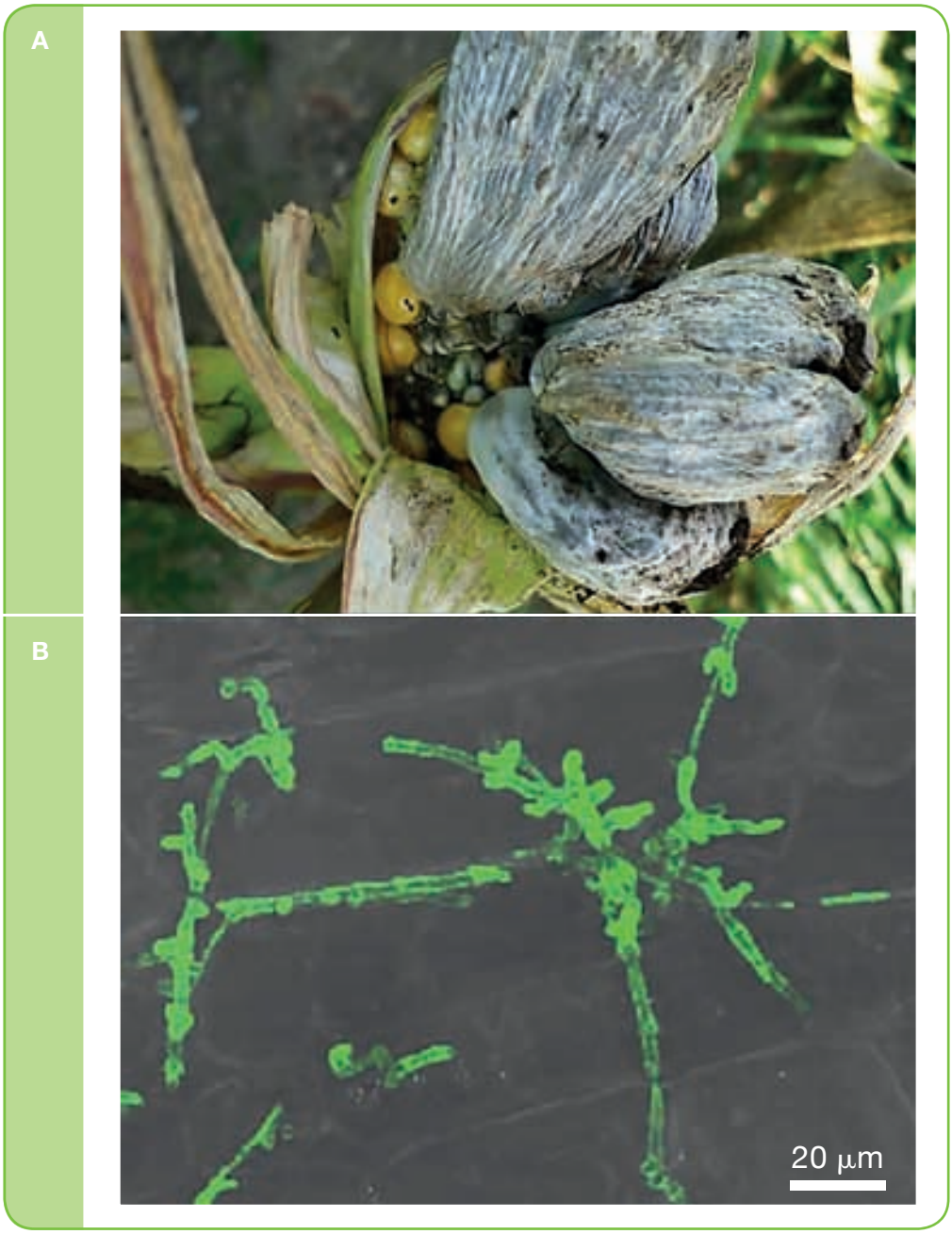


Fig. 2.

U. maydis induced tumour on maize plant in the field. Black spore material of the fungus is eponymous.

B) Microscopic picture of WGA-Alexa Fluor 488 labelled U. maydis hyphae in infected maize tissue.



culture conditions, transformation and infection protocols for *U. bromivora*. The fungal genome is currently Illumina and PacBio sequenced and preliminary data indicate a very close relation to the barley head smut fungus *U. hordei* but also to *U. maydis*.

In parallel to the analysis of *U. bromivora* we have established the transformation protocol of the host plant *Brachypodium* and are currently generating various genetic tools to enable us to study the biotrophic *U. bromivora – Brachypodium* interaction in detail at a molecular level.

1. Yi, M. and B. Valent, Communication between filamentous pathogens and plants at the biotrophic interface. Annu Rev Phytopathol, 2013. 51: p. 587-611.
2. Koeck, M., A.R. Hardham, and P.N. Dodds, The role of effectors of biotrophic and hemibiotrophic fungi in infection. Cell Microbiol, 2011. 13(12): p. 1849-57.
3. Djamei, A. and R. Kahmann, *Ustilago maydis:* dissecting the molecular interface between pathogen and plant. PLoS Pathog, 2012. 8(11): p. e1002955.
4. Brefort, T., et al., *Ustilago maydis* as a Pathogen. Annu Rev Phytopathol, 2009. 47: p. 423-45.
5. Kamper, J., et al., Insights from the genome of the biotrophic fungal plant pathogen *Ustilago maydis*. Nature, 2006. 444(7115): p. 97-101.
6. Dean, R., et al., The Top 10 fungal pathogens in molecular plant pathology. Mol Plant Pathol, 2012. 13(4): p. 414-30.
7. Barbieri, M. et al. Host Status of False Brome Grass to the Leaf Rust Fungus *Puccinia brachypodii* and the Stripe Rust Fungus *P. striiformis.* Plant Disease 95, 1339-1345, doi:10.1094/pdis-11-10-0825 (2011).
8. Mur, L. A. et al. Exploiting the *Brachypodium* Tool Box in cereal and grass research. New Phytol. 191, 334-347, (2011).

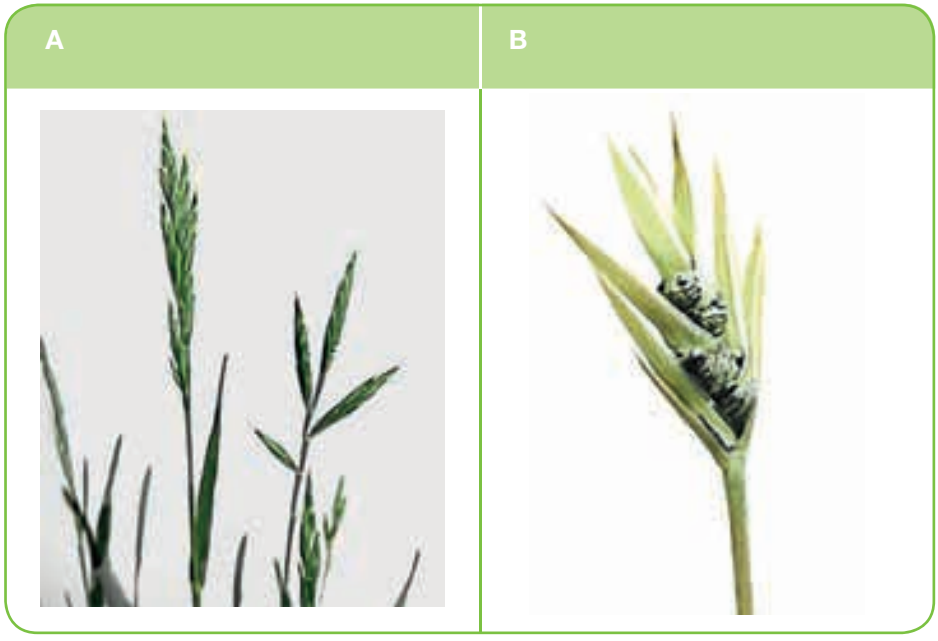


Fig. 3.

A) Brachypodium distachyon without infection symptoms.

B) Brachypodium with infection symptoms of Ustilago bromivora in the spikelets.

Growth and cell fate regulation

Lateral growth in plants is essential for the formation of extended shoot and root systems, and thus for the creation of biomass on earth. Our lab uses this process as an example to reveal principles of growth and cell fate regulation in multicellular organisms.

Multi-cellularity is a fundamental concept of life on our planet. The concept of single units (cells) taking over special functions in interaction with other units of a multicellular body is striking and requires an extreme degree of complexity with respect to cell-to-cell communication during growth and activity of such a system. Elucidating holistic concepts of the development and function of multicellular systems is therefore challenging, but also essential to understand the functionality of higher organisms. Lateral growth of plant shoots and roots is based on the tissue-forming properties of a lateral meristem called the cambium, the activity of which leads to the production of secondary vascular tissue (wood and bast, Fig. 1). Considering its function as a stem cell niche that is essential for the constant production of new tissues, as well as its dependence on environmental cues, the cambium represents an ideal model for addressing questions concerning the regulation of cell identity and how growth processes are aligned with endogenous and exogenous requirements. Given these attractive properties, our laboratory investigates lateral plant growth in order to reveal general concepts of growth and development of multicellular organisms.

Despite its herbaceous growth habit, *Arabidopsis thaliana* has been shown to be an excellent model for the analysis of secondary growth. Similarly to more woody species, secondary growth in *Arabidopsis* is initiated by the establishment of the interfascicular cambium in the elongating

THOMAS GREB

thomas.greb@gmi.oeaw.ac.at

Joined GMI in Feb 2006

PhD: Max Planck Institute for Plant Breeding Research, Cologne, Germany

Previously

– Postdoctoral Fellow, John Innes Centre, Norwich, UK, 2003-2006. Caroline Dean Lab

shoot (Fig. 2A, B). To explore the molecular control of secondary growth initiation, we concentrate on the formation of the interfascicular cambium (IC) between primary bundles, a prominent and easy to follow mark for the establishment of a closed cambium cylinder and the initiation of secondary growth. A selection of our approaches aiming at the molecular characterisation of this process is given below.

HORMONAL CONTROL OF SECONDARY GROWTH

Plant hormones play a crucial role in the long- and short-distance control of developmental processes, and secondary growth is no exception in this respect. Information about the growth stage of the plant, day length, temperature and mechanical stress are mediated by the action of auxin, ethylene, gibberellins, brassinolides and cytokinin and integrated by still unknown cambium regulators. In our research group, we revealed the influence of two additional hormones, namely strigolactones (SLs) and jasmonate (JA), further increasing our picture of the complexity of cambium regulation. SLs are connected to auxin signalling and seem to mediate information about the stage of general shoot growth. In contrast, we hypothesise that JA signalling translates tissue tension within the stem into cell division, a process essential to avoid tissue disruption during expansion of growth axes. The characterisation of the role of these hormone signalling pathways and their interactions represents a challenging but fundamental task in understanding how secondary growth is integrated into the general growth of the plant.

Group members:

Postdoctoral Fellows

Nial Rau Gursanscky
Virginie Jouannet
Branislav Kusenda (25%)
Pablo Sánchez
Stephanie Werner

Technicians

Markus Fabits
Karin Grünwald

PhD Students

Klaus Brackmann
Ivan Lebovka

Trainees

Kelly Smith
Eva Sophie Wallner

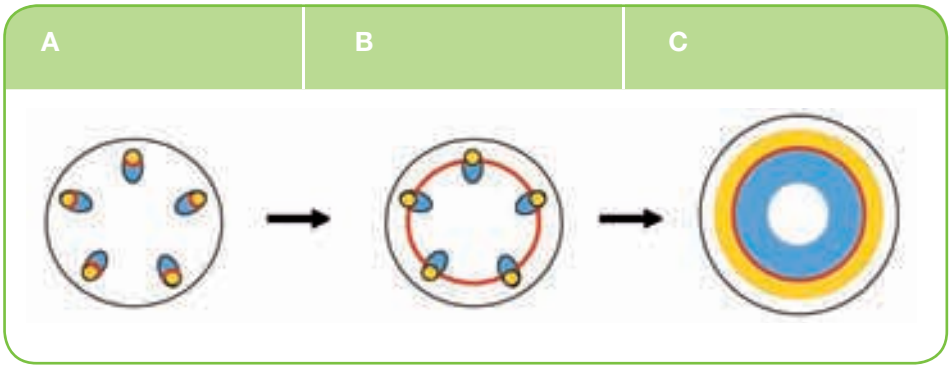


Fig. 1.

Schematic cross sections through the stem of a dicotyledonous plant. The initiation of cambium activity (red, B) between primary vascular bundles (i.e. interfascicular regions) transforms a primary stem (A) into a secondary stem (C). This process is essential for the establishment of a closed cambial cylinder which produces phloem (assimilate and signalling molecule transporting tissue, yellow) towards the outside and xylem (water transporting tissue, blue) towards the centre of the shoot axis, resulting in an increase of shoot diameter (C).

ISOLATION OF NOVEL CAMBIUM REGULATORS

The number of genes known to be involved in cambium regulation is rather limited to date. The isolation of novel regulators is therefore one essential step towards the understanding of secondary growth regulation. We established an in vitro system by which we are able to induce secondary growth in isolated stem fragments of *Arabidopsis* in a very controlled manner (Fig. 3A). For us, this system represents an invaluable tool to dissect molecular mechanisms regulating secondary growth. We took advantage of this system in particular to monitor tissue-specific changes in transcriptional profiles during the initiation of the IC and to identify regulating genes by following a Laser Capture Microdissection (LCM) approach. During this process, we collected RNA specifically from cells in interfascicular regions at three different time points during the initiation process (Fig. 3B). Micro array hybridizations with amplified RNA was performed, providing us with a repertoire of genes specifically changing expression during cambium initiation. By analysing plants defective for the identified genes, we are currently elucidating their role in cambium regulation. Here we focus primarily on factors involved in cell-to-cell signalling.

INVESTIGATION OF THE ADAPTIVE VALUE OF SECONDARY GROWTH

The process of lateral stem growth is accompanied by fundamental changes in the physiological and mechanical properties of almost all stem tissues. To gain insight into these distinct changes, we established tools for analysing changes of gene activities simultaneously in a tissue-specific and genome-wide manner. We established a set of transgenic lines expressing a nucleus-targeted histone H4-GFP fusion protein under the control of different tissue-specific promoters (Fig. 4). These lines allow us to employ fluorescence-based nucleus sorting in order to access and characterize tissue-specific mRNA. To see whether we are technically able to generate the anticipated datasets, we used the phloem tissue as a case study. We detected around 12,000 genes as being expressed, from which we classified 335 as predominantly expressed in this tissue. These results let us conclude that we are able to characterize transcriptomes from individual stem tissues, and we expect that we will gain fundamental insight into the growth dynamics of one major plant organ.

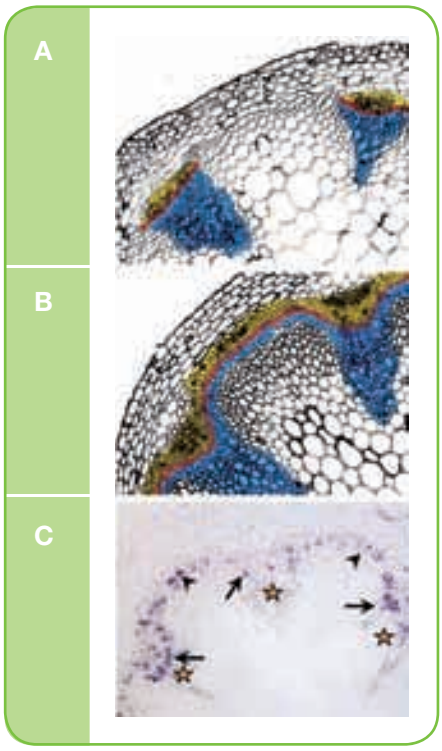


Fig. 2.

Comparison of a primary (A) and secondary (B) stem from Arabidopsis thaliana. Histological analyses show that secondary growth is initiated similarly to more woody species by initiating cambium activity in interfascicular regions. Colour coding as in Fig. 1. Molecular markers (in this case the expression of the histone H4, visualised by RNA in situ hybridisations) identify cambium cells as actively dividing. Arrows: dividing cell in primary bundles; arrowheads: dividing cells in interfascicular regions. Stars label primary vascular bundles.

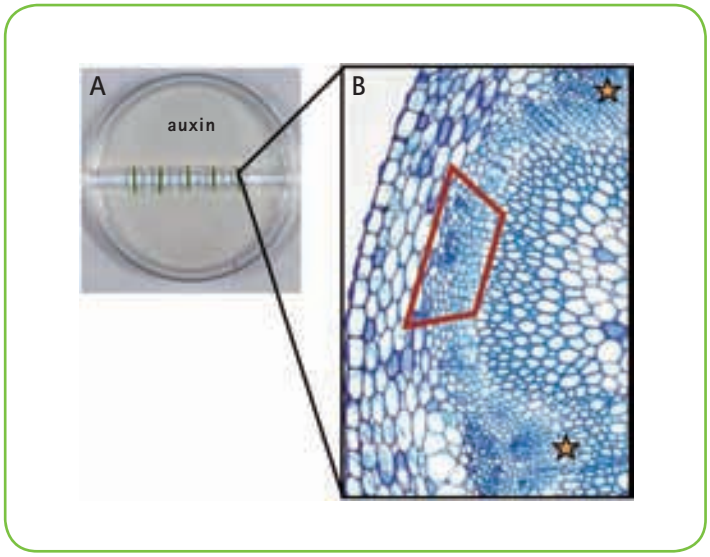


Fig. 3.

Transcriptional profiling taking advantage of an in vitro system to induce secondary growth. (A) Incubation of stem fragments on split-plates in the presence of the phytohormone auxin induces secondary growth in a very controllable manne (B) After harvesting the fragments at different time points and subsequent sectioning, cells transforming into the cambium are collected by LCM (red labelled area). Stars label primary vascular bundles.

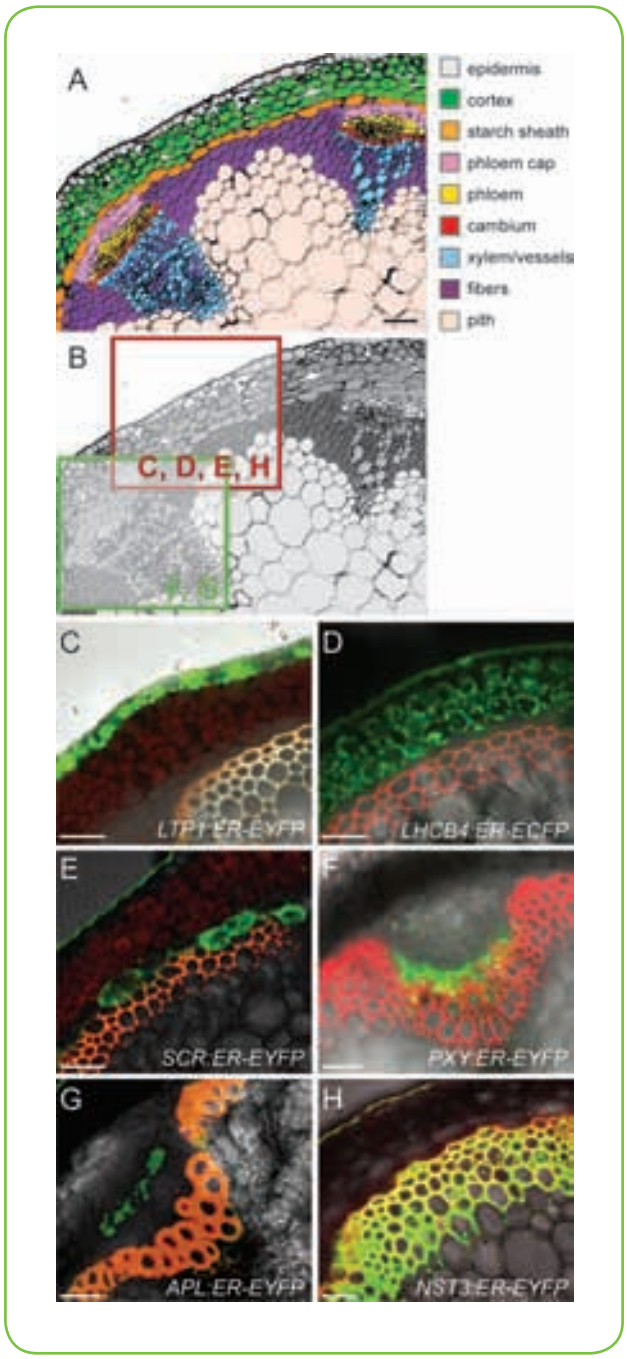


Fig. 4.

Identification of tissue-specific promoters covering the major tissue types of the stem. A) Tissue conformation in the primary inflorescence shoot. B) Position of sections shown in C-H relative to A. C – I) Different promoters are active in different tissue types. LTP1 (epidermis, C), LHCB4 (cortex, D), SCR (starch sheath, E), PXY (cambium, F), APL (phloem, G), NST3 (fibers, H), VND7 (early vessels, I). Reporter activity is visualized in green. Sections were counterstained by propidium iodide (cell walls, red). Size bars: 50 µm

Stress signal transduction and cellular responses

A key question in biology is how organisms cope with changing environmental conditions. Research in our group focuses on the mechanisms of signal transduction (intracellular information transfer system) and physiological adaptations in unfavorable environments. We take an integrative approach to better understand fundamental molecular processes at the interface between signal transduction and coordinated responses of cellular metabolism and gene expression in stress situations.

Plant growth and development largely depend on the environment. Drought, extreme temperatures, soil contamination with salts or heavy metals, and pathogen infections are examples of environmental constraints that determine the yield and reproductive success, and thus, the geographical distribution of plants. Over time, plants have evolved sophisticated inducible adaptation and defense systems. Environmental cues and pathogen infections are communicated by integrated signaling pathways, which delicately coordinate diverse cellular and physiological responses, ultimately determining stress resistance (Fig. 1). Protein kinases are key players of the signal transduction network.

ADAPTIVE REGULATION OF CELLULAR METABOLISM BY STRESS SIGNALING KINASES

In a changing environment, metabolism needs to be adjusted to enable a fast, adaptive physiological response. Protein phosphorylation represents an important means of fine tuning the activity of metabolic enzymes. However, our knowledge about how environmental stress-triggered signal transduction modulates the activity of metabolic enzymes remains limited.

We established the *Arabidopsis* GSK3/shaggy-like kinase, ASKα, as critical regulator for the cellular stress response by regulating the antioxidant system to counteract oxidative stress (Fig. 2). We showed that ASKα

is post-translationally activated by salt stress, and used a high-throughput metabolic screen to identify possible targets of ASKα. With a combination of genetic and biochemical approaches we revealed that ASKα regulates stress tolerance by activating glucose-6-phosphate dehydrogenase (G6PD), which is essential for maintaining the cellular redox balance. Loss of stress-activated ASKα leads to reduced G6PD activity, elevated levels of ROS (reactive oxygen species), and enhanced sensitivity to salt stress. Conversely, plants overexpressing ASKα have increased G6PD activity and low levels of ROS in response to stress, and are more tolerant to salt stress. ASKα stimulates the activity of a specific cytosolic G6PD isoform (G6PD6) by phosphorylating the evolutionarily conserved threonine 467. Analysis of structural data shows that the threonine residue targeted by the ASKα is in close proximity to the active site cleft of G6PD, suggesting that phosphorylation of G6PD6 might alter co-substrate binding and thus G6PD activity.

G6PD is a major determinant of cellular redox homeostasis, which plays a pivotal role in determining cellular responsiveness to stress. ROS generation and redox imbalance are closely linked to aging and a wide range of diseases including inflammation, cancer, and neurodegenerative disorders. Our data not only provide novel mechanistic insights into the regulation of G6PD6 activity by phosphorylation, but also offer a starting point for future studies beyond metabolic adaptation of plants to adverse environments.

CLAUDIA JONAK

claudia.jonak@gmi.oeaw.ac.at

Joined GMI in Feb 2004

PhD: Institute of Microbiology and Genetics, University of Vienna, Austria

Previously

- Research Assistant: Institute of Microbiology and Genetics, University of Vienna, Austria, 1994-1995
- EMBO Postdoctoral Fellow: Institute National de la Recherche Agronomique (INRA), Versailles, France, 1995-1997. Jan Traas Lab
- Research Assistant: Institute of Microbiology and Genetics, University of Vienna, Austria, 1997-2000
- Hertha Firnberg Position: University of Vienna, Austria, 2001-2004

Group members:

Postdoctoral Fellows

Branislav Kusenda (25%)
Olga Popova
Guillaume Queval
Sascha Waidmann

Technicians

Caroline Broyart
Bettina Dekrout

PhD Students

Iulia Danciu
Agnes Eder
Juliane Mayerhofer*
Bikram Pandey
Hansjörg Stampfl
Julia Krasensky

Master Student

Marion Fritz

(*left the lab in 2013)

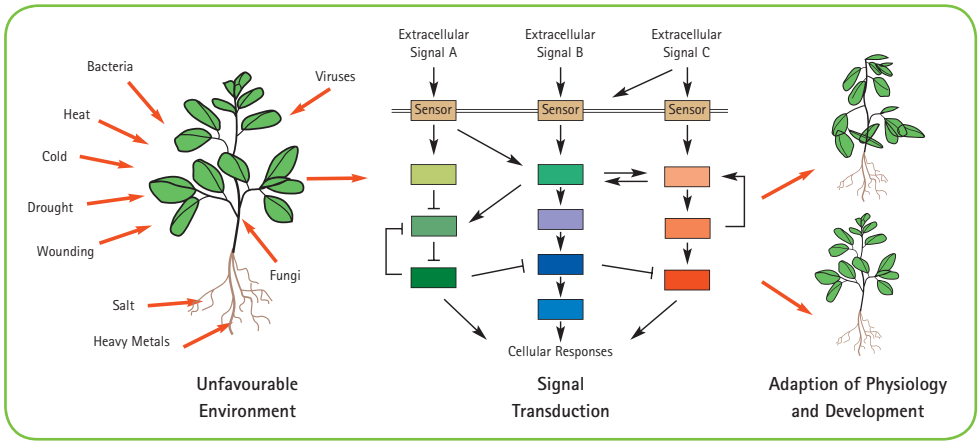


Fig. 1.

Plants respond to environmental stress. Plants are permanently exposed to a multitude of external stimuli, which plant cells have to transform into physiologically intelligible signals. Extracellular stimuli are perceived and internalized by various cellular receptors and are subsequently transduced by signaling cascades to induce appropriate cellular responses that ultimately lead to physiological and developmental modifications determining the sensitivity or tolerance of a plant.

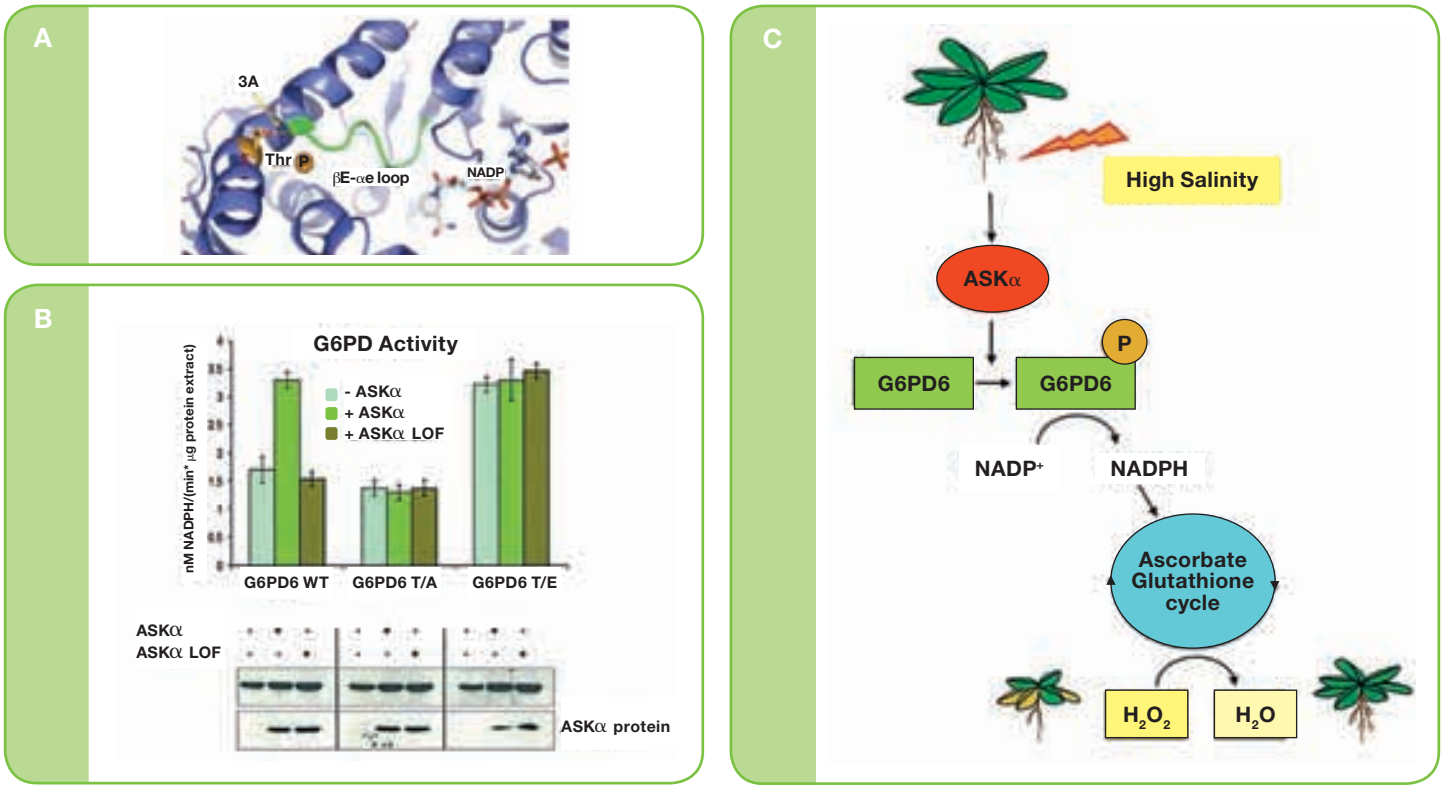


Fig. 2.
ASKα-mediated phosphorylation of G6PD contributes to maintaining the cellular redox balance under stress conditions.

(A) The crystal structure of human G6PD suggests that the threonine residue phosphorylated by ASKαα influences coenzyme binding. The threonine (stick presentation with carbon atoms colored in yellow) is positioned in close proximity to the ßE–αe loop (in green) which is part of the NADP binding region (NADP highlighted in stick representation with carbon atoms colored in white).

(B) Threonine (T) phosphorylation is necessary and sufficient for enhancing G6PD6 activity. G6PD activity was enhanced by ASKααbut not by loss-of-function ASKααLOF in cells expressing G6PD6. However, when protoplasts were transformed with the non-phosphorylatable mutant G6PD6 T/A, ASKααwas unable to stimulate G6PD activity. Cells expressing the phosphomimicking mutant G6PD6 T/E showed constitutively high G6PD activity, which could not be further stimulated by ASKα.

(C) ASKααis an important regulator of ROS detoxification and, thus, acclimation to salt stress. High salinity activates ASKαα which in turn, phosphorylates G6PD6, thereby stimulating its activity. Enhanced G6PD activity provides NADPH for the antioxidant system to remove excess ROS. Reduction of H_2O_2 to H_2O can then be mediated by the glutathione peroxidase cycle or by the ascorbate-glutathione cycle.

EPIGENETIC PATHWAY REQUIRED FOR BASAL HEAT TOLERANCE

Transcriptional reprogramming is crucial for plants to cope with fluctuating environmental conditions. Our recent work shows that a successful heat response depends on the integrity of epigenetic pathways and provides evidence that heat-dependent gene expression is influenced by closely located transposon sequences and read-through transcription.

We found that plant mutants of different components of the RNA-dependent DNA methylation (RdDM) pathway are hypersensitive to heat stress. Global comparative transcriptional analyses of plants deficient in NRPD2, a common subunit of RNA Polymerase IV and V, revealed that they mount an appropriate transcriptional response to heat but are unable to properly terminate the transcriptional stress response during recovery from heat stress, thus providing an explanation for the hypersensitivity of these plants to periods of high temperature. We studied the underlying mechanisms of several Pol IV–Pol V target loci in detail. The misexpression of protein-coding genes in *nrpd2* mutants recovering from heat correlated with defective epigenetic regulation of adjacent transposon remnants which involved the loss of control of heat stress-induced read-through transcription (Fig. 3).

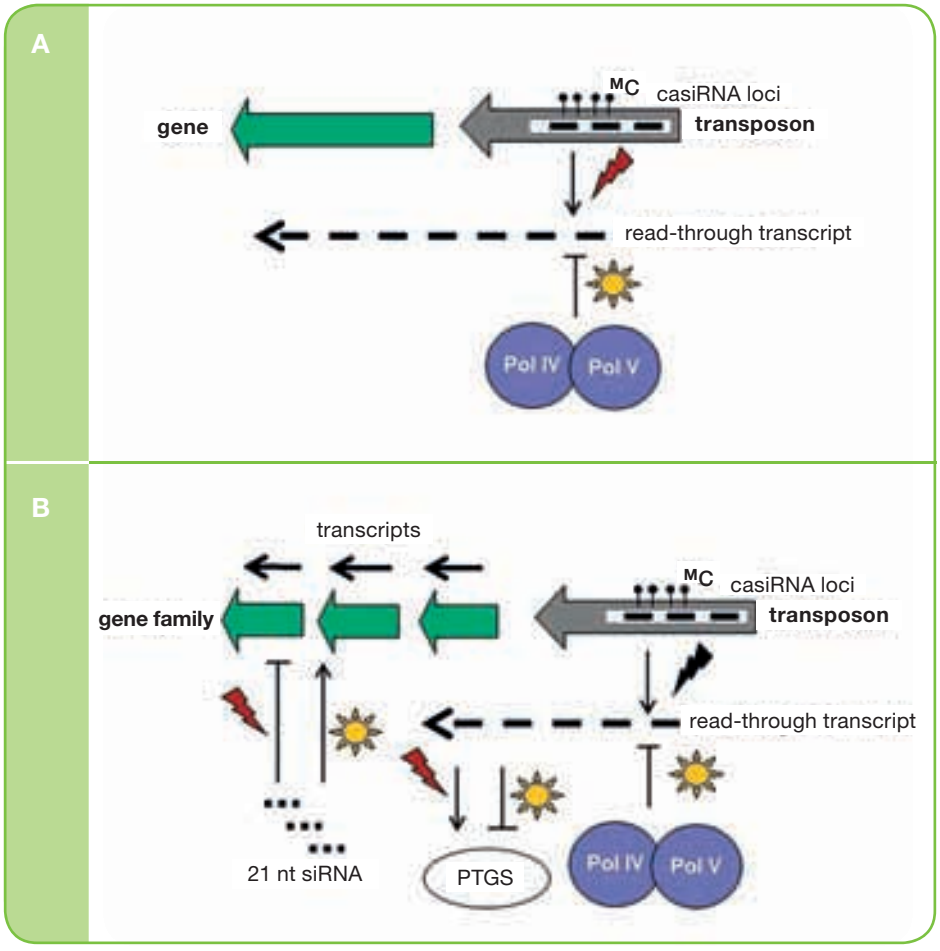


Fig. 3.

Mechanistic model of temperature-dependent regulation of RNA Polymerase IV and V (Pol IV–Pol V) target loci.

(A) Heat stress (⚡) leads to reactivation of euchromatin-dispersed RNA-dependent DNA methylation (RdDM) targets, initiating transcriptional read-through into adjacent protein-coding gene. Upon recovery (☼), re-silencing of reactivated transposons requires functional Pol IV–Pol V pathway.

(B) Transcriptional read-through of transposon might generate aberrant RNA and consequently 21 nt siRNA, thus negatively regulating expression of homologous genes by post-transcriptional gene silencing (PTGS). Upon recovery, resilencing of transposable element by RdDM will abolish a substrate for PTGS and restore expression of protein-coding genes.

Genetic and epigenetic changes in plants

The activity of genes, and thereby the characteristics of organisms, are influenced by both genetic and epigenetic information. These two components of inheritance can also mutually influence each other, and our group is interested in this interplay. Using the model plant *Arabidopsis*, we study the maintenance and modification of DNA by repair and recombination, the stability and flexibility of chromatin, and the consequences for gene expression under abiotic stress.

In addition to the DNA sequence information in the genome, epigenetic regulation represents another level of potentially heritable information that contributes to gene expression diversity in many eukaryotes. It is involved in defence against intruding DNA and RNA molecules, in stabilization, in the regulation of development and morphology and in response to environmental stimuli. Our group is interested in the interplay between genetic and epigenetic changes, in epigenetic diversity in different ecotypes and after exposure to abiotic stress. We study these aspects in *Arabidopsis thaliana* with well-established genetic, cytological and molecular methods, using mutants, reporter genes, chromatin analysis, flow sorting, fluorescence in situ hybridisation, high resolution microscopy, defined stress treatments, specific and genome-wide expression assays and bioinformatic approaches.

GENETIC AND EPIGENETIC ASPECTS OF ABIOTIC STRESS

Many exogenous conditions causing stress responses in plants can provoke genome instability, resulting in local mutations, transposon activation, or larger genome rearrangements. External factors can also result in epigenetic destabilization, changing chromatin features and expression of genes that are under epigenetic control. *Arabidopsis thaliana* has several genes and repetitive elements that are usually not expressed at ambient temperatures. However, they become transiently activated by prolonged

ORTRUN MITTELSTEN SCHEID

ortrun.mittelsten_scheid@gmi.oeaw.ac.at

Joined GMI in Jan 2004

PhD: University of Hamburg, Germany

Previously

– Postdoctoral Fellow: Max Planck Institute for Cell Biology, Ladenburg, Germany, 1985-1987. Hans-Georg Schweiger Lab

- Postdoctoral Fellow: Institute for Plant Sciences at the Federal Institute of Technology (ETH), Zurich, Switzerland, 1988-1992. Ingo Potrykus Lab

- Research Associate: Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland, 1992-2003. Jerzy Paszkowski Lab

- Interim Scientific Director: Gregor Mendel Institute of Molecular Plant Biology, Austrian Academy of Sciences, Vienna, Austria, 2007-2009

heat stress. Among them is one retrotransposon family that is transcribed after several hours of heat exposure and forms extrachromosomal DNA (Fig. 1, Cavrak et al., in press). We investigated the mechanism of its activation. Surprisingly, epigenetic regulation by DNA methylation is only a minor component: the long terminal repeat and promoter of the element is free of CG and CHG sites. However, the transposon has acquired the same heat-responsive element as plant heat shock genes. The recruitment of a major plant heat shock transcription factor to the element's promoter in periods of heat stress exploits the plant's stress response to achieve the transposon's activation, making it impossible for the host to respond appropriately to stress without losing control over the invader. Moreover, the pronounced heat response in dividing cells causes the preferential accumulation of the extrachromosomal transposon copies in meristematic tissues.

Reintegration of the transposon at new locations might be a rare event in wild type plants, but can certainly cause genetic changes as a secondary consequence of the heat exposure. Whether environmental stimuli also have the potential to directly induce stably heritable changes by modifying chromatin or other epigenetic features is a matter of intense debate. We know that heat stress can substantially modify the organization of heterochromatin within the nuclei. While most of the changes seem to be reversible, stochastic errors during the reassembly in nuclei of germ line cells could potentially be transmitted to the next generation (Fig. 2, Gutzat and Mittelsten Scheid 2012). However, the number of well-documented cases of so-called "transgenerational effects" based on epigenetic features is limited, and careful analysis is necessary to distinguish a hypothetical epigenetic memory from parental effects during seed set.

Group members:

Postdoctoral Fellows

Riccardo Aiese Cigliano*
Mattia Dona
Ruben Gutzat
Branislav Kusenda (25%)
Marie-Luise Zielinski

Technicians

Nicole Lettner
Selen Irez*

PhD Students

Jasmin Bassler
Vanja Cavrak
Tao Dumur
Meng Wang

Masters Student

Nina Daubel

Trainee

Marlene Bachleitner*

(*left the lab in 2013)

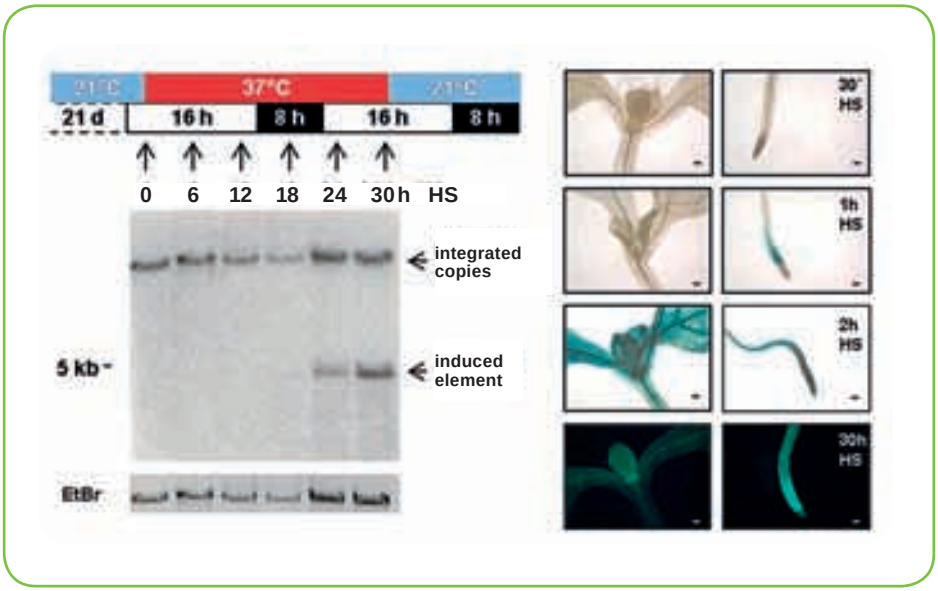


Fig. 1.

Activation of a retrotransposon during heat stress (HS). Exposure to elevated temperature induces accumulation of extrachromosomal DNA elements copied from the genomic templates (left). A reporter construct reveals increasing activity of the retrotransposon promoter in tissue with dividing cells during heat stress (right).

EPIGENETIC CONTROL OF DNA DAMAGE REPAIR AND RECOMBINATION

In contrast to the open question whether heritable chromatin-based stress effects are relevant, a role of chromatin configuration in connection with genetic changes is better documented. DNA damage, and especially breaks that occur in both DNA strands, are dangerous if not repaired before replication and cell division. Like other organisms, plants have diverse, efficient and highly interactive repair enzymes. However, DNA lesions must be accessible for these proteins even in the context of more or less densely packed chromatin. There is growing evidence that epigenetic features influence this accessibility and thereby determine genome stability, recombination and mutation rates. The density of chromatin is governed in part by multimeric chromatin remodeling complexes that can shift, remove, or insert nucleosomes, or exchange histone variants. We analyzed the role of the SWR1 complex, one of the putative remodellers and known to install one histone variant at transcriptionally active genes. We have assayed the DNA repair potential in mutants that lacked either one of three subunits of the complex (Rosa et al., 2013). All mutants showed increased sensitivity to several types of DNA damage, compared to the wild type. Combining the mutations with other defects in genes coding for known repair factors points towards a specific role of the complex in repair via homologous recombination. This was confirmed by assays

revealing reduced homologous recombination in somatic cells. Reduced fertility and impaired gametes in the mutants indicate that the chromatin remodeling complex is also required for meiosis. We are currently investigating the mechanism and kinetics of chromatin remodeling during repair and attempting to disclose more details of this vital process. Exploiting the genetic variation between *Arabidopsis thaliana* of different habitats and geographical origins, we also study factors that influence the rate of meiotic recombination between homologous chromosomes and the role of polyploidy for faithful DNA repair.

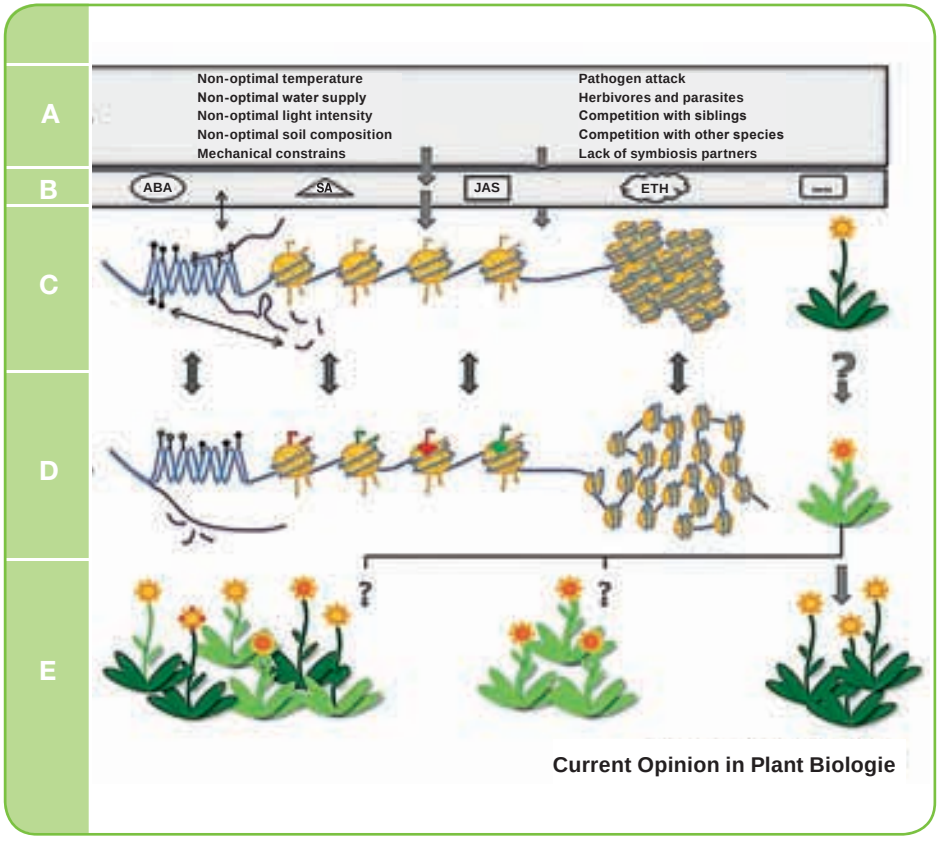
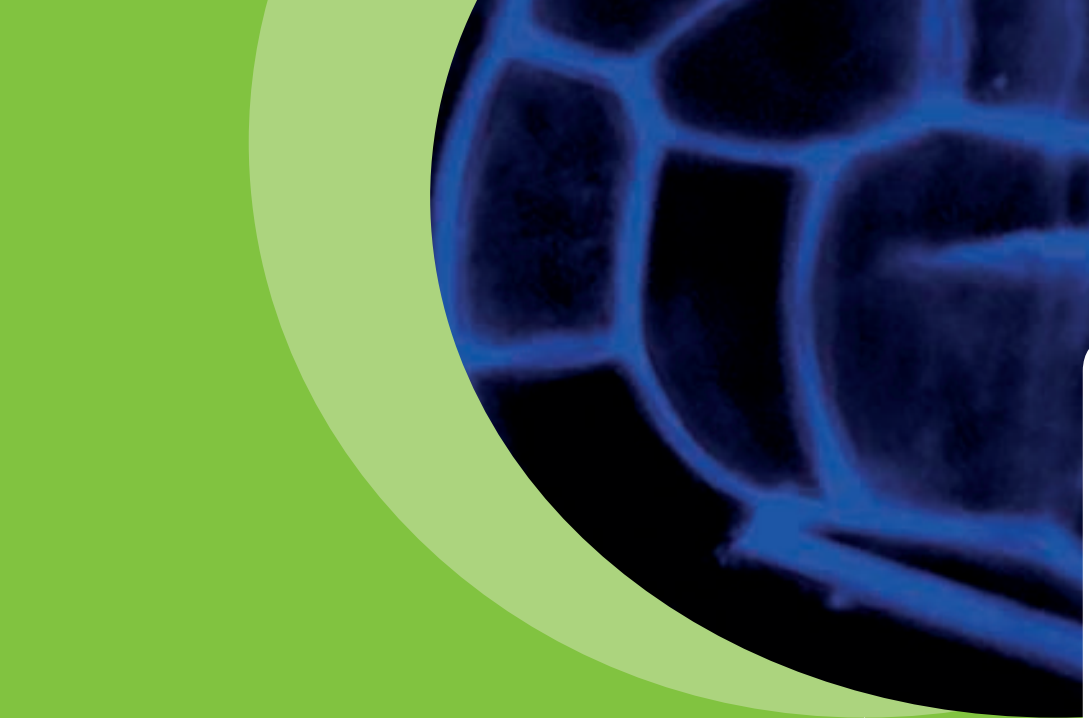


Fig. 2.

Stress conditions (A) with and without hormone signaling (B) can change gene expression and modify chromatin via DNA methylation, histone tail modifications, histone variant replacements, or nucleosome loss and chromatin de-condensation (C, D). These changes are largely reversible but can modify metabolic or morphologic plant features. Usually the new phenotypes are not transmitted to progeny. However, chromatin-associated changes have the potential to be heritable and to create epigenetic diversity (E).

Small RNA functions in plant embryos

After fertilization, the basic body plans of both plants and animals are established during early embryo development. However, despite its fundamental importance to developmental biology and agriculture, the molecular mechanisms that generate the most basic cell-types in plants remain largely uncharacterized. Short regulatory RNA molecules called microRNAs (miRNAs) are required for this formative phase of a plant's life largely for controlling when and where master regulators of cellular differentiation are active. Our major goal is to understand how these miRNAs shape the gene regulatory networks that control plant embryogenesis. We use a combination of cutting-edge experimental and computational approaches to study how these fascinating molecules regulate the earliest events in a plant's life.



MICHAEL NODINE

michael.nodine@gmi.oeaw.ac.at

Joined GMI in July 2012
PhD: University of Arizona, Tucson AZ, USA

Previously

– Postdoctoral Research Fellow, Whitehead Institute for Biomedical Research, USA, 2007-2012. David Bartel Lab

Group members:

Postdoctoral Fellows
Olga Bannikova
Divya Vashisht

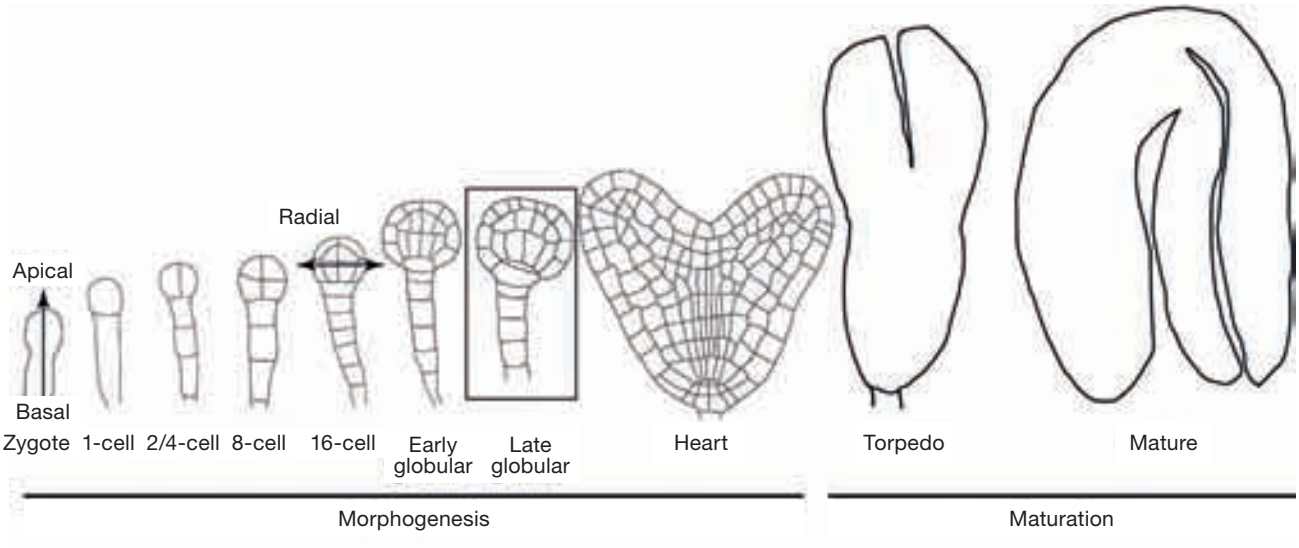
Technician
Ulf Naumann

PhD Students
Aleksandra Plotnikova

MicroRNAs are 20-24 nucleotide RNAs that regulate gene expression in both plants and animals. The DICER-LIKE1 (DCL1) protein is required for the biosynthesis of miRNAs, which are subsequently incorporated into ARGONAUTE (AGO) proteins to mediate the repression of target gene expression. Although plant miRNAs have near-perfect complementarity with binding sites of their known targets and typically mediate target RNA cleavage, recent studies suggest that plant miRNAs can repress gene expression at the translational level like their animal counterparts. Importantly, each plant miRNA family is predicted to specifically regulate only a few targets that typically encode transcription factors and other key developmental regulators.

Early *Arabidopsis* embryos undergo a series of stereotypical cell divisions to generate the basic plant body plan (Fig. 1). *Arabidopsis* embryos are therefore morphologically simple structures composed of diverse cell types, which makes them an ideal model to characterize the molecular basis of pattern formation. Previously we found that miRNA-deficient embryos exhibit widespread differentiation and developmental timing defects (Figs. 2 and 3). Because embryonic miRNAs appear to predominantly repress transcription factors, they likely have a large influence on the gene regulatory networks that control embryogenesis. Therefore, by studying embryonic miRNAs, not only will we uncover novel miRNA functions, but by identifying and characterizing their respective targets we may also discover master regulators of embryogenesis. Our research will yield insight into the molecular basis of plant embryo development, and should contribute to the general understanding of how small regulatory RNAs influence cellular differentiation.

A



B C

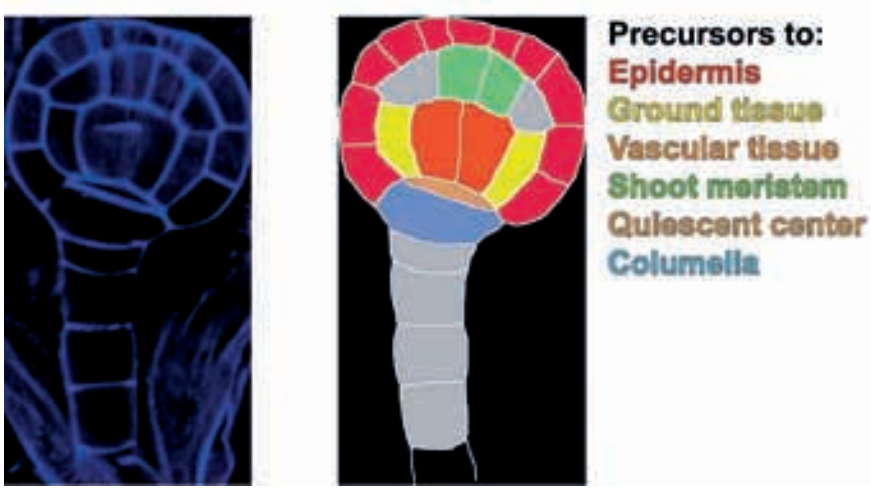


Fig. 1.

Arabidopsis embryogenesis. a) Illustrations of Arabidopsis embryos at various stages of development. Apical-basal and radial body axes are established during early embryogenesis and are labeled accordingly. Morphogenesis and maturation phases are labeled at the bottom. b) Confocal laser scanning microscopy image of late globular embryo stained with a cell wall fluorescent dye. c) Tracing of embryo shown in panel (b) with precursors to the fundamental cell-types of the plant body color-coded according to the key.

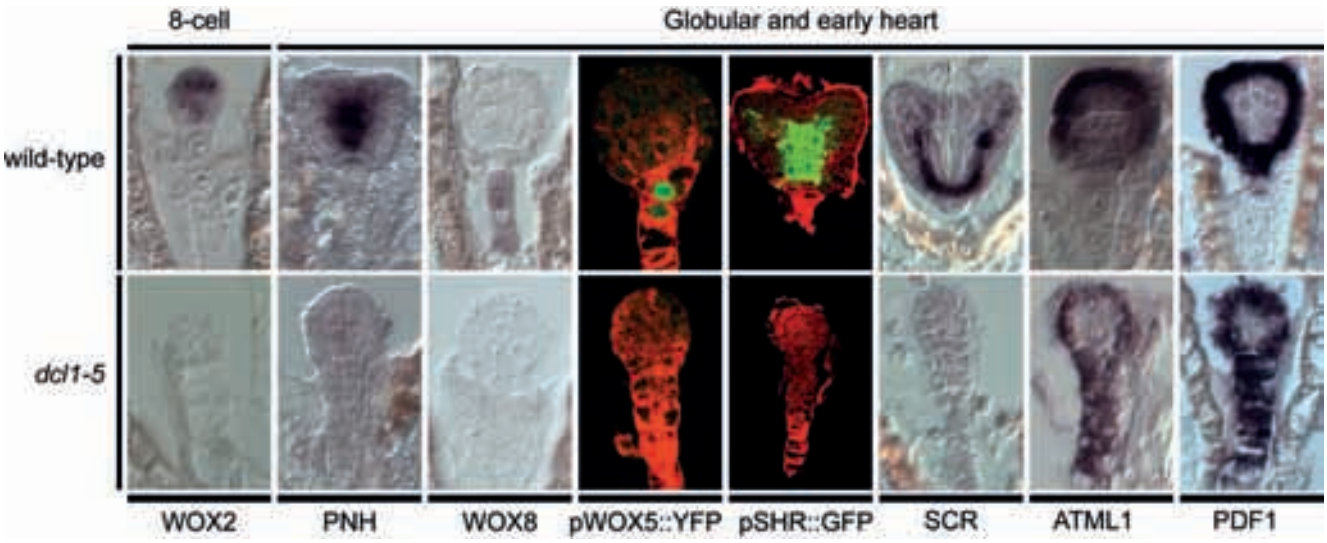


Fig. 2.

MicroRNA-deficient embryos have widespread patterning defects. Representative confocal laser scanning microscopy and RNA in situ hybridization images of cell-specific markers in wild type (top) and dcl1-5 (bottom) embryos, which lack miRNAs. Several markers are mis-expressed in dcl1 embryos indicating that miRNAs are required for multiple cell differentiation events. Adapted from Nodine and Bartel (2010) Genes & Development.

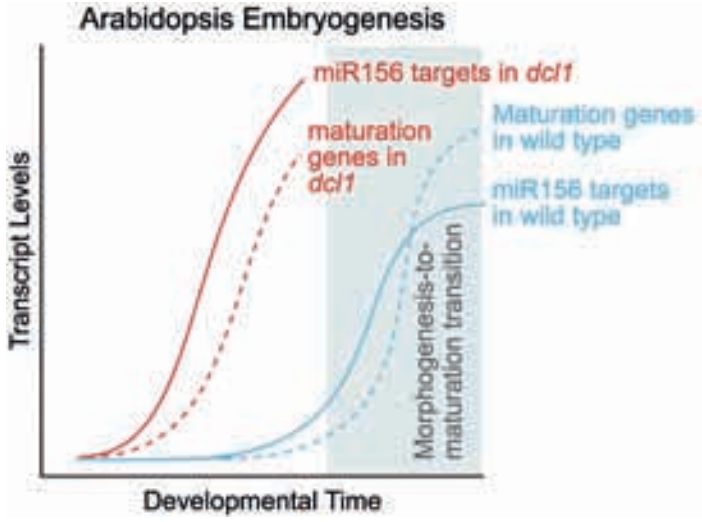


Fig. 3.

Model of plant miRNA functions during early embryogenesis. In wild-type Arabidopsis embryos, miR156-mediated repression of SPL10/11 transcription factors prevents precocious expression of maturation phase genes. Early dcl1 embryos lack miR156 and over-express SPL10/11, which in turn induce premature gene expression. We hypothesize that additional plant miRNAs also forestall expression of differentiation-promoting transcription factors. Adapted from Nodine and Bartel, Genes & Development, 2010.

Population genetics

Our group studies natural variation, the genetic basis for evolutionary change: how do differences between individuals at the level of DNA translate into differences we can see; how is this translation affected by the environment; and how do these differences affect fitness? Our research is quantitative, and involves computational analysis of genomic data in addition to field and bench work. While we focus on the model plant *Arabidopsis thaliana*, we also work on other species, including primates.

One of the most important challenges facing biology today is making sense of genetic variation. Understanding how genetic variation translates into phenotypic variation, and how this translation depends on the environment, is fundamental to our understanding of evolution, and has enormous practical implications for both medicine and agriculture. Our group studies this mapping from genotype to phenotype, primarily to understand evolution better. We also work directly at the sequence level, seeking to understand the forces that have shaped genomic variation within and between species. Our research is usually quantitative, with several group members doing exclusively computational work. The following is an overview of some of the many projects in which my group is involved.

GWAS IN *A. THALIANA* AND THE 1001 GENOMES PROJECT

Thanks to decreasing genotyping costs, there is currently great interest in so-called genome-wide association studies (GWAS), in which one attempts to identify genes responsible for variation simply by correlating genotype (typically in the form of single nucleotide polymorphisms) with phenotype. The model plant *A. thaliana* is ideally suited for such studies in that it naturally occurs as inbred lines which can be genotyped once and phenotyped repeatedly. For several years, my group has been spearheading a multi-group effort to make genome-wide association in *A. thaliana* a reality. We have genotyped of a set of roughly 1,300 lines using close to 250,000 SNPs, and play a major role in the 1001 Genomes

MAGNUS NORDBORG

magnus.nordborg@gmi.oeaw.ac.at

Joined GMI in Feb 2006

PhD: Department of Biological Sciences, Stanford University, USA

Previously

– Research Associate, Department of Ecology & Evolution, University of Chicago, USA, 1994-1997. Advisors: J. Bergelson, B. Charlesworth & D. Charlesworth

- Research Assistant Professor ("forskarassistent"), Department of Genetics, Lund University, Sweden, 1997-2000
- Assistant Professor, Molecular & Computational Biology, USC, USA, 2000-2004
- Associate Professor (tenured), Molecular & Computational Biology, USC, 2004-present

project that aims to fully sequence over 1,000 lines. In total, we will make over 2,000 densely genotyped or sequenced lines available to the *Arabidopsis* community, and we are also developing a public website that will allow anyone to carry out GWAS and coordinate as much phenotypic information as possible.

STATISTICAL METHODOLOGY FOR ASSOCIATION MAPPING

Our work on genome-wide association in *A. thaliana* has forced us to confront the problem of confounding in structured populations, which is much more severe in this organism than it is in standard human case-control studies. As the costs of genotyping and sequencing continue to decrease, genome-wide association will become an obvious choice for investigating the genetics of natural variation in many species, and methodology for dealing with confounding will be crucial. We are exploring a wide range of methods for handling this problem, focusing in particular on the effect of having several major loci under selection present.

THE GENETICS OF ADAPTATION

We are carrying out large-scale GWAS seeking to understand the genetic basis of variation for adaptively important traits like flowering time, dormancy, and cold tolerance. The GWAS results are complemented with a variety of methods to confirm results. Our goal is to achieve as complete and understanding of the genetics of these traits as is possible.

Investigating the adaptive significance of any trait also requires field studies. We are using field sites in northern and southern Sweden (Fig. 1) for reciprocal transplant competition experiments of both natural inbred lines and the offspring of crosses. The objective is to map the genes responsible for fitness differences, and to molecularly characterize them.

Group members:

Postdoctoral Fellows

Manu Dubin
Ashley Farlow
Daniele Filiault
Matthew Horton
Arthur Korte
Eriko Sasaki
Hannes Svardal
Takashi Tsuchimatsu

Technicians

Stephanie Arnoux
Pamela Korte
Viktoria Nizhynska
Viktor Voronin

Programmers/ Bioinformaticians

Alexander Platzer
Ümit Seren

PhD Students

Gökce Aköz
Envel Kerdaffrec
Dazhe Meng
Polina Novikova
Fernando Rabanal
Pei Zhang

Trainees

Rajul Garg*
Vakish Kumar*
Neha Lahri*
Ayush Maheshwari*
Joanna Jagoda
Aleksandra Lewandowska (Summer School)*

(*left the lab in 2013)

Fig. 1.
a) Common garden experiment;
b) Close-up of a dispersal experiment

GENOMIC ANALYSIS OF THE GENOTYPE–PHENOTYPE MAP

We are a major part of an NIH-funded 'Center of Excellence in Genomic Science' that aims to investigate the regulatory networks by which genetic variation leads to phenotypic variation in traits like flowering time. Our group has carried out genome-wide expression profiling of 200 lines under different environment conditions, and are complementing this information with genome-wide epigenetic profiling. The goal is to integrate the resulting multi-level data to infer causal relationships. Rather than simply finding associations between genotype and phenotype, we seek to infer how the genotype affects the phenotype.

MOLECULAR EVOLUTION OF *ARABIDOPSIS*

We are heavily involved in the comparative analysis of the genomes of *A. thaliana* and its close relatives. Questions include the evolution of genome size, the effects of polyploidy or switching to self-fertilization. For example, we are currently exploring the pattern of polymorphism in *A. suecica*, an allotetraploid hybrid between *A. thaliana* and *A. arenosa* (Fig. 2) that seems to have involved a massive bottleneck and complete loss of genetic variation.

THE GENETICS OF SPECIES DIFFERENCES IN *AQUILEGIA*

As part of an international collaboration, we are studying the genetics of species differences in the columbine genus, Aquilegia (Ranunculaceae). The genus is an excellent example of a recent, rapid adaptive radiation and offers many opportunities to study genetic changes at different stages in the speciation process. We have focused on two North American species, *A. formosa* and *A. pubescens*. As illustrated in Figure 3, the species exhibit distinct differences in floral characters that influence pollinator preference, thereby restricting gene flow between them. However, the two species are completely inter-fertile and form natural hybrid zones. We have demonstrated that the two species are very closely related at the genetic level, with most polymorphisms shared between the species, and little divergence in allele frequencies, and we are now trying to identify the genes responsible for the phenotypic differences through GWAS.

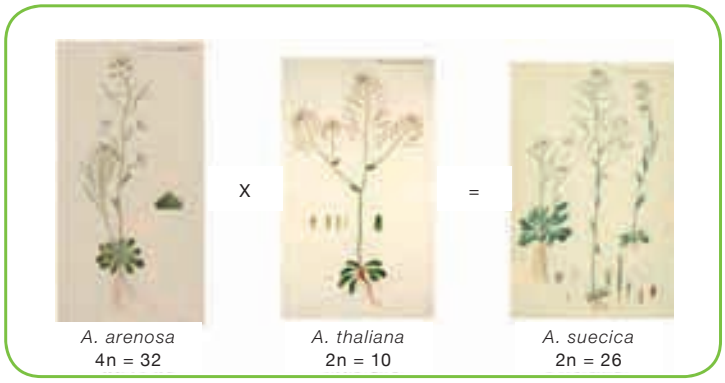
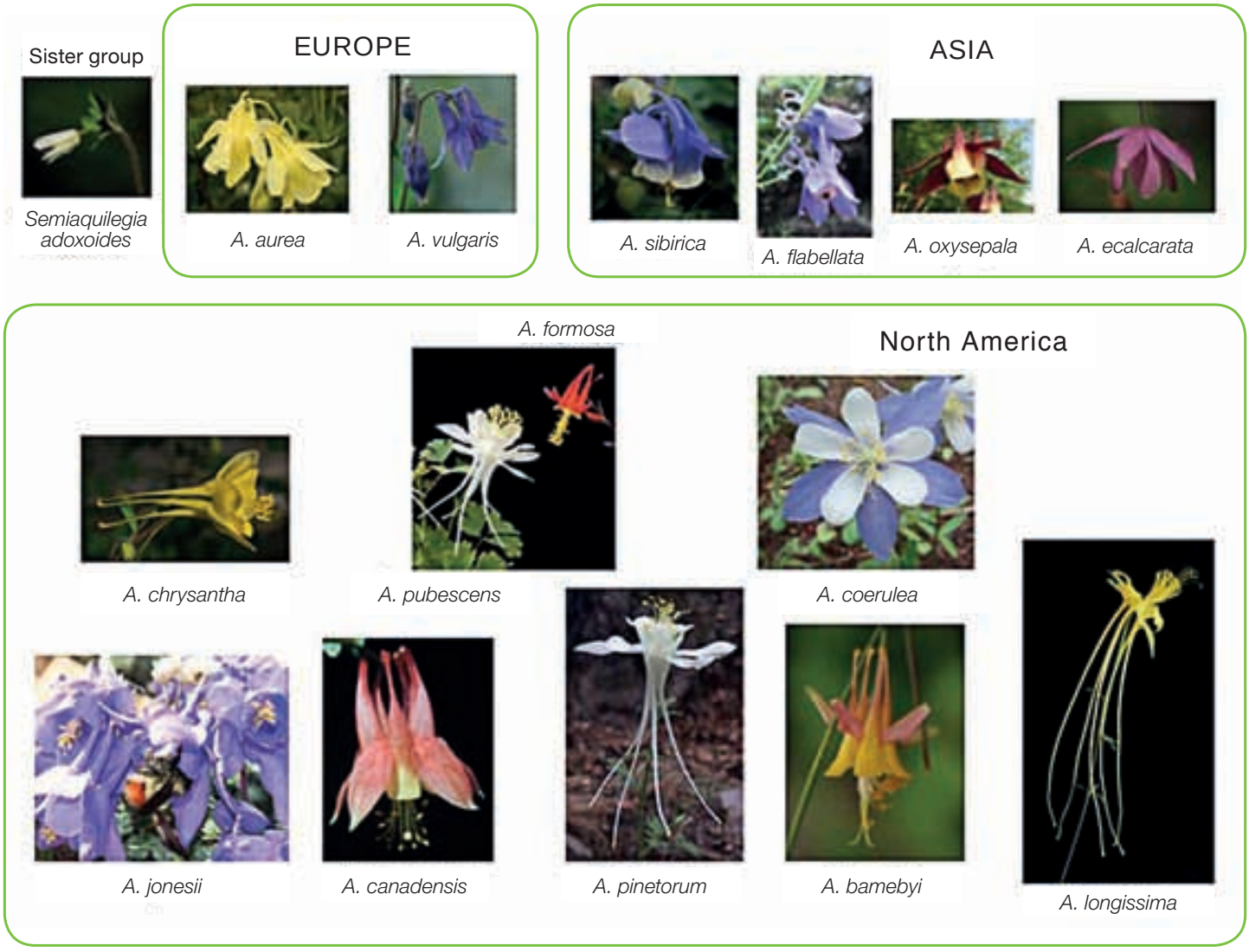


Fig. 2. The origin of A. suecica.



POPULATION GENETICS OF AFRICAN GREEN MONKEYS

The African green monkey (*Cercopithecus sp.*) is a common Old World monkey, spread throughout much of Africa, and introduced by humans to the Caribbean. It is also kept in large colonies for behavioral and biomedical research. We are part of an international consortium to develop genomic resources for African green monkeys through extensive sequencing and SNP typing of samples from wild-collected samples. Our primary interest is the genetics of subspecies differences across the African continent.

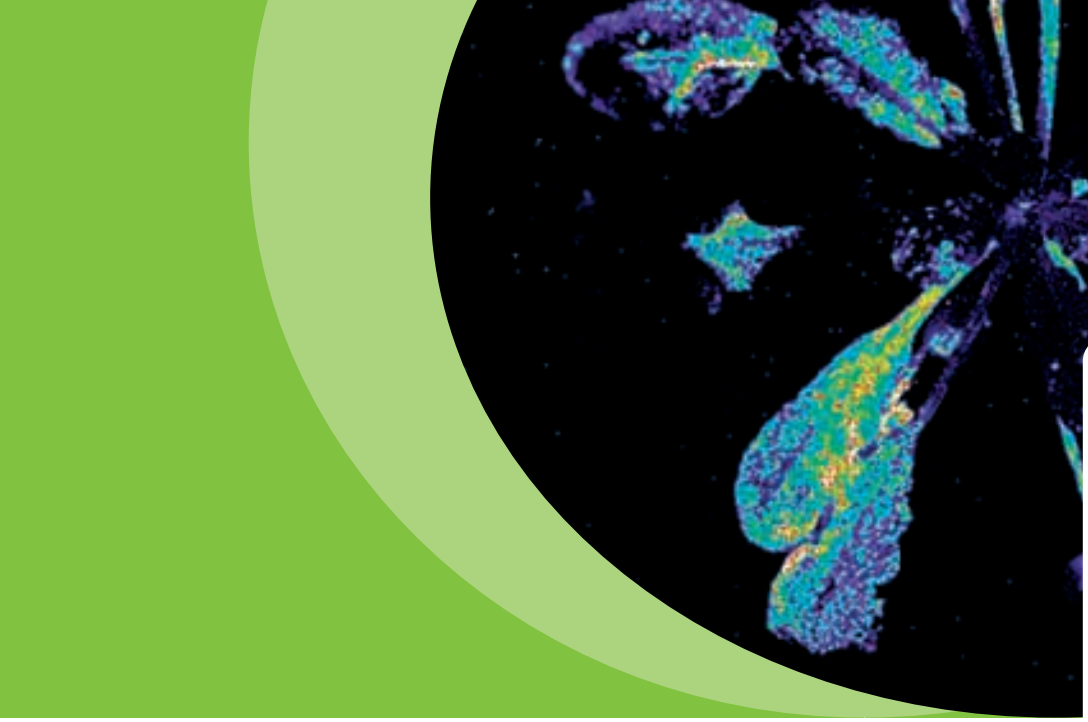
Fig. 3. Columbine species currently being sequenced by JGI.We focus in particular on the sympatric A. formosa and A. pubescens. (Courtesy of Scott Hodges, UCSB)

Genome stability: telomeres and meiosis

Chromosome integrity and their proper partitioning to daughter cells are essential prerequisites for stable inheritance of genetic information over multiple cell divisions. We study processes governing genome stability and chromosome separation during cell division. Our research aims to decipher the molecular mechanisms that stabilize and protect chromosome ends, so-called telomeres, from being perceived by the cell as DNA damage. We also study regulatory pathways that define meiosis, the cell division necessary for sexual reproduction and generation of haploid gametes.

MECHANISMS OF CHROMOSOME END PROTECTION

Telomeres are indispensable elements of eukaryotic chromosomes that are important for the complete replication of linear genomes and for chromosome end protection. These functions are essential for genome stability and long-term cell survival. The key feature of telomeres is their capability to differentiate native chromosome ends from deleterious DNA double-strand breaks. This is achieved by assembling chromosome termini in elaborate, high-order nucleoprotein structures, which in most organisms encompass telomeric DNA, specific telomere-associated proteins, and general chromatin and DNA repair factors. We developed a number of techniques for detailed structural analysis of telomeric DNA, which we use in combination with genetic tools available in *Arabidopsis* to decipher mechanisms that govern chromosome end protection. In our work we discovered that the opposite ends of a chromosome adopt different end protective structures, whose formation is dictated by the mode of DNA replication (Fig. 1). The telomeres replicated by the lagging-strand mechanism end with single stranded DNA protrusions and their maintenance depends on CST, a recently identified protein complex, mutations of which underlie several human genetic disorders. The telomeres replicated by the leading-strand mechanism terminate as blunt-ended DNA that is protected by the evolutionarily conserved DNA repair complex Ku. In our research we aim to understand how Ku mediates protection of these telomeres without triggering a DNA repair reaction.



KAREL RIHA

karel.riha@gmi.oeaw.ac.at

Joined GMI in June 2003

PhD: Masaryk University, Brno, Czech Republic

Previously

- Postdoctoral Research Associate: Department of Biochemistry & Biophysics, Texas A&M University, USA, 1999-2002. Dorothy Shippen Lab
- Senior Postdoctoral Fellow: Gregor Mendel Institute of Molecular Plant Biology, Austrian Academy of Sciences, Vienna, Austria, 2003-2005

GETTING INTO, THROUGH, AND OUT OF MEIOSIS

The alteration of haploid and diploid cell generations during the sexual life cycle requires meiosis, a specialized cell division that enables the formation of haploid gametes from diploid cells. Meiosis occurs only once during the life cycle, and the transition from the mitotic to meiotic mode of chromosome partitioning requires extensive remodeling of the cell cycle machinery. We devote part of our research efforts to deciphering mechanisms that define meiosis in plants. The cell cycle progression is driven by cyclin-dependent kinases and associated cyclins that regulate CDK activity and confer substrate specificity. The cyclin gene family has undergone a massive expansion in angiosperm plants, which has raised the question whether some of these cyclins evolved specific meiotic functions. We systematically analyzed two cyclin gene families in *Arabidopsis* and identified eight cyclins that are meiotically expressed and involved in diverse meiotic processes (Fig. 2). Furthermore, we have discovered a genetic module, consisting of SMG7 and TDM1, that inhibits meiotic CDKs and facilitates transition from meiosis to mitosis (Fig. 3). Our current work is directed towards molecular understanding of the SMG7/TDM1 function and characterization of additional genes that are involved in meiotic progression.

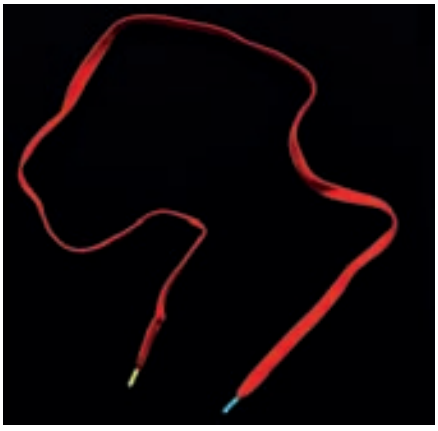


Fig. 1.

Cartoon illustrating our view on chromosome end protection in Arabidopsis. The shoelace depicts a chromosome and differently coloured aglets indicate distinct telomere architectures formed at the opposite ends of the chromosome.

Group members:

Postdoctoral Fellows

Petra Bulankova
Albert Cairó
Nick Fulcher
Anita Kazda
Branislav Kusenda (25%)
James Matthew Watson

Technician

Svetlana Akimcheva

PhD Students

Claudio Capitao
Elisa Derboven
Jiradet Gloggnitzer
Sona Valuchová
Kateryna Vashutina
Sorin Tanasa

Trainee

Andrea Plecenicova

Fig. 2.

Inactivation of cyclin B3;1 affects cell wall formation in male meiotic cells (pollen mother cells, PMC). Transversal section through the anther lobe of an Arabidopsis cycb3;1 mutant visualised by transmission electron microscopy. PMCs in the centre of the anther lobe are surrounded by the layer of tapetum cells (Tp). PMCs are characterized by a thick layer of callose (c) that forms beneath the cell wall. Arrow points to an aberrant cell wall invasion into PMC, which is one of the characteristic features of cycb3;1 mutants. Scale bar indicates 5µm.

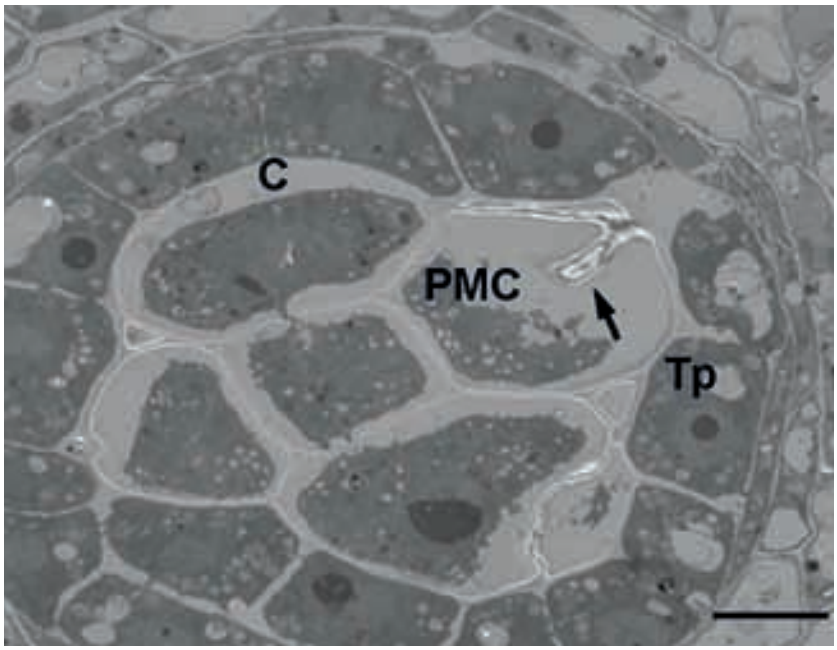
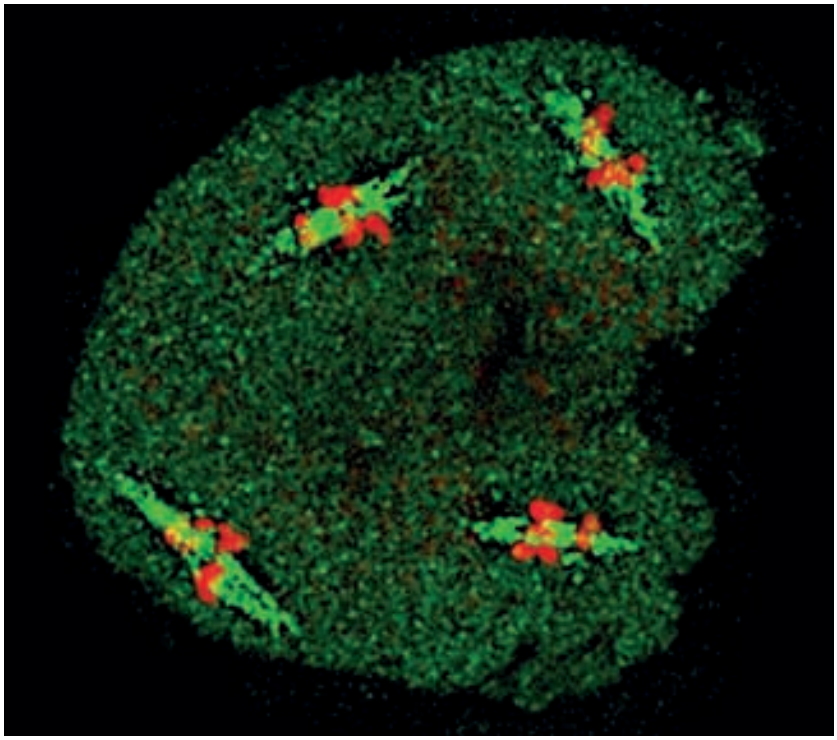


Fig. 3.

Plants with dysfunctional TDM1 protein are infertile due to an aberrant meiotic exit. Instead of leaving meiosis and entering mitotic cell cycle, tdm1 mutants initiated another meiotic division after formation of haploid nuclei. The attempt to separate unreplicated chromatids results in genome fragmentation and cell death. Picture shows third meiotic division in tdm1 mutants. Chromatin is shown in red, spindle detected with the alpha-tubulin antibody is stained in green.



NONSENSE MEDIATED RNA DECAY AND ITS ROLE IN PATHOGEN RESPONSE

Errors that occur during transcription and splicing of mRNA may lead to translation of aberrant proteins and thereby severely impair cellular metabolism. RNA quality control mechanisms are therefore important for long-term cell survival. Nonsense mediated RNA decay (NMD) is a key pathway involved in degradation of aberrant transcripts that contain premature stop codons. NMD is essential in higher eukaryotes, but its physiological function is still not fully understood. Besides its role in meiosis, SMG7 is also an important NMD factor. In the course of our functional analysis of this gene, we noticed that smg7 mutations trigger strong pathogen response in *Arabidopsis*. Our further work revealed that activation of the pathogen signaling pathway is a general physiological response to impaired NMD. In addition, we discovered that NMD efficiency is decreased upon bacterial infection, suggesting a regulatory role of NMD in the plant immune response. Considering the evolutionarily conserved nature of the NMD mechanism, modulation of this pathway may provide an attractive strategy for enhancing plant disease resistance (Fig. 4).

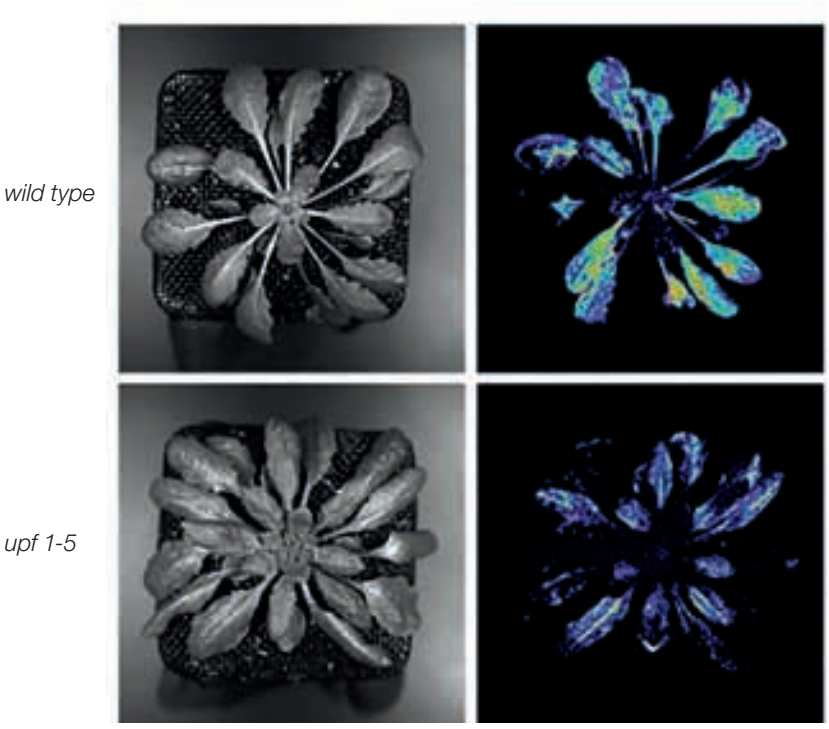


Fig. 4.

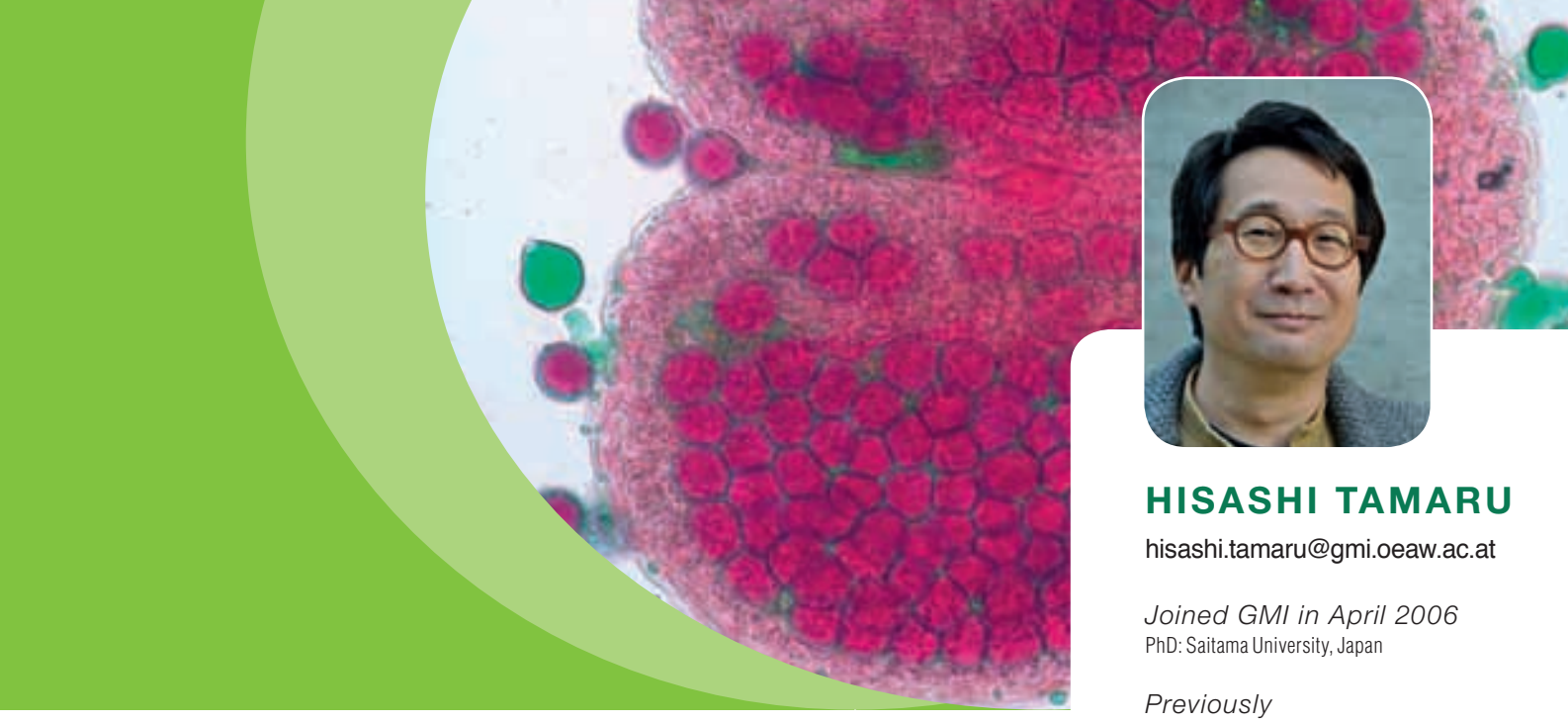
Activation of a defence response in NMD deficient plants leads to increased resistance to bacterial pathogen Pseudomonas syringae. Growth of bacteria in wild type and upf1-5 mutant plants was monitored by using a light emitting strain of P. syringae that contains the lucipherase operon from a bioluminescent bacterium Photorhabdus luminescens.

Control and function of epigenetic reconfigurations during pollen development

Research in the group focuses on investigating the molecular basis of how dynamic epigenetic reconfigurations in pollen, the male gametophyte or sexual form of a plant in the alternation of generations, contribute to development and reproduction in the model plant *Arabidopsis thaliana.* We use microscopy imaging, flow cytometry and high-throughput genomics to search for and clarify novel epigenetic mechanisms controlling pollen development and genome stability across generations.

A vital feature of gametogenesis is resetting genetic and epigenetic plans for totipotency toward the next generation. Current evidence suggests that genome-wide epigenetic reprogramming occurs in the germ cell lineage of both animals and plants, involving active DNA demethylation, *de novo* DNA methylation, and replacement of histones and their modifications. Epigenetic modifications play important roles in genomic imprinting, control of transposons, and normal development of animals and plants. Unlike the situation in animals, where the male gamete (sperm) represents the direct product of meiosis, flowering plants form the male gametophyte (pollen) by two post-meiotic mitoses. A pollen grain contains one vegetative cell and two sperm cells. The primary role for the vegetative cell in plant sexual reproduction is to germinate and form a pollen tube that brings the sperm cells to the female gametophyte for fertilization. The model plant *Arabidopsis thaliana* provides powerful genetic and genomic approaches and has solidified its status as one of the premier models for studying epigenetic control of development. Recent studies in *A. thaliana* have revealed extensive reconfigurations of chromatin dynamics, DNA methylation and small RNA synthesis in the vegetative cell that impacts on the integrity of the sperm cell genome and pollen function.

We use cytogenetic approaches to visualise gene functions in large-scale chromosome dynamics in the sperm and vegetative cell nuclei. We purify highly homogenous populations of these two nucleus types from



HISASHI TAMARU

hisashi.tamaru@gmi.oeaw.ac.at

Joined GMI in April 2006
PhD: Saitama University, Japan

Previously

– Postdoctoral Fellow, Max Planck Institute for Molecular Genetics, Berlin, Germany, 1994-1996 Vincenzo Russo Lab

- Postdoctoral Fellow, Max Planck Institute for Molecular Genetics, Germany, 1996. Thomas Trautner Lab

- Postdoctoral Fellow, University of Oregon, Eugene, OR, USA, 1996-2004. Eric Selker Lab

- Postdoctoral Fellow, National Institute of Genetics, Japan, 2004-2006. Tetsuji Kakutani Lab

wild-type and various mutant lines by fluorescence-activated cell sorting (FACS) to molecularly analyse their chromatin and transcription profiles. We employ automated fluorescence microscopy and image processing to discover genes involved in the control of chromatin dynamics.

CONTROL AND FUNCTION OF ACTIVE HETEROCHROMATIN DECONDENSATION IN POLLEN

Pollen - the flowering plant male gametophyte - is composed of two sperm cells engulfed within the cytoplasm of the vegetative cell, the companion cell of the sperm, and provides a simple attractive model to study germ cell epigenetics. The single vegetative cell nucleus demands a large quantity of ribosomes for massive protein synthesis in order to form a pollen tube that very quickly grows to a great length in the pistil and is able to transport two sperm cells to the female gametophyte for double fertilisation. Our research focuses on an unexplored mechanism of rRNA gene activation by which pollen achieves the task of forming this tube. Animal and plant genomes contain hundreds of tandem repeats of ribosomal RNA (rRNA) genes (or rDNAs) encoding rRNAs - the major structural and functional components of the ribosome. rRNA synthesis and cell growth are coupled processes. Because cellular demands for ribosomes vary during development, rDNA repeats loci form “facultative heterochromatin” that is able to revert from silent to active state, and vice versa, to control the number of active rRNA gene copies. Silent portions of rDNA loci coincide with “constitutive heterochromatin” – the densely staining condensed, constantly repressive environment for genes - and are localised at the external periphery of the nucleolus, a compartment in the cell nucleus where rRNA gene transcription and ribosome assembly take place. On the other hand, active rDNA repeats occur within the nucleolus to be transcribed. Centromeric constitutive heterochromatin is required

Group members:

Postdoctoral Fellows

Adriana Machlicova
Vera Schoft
Zsuzsanna Merai

Technicians

Janos Bindics
Lucyna Slusarz

PhD Student

Atil Saydere

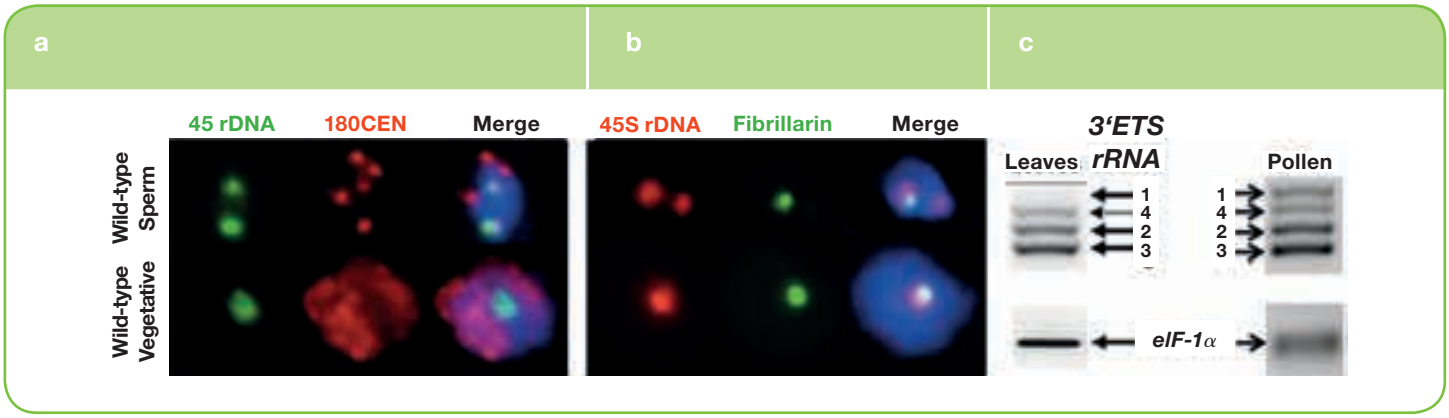


Fig. 1.
The vegetative cell actively decomposes centromeric and rDNA heterochromatin to transcribe all sets of rRNA genes in pollen. a, b) Dual fluorescence in situ hybridization (FISH) of 45S rDNA and 180-bp centromeric (180CEN) repeats (a) and FISH-immunolocalization of 45S rDNA loci and the nucleolus marker fibrillarin (b) in wild-type sperm (upper) and vegetative (lower) cell nuclei of pollen. DNA was counterstained with DAPI. c) RT-PCR detection of rRNA variants in wild-type leaves and total pollen. A subclass of long rRNA variant (arrow 1) is absent in leaves but detected in pollen.

for establishing centromeres and kinetochore assembly and chromosome segregation. We reported previously that the *A. thaliana* vegetative cell undergoes large-scale active de-condensation of centromeric heterochromatin, coincident with global loss of centromere-specific variant histone CenH3 and di-methylated histone H3 Lys9 (H3K9me2). By contrast, and for comparative purposes, chromatin in the adjacent sperm cells, which are separated from the vegetative cell by only one cell division, remains condensed (Fig. 1a). The biological significance and mechanism of this nuclear process remain unclear. Although quite a lot is known about mechanisms of heterochromatin formation and gene silencing, little is known about the reverse process of active heterochromatin decondensation.

We have now shown that two unlinked rDNA loci are invariably clustered together (Fig. 1a) and cololalise with the nucleolus (Fig. 1b). Unlike in somatic leaf nuclei in which a class of long rRNA gene repeats representing ~50% of the total rDNA pool is silenced, all four rRNA variants are expressed in the vegetative cell in pollen (Fig. 1c). We used state-of-the-art semi-automated fluorescence microscopy and image processing systems and identified a gene *IZANAGI (IGI)*, named after a Nipponese god of fertility, in which mutations affect both the active heterochromatin decondensation and pollen tube formation. *IGI* encodes an AAA (ATPases Associated with diverse cellular Activities) molecular chaperone homologous to human p97, which is implicated in a variety of essential biological processes and diseases including motor neuron degeneration and dementia. The *igi* mutation regains condensed CenH3-containing centromeres (Fig. 2a, c) and its flanking H3K9me2-enriched pericentromeric heterochromatin (Fig. 2c) in the vegetative cell. AAA are highly conserved from archaebacteria to mammals, supporting the view that the *IGI*-mediated heterochromatin decondensation has a positive function(s) in pollen. Although *igi* pollen undergo mitoses normally, *igi* mutant alleles are consistently not transmitted paternally, which primarily reflects defective pollen tube formation (Fig. 2b). In *igi* mutant vegetative cell nuclei, two condensed heterochromatic domains of rDNA loci frequently coincide with centromeric heterochromatin (Fig. 2d) at the external periphery of the nucleolus (Fig. 2e). Taken together, our results suggest a novel mechanism of bulk rRNA gene activation in pollen. The vegetative cell likely benefits from not

needing a centromere function and operates the *IGI* AAA-ATPase to actively disassemble centromeric constitutive and rDNA facultative heterochromatin complex, thereby releasing vast portions of rDNA loci into the nucleolus to fuel pollen tube formation. Our finding is a milestone because it reveals that IGI links heterochromatin decondensation to rRNA gene activation to pollen development. We anticipate this IGI function of full rRNA gene activation to be relevant to other terminally differentiated cell types such as neurons in which a single nucleus drives tube growth.

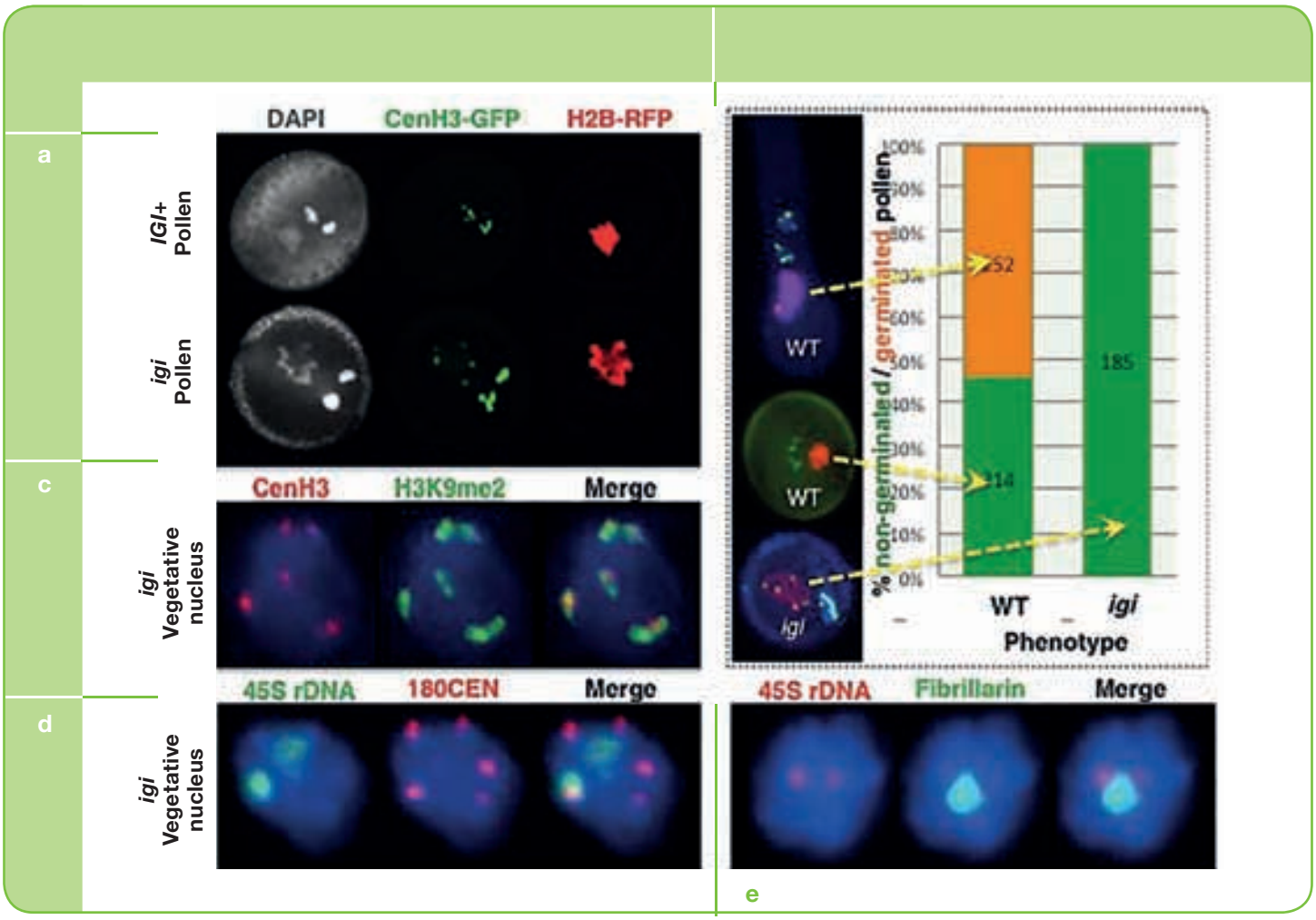


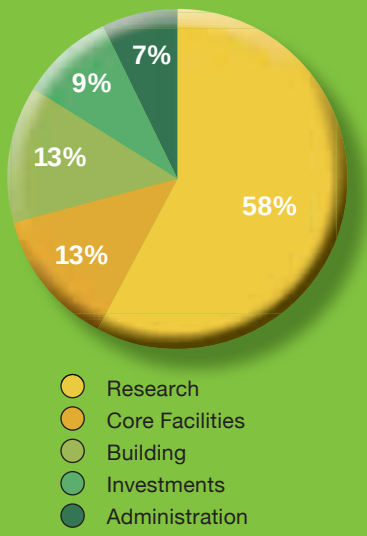
Fig. 2.

IGI/p97 mediates active decondensation of centromeric and rDNA heterochromatin complex and is required for pollen tube formation. a) Fluorescence microscopy of IGI wild-type (upper) and igi mutant (lower) pollen grain carrying a GFP-tagged CenH3 under the control of its native promoter (pCenH3::CenH3::GFP) and a RFP-tagged H2B driven by a vegetative cell-specific LAT52 promoter (pLAT52::H2B::RFP). The wild-type vegetative cell undergoes decondensation of centromeric heterochromatin, thus showing no CenH3-GFP signals in the RFP-positive vegetative cell nucleus, whereas five condensed CenH3-GFP centromeric foci are detected in the igi vegetative cell nucleus. b) Percentage of germinated (orange bar) and non-germinated (green bar) pollen grains from IGI/igi plants were inspected for the igi phenotype. Numbers on the bars indicate the number of pollen examined. c-e) Dual immunolocalisation of CenH3 and H3K9me2 (c), dual FISH of 45S rDNA and 180-bp centromeric (180CEN) repeats (d), and FISH-immunolocalization of 45S rDNA loci and nucleolar fibrillarin (e) in igi mutant vegetative cell nuclei. DNA was counterstained with DAPI.

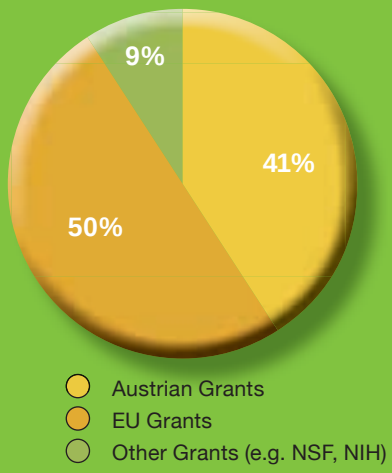
Key Facts

(as of 31 December 2013)

GMI Expenditures %



Research Grants %



Publications

Busch Group

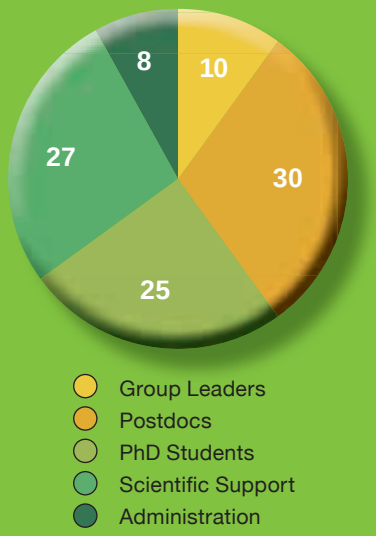
Meijón M, Satbhai S, Tsuchimatsu T, Busch W (2013) Genome-wide association study using cellular traits identifies a new regulator of root development in *Arabidopsis*. Nat. Genet. doi: 10.1038/ng.2824

Kaufmann K, Busch W (2013) Plant genomics: from weed to wheat. Genome Biol. 14(6):308. Abstract: A report on the first 'Plant Genomics Congress' meeting, held in London, UK, 12-13 May 2013.

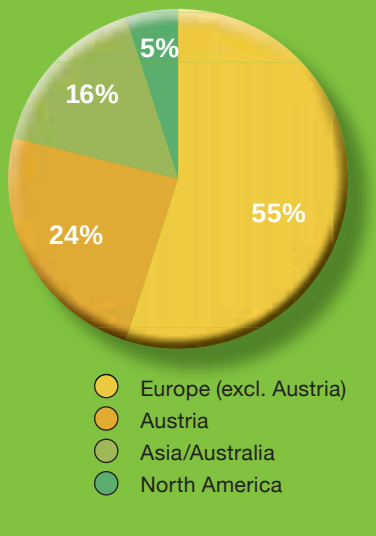
Book chapter: Brand LH, Satbhai SB, Kolukisaoglu Ü, Wanke D (2013) Limits And Prospects Of Methods For The Analysis Of DNA-Protein Interaction. In: The Analysis of Regulatory DNA: Current Developments, Knowledge and Applications Uncovering Gene Regulation. eISBN: 978-1-60805-492-3, ISBN: 978-1-60805-711-5, Berendzen (ed.), Kilian, Wanke (co-eds.): Bentham Science.

Ischebeck T, Werner S, Krishnamoorthy P, Lerche J, Meijón M, Stenzel I, Löfke C, Wiessner T, Im YJ, Perera IY, Iven T, Feussner I, Busch W, Boss WF, Teichmann T, Hause B, Persson S, Heilmann I (2013) Phosphatidylinositol 4,5-Bisphosphate Influences PIN Polarization by Controlling Clathrin-Mediated Membrane Trafficking in *Arabidopsis*. Plant Cell. doi: 10.1105/tpc.113.116582

GMI Staff by Function (Head Count)



GMI Staff - Nationalities %



Greb Group

Brackmann K, Greb T (2013) Long- and short-distance signaling in the regulation of lateral plant growth. Physiol Plant.

Agusti J, Greb T (2013) Going with the wind - adaptive dynamics of plant secondary meristems. Mech Dev 130(1):34-44. doi: 10.1111/ppl.12103

Ischebeck T, Werner S, Krishnamoorthy P, Lerche J, Meijón M, Stenzel I, Löfke C, Wiessner T, Im YJ, Perera IY, Iven T, Feussner I, Busch W, Boss WF, Teichmann T, Hause B, Persson S, Heilmann I (2013) Phosphatidylinositol 4,5-Bisphosphate Influences PIN Polarization by Controlling Clathrin-Mediated Membrane Trafficking in *Arabidopsis*. Plant Cell. doi: 10.1105/tpc.113.116582

Jonak Group

Popova O, Dinh H, Aufsatz W, Jonak C (2013) The RdDM pathway is required for basal heat tolerance in *Arabidopsis*. Mol Plant 6(2):396-410.

Khan M, Rozhon W, Bigeard J, Pflieger D, Husar S, Pitzschke A, Teige M, Jonak C, Hirt H, Poppenberger B (2013) Brassinosteroid-regulated GSK3/Shaggy-like kinases phosphorylate mitogen-activated protein (MAP) kinase kinases, which control stomata development in *Arabidopsis thaliana*. J. Biol. Chem. 288(11):7519-27.

Matzke Group

You W, Lorkovic Z, Matzke A, Matzke M (2013) Interplay among RNA polymerases II, IV and V in RNA-directed DNA methylation at a low copy transgene locus in *Arabidopsis thaliana*. Plant Mol. Biol. 82(1-2):85-96



Mittelsten Scheid Group

Cigliano R, Cremona G, Paparo R, Termolino P, Perrella G, Gutzat R, Consiglio M, Conicella C (2013) Histone deacetylase AtHDA7 is required for female gametophyte and embryo development in *Arabidopsis*. Plant Physiol. 163(1):431-40.

Long Q, Rabanal F, Meng D, Huber C, Farlow A, Platzer A, Zhang Q, Vilhjálmsson B, Korte A, Nizhynska V, Voronin V, Korte P, Sedman L, Mandáková T, Lysak M, Seren Ü, Hellmann I, Nordborg M (2013) Massive genomic variation and strong selection in *Arabidopsis thaliana* lines from Sweden. Nat. Genet. 45(8):884-90.

Rosa M, Von Harder M, Cigliano R, Schlögelhofer P, Mittelsten Scheid O (2013) The Arabidopsis SWR1 chromatin-remodeling complex is important for DNA repair, somatic recombination, and meiosis. Plant Cell 25(6):1990-2001.

Nordborg Group

Debieu M, Tang C, Stich B, Sikosek T, Effgen S, Josephs E, Schmitt J, Nordborg M, Koornneef M, de Meaux J (Epub: 2013) Co-variation between seed dormancy, growth rate and flowering time changes with latitude in *Arabidopsis thaliana.* PLoS ONE 8(5):e61075.

Ngo Q, Albrecht H, Tsuchimatsu T, Grossniklaus U (Epub: 2013) The differentially regulated genes TvQR1 and TvPirin of the parasitic plant Triphysaria exhibit distinctive natural allelic diversity. BMC Plant Biol. 13:28.

Juraniec M, Lequeux H, Hermans C, Willems G, Nordborg M, Schneeberger K, Salis P, Vromant M, Lutts S, Verbruggen N (2013) Towards the discovery of novel genetic component involved in stress resistance in *Arabidopsis thaliana*. New Phytol. doi: 10.1111/nph.12554.

Tsuchimatsu T, Shimizu K (2013) Effects of pollen availability and the mutation bias on the fixation of mutations disabling the male specificity of self-incompatibility. J. Evol. Biol. 26(10):2221-32.

Sasaki E, Sugino R, Innan H (2013) The linkage method: a novel approach for SNP detection and haplotype reconstruction from a single diploid individual using next-generation sequence data. Mol. Biol. Evol. 30(9):2187-96.

Long Q, Rabanal F, Meng D, Huber C, Farlow A, Platzer A, Zhang Q, Vilhjálmsson B, Korte A, Nizhynska V, Voronin V, Korte P, Sedman L, Mandáková T, Lysak M, Seren Ü, Hellmann I, Nordborg M (2013) Massive genomic variation and strong selection in *Arabidopsis thaliana* lines from Sweden. Nat. Genet. 45(8):884-90.

Slotte T, Hazzouri K, Ågren J, Koenig D, Maumus F, Guo Y, Steige K, Platts A, Escobar J, Newman L, Wang W, Mandáková T, Vello E, Smith L, Henz S, Steffen J, Takuno S, Brandvain Y, Coop G, Andolfatto P, Hu T, Blanchette M, Clark R, Quesneville H, Nordborg M, Gaut B, Lysak M, Jenkins J, Grimwood J, Chapman J, Prochnik S, Shu S, Rokhsar D, Schmutz J, Weigel D, Wright S (2013) The Capsella rubella genome and the genomic consequences of rapid mating system evolution. Nat. Genet. 45(7):831-5.

Platzer A (2013) Visualization of SNPs with t-SNE. PLoS ONE 8(2):e56883.

Long Q, Zhang Q, Vilhjalmsson B, Forai P, Seren Ü, Nordborg M (2013) JAWAMix5: an out-of-core HDF5-based java implementation of whole-genome association studies using mixed models. Bioinformatics 29(9):1220-2.

Rehmsmeier M (2013) A computational approach to developing mathematical models of polyploid meiosis. Genetics 193(4):1083-94.

Beleza S, Johnson N, Candille S, Absher D, Coram M, Lopes J, Campos J, Araújo I, Anderson T, Vilhjálmsson B, Nordborg M, Correia E Silva A, Shriver M, Rocha J, Barsh G, Tang H (2013) Genetic architecture of skin and eye color in an African-European admixed population. PLoS Genet. 9(3):e1003372.

Riha Group

Göhring J, Fulcher N, Jacak J, Riha K. TeloTool: a new tool for telomere length measurement from terminal restriction fragment analysis with improved probe intensity correction. Nucleic Acids Res. 2013 Dec 23 [Epub ahead of print]

Samanić I, Simunić J, Riha K, Puizina J (Epub: 2013) Evidence for Distinct Functions of MRE11 in Arabidopsis Meiosis. PLoS ONE 8(10):e78760.

Fulcher N, Derboven E, Valuchova S, Riha K (2013) If the cap fits, wear it: an overview of telomeric structures over evolution. Cell. Mol. Life Sci.

Bulankova P, Akimcheva S, Fellner N, Riha K (2013) Identification of *Arabidopsis meiotic* cyclins reveals functional diversification among plant cyclin genes. PLoS Genet. 9(5):e1003508.

Tamaru Group

Nyikó T, Kerényi F, Szabadkai L, Benkovics A, Major P, Sonkoly B, Mérai Z, Barta E, Niemiec E, Kufel J, Silhavy D (2013) Plant nonsense-mediated mRNA decay is controlled by different autoregulatory circuits and can be induced by an EJC-like complex. Nucleic Acids Res. 41(13):6715-28.

Grants

Busch Group

The role of KUK in root development
FP7 Marie Curie Actions - Research Fellowship (Daniela Ristova): European Commission (2013 – 2015)

Djamei Group

Effectomics: elucidating the toolbox of biotrophic pathogens. ERC: European Research Council - Starting Grant (2014 - 2018)

Greb Group

The role of strigolactones in secondary growth regulation
FWF: Austrian Science Fund (2011 – 2014)

Identification and Characterization of Plant Vascular Regulators
FWF: Austrian Science Fund (2013 – 2016)

Identification and characterization of CBI1
DFG fellowship (Stefanie Suer): German Research Foundation (2012 – 2013)

Identification of the WOX4 downstream network essential for the regulation of lateral plant growth
EMBO Fellowship (Virginie Jouannet): European Molecular Biology Organization (2012 – 2014)

CEB gene function
FFG/FEMTECH Fellowship (Eva-Sophie Wallner): Austrian Research Promotion Agency (2013 – 2014)

The role of MOL1 in the regulation of lateral growth in angiosperms FP7 Marie Curie Actions - Research Fellowship (Nial Rau Gursanscky): European Commission (2013 – 2015)

Jonak Group

Arabidopsis GSK3/SHAGGY-LIKE KINASE β in drought stress signalling
FWF: Austrian Science Fund (2010 – 2013)

Characterization of a novel salt stress signaling component from *Arabidopsis thaliana*
FWF: Austrian Science Fund (2013 – 2015)

Calcium- and light signals in photosynthetic organisms
FP7: European Commission, 7th Framework Programme on Research, Technological Development and Demonstration (2013 – 2017)

Stresstoleranz
FFG/FEMTECH Fellowship (Marion Fritz): Austrian Research Promotion Agency (2012 – 2013)

Mittelsten Scheid Group

EPICOL – Ecological and evolutionary plant epigenetics
FWF: Austrian Science Fund (2010 – 2015)

Graduate program “Chromosome Dynamics”
FWF: Austrian Science Fund (2012 – 2016)

Stability of epigenetic information in the shoot apical meristem
FP7: European Commission Marie Curie Actions - Research Fellowship (Ruben Gutzat) (2013 – 2015)

SINUDYN - Stress-induced nucleosome dynamics in plants
FWF: Austrian Science Fund (2013 – 2016)

An epigenome-wide association study in plants
Lise Meitner fellowship (Manu Dubin)
FWF: Austrian Science Fund (2012 – 2013)

DAAD Erasmus fellowship (Suraj Jamge): German Academic Exchange Service (2012 – 2013)

Microscopic observation of plant chromatin under stress
FFG/FEMTECH Fellowship (Nina Daubel): Austrian Research Promotion Agency (2013)

Nordborg Group

The molecular basis of local adaptation in *Arabidopsis thaliana*
NIH: National Institutes of Health (2008 – 2013)

Genomic analysis of the genotype-phenotype map / Nordborg
NIH: National Institutes of Health (2009 – 2014)

Starting from scratch: adaptation to variable environments after an extreme bottleneck
DFG fellowship: German Research Foundation (2011 – 2014)

Trans-national Infrastructure for Plant Genomic Science
FP7: European Commission, 7th Framework Programme (2011 – 2015)

Developing maximum-resolution genotype-phenotype maps using whole-genome polymorphism data
ERC: European Research Council (2011 – 2016)

Integrated Genetic and Genomic Resources for a Model System / Nordborg
NICD, NIH: Laboratory of Molecular Genetics, National Institutes of Health (2012 – 2017)

Genome-wide association analysis of drought tolerance in seedlings of *A. thaliana*
DFG fellowship (Arthur Korte): German Research Foundation (2011 – 2013)

Genetic adaptions to climate in *Arabidopsis thaliana*
FP7: European Commission Marie Curie Actions - Research Fellowship (Angela Hancock) (2012 – 2016)

The genomics of buffering and canalization in Arabidopsis
Lise Meitner fellowship (Eriko Sasaki),
FWF: Austrian Science Fund (2012 – 2014)

EMBO Longterm fellowship (Takashi Tsuchimatsu): European Molecular Biology Organization (2012 – 2013)

Riha Group

Mechanisms of Chromosome end Protection
FWF: Austrian Science Fund (2009 – 2014)

Dissecting the mechanisms governing meiotic progression
FWF: Austrian Science Fund (2011 – 2014)

Graduate program “Chromosome Dynamics”
FWF: Austrian Science Fund (2012 – 2016)

Tamaru Group

Control and function of epigenetic reconfiguration in pollen
FWF: Austrian Science Fund (2012 – 2015)

FP7

Vienna Biocenter International PhD Program

The GMI offers PhD positions within the framework of the prestigious Vienna Biocenter (VBC) International PhD Program, providing students the opportunity to undertake research at the cutting edge of modern plant biology. Modest group sizes ensure students receive excellent supervision, plenty of interaction with fellow students, and unhindered access to top-notch infrastructure.

Students are selected twice-yearly with an emphasis on academic and technical excellence. The official language of the program is English, and students are enrolled through the University of Vienna. PhD salaries are offered at an internationally competitive level for up to 4 years.

A number of GMI faculty are also involved in giving lectures, seminars, and practical courses in Molecular Plant Biology in the context of this program, all in English language.

The Institute of Molecular Biotechnology (IMBA), the Research Institute of Molecular Pathology (IMP), and the Max F. Perutz Laboratories (MFPL) also participate in the program. For detailed information and application procedure, please consult the program's website (www.vbcphdprogramme.at).

GMI
GREGOR MENDEL INSTITUTE
OF MOLECULAR PLANT BIOLOGY

IMBA
Institute of Molecular Biotechnology
of the Austrian Academy of Sciences

IMP
Research Institute of Molecular Pathology

mfpl
MAX F. PERUTZ LABORATORIES

Seminars

February

Viktor Žárský, Department of Experimental Plant Biology, Charles University Prague
Functions of plant exocyst complexes in land plants
Host: Wolfgang Busch

Mattia Doná, Department of Biology and Biotechnology, University of Pavia
Silencing of the DNA repair gene Tdp1a triggers premature senescence and nucleolar dysfunction in *Medicago truncatula*
Host: Ortrun Mittelsten Scheid

March

Markus Schmid, Max Planck Institute for Developmental Biology, Tübingen
Integration of flowering time signals in *Arabidopsis thaliana*
Host: Wolfgang Busch

Thomas Brabbs, University of York, UK
Identification and characterisation of MORC6 as a component of the RNA-directed DNA methylation pathway in *Arabidopsis thaliana*
Host: Ortrun Mittelsten Scheid

Diana Santelia, Institute of Plant Biology, University of Zürich
The metabolism of starch and its role in abiotic stress tolerance
Host: Claudia Jonak

Marcus Koch, University of Heidelberg, Department of Biodiversity and Plant Systematics
The evolutionary history of the genus *Arabidopsis* and the impact of hybrid speciation and introgression - rare exception or simply overlooked
Host: Magnus Nordborg

Jieun Shin, Department of Plant Developmental Biology, Max Planck Institute for Plant Breeding Research, Cologne
Translation of environmental stress signals to plant growth and development by the circadian clock
Host: Magnus Nordborg

Tuncay Baubec, Schuebeler Lab, Friedrich Miescher Institute for Biomedical Research
A genomic binding atlas for MBD proteins in ES and neuronal cells reveals their complex binding preferences to chromatin
Host: Ortrun Mittelsten Scheid

April

Armin Djamei, Max Planck Institute for Terrestrial Microbiology, Department of Organismic Interactions, Marburg, Germany
EFFECTOMICS - elucidating the toolbox of fungal plant pathogens
Host: Magnus Nordborg

Joop Vermeer, Department of Plant Molecular Biology, University of Lausanne
Mechanical signalling between pericycle and endodermis regulate lateral root formation
Host: Magnus Nordborg

Ivan Acosta, Department of Plant Molecular Biology, University of Lausanne
Jasmonate signaling in plant reproductive development and defense
Host: Magnus Nordborg

Christian Hardtke, Department of Plant Molecular Biology, University of Lausanne
Molecular genetic control of root system architecture - from the wild to the lab and back again
Host: Wolfgang Busch

Stéphanie Robert, SLU/Umeå Plant Science Center, Dept of Forest Genetics and Plant Physiology
Discovery of novel growth regulators to better understand plant development
Host: Magnus Nordborg

Oliver Stegle, EMBL - European Bioinformatics Institute, Cambridge, UK
Harnessing gene-environment interactions to identify functional targets for molecular intervention in phenotype
Host: Magnus Nordborg

Xiaoqi Feng, Zilberman Lab, Plant & Microbial Biology, UC Berkley
Mechanism and significance of DNA methylation reprogramming in plant sexual lineage
Host: Magnus Nordborg

Anna Jehle, Zilberman Lab, Plant & Microbial Biology, UC Berkley
The receptor-like protein reMAX of *Arabidopsis thaliana* detects the novel MAMP emax of *Xanthomonas*
Host: Claudia Jonak

Bernhard Wurzinger, Max. F. Perutz Laboratories, Vienna
The Ca2+ dependent protein kinase CPK3 is required for salt stress acclimation in *Arapidopsis*
Host: Claudia Jonak

Guillaume Queval, Faculty of Biological Sciences, University of Leeds
Transport of glutathione between the cytosol and the nucleus: investigation of candidate proteins in *Arabidopsis thaliana*
Host: Claudia Jonak

Madlen Vetter, Bergelson Lab, Department of Ecology and Evolution, University of Chicago
Molecular integration of growth and defense
Host: Magnus Nordborg

Eva Benkova, IST Austria
Auxin - cytokinin network regulating root architecture
Host: Wolfgang Busch

Andreas Houben, Leibniz Institute of Plant Genetics & Crop Plant Research (IPK) Gatersleben
How to get rid of your partner
Host: Ortrun Mittelsten Scheid

May

Ronny Völz, Centre for Plant Molecular Biology, Eberhard Karls University, Tübingen
Cell-cell communication at the interface between male and female gametophyte
Host: Thomas Greb

Stephanie Werner, Department of Cellular Biochemistry, Martin-Luther-University Halle-Wittenberg
The role of phosphoinositides in auxin signaling in *Arabidopsis thaliana*
Host: Thomas Greb

Anja van Haperen, Institute for Biology III, Freiburg University
An enhancer screen for regulators of shoot apical meristem development
Host: Thomas Greb

Jo Hepworth, University of Potsdam
Growth control, evolution and mystery mobile signals: strigolactone biosynthesis evolution and KLU-dependent signaling
Host: Thomas Greb

June

Moritz Nowack, VIB Department of Plant Systems Biology, Ghent University
So many smart ways to die – The regulation of programmed cell death in plants
Host: Thomas Greb

Wojciech Pawlowski, Department of Plant Breeding and Genetics, Cornell University
The genetics of genetics: mechanisms of chromosome interactions and recombination during meiosis in plants
Host: Karel Riha

Andrew Lloyd, INRA Versailles, France
Meiotic gene fate following polyploidy in angiosperms: Can you teach a (duplicated) old dog new tricks?
Host: Ortrun Mittelsten Scheid

Kentaro Shimizu, Institute of Evolutionary Biology and Environmental Studies, University of Zurich
Ecological genomics and transcriptomics of polyploid *Arabidopsis* relatives and of tropical trees
Host: Magnus Nordborg

Emma Huang, Mathematical and Information Sciences, CSIRO, Australia
Finding common ground for analysis in wheat, rice and *Arabidopsis* MAGIC populations
Host: Magnus Nordborg

July

Christian Hermans, Lab of Plant Physiology and Molecular Genetics, Université Libre de Bruxelles
Plant nutrition: from root architecture to nutrient rich food
Host: Wolfgang Busch

Steve Jacobsen, Department of Molecular, Cell and Developmental Biology, UCLA
Genetics and genomics of gene silencing in Arabidopsis
Host: Ortrun Mittelsten Scheid

August

Philip Wolff, (Köhler's lab), Swedish University of Agricultural Sciences
Genomic imprinting in *Arabidopsis thaliana*
Hosts: GMI Postdocs

October

Jan Lohmann, Dept. for Stem Cell Biology, Centre for Organismal Studies, University Heidelberg
A regulatory framework for shoot stem cell control
Host: Wolfgang Busch

Claus Schwechheimer, Department of Plant Systems Biology, Technical University Munich
The polarly localized D6PK protein kinases promote auxin transport in *Arabidopsis thaliana*
Host: Wolfgang Busch

Aline Probst, Génétique Reproduction & Développement, CNRS/INSERM, Clermont-Ferrand, France
Heterochromatin organization and dynamics during development
Host: Ortrun Mittelsten Scheid

Martin Lysak, Laboratory of Plant Cytogenomics, Central European Institute of Technology (CEITEC), Brno
Principles and trends of genome evolution in crucifers *(Brassicaceae)*
Host: Karel Riha

Antje von Schaewen, Institute for Biology and Biotechnology of Plants, Westfälische Wilhelms-Universität Münster
Role of primary CHO metabolism for plant development & stress responses
Host: Claudia Jonak

November

Juliette de Meaux, Institute for Evolution and Biodiversity, Westfälische Wilhelms-Universität Münster
The molecular underpinnings of genetic adaption in *Arabidopsis thaliana*
Host: Magnus Nordborg

Ales Pecinka, Department of Plant Breeding and Genetics, MPIPZ, Cologne
ATR and ATM dependent repair of nucleoprotein adducts in *Arabidopsis*
Hosts: Ortrun Mittelsten Scheid & Vanja Cavrak

Annabelle Haudry, Laboratoire de Biométrie et Biologie Évolutive (LBBE), University of Lyon
Selection on noncoding DNA in *Brassicaceae*
Host: Magnus Nordborg

Trude Schwarzacher, Department of Biology, University of Leicester
The genome landscape: molecular cytogenetics and repetitive DNA evolution in hybrids including polyploids
Host: Ortrun Mittelsten Scheid

Angela Sessitsch, Head of Bioresources, AIT – Austrian Institute of Technology
The plant microbiome: ecology and functionality of bacterial endophytes and how plants can benefit
Host: Ortrun Mittelsten Scheid

December

Naomi Nakayama, Institute of Molecular Plant Sciences, University of Edinburgh
Mechanical regulation of morphogenesis at the shoot apex
Host: Thomas Greb

Chris Pires, Interdisciplinary Plant Group, University of Missouri, USA
Whole genome duplications and the origins of novelty: impact of ancient and recent polyploidy
Host: Ortrun Mittelsten Scheid

Olivier Voinnet, Department of Biology, ETH Zurich
A sensitized genetic screen reveals a novel RNA-mediated antiviral pathway in plants
Host: Ortrun Mittelsten Scheid

Peter Doerner, Institute for Molecular Plant Sciences, Edinburgh University
Control of root growth by phosphate limitation
Host: Wolfgang Busch

Doris Bachtrog, Center for Theoretical Evolutionary Genomics, University of California, Berkeley
The epigenome of evolving sex chromosomes in Drosophila: dosage compensation and heterochromatin formation
Host: Magnus Nordborg

Professional Training & Personal Development

As part of the responsibility of a leading international research institute, the Gregor Mendel Institute fosters the development of our scientists' research skills and careers by providing a range of training and development opportunities, specifically tailored for PhD students, postdoctoral fellows, and group leaders. Through external partners and on-campus specialist services we thereby aim to develop our employees' research performance, future employability, professionalism and social engagement:

General training

- German language courses

Training for PhD Students and Postdoctoral Fellows

- Scientific writing
- Methodologies/expertise (statistics, bioinformatics, software)

Special training for Postdoctoral Fellows

- Successful grant writing
- Presentation skills

Special leadership and management training for group leaders

- Leadership in science
- Personal coaching
- Media training
- Negotiation skills
- Training in Intellectual Property and Patent Law

Alumni

The Gregor Mendel Institute views the furthering of our employees' careers as an important part of our mission. Naturally, their next career stop also reflects on the quality of our research and our reputation in the international plant research community. Thus, in 2013, with pride and a little melancholy, we said "auf Wiedersehen und viel Glück!" to:

Stefanie Suer
Baxter AG, Austria

Riccardo Aiese Cigliano
Founder/Scientific Director Sequentia-biotech, Barcelona, Spain

Wanhui You
Postdoc, University of Zurich, Switzerland

Events

Summer School 2013

GMI SCIENCE RETREAT

The 3rd annual scientific retreat for all GMI staff was held in June 2013, for the first time at the beautiful medieval Schloss Krumbach south of Vienna. Over three days, each lab had time to present their research to the rest of the Institute, with evening poster sessions and free time for spontaneous discussion filling in the program. This annual event provides GMI researchers with an important opportunity to receive fresh ideas and creative feedback from colleagues, including those working in less related fields. Administrative staff joined for most of the retreat, holding their own team sessions, and participating in the all-GMI 'team-building' event, this year a team competition in suitably medieval style!

Krumbach

VBC PHD SYMPOSIUM: "TIME – HOW NATURE SETS THE CLOCK"

A highlight event in 2013 was the 11th annual two-day VBC PhD Symposium in November, organized by students of the Vienna Biocenter PhD program, including PhD students from the GMI. This year, eighteen speakers provided insight into the huge range of species from cyanobacteria to plants to humans that have evolved an internal self-sustained ticker to tune themselves into environmental changes and adapt to local environments. Participants learned how an internal clock is not only required at an organismal level for proper

physiology and behavior, but also in order for single cells themselves to know how to exert their functions in a timely manner. A further aspect of the talks involved the subjective perception of time; time cannot be sensed like traditional senses, but rather time is indirectly perceived by reconstructing it in the organism's nervous system.

VIENNA BIOCENTER SUMMER SCHOOL

In 2013 the GMI participated for the 4th year in the VBC Summer School, a program to provide high school students the exciting chance to carry out own projects within research groups at the Vienna Biocenter. Lectures and social events were included in the program, which concluded with a symposium where all students could present their results.

INTERNATIONAL FASCINATION OF PLANTS DAY 2013: MOVIE NIGHT AT THE GMI

In May 2013, the GMI participated for the second time in this international outreach event to get the Viennese public, and young people in particular, enthused about the importance of plants in our daily lives: from the clean air they provide us, to the food we eat, the clothes we wear, and the joy we derive from their beauty. A free "Movie Night" was organized at the Institute, where three excellent documentaries on some unusual and fascinating aspects of plants and plant research were shown in our own auditorium to a full house of spectators.

GMI Science Retreat 2013

Management

Dr Magnus Nordborg
Scientific Director

Dr Markus Kiess
Business Director

Administration & Services

Dr Borries Luberacki
Head of Lab Management & Services

Thomas Friese BSc
Head of Science Support

Mireia Verdaguer MSc
Head of Finance

Mag. Carmen Ilic
Human Resources Officer

Eckehard Siegmann
Head of IT Services

Martina Gsur
Assistant to the Directors

Lab Management & Services

Jens Aberlin Schaich, Anneliese Auer, Borries Luberacki, Stefan Ferscha

Aaron Zauner, Petar Forai, Eckehard Siegmann, Thomas Ciganek

IT Services

Administration

Back row: **Thomas Ciganek, Petar Forai, Jens Aberlin Schaich, Anneliese Auer, Stefan Ferscha**
Middle row: **Carmen Ilic, Gabriele Nestyak, Markus Kiess, Ines Crisostomo, Barbara Weigel, Heidi Fürnkranz, Mireia Verdaguer, Johanna Ostah**
Front row: **Claudia Oriold, Martina Gsur, Thomas Friese, Borries Luberacki, Eckehard Siegmann**

GMI Scientific Advisory Board

Prof. Philip N. Benfey
Duke University,
Durham,
North Carolina, USA

Prof. Edward Buckler
Institute for Genomic Diversity, Cornell University, Ithaca, NY, USA

Prof. Joseph Ecker
Salk Institute for Biological Studies,
La Jolla, CA, USA

Prof. George Coupland
Max Planck Institute for Plant Breeding Research,
Cologne, Germany

Prof. Ueli Grossniklaus
Institute of Plant Biology,
University of Zurich,
Switzerland

Dr Michael Metzlaff
Bayer BioScience,
Ghent, Belgium

Prof. Elizabeth Vierling
University of Massachusetts, USA

Prof. Ottoline Leyser
University of Cambridge,
Cambridge, UK

"We cannot overemphasize the dramatic and positive transition that has occurred at the GMI [...]. The facilities are now outstanding, due both to the essential development of GMI resources as well as enhanced integration and access to other advanced technologies on the VBC campus. All group leaders and their group members commented on this situation and how it enables creative and world-class, basic plant science possible at only a very few institutions."

GMI Scientific Advisory Board Report 2013

The Austrian Academy of Sciences

The Austrian Academy of Sciences (originally the Imperial Academy of Sciences in Vienna) was founded in 1847 to promote scientific research and freedom. Its headquarters are located in Vienna's city center in the former assembly hall of the University of Vienna built between 1753 and 1755 by the French architect Jean Nicolas Jadot. The Austrian Academy of Sciences has two sections, the Section for Mathematics and Natural Sciences, and the Section for the Humanities and Social Sciences. Today, the Academy fulfils two main functions. On the one hand, its 90 elected full members and 250 appointed corresponding members form a scholarly society and, on the other, it is Austria's major supporter of research outside the university system, funding some 70 research institutions both in the natural sciences and the humanities. The Academy also organizes various events and lecture series, and supports established and young talented scientists alike through its awards and scholarships programs.

The City of Vienna

Vienna is simply a fantastic city to live in – in fact, in the annual Mercer livability survey of 215 cities, it has now taken top rank for four years in a row (2010-2013)! Why is it the best city in the world to live in? Ask GMI employees from around the world and they might give these reasons:

Its location – in the heart of Europe, with easy connections in all directions, whether to go home or on a weekend excursion.

The lifestyle – Vienna combines the elegant splendor of the former Austro-Hungarian capital with a modern infrastructure, lots of nearby countryside for outdoor excursions, and one of the richest cultural offerings of any European city.

It's safe, clean and practical – walk anywhere in Vienna, even at night, and you feel safe. The air, the streets, everything is clean. And public transport, housing, schooling, health care and all the other everyday needs work well and are affordable.

Cosmopolitan – with the United Nations, OPEC, and a number of other international corporations and organizations, Vienna has become a dynamic, multicultural, and cosmopolitan city in the last two decades.

Location & Travel Directions

Gregor Mendel Institute of Molecular Plant Biology
Dr. Bohr-Gasse 3
1030 Vienna
Austria

From the Airport
by city train (S-Bahn): S7 to Sankt Marx-Vienna Biocenter

From the City
by city train (S-Bahn): S7 to Sankt Marx-Vienna Biocenter
by tram: 71, 18 to Sankt Marx
by bus: 74A to Sankt Marx
by underground: U3 to Schlachthausgasse (7 minute walk or three stops with tram 18)

www.gmi.oeaw.ac.at