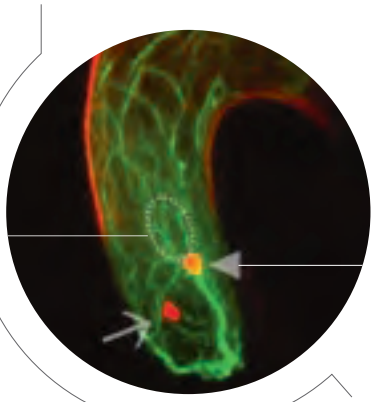
annual report 15



GREGOR MENDEL INSTITUTE
OF MOLECULAR PLANT BIOLOGY

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: J. Matthew Watson
Photographers: Christian Huttar, Herbert Blazejovsky,
Ruben Gutzat, Oliver Zehner, Envel Kerdaffrec
GMI logo: Lo Breier
Graphic design: floorfour.at
Printing house: Riedel Druck GmbH, 2214 Auersthal

ÖAW AUSTRIAN ACADEMY OF SCIENCES

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

annual report 15

GMI
GREGOR MENDEL INSTITUTE
OF MOLECULAR PLANT BIOLOGY

CONTENTS

15 Directors' statement

Dr Magnus Nordborg
Scientific Director

Dr Markus Kiess
Business Director

We are proud to be one of a relatively small number of institutions worldwide devoted to basic research in plant biology. The decision to establish such an institute well over a decade ago is looking increasingly visionary given the mounting evidence that human activities, in particular fossil-fuel usage, are rapidly changing the global climate. The importance of understanding the biology of the world's primary producers is difficult to overstate.

Our goal is to demonstrate the importance of plant biology by establishing the GMI as a world-class research institute, but we also seek to contribute to securing the position of the Vienna Biocenter as one of Europe's leading research locations. We strive for scientific excellence at every level. As directors, one of our most important (and rewarding) tasks is recruiting promising young scientists as group leaders, and providing them with an environment that allows them to develop into established researchers capable of competing for senior scientific positions worldwide. The last year marked a milestone in that Claudia Jonak, the last of several Junior Group Leaders recruited rapidly during the establishment phase of the GMI, left the institute. Going forward, we aim for a constant turnover of group leaders at a rate of about one per year. As always, the success of departing researchers (at any level, including, of course, doctoral students and postdocs) is one of the most important indicators of our success as a research institute.

Despite our emphasis on basic research, we recognize that academic careers are not for everyone. This year we organized a two-day career workshop that was offered to all students and postdocs at the Vienna Biocenter, as well as a career day that included high-level participation from several potential employers, notably Nestlé, Novartis, and Syngenta. These events were well received and provided the scientists on campus with a broader view of career opportunities.

The year also saw the full establishment of two new groups, namely those of Fred Berger and Youssef Belkhadir, working on chromatin structure and plant defense, respectively. There are enormous potential for fruitful interactions during the coming years, and we look forward to great things!

As always, we want to thank the Austrian Academy of Sciences for its continued support, without which the Gregor Mendel Institute 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

15 Introducing the GMI

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 throughout the world that focuses on basic plant biology. The GMI is located in the purpose-built ÖAW Life Sciences Center, completed in 2006, in the heart of Vienna's most important life sciences research complex, the Vienna Biocenter (VBC). The VBC includes three other important research institutes the IMP, IMBA, and MFPL, as well as several biotechnology companies, which provide an environment of powerful research synergies for the GMI.

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 defense. During the last 20 years, the model plant *Arabidopsis thaliana* has emerged as the primary experimental system for plant molecular biology and is the main model organism used at the GMI. Research is carried out by independent research groups, led either by senior group leaders with contracts of unlimited duration, or junior group leaders with limited appointments. Our focus is on scientific excellence and, as a testament to this focus, GMI researchers have one of the highest publication rates in high-impact 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 computing cluster, joint services with the IMP and IMBA, and other core services offered by the CSF. Block funding is received from the Austrian Academy of Sciences with additional resources provided by a variety of national, European Union, and 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 that is receiving new attention due to 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.

Research on plants can also lead to fundamental scientific breakthroughs beyond plant biology, including many that can be applied to human medicine. 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 strength of the GMI), 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 international VBC PhD Programme, and is also involved in several externally funded doctoral programs. During the summer, GMI research groups host students through 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 to the general public.

Working at the GMI

The GMI provides a lively, international working environment with around 120 staff from over 30 countries. The working language is English. The GMI offers an excellent, subsidized child daycare center through the CSF. Day care is available for children from 3 months old with extended opening hours. Research is complemented by scientific events, including a packed seminar series, an annual scientific retreat, GMI-organized conferences, and social events such as a ski trip to the nearby Alps, sports events, and festivities.

Career

The GMI focuses on providing a perfect environment for excellent science as well as education, which makes it an excellent place to develop a scientific career. We offer an exciting setting for undergraduates, PhD students, postdocs, and principal investigators alike. All researchers have access to superb infrastructure and generous funding, allowing for enormous intellectual freedom.

At the GMI we see the career development of our junior researchers as a priority. The faculty aims to provide effective mentoring to PhD students and postdocs in order for them to progress and be successful. While most of these mentoring efforts are involved in promoting a research career, we organize events to promote the interaction of young researchers with people from many different career paths.

GMI alumni have gone on to a broad range of careers, with members of this year's alumni going on to group leader positions, postdocs in industry and academia, the biotech and pharmaceutical industry, and even as far afield as Google.

15 GMI Research Groups

Belkhadir Group

Berger Group

Busch Group

Djamei Group

Jonak Group

Mittelsten Scheid Group

Nordborg Group

Cell surface control of growth and defense in Arabidopsis

BELKHADIR GROUP

Plants must grow fast enough to compete with their neighbors, while maintaining appropriate defenses to survive in the presence of pathogens. To this end, plants exploit phylogenetically related cell surface Receptor Like Kinases (RLKs) to control developmental and defense programs. The central goal of our laboratory is to provide an increased understanding of RLK-controlled "growth-defense" decision-making processes in plants.

YOUSSEF BELKHADIR

youssef.belkhadir@gmi.oeaw.ac.at

Joined GMI in Jan 2014

PhD: University of North Carolina-Chapel Hill, NC, USA

Previously

- Chief Scientific Officer: Atlas Genomics, Casablanca, Morocco 2011–2013
- Research Associate: SALK Institute for Biological Studies, La Jolla, CA, USA 2006–2011, Laboratory: Prof. Joanne Chory

GROUP MEMBERS

PhD Student
Stephanie Arnoux* (50%)

Postdocs
Jixiang Kong
Marcal Gallemi Rovira*
Elwira Smakowska

Technician
Karin Grünwald
Natascha Weinberger

Trainee
Anna-Maria Gamper*
Katarzyna Parys*
Valentina Zehetbauer*

Visitor
Mehdi Doumane*

*(*left the lab in 2015)*

A key question in biology is how organisms "adapt", or acquire environment-dependent fitness advantages. Plants are rooted in the ground and, unlike animals, must adapt to their environment rather than change it through relocation. Adaptation involves adjustment in the plant body plan and requires mechanisms for sensing the environment and reacting effectively.

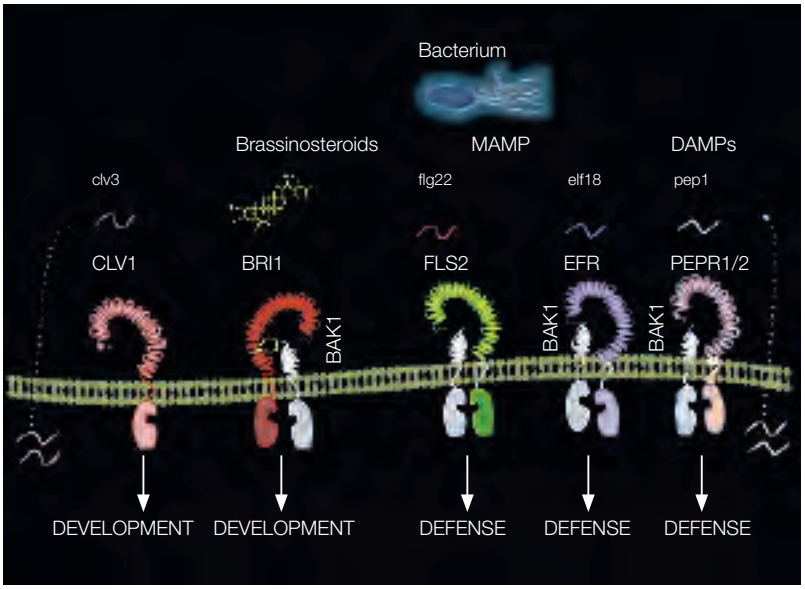
Intercellular communication in multicellular organisms depends upon the relay of extracellular signals to intracellular mediators often through activation of membrane-embedded proteins called receptors. Receptors represent the gateway through which a cell senses and responds to its environment. The mechanisms of cell surface receptor activation are highly diverse, particularly in plants. Receptor activation is usually initiated by the engagement of an extracellular molecule with the extracellular regions of either one or many cell surface receptors. This engagement, in turn, activates intracellular signal transduction cascades and elicits downstream gene expression programs. The availability of genome sequences from several model organisms has facilitated the identification of many plasma membrane receptor families. The Receptor Protein Kinases (RPKs) comprise one of the largest subfamilies of transmembrane receptor kinases in metazoans. Higher plants possess a multitude of genes coding for putative Receptor-Like Kinases (RLKs). For instance, the genome of the model plant Arabidopsis contains 400 genes predicted to encode proteins displaying the architectural hallmarks of RPKs. In plants, all of the RLKs identified thus far contain signature sequences indicative of ser/thr- and tyr-specific protein kinases. Thus, like animals, higher plants broadly employ receptor kinase signaling to regulate vital plant functions from pathogen sensing to development. While information is emerging about the range of biological processes RLKs control, the mechanisms by which they exert their function has remained unknown. Whereas the structural features of the LRR-RLKs suggest that these proteins may act as receptors for extracellular signals, the vast majority of these proteins remain orphan receptors with respect to their *in vivo* functions and/or associated ligands.

Clear evidence for direct, receptor-ligand interactions is known for only a few of these perception systems (→ Fig.1)

By far the most abundant class in plants, over 230 members in *Arabidopsis thaliana* alone, contains leu-rich repeat sequences commonly referred to as LRR-RLKs. Research during the past decade led to the cloning and identification of plant RLKs from both model and agriculturally important crop species. Within the last few years, genetic analyses, along with gene expression studies, uncovered the involvement of LRR-RLK proteins in a wide variety of developmental and defense-related processes including stem cell maintenance, cell proliferation, stomata development, hormone perception, and symbiosis.

The major goal of the laboratory is to understand how RLKs allow plants to optimize the use of their growth and defense systems. For this, we use the signaling pathways governing defense and growth to uncover RLKs hubs that mold 'growth-defense' dynamics and function.

Fig.1
Paradigms of LRR-RK signaling in Arabidopsis



In the past year, we established two systematic approaches for network analysis of cell surface receptors in Arabidopsis. First, we exhaustively dissected the extent to which RLKs can establish functional networks by mapping more that 20.000 unique pairwise interactions (→ Fig.2). Second, we used genome wide association (GWA) mapping to identify cell surface receptors involved in the regulation of both growth and defense among natural strains of *A. thaliana* (→ Fig.3). These screens allowed us to identify new RLKs involved in the control of growth and defenses. Third we used biochemistry, reverse genetics, and cell biology approaches to validate predictions unraveled by our system proteomic and quantitative genetics approaches. In sum, by combining the knowledge gained from our RLK interaction networks with the results of our GWA studies, we have reached a position where we can now begin to understand the biological processes controlled by specific RLKs.

Fig. 2
Novel RLK networks

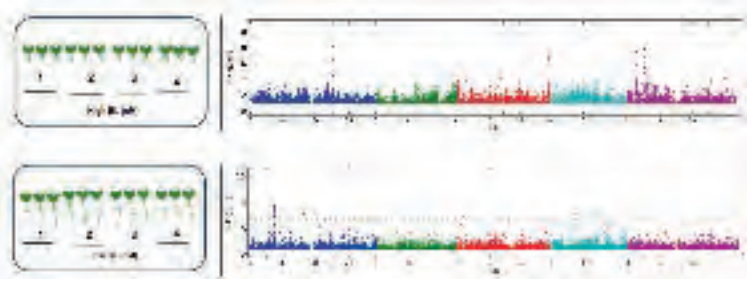


Fig. 3.
Results from Brassinosteroid GWA mapping

Chromatin Architecture and Function

BERGER GROUP

The genetic information contained in DNA is organized into functional units that are assembled as domains within the space of the nucleus. We are investigating how these levels of genome organization depend on variants of the histone proteins. Eight histone proteins, two copies each of H2A, H2B, H3, and H4, form an octamer called the nucleosome, which is the basic unit of the architecture supporting DNA. We use plants as models because, like vertebrates, they have evolved a remarkable diversity of histone variants. This year we made advances in our understanding of the evolution of the H2A family and obtained evidence for the diversification of its functions. We also made major advances in determining the properties conferred to chromatin by the variants from the H2A family. This led us to propose a new concept of genome organization.

Evolution of H2A variants and identification of a new class.

The H2A family has shown a high degree of diversification into distinct classes during evolution. In flowering plants, we identified four classes of H2A variants including the seed-plant specific H2A.W that localizes specifically to heterochromatin, and is enriched in transposons and silenced genes. In depth molecular phylogenetic analyses using newly sequenced genomes allowed us to define the additional class H2A.M which was present in the first land plants. Our data support the hypothesis that H2A evolved with a gradual selection of specific sequences at the L1 region, which connects the two H2A proteins inside the nucleosome. Further acquisition of a C-terminal specific motif completed the evolution of H2A.M and H2A.W. H2A.M is present in the liverwort *Marchantia polymorpha,* a new model system that we will use for further functional studies to investigate how H2A.W acquired its localization in heterochromatin and its function in 3D organization of heterochromatin.

In flowering plants we observed that a member of the H2A.W family, the variant H2A.W.7 possesses an additional C-terminal motif similar to that found in H2A.X. This variant is important for DNA repair in the heterochromatin region, where it is enriched at the expense of H2A.X.

These findings show the dynamics and importance of histone variants in the functional organization of the eukaryotic genome. (→ Fig.1).

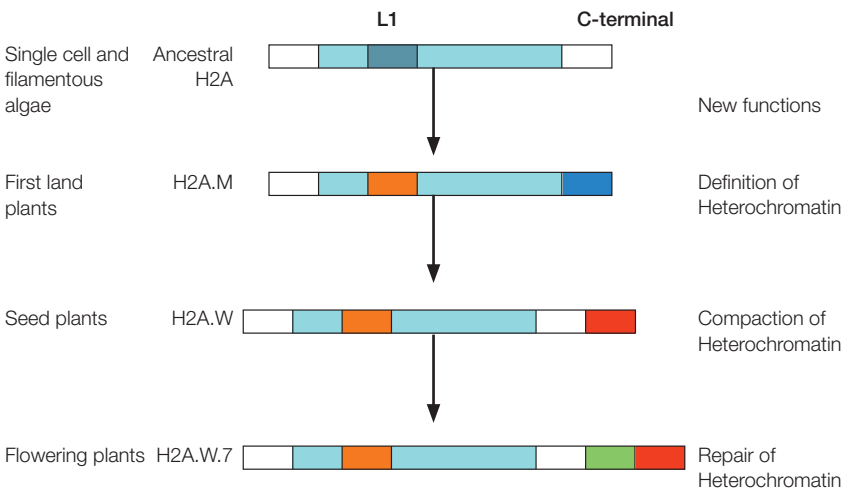


Fig.1
Schematic evolution of H2A.M and H2A.W and the potential functions acquired during plant evolution. The L1 domain became specialized (blue to orange) and likely conferred the heterochromatin localization. C-terminal motifs evolved, providing novel functions.

FREDERIC BERGER

fred.berger@gmi.oeaw.ac.at

Joined GMI in Jan 2014

PhD: Marine Biological Association, Plymouth, U.K.

Previously
- Group Leader: Temasek Life Sciences Laboratory, Singapore 2004–2014
- Research assistant professor: Institut National de la Recherche Agronomique (INRA) Lyon, France 1997–2004

GROUP MEMBERS

Bioinformatician
Elin Axelsson

Postdocs
Michael Borg
Danhua Jiang
Tomokazu Kawashima
Bingkun Lei
Chulmin Park
Haifeng Wang
Ramesh Yelagandula*

Staff Scientist
Zdravko Lorkovic

Technicians
Svetlana Akimcheva
Bhagyshree Jamge

Visitors
Pao-Yang Chen
Asuka Higo*
Aleksia Vaattovaara*

(*left the lab in 2015)

H2A variants contribute specific physical properties to chromatin.

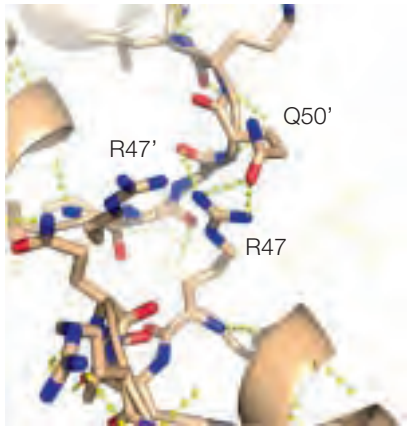
H2A variants contribute specific physical properties to chromatin. In collaboration with the laboratory of H. Kurumizaka, we analyzed the structure of nucleosomes containing different H2A variants. We showed that each nucleosome contains two H2A of the same type. A combination of different H2A variants within a single nucleosome is very rare, and supports the hypothesis that specific machineries assemble distinct types of nucleosomes based on the H2A variant they contain. We also hypothesized that H2A variants confer specific properties to the nucleosome. Comparison of crystal structures of nucleosomes containing H2A and H2A.W indicates that H2A.W leads to a more stable association between the nucleosome and the DNA, and further biochemical tests showed that arrays of H2A.W nucleosomes are more compact than H2A nucleosomes, further supporting the idea that H2A.W confers specific properties to the chromatin domains where it is enriched. (→ Fig.2).

A new functional definition of chromatin: the barcoding hypothesis.

We extended the results we obtained for H2A.W, and established that each variant of the H2A family marks functional domains along the genome. Biochemical analyses further suggest that H2A variants likely confer specific properties to entire regions of the chromatin. Therefore we **propose the idea of a barcode defined by H2A variants that not only identifies specific genomic features but also participates in their function.** We are in the process of testing whether this barcode hypothesis extends to other eukaryotes. (→ Fig.3).

Fig. 2
Impact of H2A.W on nucleosome properties.

Structure of H2A.W nucleosome



AtH2A.W6: 47 **R**YA**Q**R**L**GG 54
AtH2A.1: 39 KYAERVGA 46

Sequences and structures of the L1 loop Compared in H2A and H2A.W

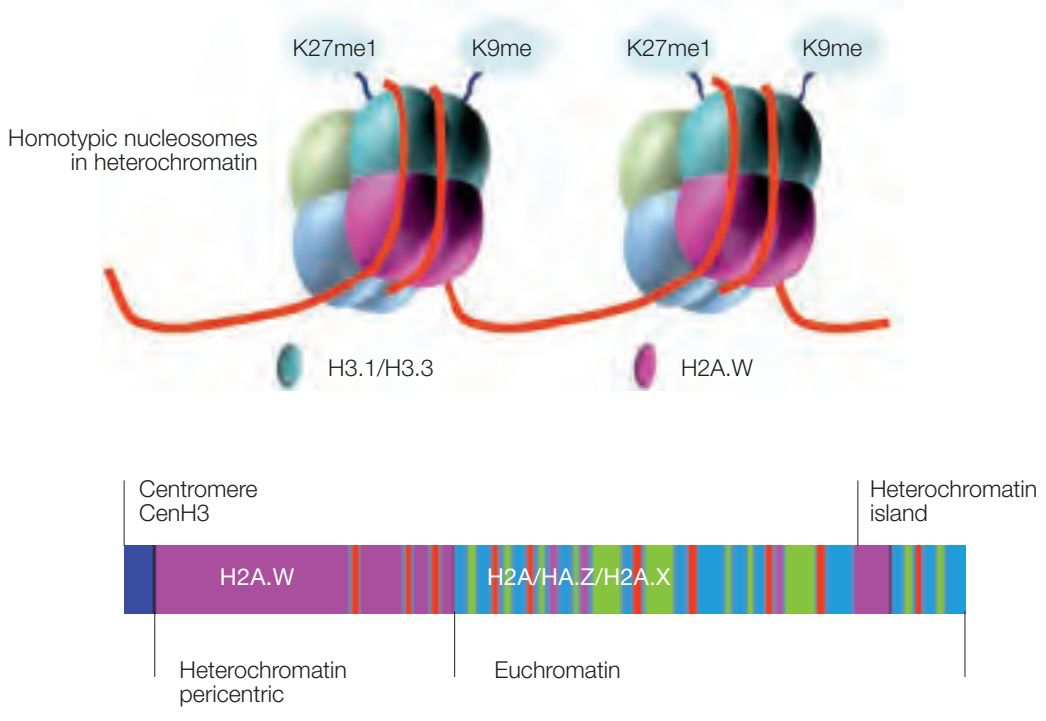
Outlook for 2016

H2A.W is both necessary and sufficient to promote heterochromatin condensation into higher order nuclear domains participating in maintaining transposon silencing and genome integrity. We have now realized that heterochromatin marked by H2A.W can be further subdivided into distinct domains marked by chromatin modifications and histone variants from multiple families. We are investigating the function of these new domains.

We will pursue analyses of H2A.M and H2A.W functions and properties based on structural, biochemical, and molecular analyses. The Marchantia genome will be published in 2016 and we have already obtained preliminary chromatin profiles of some histone variants and modifications. We will need to extend genomic sequencing and assembly in Marchantia and other land plant ancestors to investigate how the chromatin landscape has evolved in plants. This will be the first comprehensive attempt to understand the origin of chromatin-mediated genome organization and to which degree it enabled the diversification of genomic functions during the evolution of Eukaryotes.

Fig. 3.

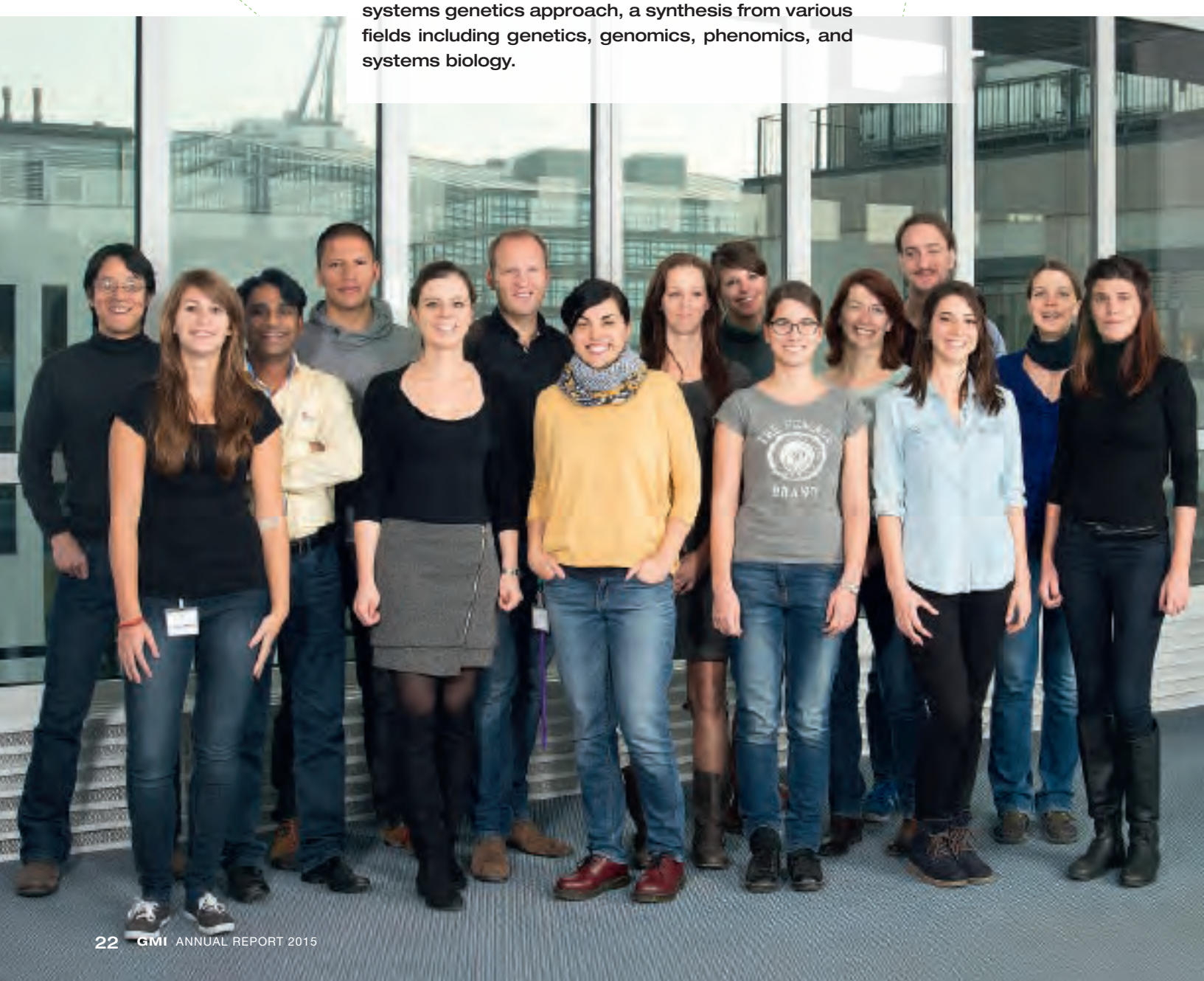
Barcoding of chromatin: Each H2A variant ascribes a specific composition to the nucleosomes. Shown is a typical H2A.W nucleosome that marks heterochromatin. The four H2A variants organize the genome into distinct functional units. Based on biochemical analyses and genomic profiling we propose that H2A variants make homogenous building blocks of chromatin with distinct properties, producing a specific barcode that can be read by yet unknown protein complexes.



Systems Genetics of Root Growth

BUSCH GROUP

Although the roots of plants are hidden from view, they are of utmost importance. Roots anchor plants in the ground, explore the soil, and gather all essential nutrients. Regulating the continuous and highly plastic development of the root is therefore essential to any plant. While root growth and development is genetically determined, it is also strongly impacted by environmental factors. Our long-term goals are to understand how, and through which molecular and cellular mechanisms, root growth is quantitatively determined by the genotype and different environmental conditions. To accomplish this we use a systems genetics approach, a synthesis from various fields including genetics, genomics, phenomics, and systems biology.



The root system enables plants to anchor themselves in the soil and forage their environment for nutrients and water. The evolution of this system 400 million years ago allowed plants to efficiently colonize and transform the land surface of our planet and paved the way for the highly diverse ecosystems that occupy its landmasses today. The distribution of roots in the soil, root system architecture (RSA), determines to a large extent how water and nutrients can be taken up. RSA is genetically determined; it differs between species and displays a high level of natural variation within a species. However, it is also strongly impacted by environmental parameters.

The genetic and environmental control of RSA allows our lab to address highly important questions in biology, such as: How does the genotype of an organism give rise to its phenotype? And how is this relationship impacted by interactions with the environment? Major progress in this area would not only bring about fundamental insights into biology, but also enable breakthroughs in fields such as breeding and biological engineering.

We address these questions using powerful systems genetics approaches in the root of the model plant *Arabidopsis thaliana.* Here, broad phenotypic variation exists in different Arabidopsis accessions (strains) that display high variation in processes that are relevant for root growth (→ Fig.1). These processes range from cell division and cell elongation to the response of the whole root system to different growth environments. Importantly, we have developed methods for measuring root traits with high-throughput in Arabidopsis, enabling large-scale association genetics in which phenotypic variability is mapped to causal regions of the genome. Moreover, large systems-type data sets such as cell-type specific transcriptome, proteome, and metabolomics data sets are available. These depict molecular states, and represent important intermediates between genotypes and phenotypes which can not only be used to increase the success of identifying causal genes but also to gain fundamental insights into the quantitative regulation of root traits at the molecular level.

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 Associate:
IGSP Center for Systems Biology, Duke University, Durham, NC, USA, 2008-2011
Laboratory: Dr. Philip Benfey

GROUP MEMBERS

PhD Student
Radka Slovak

Postdocs
Elke Barbez
Takehiko Ogura
Daniela Ristova
Santosh Satbhai

Programmer
Christian Göschl

Summer School
Joanna Nosarzewska*

Technicians
Angelika Gaidora
Katharina Jandrasits (50%)
Kristina Metesch
Madalina Mirea
Santiago Perez
Claudia Setzer
Delyana Stoeva
Franziska Stritzinger
Bonnie Wolhrab*

Trainees
Ceren Tabak

Visitors
Alejandro Alonso*
Sandra Cortijo*
Han Wang*
Miori Yoshida*

*(*left the lab in 2015)*

Using such approaches, we have generated a very large atlas of natural variation of root growth traits that range from the cellular to the organ level and span different growth conditions. Using these data we are able to identify genes at which sequence variation causes phenotypic variation.

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 micros-

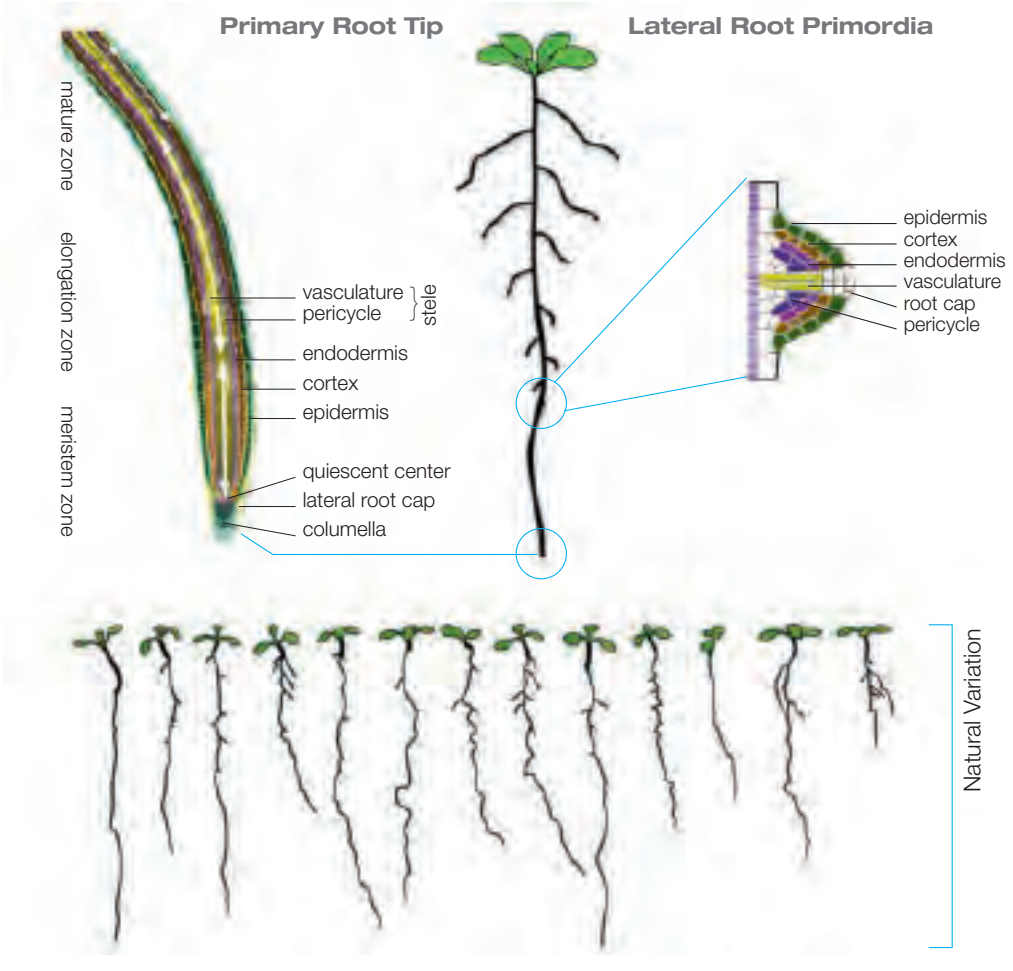


Fig. 1
Tissue architecture and natural variation of the root of Arabidopsis.
The Arabidopsis root and its developing tissues. Schematic of a young Arabidopsis root (center). The developmental zones of the primary root tip and its tissue architecture (left) and lateral root primordium (right). Different tissue types are indicated by different colors.

copy 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 used this information to identify genomic regions associated with variations in cellular architecture such as the size of the cells or of the root apical meristem (the zone in which cells divide; → Fig.1). The most significant genome region was located in the coding region of an uncharacterized F-box gene. In 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. Based on the mutant phenotype, we named the gene *KURZ UND KLEIN (KUK).* Using a transgenic approach, we were able to show that polymorphisms in the coding region account for the majority 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 coming years. For instance, how do 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?

Regulation of root system architecture

Much of the remarkable capability of plants to adjust to local environments is due to the fact that plants are modular organisms that can tune their organ number as well as the growth of these

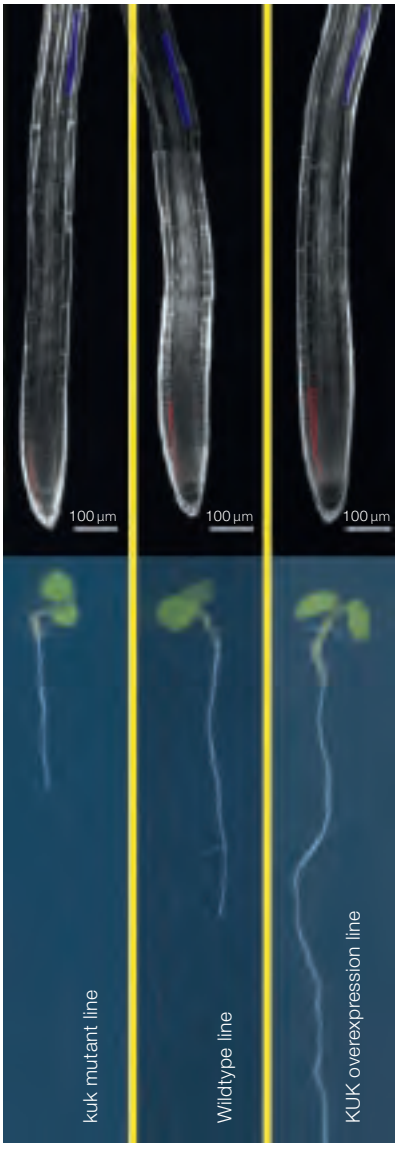


Fig. 2
The role of KUK. Meristem length (upper panel; highlighted in red), mature cell length (upper panel; highlighted in blue) and root length (lower panel) in representative plants of kuk-1 mutant, Col-0 wild type and 35S::KUK overexpression lines.

organs. This allows for a remarkable plasticity in plant architecture. In the root system, root system architecture (RSA) determines crucial parameters for plant survival, such as the ability to take up water, forage the soil for nutrients, and anchor the plant. RSA is mainly shaped by the processes of root branching, root elongation, and root growth direction (→ Fig.3). Central regulators of RSA are plant hormones. To identify the genetic bases that lead to variations in root system architecture, we have used chemical genomic approaches in which we perturb processes relating to phytohormonal signaling, quantify the phenotypic consequences in different accessions, map this variation of the root growth responses to the genome, and then study the genetic and molecular mechanisms of the genes that have the largest impact on the phenotype.

For instance, to understand which genetic and molecular components specifically modulate auxin dependent root growth traits, we applied a chemical genetics approach using a moderate concentration of the auxin transport inhibitor 1-N-naphtylphthalamic acid (NPA) and assessed root growth in more than 200 natural accessions of Arabidopsis. We observed the most striking natural variation in traits related to the root growth direction (→ Fig.4). 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 and root gravitropism and consequently control of root growth direction. This control of root growth direction over time translates into drastic differences in RSA. We are in the process

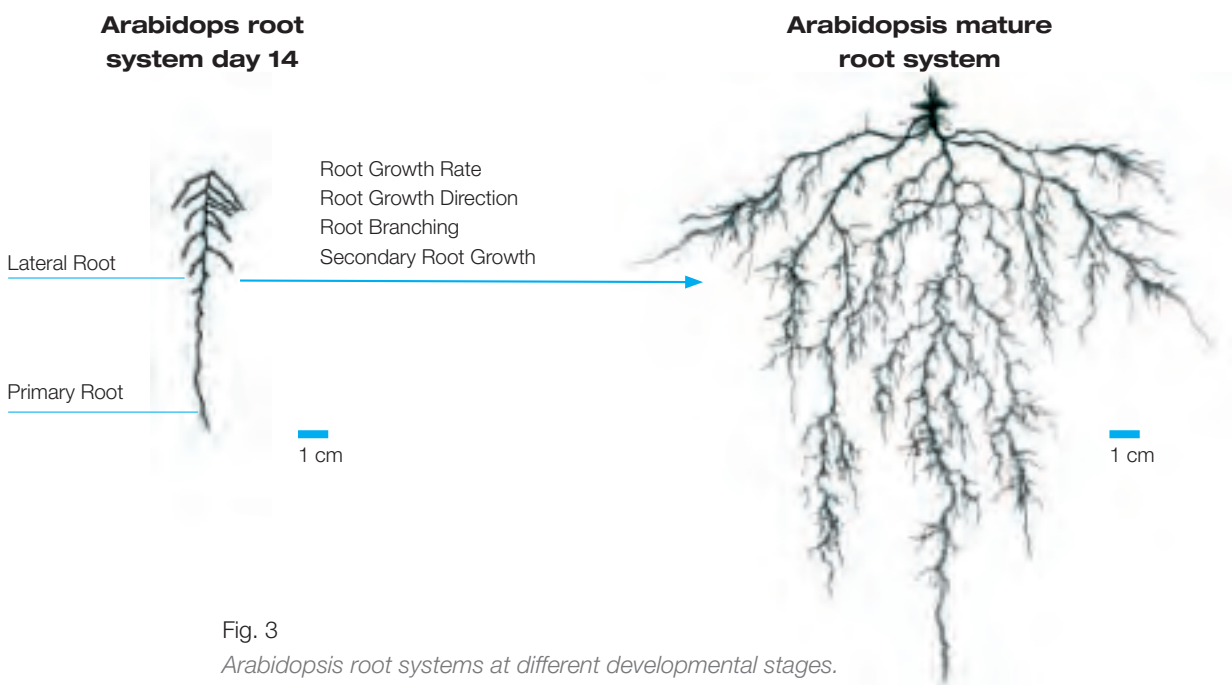


Fig. 3
Arabidopsis root systems at different developmental stages. Schematic representations of the Arabidopsis root system of a 14 day old seedling grown in vitro on an MS - agar plate (left) and a mature Arabidopsis root system in clay soil, Klagenfurt, Austria (right, based on Figure 135 in Lore Kutschera und Ernst Lichtenegger, 2010 Wurzelatlas mitteleuropäischer Ackerunkräuter und Kulturpflanzen. Unveränderter Nachdruck ISBN 978-3-7690-0758-9)

of 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 content. Root architecture is the outcome of local developmental decisions, such as lateral root outgrowth and growth rate modulation of primary and lateral roots (→ Fig.3). However, little is known about how this quantitative regulation is achieved. Using our large-scale phenotyping pipeline we have phenotyped hundreds of *A. thaliana* accessions for root growth traits in different stress conditions. We observed 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.5), indicating that accessions respond to different environmental cues in a specific, genetically determined manner. Using this variation for genome wide association mapping and in conjunction with advanced data mining of transcriptome and interactome data, we are uncovering the genes, their alleles and the gene networks that mediate the observed specificity in tuning growth responses.

Fig. 4
Differential response of 4 different accessions to NPA treatment.

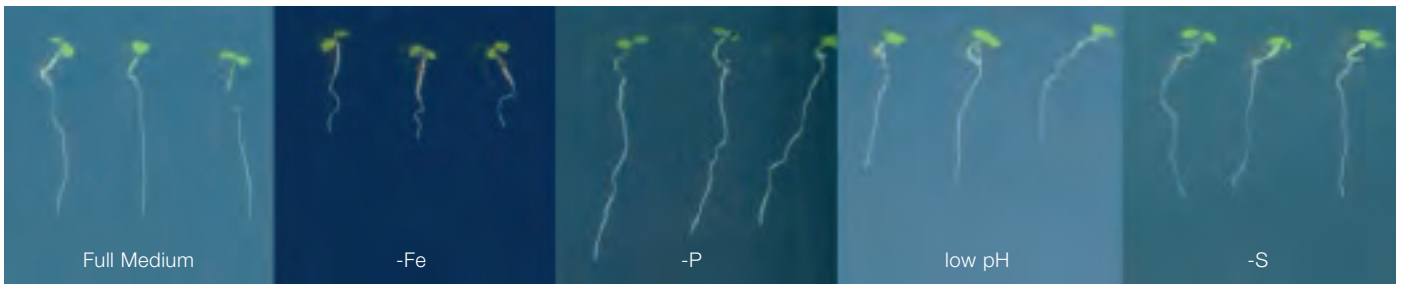


Fig. 5
Root growth response of an Arabidopsis accession to different growth conditions. Plants 5 days after germination; –Fe: Iron deficient medium; -P: Phosphorus deficient medium; low pH: medium adjusted to pH 4.6; -S: Sulfur deficient medium.

Effectomics – exploring the toolbox of biotrophic plant pathogens

DJAMEI GROUP

Plant pathogenic fungi, like smuts, are biotrophs that live and feed on their living host. They evolved a set of manipulative secreted molecules, so called effectors, with which they suppress their host's immune defense responses and redirect its metabolism and development. In our group, we study effectors to learn which plant pathways are targeted by the pathogen. As models, we employ the smut fungi *Ustilago maydis,* which infects the important crop plant maize, and its relative *Ustilago bromivora,* which infects the emerging grass model *Brachypodium distachyon*. In a systematic approach we characterize the effectome of these pathogens on the molecular level to provide a toolset for plant biologists to manipulate and learn about various metabolic pathways in plants.

ARMIN DJAMEI

armin.djamei@gmi.oeaw.ac.at

Joined GMI in Sep 2013

PhD: University of Vienna, Vienna, Austria

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

PhD Students
Jason Bosch
Fernando Navarrete
Franziska Rabe
Denise Seitner
Alexandra Stirnberg
Simon Uhse

Postdocs
Janos Bindics
Angelika Czedik-Eysenberg
Zhuoyu Wang*

Programmer
Tajamul Hussain*

Summer School
Laura Baggaley*

Technicians
Lisa Bauer*
Klaus Ehrlinger
Michelle Gallai
Tilo Guse
Daniel Player
Daniel Reumann*
Julia Riefler
Sebastian Seitner

Trainees
Meritxell Amigo*
Fahimeh Nazari*

*(*left the lab in 2015)*

Successful plant biotrophic pathogens must constantly sense and adapt the molecular manipulation of their host's metabolism to balance their interaction and keep the host alive. To suppress the highly evolved plant defense system and divert the host metabolism, plant pathogenic biotrophs coevolved fascinating strategies. The molecular basis for manipulation of the host plant is encoded in a versatile secreted effector repertoire found in biotrophic pathogens. 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 lacking known motifs which could otherwise suggest a putative function. Nevertheless, characterization of these effectors and their host target sites give fundamental insights into the requirements of the pathogen and point to key-nodes in the host metabolic network. Effector studies may thus prove rewarding for pest control and plant breeding in the field.

Ustilago maydis – Maize, an established model pathosystem

The *Ustilago maydis* - *Zea mays* pathosystem has emerged as a versatile model for studying biotrophic grass - fungal pathogen interactions. The corn smut fungus *U. maydis* causes prominent galls on all aerial parts of the maize plant (→ Fig.2A) and has been studied for more then 100 years. One important breakthrough for molecular studies is the well annotated genome sequence that was published in 2006.

With the small genome size, the ease of symptom recognition (forms local galls within a week of infection), its amenability to molecular genetic manipulation, and its relevance as a pathogen of an important crop plant, *U. maydis* is a fantastic pathogen to study biotrophic interactions (→ Fig.1).

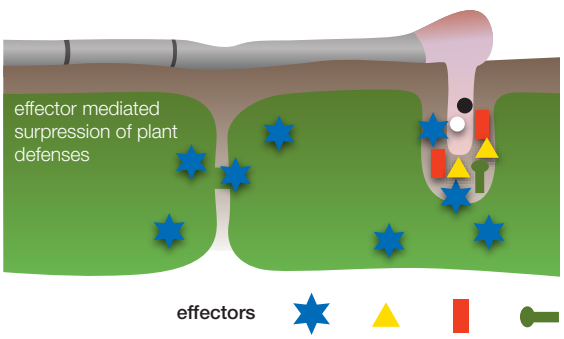


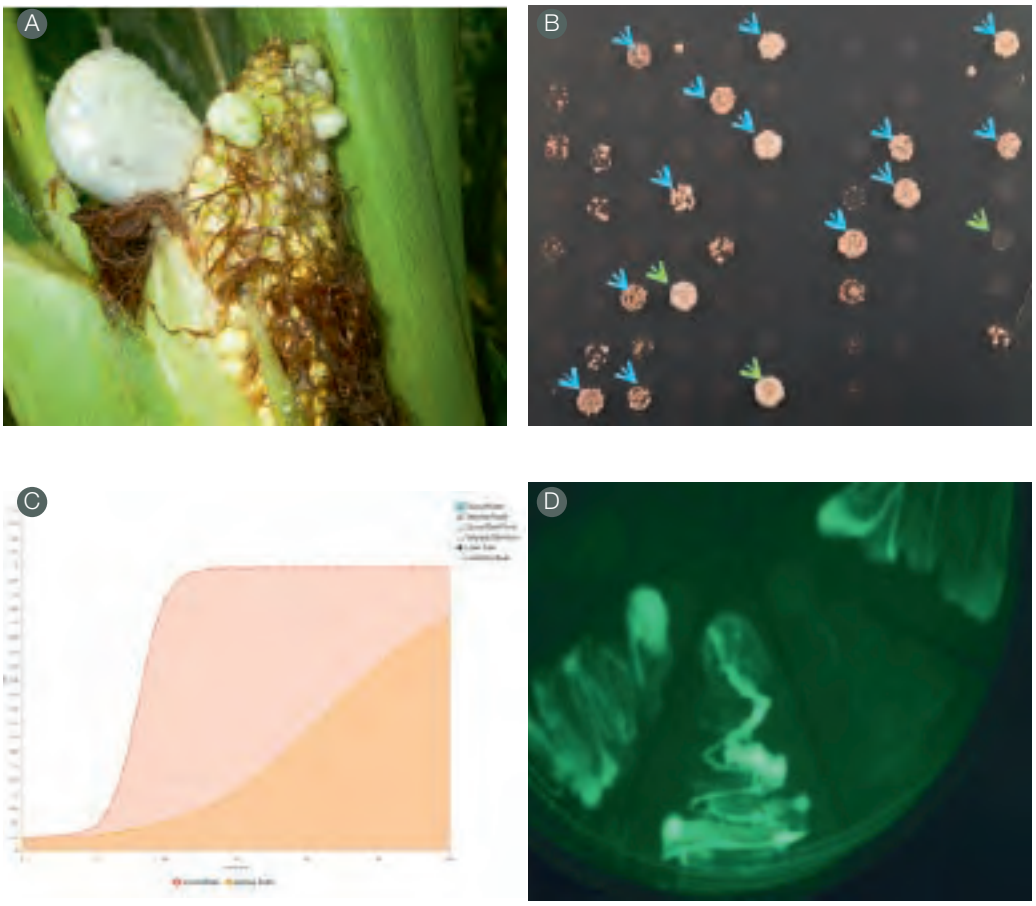
Fig.1
Scheme of fungal hyphae penetrating and secreting effector proteins into the host cell.

As most effector proteins do not show any sequence similarity with characterized proteins, our group decided to follow a systematic approach whereby all ~300 putative effector genes of *U. maydis* were cloned in a gateway compatible library to perform various screens (→ Fig.2).

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. Part of the characterization of the effector proteins is to delete them one by one and to test the fungal mutant strains for their virulence on the host plant. We have identified a number of putative effector proteins which, upon deletion, show a reduced or even abolished virulence. These interesting candidate proteins are currently being characterized in more detail. Unfortunately, the host plant of *U. maydis,* maize, is much less suitable for molecular functional studies due to its long generation time, enormous space requirements, and non-selfing nature. Therefore,

Fig. 2
A) *U. maydis induced tumour on a maize plant in the field. Black spore material of the fungus is eponymous.* **B – D** *representative data from effector screens.* **B**) *Homodimerisation assay in yeast for the putative effector library.* **C**) *growth curve of a yeast mutant without effector expression (pink) or effector expression (orange) as an example for the ongoing synthetic lethality screen.* **D**) *heterologous effector protein expression in fusion with the green fluorescent protein in bacteria.*



we are currently exploring an alternative grass-pathosystem with special emphasis on the plant side.

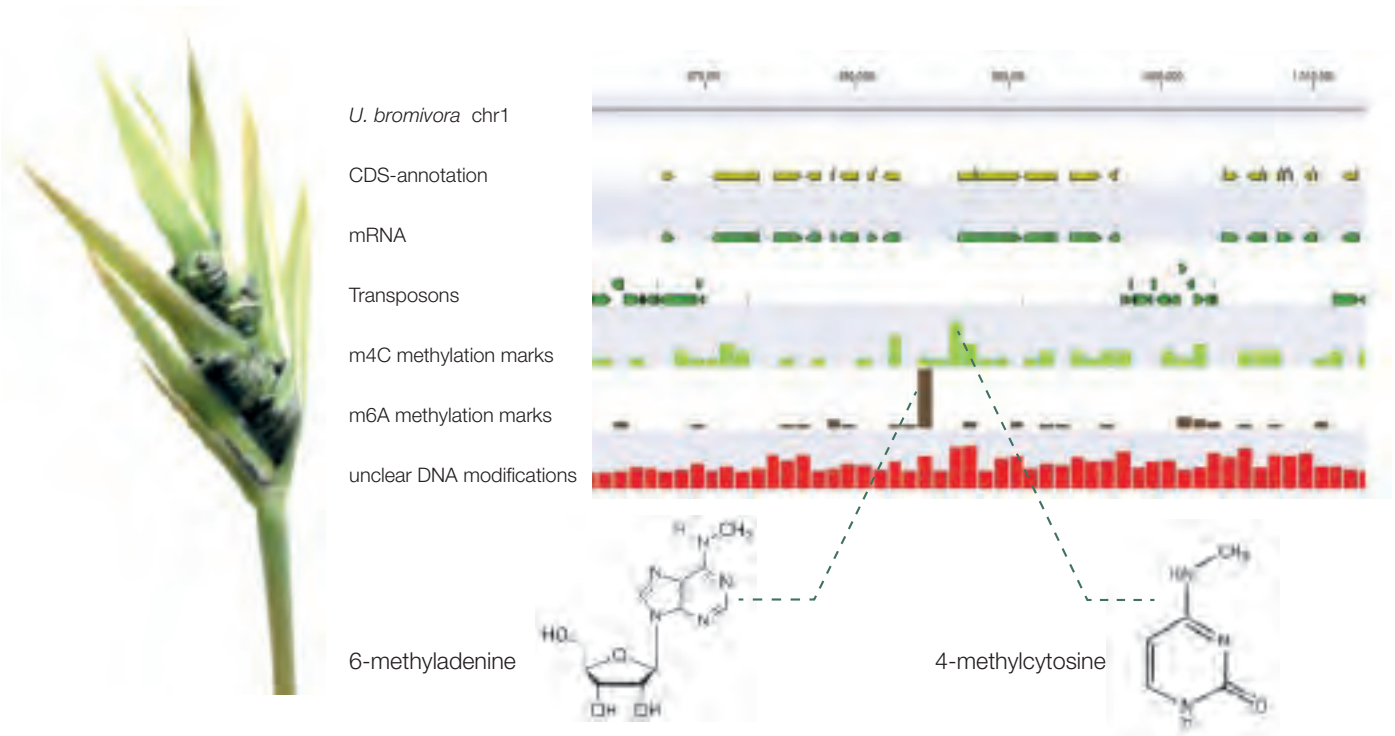
Ustilago bromivora – Brachypodium distachyon, an emerging model pair

In a recent report, the smut *Ustilago bromivora* was shown to infect *Brachypodium distachyon*. This model grass has a short generation time of 6-8 weeks, and stable transformations take only a few months. Spores of *U. bromivora* were kindly provided by Dr Thierry Marcel (Grignon, France). Over the past year we have been establishing the culture conditions, transformation, and infection protocols for *U. bromivora* (→ Fig.3). The fungal genome has been sequenced, assembled, and annotated, and our data indicate a very close evolutionary relationship to the barley head smut fungus *U. hordei* but also to *U. maydis* (→ Fig.3).

In parallel to our analysis of *U. bromivora* we have established the transformation protocol of the host plant *Brachypodium distachyon.* CRISPR/Cas9 technology is currently being tested in both *Brachypodium* and *U. bromivora* to enhance functional effector studies in this novel system in the future.

Fig. 3.

(Left) A spikelet of the model grass Brachypodium distachyon with sori filled with black spores of the smut fungus Ustilago Bromivora. (Right) A view from the genome browser showing the different information available for the emerging model smut U. bromivora.



Stress signal transduction and cellular responses

JONAK GROUP

Plants are constantly challenged by unfavorable environmental conditions. Our group studies the mechanisms that plants use to cope with environmental stress. A multitude of stress-induced responses at all levels of organization are required for acclimation to stress. We take an integrative approach to better understand how information transfer within cells (signal transduction) regulates the coordinated response of metabolism and gene expression that is vital to acquiring stress tolerance.

CLAUDIA JONAK

claudia.jonak@gmi.oeaw.ac.at

Joined GMI in Feb 2004

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

Previously

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

Laboratory: Prof. Jan Traas

GROUP MEMBERS

PhD Students
Iulia Danciu*
Bikram Pandey*
Hansjörg Stampfl*

Postdocs
Guillaume Queval*
Sascha Waidmann*

Technicians
Caroline Broyart*
Bettina Dekrout*

*(*left the lab in 2015)*

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. 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).

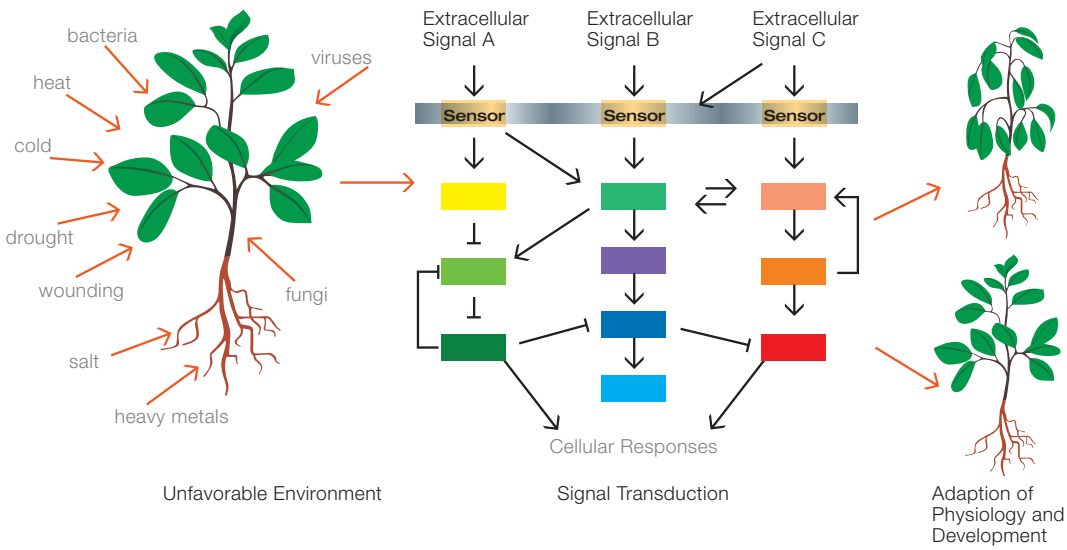


Fig. 1

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.

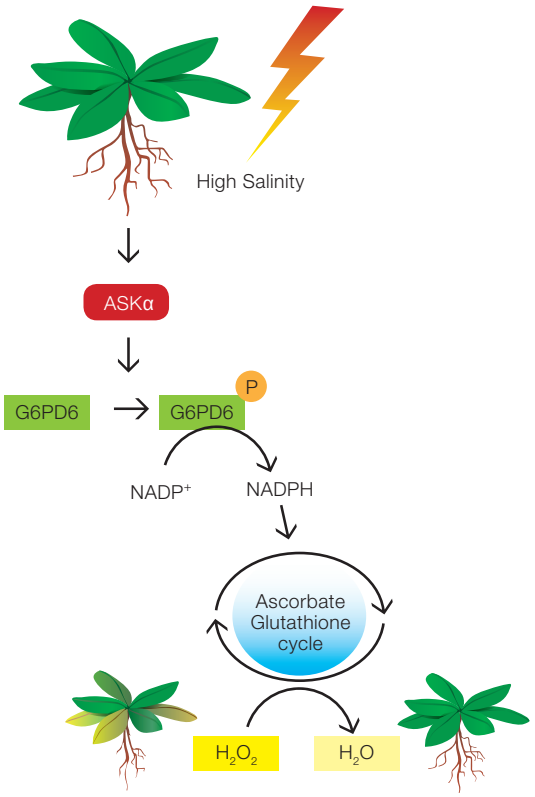


Fig. 2

ASKαis an important regulator of ROS detoxification and, thus, acclimation to salt stress. High salinity activates ASKα 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.

Adaptive regulation of cellular metabolism

A change in redox metabolism is a key phenomenon in response to abiotic and biotic stress. We provided novel mechanistic insight into how a key component of the antioxidant system, glucose-6-phosphate dehydrogenase (G6PD), is regulated. G6PD is the entry point into the pentose phosphate pathway, which provides reducing equivalents essential for maintaining the cellular redox balance. Combining genetic, molecular, and biochemical analyses, we identified an unexpected role for the Arabidopsis kinase ASKα in modulating levels of ROS (reactive oxygen species) and thereby salt stress tolerance. Significantly, we discovered G6PD as an *in vivo* substrate of ASKα. ASKα stimulates the activity of a specific cytosolic G6PD isoform (G6PD6) by phosphorylating an evolutionarily conserved threonine residue which is implicated in co-substrate binding (→ Fig. 2). This novel mechanism of G6PD adaptive regulation is critical for the cellular response to salinity stress. Currently, we are investigating the role of ASKα-G6PD6 in response to pathogen infection.

Redox-regulation is an important means to adjust cellular metabolism to environmental changes. We recently discovered a novel redox-sensitive mechanism that enables plants to rapidly adjust trehalose metabolism to prevailing environmental and developmental conditions. Plant trehalose metabolism is central to plant development and stress tolerance. It plays a vital role in communicating the sugar/energy status and regulating its use. We found that the activity of trehalose-6-phosphate phosphatases (TPPs, which catalyze the final step of trehalose synthesis), is redox sensitive (→ Fig. 3B). The evolutionary conservation of the two redox regulatory cysteine residues of TPPs in spermatophytes indicates that redox

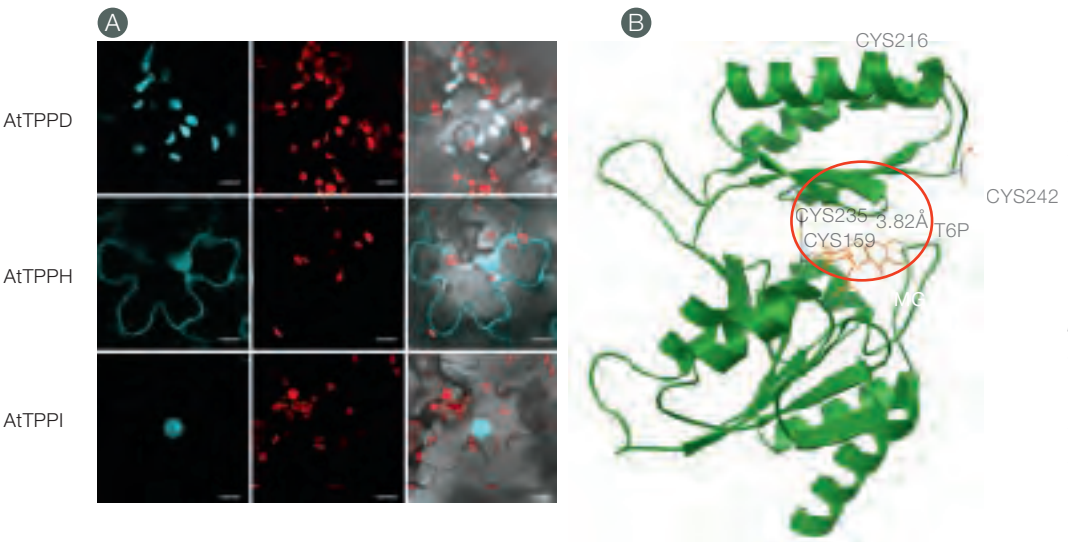


Fig. 3

Redox-regulation of trehalose metabolism present in different subcellular compartments. **A**) *Subcellular localization studies with fluorescent-tagged proteins show that different isoforms of the metabolic enzyme trehalose-6-phosphate phosphatase (TPP) are localized to plastids, cytoplasm and nucleus/nucleolus.* **B**) *TPP activity can be regulated by formation of an intramolecular disulfide bridge between two evolutionarily conserved redox sensitive cysteine residues in the substrate pocket.*

regulation of TPPs might be a common mechanism enabling plants to rapidly adjust trehalose metabolism to environmental and developmental conditions. Analysis of the subcellular localization of different Arabidopsis TPP isoforms revealed cytoplasmic, nuclear and chloroplast-localization (→ Fig. 3A). This result is surprising as trehalose metabolism is currently thought to be mainly cytosolic and it opens new perspectives to better understand the multitude of processes regulating trehalose metabolism.

Modulation of chromatin structure and function

Chromatin, the complex of DNA and proteins, is a major determinant in regulating gene expression. In our recent work, we identified the evolutionarily conserved protein DEK3 as a novel Arabidopsis chromatin-associated protein. A combination of global approaches with detailed biochemical, molecular and genetic analyses revealed that DEK3 is a chromatin architectural protein capable of modulating DNA topology, DNA accessibility, and gene expression. Genome-wide mapping of DEK3 binding sites by chromatin immunoprecipitation followed by deep sequencing revealed an enrichment of DEK3 at protein coding genes. Analysis of plants with altered DEK3 levels provided evidence that AtDEK3 contributes to transcriptional control as a repressor, probably by modulating DNA accessibility (→ Fig. 4).

Chromatin organization plays a key role in stress responses. Interestingly, fine-tuned DEK3 levels are critical for tolerance to high salinity and heat stress tolerance. Our ongoing research investigates the mechanism of how DEK3 function is regulated under stress conditions and how DEK3 contributes to stress-responsive gene expression.

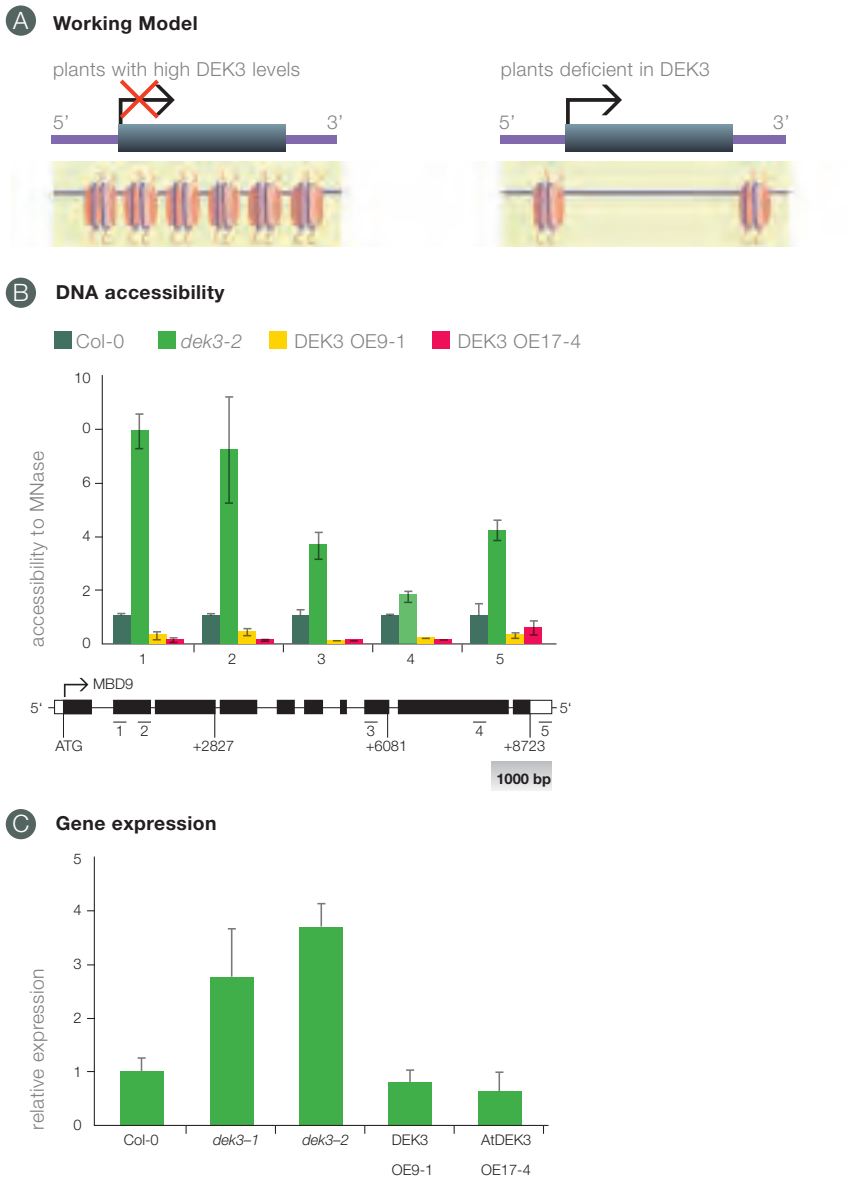


Fig. 4

The chromatin architectural protein DEK3 modulates DNA accessibility and gene expression. **A**) *Working model: In plants with elevated levels of DEK, target loci are more compact and gene expression is repressed while in plants deficient in DEK3, target loci are less compacted, allowing gene expression.* **B**) *DNA accessibility (monitored by accessibility of DNA to MNase) of the DEK3 tagtet locus MBD9 is enhanced in DEK3 knockout plants (dek 3-2) and reduced in Arabidopsis plants overexpressing DEK3 (DEK3 OE).* **C**) *Influence of DEK3 on gene expression. Transcript levels of MBD9 are elevated in plants deficient in DEK3 but reduced in plants with elevated DEK3 levels (DEK3 OE).*

Genetic and epigenetic changes in plants

MITTELSTEN SCHEID GROUP

The characteristics of organisms are influenced by two components of inheritance: genetic and epigenetic information, which mutually influence each other. Our group is interested in their interplay. We study the maintenance and modification of DNA by repair and recombination, the stability, flexibility and architecture of chromatin in the nucleus, and its connection with gene expression under abiotic stress and during development.

ORTRUN MITTELSTEN SCHEID

ortrun.mittelsten_scheid@gmi.oeaw.ac.at

Joined GMI in Jan 2004

PhD: University of Hamburg, Germany

Previously

- Research Associate: Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland, 1992-2003
  Laboratory: Prof. Jerzy Paszkowski
- Postdoctoral Fellow:
  Institute for Plant Sciences at the Federal Institute of Technology (ETH), Zurich, Switzerland, 1988-1992
  Laboratory: Prof. Ingo Potrykus
- Postdoctoral Fellow:
  Max Planck Institute for Cell Biology, Ladenburg, Germany, 1985-1987
  Laboratory: Prof. Hans-Georg Schweiger

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 defense against intruding DNA and RNA molecules, in genome 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 and in modes of epigenetic inheritance. We study these aspects in *Arabidopsis thaliana* and *Aethionema arabicum,* with 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.

The long chromosomal DNA molecules containing the majority of the genetic information are organized in a complex and inconceivably condensed way within the nucleus. Here they associate with RNA and proteins, including histones that contain much of the epigenetic information. This organization needs to be dynamic to allow for cell division, differentiation, metabolic activities, and stress responses. We follow changes in this architecture with molecular tools and study the interaction of DNA with differentially modified histones during and after heat stress. In parallel, we are developing tools to image these changes in real time in living cells. In the transparent roots of young plants, we track individual nuclei during the process of cell growth and differentiation, which is associated with visible changes in nuclear morphology (→ Fig. 1) Together with the microscopy experts on campus and in collaboration with

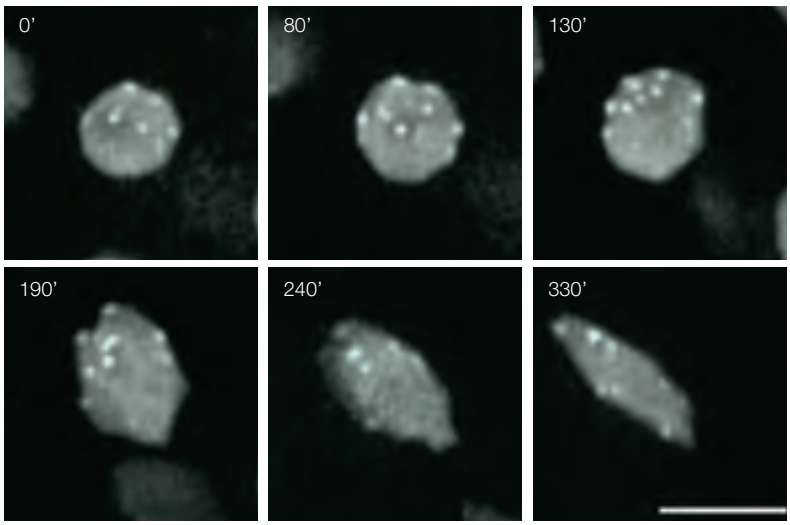


Fig.1
Changes in shape, size, number, and position of chromocenters can be tracked in a time series for individual nuclei in the growing root of Arabidopsis thaliana by live imaging. Chromatin is visualized with RFP-fused histones (line from the Berger lab). Scale bar = 10 µm (Photo Tao Dumur).

GROUP MEMBERS

Bachelor Student
Benjamin Kogelmann

Masters Students
David Schlager
Julia Thoma*

PhD Students
Jasmin Bassler
Claudio Capitao
Tao Dumur

Postdocs
Mattia Donà
Ruben Gutzat
Zsuzsanna Mérai

Programmer
Malgorzata Goiser

Technicians
Nina Daubel*
Katharina Jandrasits (50%)
Nicole Lettner

Trainees
Anita Banyai*
Alina Pröll

*(*left the lab in 2015)*

the Busch group, we developed a custom-made setup to monitor root nuclei over long periods under environmentally controlled conditions, including exposure to heat stress.

While the transmission of genetic information between generations is reliable, epigenetic information is more dynamic and apt to undergo reversible modifications upon internal and external stimulus. Whether environmentally induced epigenetic changes have the potential to be transmitted from one generation to the next, thereby becoming permanent, is a matter of intense debate. If so, the changes have to occur in the stem cells from which the progeny originates. The germ line in plants is less strictly defined than in most animals, and the corresponding stem cells separate from other somatic cells late in development. Nevertheless, there are only very few cells that contribute to flowers and seeds. To study the epigenetic configuration in these exact cells within the meristematic regions, we label their nuclei (→ Fig. 2) in order to sort them by fluorescence-activated nuclei sorting. We have constructed a reporter system to induce epigenetic changes at specific developmental stages and to subsequently follow the maintenance of the resulting modifications.

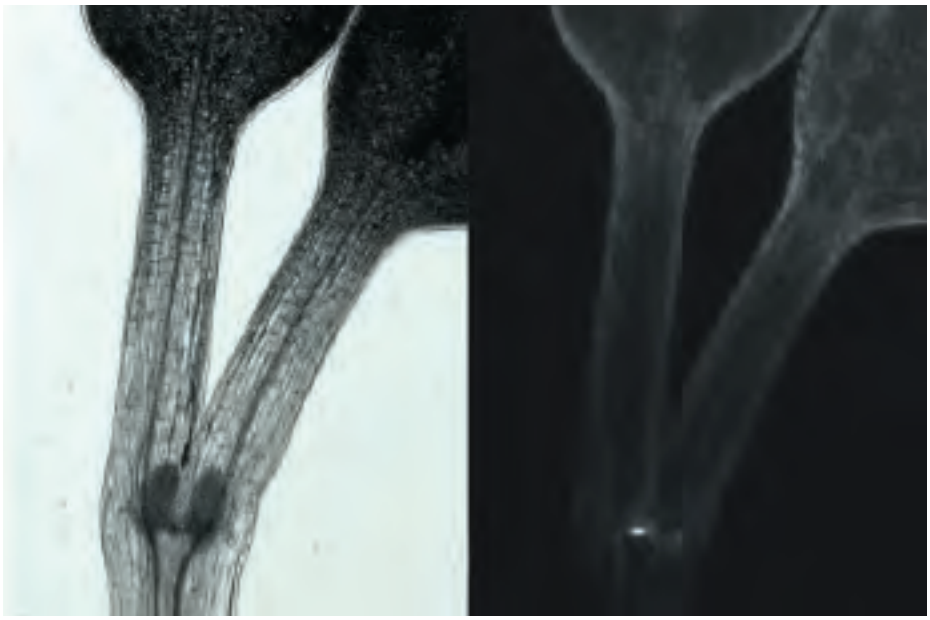


Fig. 2
Nuclei of germ line cells in the shoot apical meristem of Arabidopsis thaliana are labelled with fluorescent histone variants expressed from a specific promoter. Left: detail of an 8 day-old seedling in visible light; right: image in fluorescence optics (Photo Ruben Gutzat).

While less variable than epigenetic features, the conservation of DNA sequence information is constantly challenged by external genotoxic factors. There are multiple types of DNA lesions, and all organisms have developed several DNA damage repair pathways to restore and maintain genome integrity. In eukaryotes, the sites of DNA damage can be located in dense chromatin and must be made accessible for repair enzymes. Several multimeric chromatin remodelling complexes can shift, remove, or insert nucleosomes, or exchange histone variants. We are characterizing the action of the SWR1 complex that installs a specific histone variant at transcriptionally active genes but is also important for efficient DNA damage repair by homologous recombination. Plant lines expressing labelled subunits of the complex are used to identify interacting proteins, and to study epistastic relationships with repair enzymes together with the kinetics of repair.

Aethionema arabicum, a distant relative of Arabidopsis, forms two different types of both fruit and seed on the same plant. This likely evolved as a strategy to diversify the mode of distribution. In a collaborative project with 6 other labs, we aim to elucidate the molecular basis of this dimorphism. Genetically similar accessions from distinct geographical regions reveal differences in morphology and development (→ Fig. 3), germination biology, gene expression, and epigenetic features. We have adapted protocols for epigenetic analysis and aim to elucidate if, when, and how epigenetic regulation contributes to the decision about the type of fruit and seed formation. These data are combined with anatomical, genomic, transcriptional, developmental, and hormonal information in order to understand this fascinating developmental process.

Fig. 3
Aethionema arabicum, a cruciferous plant with dimorphic seeds and fruits, features natural variation between different accessions. Plant with the same age from Turkey (left) and Cyprus (right) (Photo David Schlager).

Small RNA functions in plant embryos

NODINE GROUP

After fertilization, the basic body plans of both plants and animals are established during early embryo development. However, despite the fundamental importance of this formative phase of the plant's life to developmental biology and agriculture, the molecular mechanisms that generate the most basic cell-types in plants remain largely uncharacterized. Our group's research is helping elucidate the molecular basis of plant body plan formation during early embryogenesis.

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
Laboratory: Prof. David Bartel

GROUP MEMBERS

PhD Students
Falko Hofmann
Ping Kao
Stefan Lutzmayer
Katalin Paldi
Aleksandra Plotnikova
Michael Schon

Postdocs
Balaji Enugutti
Divya Vashisht

Technicians
Magdalena Mosiolek
Subramanian Paulraj
Lucyna Slusarz

Trainees
Florian Hödlmaier
Max Kellner
Tobias Riedl
Sandra Tietscher*

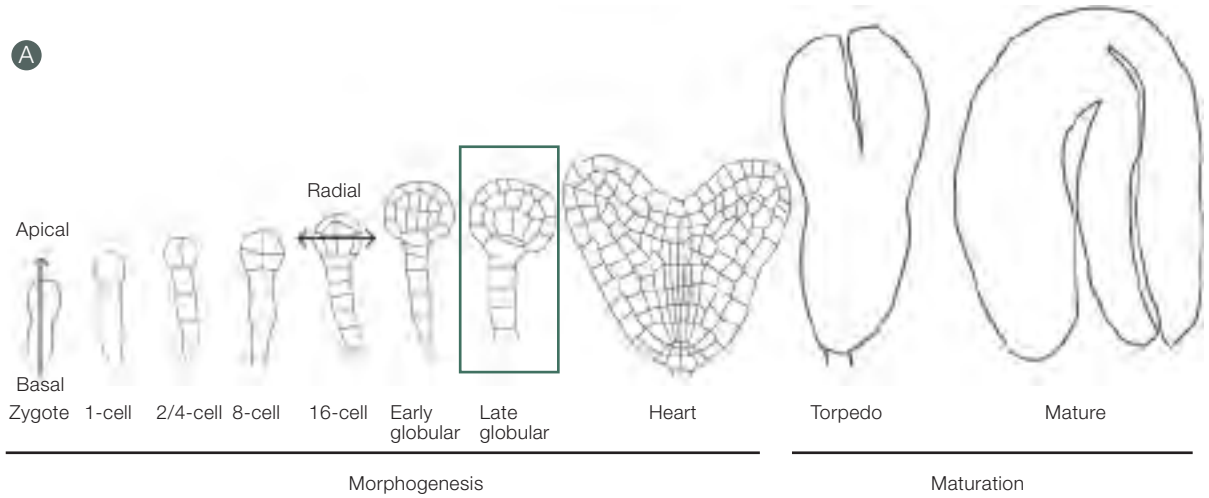
*(*left the lab in 2015)*

A class of short regulatory RNA molecules called microRNAs (miRNAs) is required for both pattern formation and timing during plant embryo development by 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.

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. Plant miRNAs have near-perfect complementarity with binding sites in their target RNAs and typically mediate target RNA cleavage. Although each plant miRNA family is predicted to specifically regulate only a few target RNAs, these targets typically encode transcription factors and other key developmental regulators, and thus regulate many downstream genes themselves.

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.1 and 2). 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 are we uncovering novel miRNA functions, but by identifying and characterizing their respective targets we are also discovering novel transcription factor functions during embryogenesis.

Over the past year, we have identified new miRNA functions during early embryogenesis and our research is yielding insights into the molecular basis of plant embryo development, as well as the general understanding of how small regulatory RNAs influence cellular differentiation.



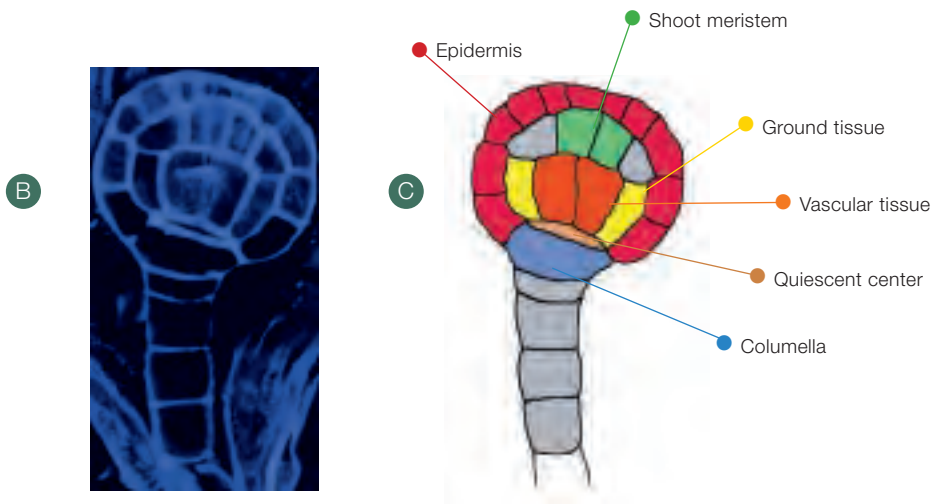


Fig. 1 *Arabidopsis embryogenesis.*
A) *Illustrations of Arabidopsis embryos at various stages of development. Apical-basal and radial body axes are established during early embryogenesis and are labeled accordingly. Morphogenesis and maturation phases are labeled at the bottom.* B) *Confocal laser scanning 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.*

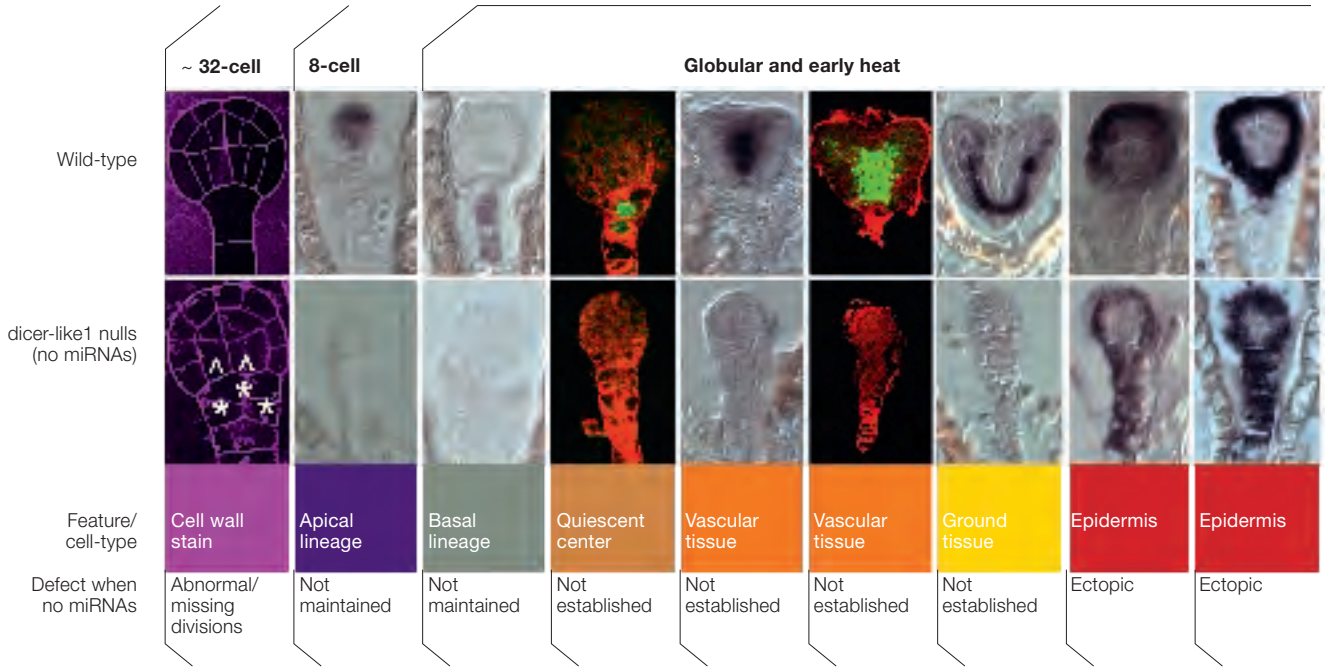


Fig. 2

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 dicer-like1 null (dcl1-5) (bottom) embryos, which lack miRNAs. Embryos deficient in miRNAs exhibit morphological defects (see cell wall dye in left-most panels) and mis-express several cell-specific markers including those for the first two cell lineages (apical and basal) and along the radial axis, which indicates that miRNAs are required for multiple cell differentiation events. Unpublished and adapted from Nodine and Bartel (2010) Genes & Development.

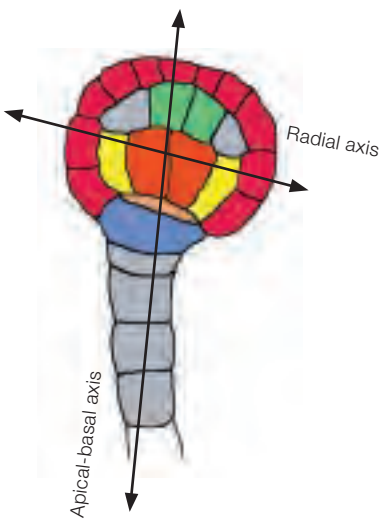
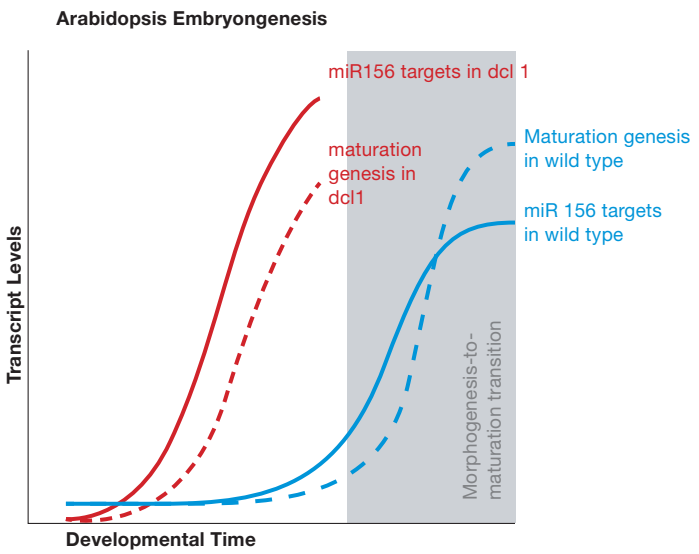


Fig. 3

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

NORDBORG GROUP

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 does the environment affect this translation; 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 — as well as the genome itself. Our research is 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 an international effort to make genome-wide association in *A. thaliana* a reality. We have sequenced over 1000 natural inbred lines and are making the results available to the *Arabidopsis* community. We are also developing a public website that will allow anyone to carry out GWAS and coordinate as much phenotypic information as possible.

MAGNUS NORDBORG

magnus.nordborg@gmi.oeaw.ac.at

Joined GMI in Feb 2009

PhD: Department of Biological Sciences, Stanford University, USA

Previously

- Associate Professor: Molecular & Computational Biology, USC, USA 2004-2015
- Assistant Professor: Molecular & Computational Biology, USC, USA, 2000–2004
- Research Assistant Professor ("forskarassistent"): Department of Genetics, Lund University, Sweden, 1997–2000
- Postdoctoral Associate: Department of Ecology & Evolution, University of Chicago, USA, 1994-1997
  Laboratory: J. Bergelson, B. & D. Charlesworth

GROUP MEMBERS

PhD Students

Gökce Aköz | Robin Burns
Envel Kerdaffrec | Dazhe Meng*
Polina Novikova | Fernando Rabanal
Mayela Soto | Pei Zhang*

Postdocs

Pieter Clauw
Manu Dubin*
Ashley Farlow*
Daniele Filiault
Matthew Horton
Benjamin Jaegle
Arthur Korte*
Cheng-Ruei Lee
Eriko Sasaki
Hannes Svardal*

Programmers

Rahul Pisupati | Ümit Seren

Technicians

Selen Irez*
Stefanie Koemeda*
Pamela Korte*
Viktoria Nizhynska
Ilka Reichardt-Gomez
Viktor Voronin

*(*left the lab in 2015*

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 methodologies for dealing with confounding will be crucial. We are exploring a wide range of methods for handling this problem.

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 an 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 characterize them at the molecular level.

A

Fig. 1
A) *Common garden 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 environmental 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, and understand the role of epigenetic inheritance in natural variation.

Evolution of *Arabidopsis*

We are heavily involved in the comparative analysis of the genus *Arabidopsis.* Long-term questions include the evolution of genome size, the effects of polyploidy or switching to self-fertilization, but our immediate goal is to understand how genetic variation is distributed across a diverse group of plant species. To this end, we have sequenced over a hundred individuals from all taxa in the genus, and discovered that speciation in the genus is a messy (and ongoing) process involving long periods of partial reproductive isolation.

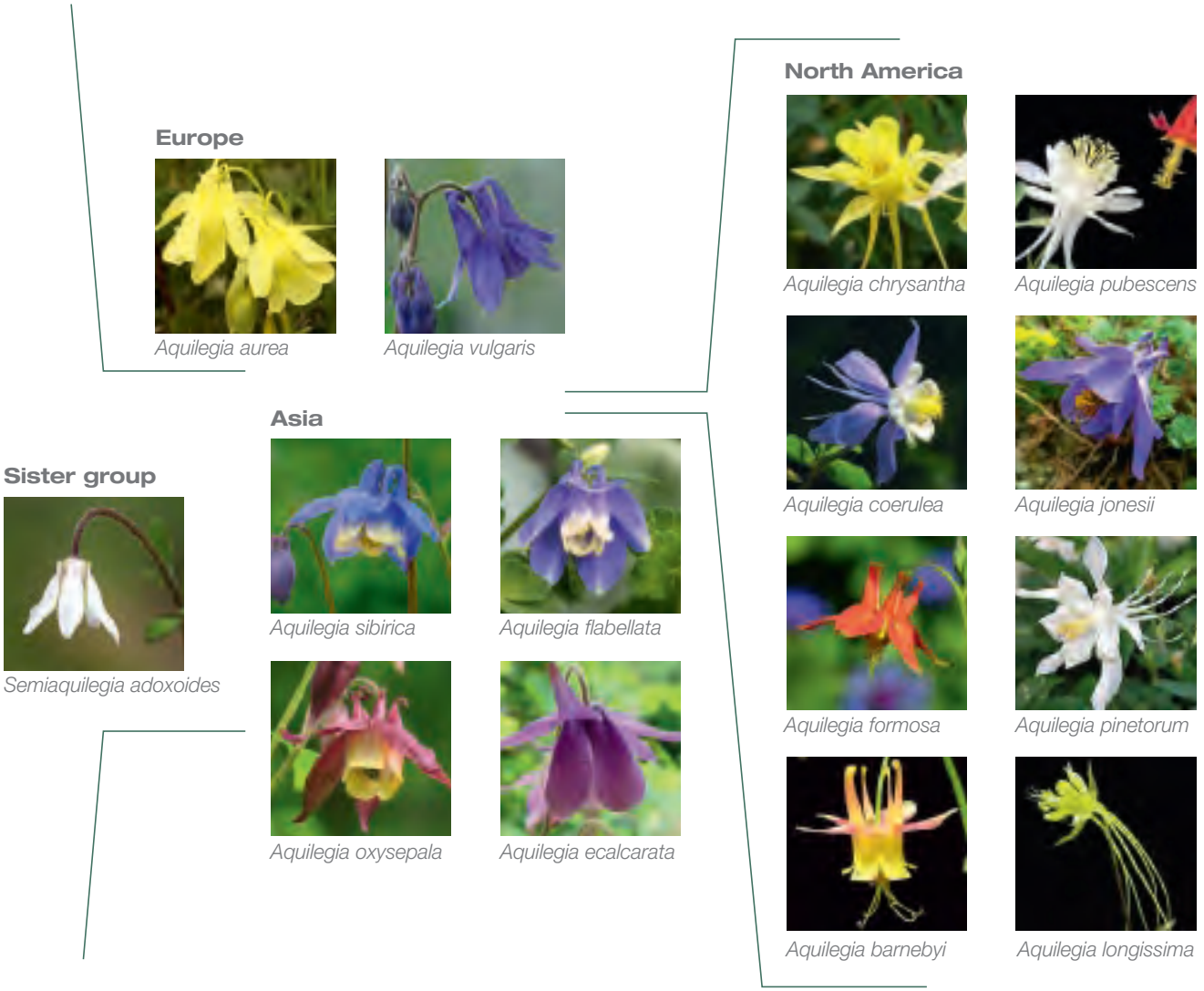
B

Fig. 1
B) *Close-up of a dispersal experiment*

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 (→ Fig. 2), 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
Columbine species currently being sequenced by JGI. We focus in particular on the sympatric A. formosa and A. pubescens.
(Courtesy of Scott Hodges, UCSB)

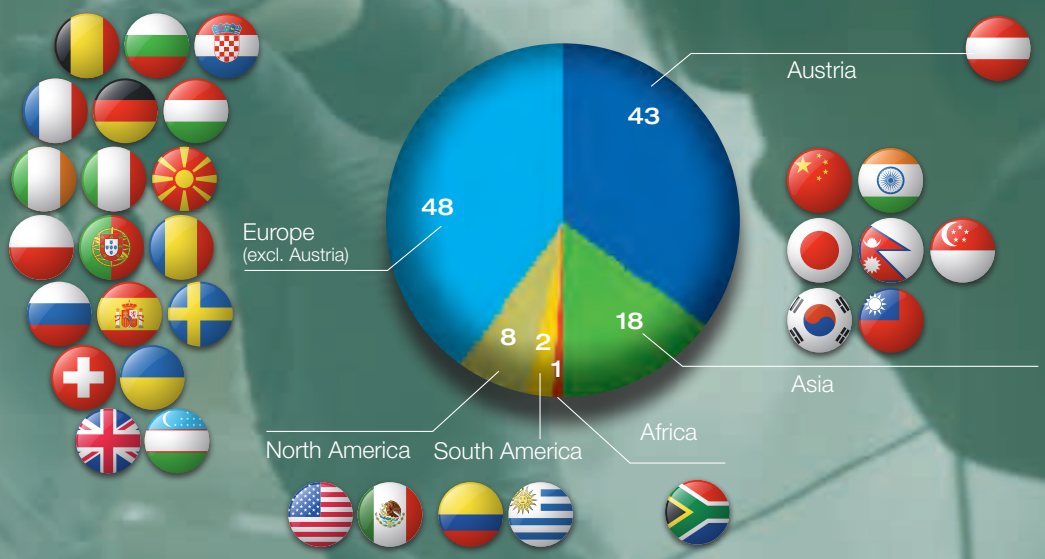


Population genetics of African green monkeys

The African green monkey *(Cercopithecus sp.)* is a common Old World monkey, spread throughout much of Africa, and introduced by humans to the Caribbean (→ Fig. 3). It is also kept in large colonies for behavioral and biomedical research, in particular for understanding HIV resistance. We are part of an international consortium developing 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.

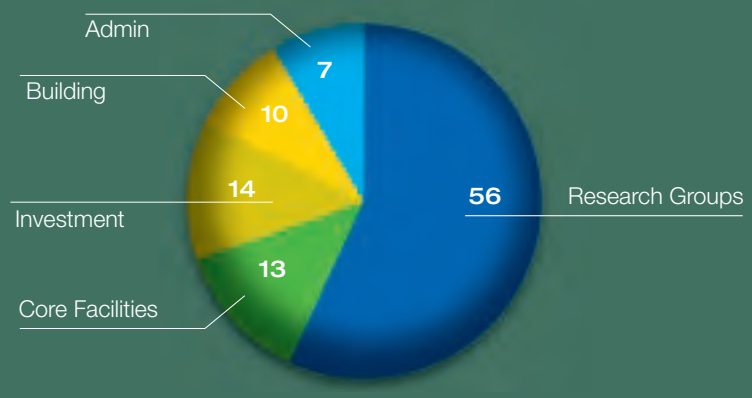
Fig. 3

Staff - Nationalities (Head Count)

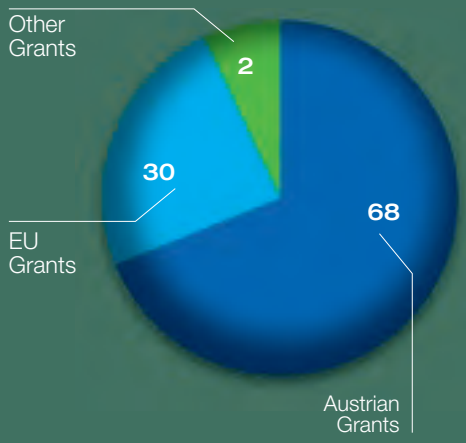


15 Key Facts *(AS OF DEC 31, 2015)*

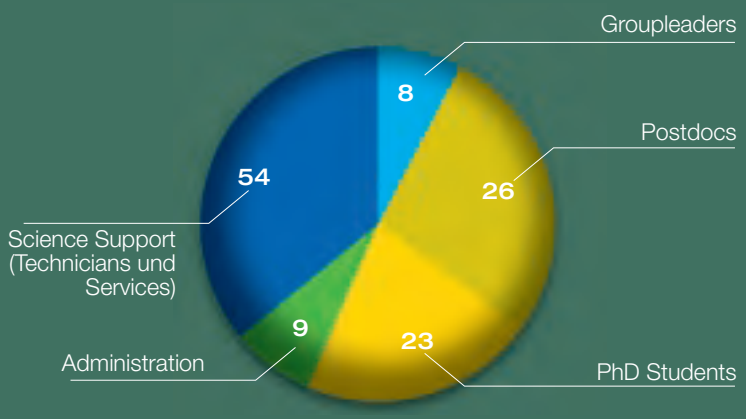
Expenditures (%)



Research Grants (%)



Staff by Function (Head Count)



15 Publications

BELKHADIR GROUP

Belkhadir Y, Jaillais Y *(2015)* **The molecular circuitry of brassinosteroid signaling.** *New Phytol. 206(2):522-40.*

BERGER GROUP

Borg M, Berger F *(2015)* **Chromatin remodelling during male gametophyte development.** *Plant J. 83(1):177-88.*

Bowman JL, Araki T, Arteaga-Vazquez MA, Berger F, Dolan L, Haseloff J, Ishizaki K, Kyozuka J, Lin SS, Nagasaki H, Nakagami H, Nakajima K, Nakamura Y, Ohashi-Ito K, Sawa S, Shimamura M, Solano R, Tsukaya H, Ueda T, Watanabe Y, Yamato KT, Zachgo S, Kohchi T *(2015)* **The naming of names: guidelines for gene nomenclature in *Marchantia.*** *Plant Cell Physiol. epub.*

Kawashima T, Berger F *(2015)* **The central cell nuclear position at the micropylar end is maintained by the balance of F-actin dynamics, but dispensable for karyogamy in *Arabidopsis.*** *Plant Reprod. 28(2):103-10.*

Kawashima T, Lorkovic ZJ, Nishihama R, Ishizaki K, Axelsson E, Yelagandula R, Kohchi T, Berger F *(2015)* **Diversification of histone H2A variants during plant evolution.** *Trends Plant Sci 20(7):419-25.*

Maruyama D, Kawashima T, Higashiyama T *(2015)* **Selective nuclear elimination in multinucleate cells.** *Oncotarget 6(31):30447-8.*

Maruyama D, Völz R, Takeuchi H, Mori T, Igawa T, Kurihara D, Kawashima T, Ueda M, Ito M, Umeda M, Nishikawa S, Groß-Hardt R, Higashiyama T *(2015)* **Rapid Elimination of the Persistent Synergid through a Cell Fusion Mechanism.** *Cell 161(4):907-18.*

Roscoe T, Guilleminot J, Bessoule J, Berger F, Devic M *(2015)* **Complementation of Seed Maturation Phenotypes by Ectopic Expression of ABSCISIC ACID INSENSITIVE3, FUSCA3 and LEAFY COTYLEDON2 in *Arabidopsis.*** *Plant Cell Physiol. 56(6):1215-28.*

BUSCH GROUP

Brady S, Burow M, Busch W, Carlborg Ö, Denby K, Glazebrook J, Hamilton E, Harmer S, Haswell E, Maloof J, Springer N, Kliebenstein D *(2015)* **Reassess the t Test: Interact with All Your Data via ANOVA.** *Plant Cell 27(8):2088-94.*

Satbhai S, Ristova D, Busch W *(2015)* **Underground tuning: quantitative regulation of root growth.** *J. Exp. Bot. 66 (4):1099-112.*

Slovak R, Göschl C, Seren Ü, Busch W *(2015)* **Genome-wide association mapping in plants exemplified for root growth in Arabidopsis thaliana.** *Methods Mol. Biol. 1284:343-57.*

Slovak R, Ogura T, Satbhai SB, Ristova D, Busch W *(2015)* **Genetic control of root growth: from genes to networks.** *Ann Bot. epub.*

MITTELSTEN SCHEID GROUP

Donà M, Mittelsten Scheid O (2015) **DNA Damage Repair in the Context of Plant Chromatin.** *Plant Physiol. 168(4):1206-18.*

Mittelsten Scheid O *(2015)* **Editorial.** *Semin Cell Dev Biol. 44:1*

Probst A, Mittelsten Scheid O *(2015)* **Stress-induced structural changes in plant chromatin.** *Curr. Opin. Plant Biol. 27:8-16.*

NORDBORG GROUP

Dubin M, Zhang P, Meng D, Remigereau M, Osborne E, Paolo Casale F, Drewe P, Kahles A, Jean G, Vilhjálmsson B, Jagoda J, Irez S, Voronin V, Song Q, Long Q, Rätsch G, Stegle O, Clark R, Nordborg M *(2015)* **DNA methylation in Arabidopsis has a genetic basis and shows evidence of local adaptation.** *Elife 4:e05255.*

Farlow A, Long H, Arnoux S, Sung W, Doak T, Nordborg M, Lynch M *(2015)* **The Spontaneous Mutation Rate in the Fission Yeast Schizosaccharomyces pombe.** *Genetics 201(2):737-44*.

Ito S, Nozoye T, Sasaki E, Imai M, Shiwa Y, Shibata-Hatta M, Ishige T, Fukui K, Ito K, Nakanishi H, Nishizawa N, Yajima S, Asami T *(2015)* **Strigolactone regulates anthocyanin accumulation, acid phosphatases production and plant growth under low phosphate condition in Arabidopsis.** *PLoS ONE 10(3):e0119724.*

Muir G, Ruiz-Duarte P, Hohmann N, Mable B, Novikova P, Schmickl R, Guggisberg A, Koch M *(2015)* **Exogenous selection rather than cytonuclear incompatibilities shapes asymmetrical fitness of reciprocal Arabidopsis hybrids.** *Ecol. Evol. 5(8):1734-45.*

Provart N, Alonso J, Assmann S, Bergmann D, Brady S, Brkljacic J, Browse J, Chapple C, Colot V, Cutler S, Dangl J, Ehrhardt D, Friesner J, Frommer W, Grotewold E, Meyerowitz E, Nemhauser J, Nordborg M, Pikaard C, Shanklin J, Somerville C, Stitt M, Torii K, Waese J, Wagner D, McCourt P *(2015)* **50 years of Arabidopsis research: highlights and future directions.** *New Phytol. epub.*

Sasaki E, Zhang P, Atwell S, Meng D, Nordborg M *(2015)* **"Missing" G x E Variation Controls Flowering Time in Arabidopsis thaliana.** *PLoS Genet. 11(10):e1005597.*

Warren W, Jasinska A, Garcia-Perez R, Svardal H, Tomlinson C, Rocchi M, Archidiacono N, Capozzi O, Minx P, Montague M, Kyung K, Hillier L, Kremitzki M, Graves T, Chiang C, Hughes J, Tran N, Wang Y, Ramensky V, Choi O, Jung Y, Schmitt C, Juretic N, Wasserscheid J, Turner T, Wiseman R, Tuscher J, Karl J, Schmitz J, Zahn R, O'Connor D, Redmond E, Nisbett A, Jacquelin B, Müller-Trutwin M, Brenchley J, Dione M, Antonio M, Schroth G, Kaplan J, Jorgensen M, Thomas G, Hahn M, Raney B, Aken B, Schmitz J, Churakov G, Noll A, Stanyon R, Webb D, Thibaud-Nissen F, Nordborg M, Marques-Bonet T, Dewar K, Weinstock G, Wilson R, Freimer N *(2015)* **The genome of the vervet (Chlorocebus aethiops sabaeus).** *Genome Res. epub.*

Weigel D, Nordborg M *(2015)* **Population Genomics for Understanding Adaptation in Wild Plant Species.** *Annu. Rev. Genet. epub.*

Yoshida K, Sasaki E, Kamoun S *(2015)* **Computational analyses of ancient pathogen DNA from herbarium samples: challenges and prospects.** *Front. Plant Sci. 6:771.*

15 Grants

BELKHADIR GROUP

Brassignal
The Austrian Research Promotion Agency - FEMTECH
2014 - 2015

BERGER GROUP

EMBO Long-term fellowship
European Molecular Biology Organization
2014 – 2016

Impact of the new histone H2a on chromatin structure and dynamics
Austrian Science Fund
2014 – 2017

Epigenetic reprogramming of the plant paternal genome
Austrian Science Fund
2015 – 2016

Evolution of sexual reproduction in plants
Austrian Science Fund
2015 – 2018

Evolution of the chromatin organization in plants
Austrian Science Fund
2016 – 2018

The histone variant H2A.W: a novel component that structures chromatin domains
Austrian Science Fund
2016 – 2017

BUSCH GROUP

The role of KUK in root development (Plant Fellows)
EU-FP7-Marie Curie Actions – COFUND Research Fellowship
2013 – 2015

Quantitative live imaging to determine the regulatory impact of chromatin dynamics
Vienna Science and Technology Fund
2014 – 2017

EXO70 exocyst subunits in morphogenesis and adaptation
Austrian Science Fund
2015 – 2018

Growth control
The Austrian Research Promotion Agency - FEMTECH
2015

Root-gene-networks
The Austrian Research Promotion Agency - FEMTECH
2015

Root growth control and epistasis
Austrian Science Fund
2015 – 2017

The role of PLD zeta1 in iron dependent root growth regulation
Austrian Science Fund
2016 – 2018

DJAMEI GROUP

Effectomics – elucidating the toolbox of plant pathogens
European Research Council (ERC)
2014 – 2019

Functional Characterization of putative translocated effector Flip3 of pathogenic biotrophic smut fungus Ustilago maydis
OeAD Austrian Agency for International Cooperation in Education and Research Ltd.
2014 – 2015

Characterization of an essential virulence factor in the maize pathogen Ustilago maydis
Austrian Science Fund
2015 – 2018

Elucidating salicylic acid sensing in biotrophic smut fungi
Austrian Science Fund
2015 – 2017

JONAK GROUP

CALIPSO - Calcium- and light signals in photosynthetic organisms
EU-FP7-Marie Curie Actions - ITN
2013 – 2017

Characterization of a novel salt stress signaling component from Arabidopsis thaliana
Austrian Science Fund
2013 – 2015

MITTELSTEN SCHEID GROUP

EPICOL – Ecological and evolutionary plant epigenetics
Austrian Science Fund
2010 – 2015

Graduate program "Chromosome Dynamics"
Austrian Science Fund
2012 – 2016

SINUDYN – Stress-induced nucleosome dynamics in plants
Austrian Science Fund
2013 – 2016

Stability of epigenetic information in the shoot apical meristem (Plant Fellows)
EU-FP7-Marie Curie Actions – COFUND Research Fellowship
2013 – 2015

Dimorphic fruits, seeds and seedlings as adaptation mechanisms to abiotic stress in unpredictable environments
ERA-CAPS / Austrian Science Fund
2014 – 2017

Quantitative live imaging to determine the regulatory impact of chromatin dynamics
Vienna Science and Technology Fund
2014 – 2018

Plant stem cell ATAC
The Austrian Research Promotion Agency - FEMTECH
2015 – 2016

NODINE GROUP

European plant embryology consortium
ERA-CAPS / Austrian Science Fund
2014 – 2017

Graduate program "RNA Biology"
Austrian Science Fund
2014 – 2016

Small RNA directed reprogramming of lineage-specific epigenomes in plant embryos
Austrian Science Fund
2015 – 2019

sRNA-EMB: Small RNA regulation of the body plan and epigenome in Arabidopsis embryos
European Research Council (ERC)
2015 – 2020

NORDBORG GROUP

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

Starting from scratch: adaptation to variable environments after an extreme bottleneck
German Research Foundation
2011 – 2017

transPLANT: Trans-national infrastructure for plant genomic science
EU-FP7-Collaborative Project & Coordination and Support Action
2011 – 2015

CLIMATE_ADAPTATION: Genetic adaptions to climate in Arabidopsis thaliana
EU-FP7-Marie Curie Actions - CIG
2012 – 2016

EMBO Long-term fellowship
European Molecular Biology Organization
2014 – 2015

15 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.

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).

15 Seminars

January

Sebastian Schornack, *The Sainsbury Laboratory, University of Cambridge, UK*
Common and contrasting processes during plant colonisation by mycorrhiza fungi and oomycetes

Tan Ek Han, *Plant Biology & Genome Center, University of California, Davis, US*
Genomic Catastrophes during Genome Elimination in Plants

Karol Mikula, *Dept. of Mathematics and Descriptive Geometry, Slovak University of Technology, SK*
Numerical methods for early embryogenesis computational reconstruction

On Sun Lau, *Department of Biology, Stanford University, US*
Stomatal development as a model system for cell specification and environmental signaling

Martin Parniske, *Ludwig Maximilian University of Munich, DE*
Molecular communication between plant roots and their microbial symbionts: the enigmatic role of the symbiosis receptor kinase SYMRK

February

Abidur Rahman, *Cryobiofrontier Research Center, Iwate University, JP*
Auxin homeostasis under temperature stress: a cellular perspective

Seong Wook Yang, *Department of Plant and Environmental Sciences, University of Copenhagen, DK*
COP1 E3 ligase protects HYL1 to retain microRNA biogenesis

Daisuke Urano, *Biology Department, University of North Carolina, US*
Flexibility of G-protein network architecture during evolution

Alexander Jones, *Carnegie Institution for Science, Stanford, US*
A closer look at the master regulators – phytohormones at high resolution

Niko Geldner, *Department of Plant Molecular Biology, University of Lausanne, CH*
The endodermis - a tale of two cell types

March

Ross Sozzani, *Department of Plant & Microbial Biology, NCSU, US*
Integration of imaging tools with genome-wide approaches and modeling to understand network dynamics regulating stem cells

Rüdiger Simon, *Heinrich Heine University, DE*
Dynamics of stem cell signalling pathways in meristems

April

Thomas Schmülling, *Institute of Biology, Free University of Berlin, DE*
Regulation of plant growth and development by cytokinin - Fundamental and applied aspects

Sarah Otto, *Department of Zoology, University of British Columbia, CA*
Inferring the impact of dioecy and polyploidy on speciation and extinction rates

Thorsten Hamann, *Department of Biology, Norwegian University of Science and Technology, NO*
Mapping the plant cell wall integrity maintenance network

May

Anne Knowlton, *Editor of Current Biology and Developmental Cell*
Publishing in Current Biology

Justin Borevitz, *Center of Excellence in Plant Energy Biology, Australian National University, AU*
Plant Genomics and Phenomics for Climate Adaptation: From model organisms to foundation species

Nicolaus von Wirén, *Leibniz Institute of Plant Genetics and Crop Plant Research (IPK Gatersleben), DE*
Modulation of root system architecture by nutrient signals

June

VBC Seminar: Mark Estelle, *University of California San Diego, US*
Auxin: A Versatile Regulator of Plant Growth and Development

Sigal Savaldi-Goldstein, *Faculty of Biology, Technion, Haifa, IL*
Growth coordination through differential spatio-temporal brassinosteroid activity

Nancy Eckardt, *Senior Features Editor, The Plant Cell*
The New Face of The Plant Cell and the Road to Publication

July

Yee-yung Charng, *Agricultural Biotechnology Research Center, Academia Sinica, TW*
Towards a molecular understanding of thermo-tolerance diversity in plants - from genotypes, phenotypes to envirotypes

Rens Voesenek, *Plant Ecophysiology, Utrecht University, NL*
Ethylene priming: a new mechanism that confers flooding tolerance

Sarah Schmidt, *Faculty of Science, University of Amsterdam, NL*
What makes a pathogen pathogenic? Virulence genes and accessory chromosomes in the plant pathogenic fungus Fusarium oxysporum'

August

Quentin Gouil, *University of Cambridge, UK*
Paramutation in tomato: infectious memories. Insights from old and new cases

September

Nathalie Durut, *University of Perpignan, FR*
Characterization of NUC2: Role in rDNA organization and in response to heat stress in A. thaliana

VBC Regular Seminar: Dominique Bergmann, *Stanford University, US*
Birth, life and death of a plant epidermal stem cell lineage

Julia Engelhorn, *Plant and Cell Physiology Laboratory, Grenoble, FR*
Genome-wide analysis of chromatin changes during trithorax-associated gene activation in Arabidopsis

Siobhan Brady, *University of California, Davis, US*
Regulation of root morphogenesis in tomato species in the face of a changing environment

Hironaka Tsukagoshi, *Nagoya University, JP*
The regulation mechanism of root development by ROS

Marie Mirouze, *Laboratory of Plant Genome and Development, University of Perpignan, FR*
Epigenetic control of plant mobilomes

Grégory Vert, *Institute for Integrative Biology of the Cell (I2BC), Paris, FR*
Deconstructing K63 polyubiquitination in plants

October

Beatriz Vicoso, *IST Austria, Tulln, AT*
Frequent sex chromosome turnover in dipteran insects

Paul Kersey, *EMBL-EBI, Wellcome Trust Genome Campus, Hinxton, UK*
Adventures in Cereal Genomics

Ben Scheres, *Wageningen University, NL*
Signal and Noise in Plant Stem Cell Networks

Hitoshi Kurumizaka, *Faculty of Science & Engineering, Waseda University, Tokyo, JP*
Structural basis of epigenetic regulation of chromatin

November

Tim Paape, *Institute of Evolutionary Biology and Environmental Studies, University of Zurich, CH*
Developing new plant models for evolutionary and ecological genomics

Sandra Cortijo, *Sainsbury Laboratory, University of Cambridge, UK*
Interplay between H2A.Z and HSF1 facilitates controlled transcriptional response to ambient temperature variation

Claude Becker, *Max Planck Institute for Developmental Biology, Tübingen, DE*
Epigenome-environment interactions: shaping and breaking of chromatin configurations by stress

December

Marco Todesco, *Department of Botany, University of British Columbia, CA*
The genetic basis of adaptation in plants: trade-offs and camouflage

15 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

15 Alumni

The Gregor Mendel Institute believes that training new scientists is an important part of our mission. Naturally, our employees' next career stop also reflects on the quality of our research and our reputation in the international plant research community. 2015 saw the departure of the last of the GMI'S original junior group leaders, Claudia Jonak. Thus, we said "Auf Wiedersehen und viel Glück!" in 2015 to:

Stephanie Arnoux
PhD Student, INRA, France

Klaus Brackmann
writing thesis

Manu Dubin
Postdoc, Bayer Crop Sciences, Ghent, Belgium

Ashley Farlow
Research Associate, University Melbourne, Australia

Marcal Gallemi
Postdoc, IST, Austria

Nial Gursansky

Claudia Jonak
Group Leader, Austrian Institute of Technology (AIT), Tulln, Austria

Virginie Jouannet
COS Heidelberg, Germany

Arthur Korte
Assistant Professor, University of Würzburg, Germany

Ivan Lebovka
COS Heidelberg, Germany

Dazhe Meng
Google, USA

Bikram Pandey
PhD, AIT, Austria

Olga Popova
Octopharma Vienna, Austria

Guillaume Queval
Postdoc, AIT, Austria

Hansjörg Stampfl
PhD, AIT, Austria

Hannes Svardal
Postdoc, Sanger Institute, Cambridge, UK

Sascha Waidmann
Postdoc, BOKU, Austria

Ramesh Yelegandula
Postdoc, IMBA, Austria

Pei Zhang
Astrazeneca, UK

15 The Vienna Biocenter

Around 25 research institutes and companies, 2,100 scientific employees and students, over 90,000 m² lab and office space for Life Sciences – the Vienna Biocenter at Neu Marx is one of Europe's leading Life Science hubs.

The success story of the Vienna Biocenter (VBC) began in the 1980s with the foundation of the Research Institute of Molecular Pathology (IMP), the basic research center of Boehringer Ingelheim. Following the relocation of five university departments – that are now under the umbrella of the Max F. Perutz Laboratories (MFPL) – to the Neu Marx area in Vienna's Third District, the VBC has grown continuously. Profiting from the assets offered at the location, the University of Applied Sciences and two flagship institutes of the Austrian Academy of Science round off the academic institutions at the VBC. Since their founding by the Academy, the Institute of Molecular Biotechnology (IMBA) and the Gregor Mendel Institute for Molecular Plant Biology (GMI) have developed rapidly into two of the most renowned Austrian research institutes in their respective fields.

A growing number of biotech-companies complement the training and research activities at the Vienna Biocenter. Currently, eighteen

ONE OF EUROPE'S LEADING LIFE SCIENCE LOCATIONS

4 Academic research centers
18 Biotech companies
3 Universities

90,000 m² lab and office space
45,000 Vienna Open Lab visitors

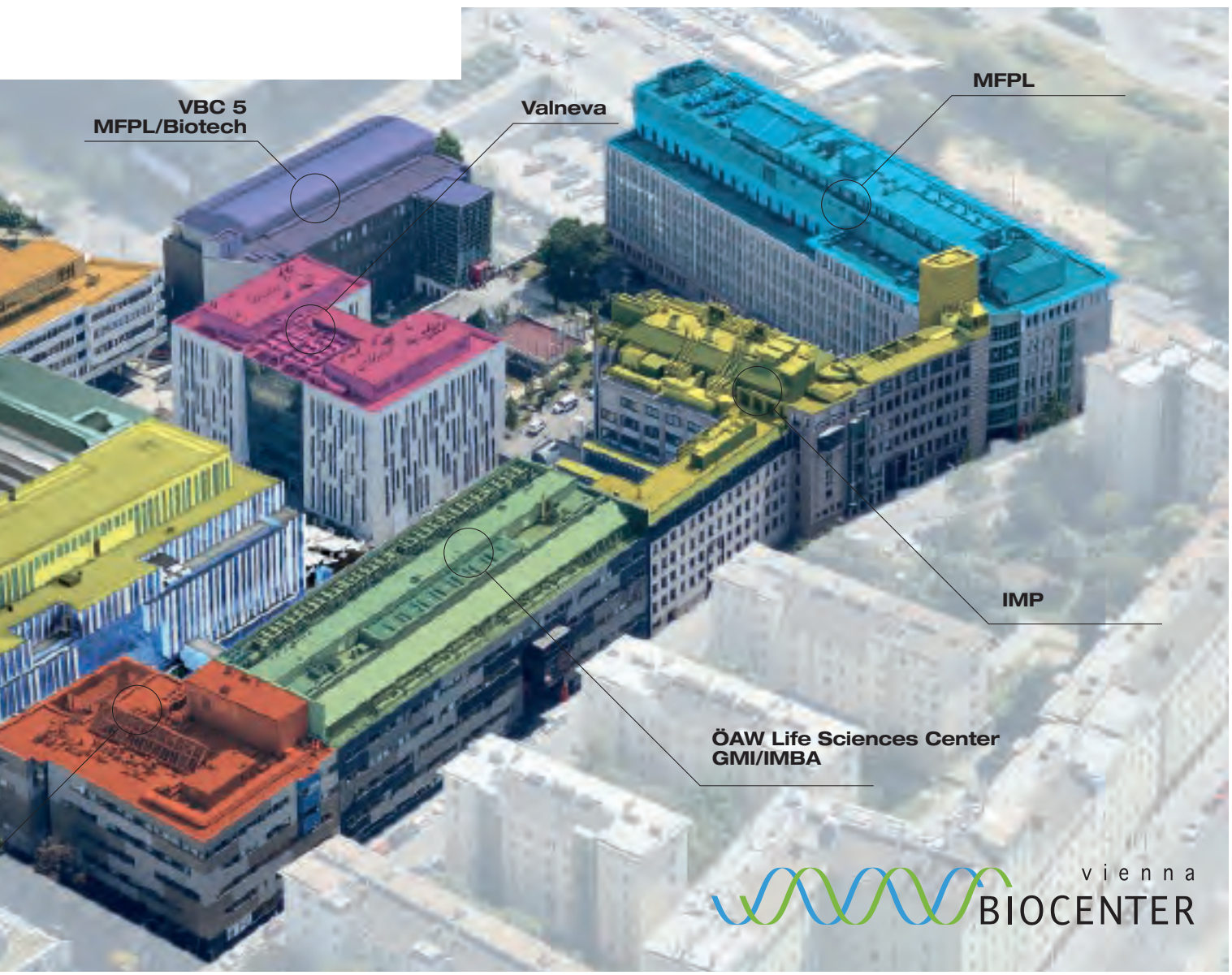
1,400 Employees
250 PhD students
100 Scientific groups
40 Nationalities

32 ERC Grants
11 Wittgenstein Awards
350 Publications / Year

commercial companies reinforce the collaborative potential of academic and applied research at the Vienna Biocenter.

Moreover, the VBC hosts institutes and companies dedicated to science communication. The publicly funded organization Open Science aims at fostering the dialogue between the world of science and the public, and it also runs the Vienna Open Lab (a joint initiative with IMBA), which has already provided 45,000 visitors with an interactive glimpse into the Life Sciences. Biolution has established a reputation as a professional agency for science PR and EU-project application in the field of Life Siences.

The research institutes at the VBC are home to 1,400 experts and 700 students enrolled at the University of Vienna, the Medical University of Vienna and the University of Applied Sciences. The passionate and creative scientists in over 100 scientific groups and from 40 nations have acquired 32 ERC grants, 11 Wittgenstein Awards and publish around 350 scientific papers per year. They are supported by the Campus Science Support Facilities (CSF), providing first class scientific infrastructure. The successful cooperations, the broad expertise of the researchers and the established infrastructure offer unique working conditions that enable the VBC members to be at the forefront of Life Science research.



15 Vienna Biocenter Core Services

The GMI is a member of the IMP/IMBA/GMI core services, providing cutting edge services to the three institutes.

BioOptics

The services offered by the BioOptics Facility to researchers at IMP, IMBA and GMI encompass analytical flow cytometry and cell sorting, as well as a large variety of microscopy techniques, image processing and analysis. We provide instrumentation, education and expertise for flow cytometry experiments, manage more than twenty microcopy systems, including wide-field, confocal laser scanning and airyscan, two-photon, light sheet, total internal reflection, and structured illumination microscopy techniques, automated slide scanning as well as access to laser microdissection and fluorescent lifetime imaging microscopy, and offer five state-of-the-art computer workstations operating most of the common commercial and open-source image processing and visualization software. The facility provides assisted use and training on instrumentation, consultation concerning experimental design, including project planning, staining, microscope selection, etc. Additionally intense basic as well as advanced practical microscopy courses are organized including hands-on sessions as well as lectures by internal and external faculty.

Max Perutz Library

The Max Perutz Library is a specialized reference library located at the Vienna Biocenter (VBC) whose mission is to develop and maintain collections and services that support research at the IMP, IMBA and GMI. The main task of the library is to provide comprehensive scientific literature pertaining to the areas of research pursued at the institutes.

Molecular Biology Services

The facility offers a wide variety of standard services to all scientists at IMP/IMBA and GMI. These include the Media Lab and Dish Washing Unit, Sanger Sequencing, the preparation of competent cells of various E. coli strains, production of monoclonal antibodies, and plasmid prep in 96 well among many others. In addition, we provide instrumentation and expertise for lab automation and high-throughput methods.

Protein Chemistry Facility

The protein chemistry facility is a core unit offering protein analyses. We offer services such as protein identification, characterization of posttranslational modifications, protein quantitation and the respective data interpretation. Additionally, our facility provides peptide synthesis and affinity purification of antibodies. We operate several chromatography systems for both protein and peptide separations and a number of state-of-the-art mass spectrometers.

Members of the Molecular Biology Services

Campus Science Support Facilities

The CSF provides advanced scientific services to the GMI, and also runs the campus child care center. The CSF is divided into different units, including:

Advanced Microscopy

The Advanced Microscopy Facility offers users access to a selection of cutting-edge optical microscopy and spectroscopy techniques, along with assistance in their implementation and data analysis. They also offer the development or customization of microscopes for applications where commercial solutions are not available.

Next Gen Sequencing

The goal of the Next Generation Sequencing Facility is to provide cutting edge next generation sequencing technology to its users. Advice and guidance of sequencing projects are offered by our team that relies on years of experience with sequencing systems and sequencing data analysis. All common sequencing applications are supported and the development of novel methods and protocols encouraged. Currently, requests are processed on Illumina HiSeq2500 and MiSeq instruments.

Plant Sciences

The Plant Sciences Facility (PlantS) operates 22 high quality state-of-the-art and highly specialized plant growth chambers and provides professional support to research groups at the VBC. Several chambers are capable of providing exceptional environmental conditions i.e. low temperature (frost), high temperature, different light intensities, different light spectra and different gas conditions, allowing precise environmental simulation across different climate zones and the simulation of various environmental stress conditions. Additionally, one of our chambers is equipped with a robotic plant phenotyping system linked to LemnaTec image analysis software.

ProTech

The mission of the Protein Technologies Facility (ProTech) is to help researchers at the Vienna Biocenter overcome two major experimental bottlenecks: protein production and purification. In addition, we offer services upstream and downstream of these areas, including molecular cloning and biophysical protein characterization, and can provide expertise and advice on most protein-related technologies. We also provide consulting and reagent generation for CRISPR/Cas9 genome engineering through CRISPR Lab.

Child Care Center

The Child Care Center's highly motivated team provides a loving and caring atmosphere for children from the VBC. They offer extended opening hours, the possibility to attend a crèche from 3 months on, and English lessons with native speakers. The Child Care Center is a creative place for children where they undertake excursions into the countryside, visit kids theatre, grow vegetables, go ice skating and do everything else a children's heart desires.

Illumina Flowcell

"Going for a walk"

15 Events

GMI Science Retreat

We held our 5th annual scientific retreat for all GMI staff in June 2015, at Steinschalerhof in the Dirndl valley West 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 step back from the everyday work in the lab and discuss the projects currently running at the GMI. The administration joined as well, and held their own sessions on optimizing processes workflows. The event was capped by a team-cooking event, where employees were split into teams and, together, we managed to prepare a delicious meal for ourselves!

VBC PhD Symposium: "Communication – let's talk about it"

The annual two-day Vienna Biocenter PhD Symposium in November, organized by students of the Vienna Biocenter PhD program including PhD students from the GMI, is a highlight of the year. This year, eighteen invited speakers from around the world discussed communication in all of its forms, from communication within and between cells to communication within and between individuals. This symposium is unique in always finding an extremely interdisciplinary topic, bringing together researchers from disparate disciplines that still manage to have commonalities in their work. Over 300 participants registered for the symposium, with nearly half of them coming from outside the VBC to take part.

Career Workshops

With more and more students and postdocs interested in pursuing careers outside of academics, the GMI made a strong push this year to expand the career training opportunities for our staff. In addition to a yearly intellectual property seminar, the GMI helped to organize a career workshop and a career day. In the workshop, a team from Mediatum put together a program to introduce scientists to the process of applying for non-academic positions. They presented the different skills necessary to succeed outside of academia, and discussed CV, interview, and contract negotiation techniques. The career symposium featured speakers ranging from pharmaceutical to medical to agriculture to government, highlighting their organizations and the possibilities available for PhD level employees.

Fascination of Plants Day

In the GMI's largest outreach event of the year, we collaborated with the Botanical Gardens of the University of Vienna as part of the International Fascination of Plants Day on May 18th. Our event, "Making the Invisible Visible" took place in the main greenhouse of the Botanical Garden and included several participants from the University as well as the GMI. The GMI presented an international root-race, where we measured Arabidopsis accessions from around the world to see which one would most quickly re-orient itself to a change in gravity. We presented work from the lab of Wolfgang Busch, and invited members of the public to bet which root would win our race. The winner won a new Motorola G smart phone, and the second place winners were invited for a tour of the GMI hosted by Busch himself. Well over 500 people took part in the event, including Christian Oxonitsch, the Viennese Councilman for Youth, Education, and Sports, who opened the event.

VBC Summer School

In 2015 the GMI participated for the 6th year in the Vienna Biocenter Summer School, a program to provide undergraduate students an exciting opportunity to carry out their own projects within research groups at the Vienna Biocenter. In doing so, these students gain a feel for what an academic career entails. Lectures and social events were included in the program, which concluded with a symposium where all students could present their results.

15 Finance & Administration

Dr Markus Kiess
Business Director

HEADS OF FINANCE & ADMINISTRATION

Dr Borries Luberacki
Head of Lab Services

Dr J. Matthew Watson
Head of Science Support

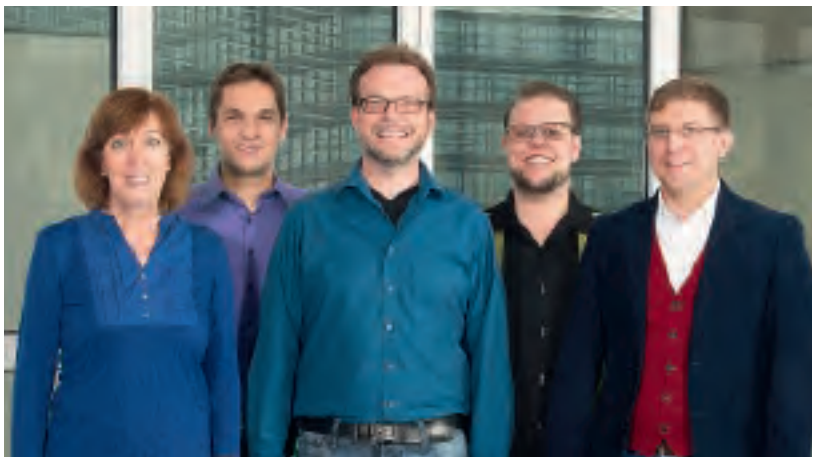
Mireia Verdaguer MSc
Head of Finance

Mag. Carmen Hügel
Human Resources Officer

Eckehard Siegmann
Head of IT Services

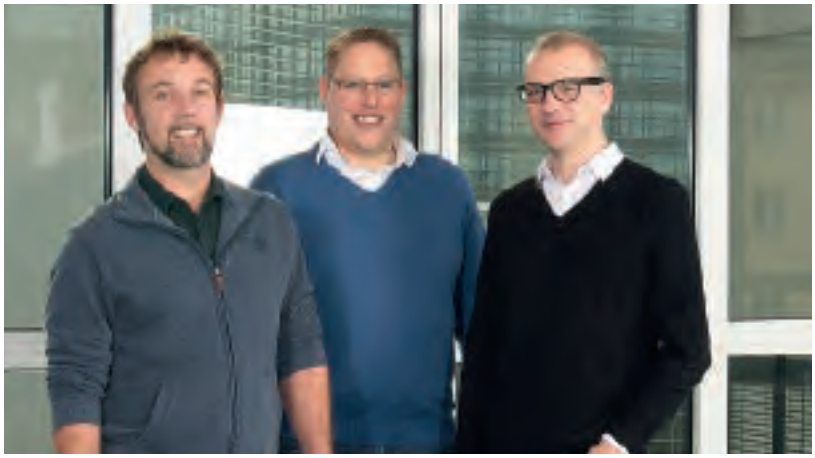
Martina Gsur
Assistant to the Directors

from left to right: Erich Birngruber, Martina Gsur, Thomas Ciganek, Eckehard Siegmann, Borries Luberacki, Carmen Hügel, Matt Watson, Markus Kiess, Gerhard Dürnberger, Anneliese Auer, Marion Wohlmuth, Ines Crisostomo, Barbara Weigel, Mirea Verdaguer, Johanna Ostah, Heidi Fürnkranz, Stefan Ferscha, Jens Schaich



LAB SERVICES

Anneliese Auer
Stefan Ferscha
Borries Luberacki
Jens Schaich
Erich Birngruber



IT SERVICES

Eckehard Siegmann
Thomas Ciganek
Gerhard Dürnberger

15 GMI Scientific Advisory Board

Research at the GMI is annually evaluated by the GMI Scientific Advisory Board (SAB). The SAB comprises independent international experts whose primary role is to provide the institute's management, and the Austrian Academy of Sciences, with feedback on the quality of the science being undertaken. The SAB meet over a two-day period (typically each November) during which time they conduct in-depth discussions with all Research Groups as well as Postdoc, PhD and technical staff representatives.

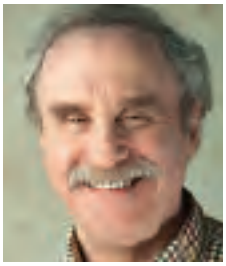
"The GMI continues to go from strength to strength, guided by superb leadership and management. There is no doubt that it is a world leading institute, with Group Leaders making the most of the opportunity to undertake innovative high risk research....morale at the institute is high, with palpable dynamism and energy."
GMI Scientific Advisory Board Report 2015

Prof. Elizabeth Vierling
Chair of Scientific Advisory Board University of Massachusetts, USA

Prof. Dominique Bergmann
Stanford University, Stanford, USA

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

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



Prof. Steven Henikoff
Fred Hutchinson Cancer Research Center, Seattle, USA

Prof. Sophien Kamoun
The Sainsbury Laboratory, Norwich, UK

Prof. Ottoline Leyser
University of Cambridge, Cambridge, UK

Prof. Craig Pikaard
Indiana University, Bloomington, Indiana, USA.

The Austrian Academy of Sciences

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

The Austrian Academy of Sciences (ÖAW) is Austria's central institution for science and research. Founded in 1847 as a learned society in Vienna, the Academy currently has over 750 members and 1,300 employees; it stands for the transdisciplinary exchange of knowledge, innovative basic research, and progress for society as a whole. 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 750 members form a scholarly society, advising decision-makers from politics, industry, and society and conveying scientific insights to the public, and, on the other, it is Austria's major supporter of research outside the university system, funding some 28 research institutions in both the natural sciences and humanities. The Academy also organizes various events and lecture series, and supports established and young talented scientists alike through its awards and scholarships programs.

ÖAW AUSTRIAN ACADEMY OF SCIENCES

15 The City of Vienna

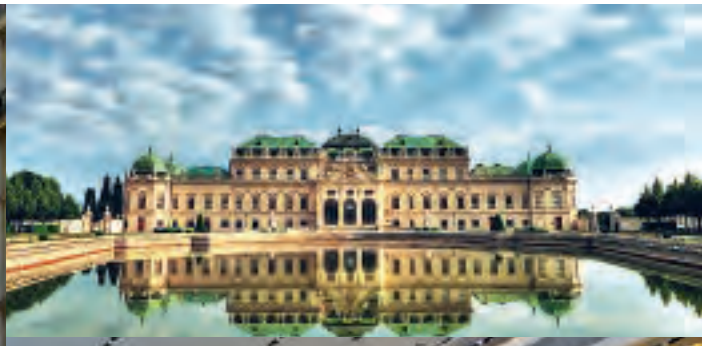
Vienna is a fantastic city to live in – and that's not just our claim: in the annual Mercer livability survey of 215 cities, it has taken top rank for six years in a row (2010-2015)! Why is it the best city in the world to live in? Ask GMI employees from around the world and they might give these reasons:

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

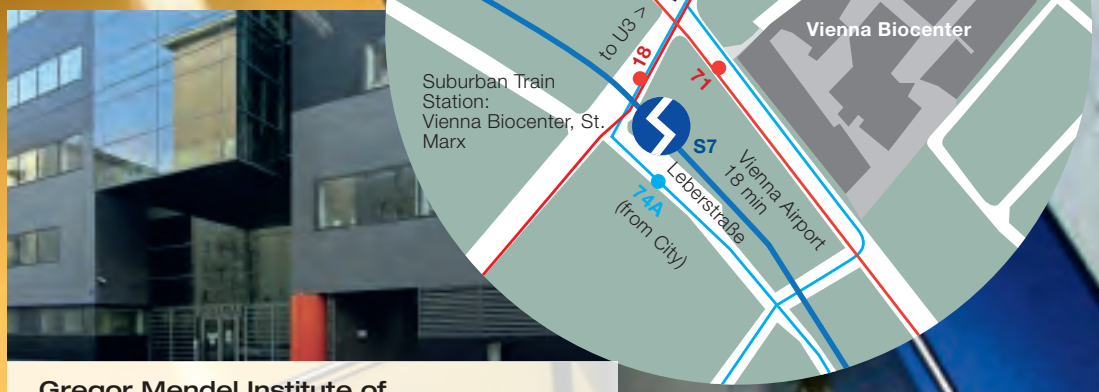
The lifestyle – Vienna combines the elegant splendor of the former Austro-Hungarian capital with a modern infrastructure, lots of nearby countryside for outdoor excursions, and one of the richest cultural offerings of any European city.

It's safe, clean and practical – walk more or less 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 several decades.



Location and 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)

The Gregor Mendel Institute is located in the Vienna Biocenter (VBC), the premier location for life sciences in Central Europe and a world-leading international bio-medical research center (www.viennabiocenter.org).

vienna BIOCENTER

GMI

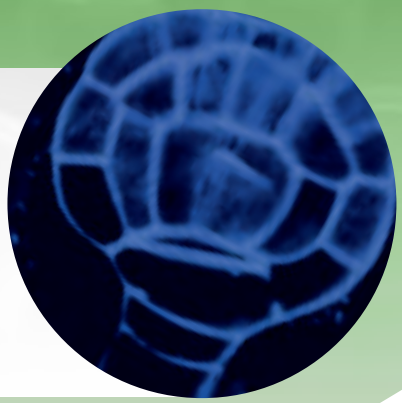
15

GREGOR MENDEL INSTITUTE OF MOLECULAR PLANT BIOLOGY
DR. BOHR-GASSE 3
1030 VIENNA, AUSTRIA

OFFICE@GMI.OEAW.AC.AT
WWW.GMI.OEAW.AC.AT

GMI
GREGOR MENDEL INSTITUTE
OF MOLECULAR PLANT BIOLOGY

ÖAW
AUSTRIAN ACADEMY OF SCIENCES



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