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ANNUAL REPORT 2017

GMI

GREGOR MENDEL INSTITUTE OF MOLECULAR PLANT BIOLOGY

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

GMI
GREGOR MENDEL INSTITUTE
OF MOLECULAR PLANT BIOLOGY

17 ANNUAL REPORT

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17 DIRECTORS' STATEMENT

Dr. Magnus Nordborg
Scientific Director

Dr. Markus Kiess
Business Director

We are proud to be one of very few 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 in this context.

The goal of the GMI is to contribute to our understanding of plants (and biology in general) by carrying out world-class research, in particular the kind of fundamental research that is poorly supported elsewhere. Like the other institutes that are part of the Vienna BioCenter (VBC), we strive for excellence and emphasize creativity and independent thinking at every level. As directors, our most important task is to create a fantastic research environment and to recruit and promote young scientists, allowing them to develop into researchers capable of securing scientific positions worldwide. This year, we congratulate Wolfgang Busch on his successful transition from Junior Group Leader at the GMI to Associate Professor at the Salk Institute in La Jolla, California. 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.

We also welcome two new Junior Group Leaders, Claude Becker and Yasin Dagdas, who are currently building their research groups. To bring the institute back to full-strength, we are in the process of recruiting two additional junior group leaders, one of which will be a joint, tenure-track position with the Max F. Perutz Laboratories of the University of Vienna, the first position of its kind at the VBC.

Our main indicator is, of course, scientific productivity, and on this front, we believe our publications speak for themselves. The quality of publications from the GMI continues to increase every year, and this is evident even in crude numerical terms: two-thirds of our publications this year were published in the top 10% of scientific journals by category-ranked impact factor.

As always, we want to thank the Austrian Academy of Sciences for its support (without which the Gregor Mendel Institute would not exist); the Federal Ministry of Science, Research and Economy, and the City of Vienna for their general support of the VBC; and all our colleagues at the VBC for making this an amazing place to work.

Magnus Nordborg, Markus Kiess

17 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 January 2006, in the heart of Vienna's most important life sciences research location, the Vienna BioCenter (VBC). The VBC includes three other research institutes: 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, notably, 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 high-performance computing cluster, joint services with the IMP and IMBA, and other core services offered by the VBCF. Block funding is received from the Austrian Academy of Sciences with additional resources provided by a variety of Austrian, EU, and international funding agencies.

> *Plants are the basis of the food we eat, the oxygen we breathe, and most of the energy we consume. To me, it is obvious that we should try to understand them in every possible way.*
>
> (Claude Becker)

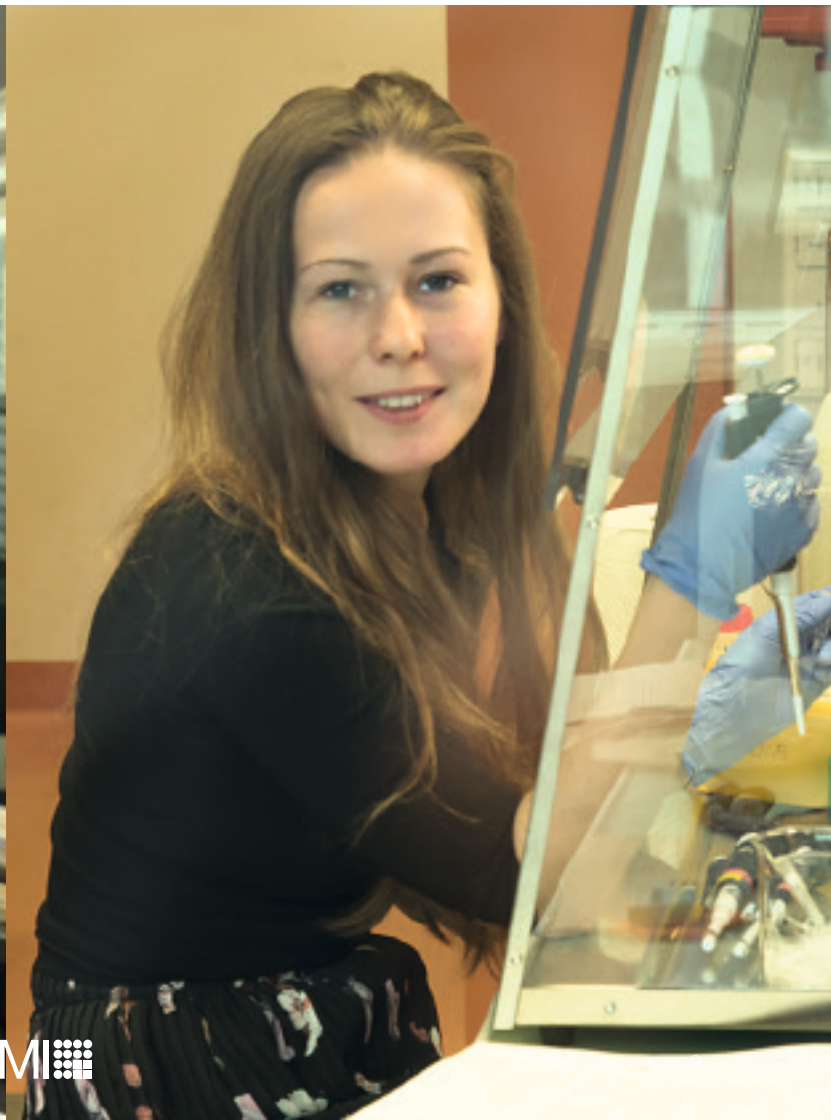
IMPORTANCE OF EXPERIMENTAL PLANT RESEARCH

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 like 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 network interactions of receptor kinases 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.

> *It's estimated that food for 600 million people is lost annually due to fungal infections. That's why I think it's important that we learn as much as possible about fungal pathogens and how they infect plants so we can find solutions to stop this loss.*
>
> (Angelika Czedik-Eysenberg L'Oreal Women in Science Awardee)

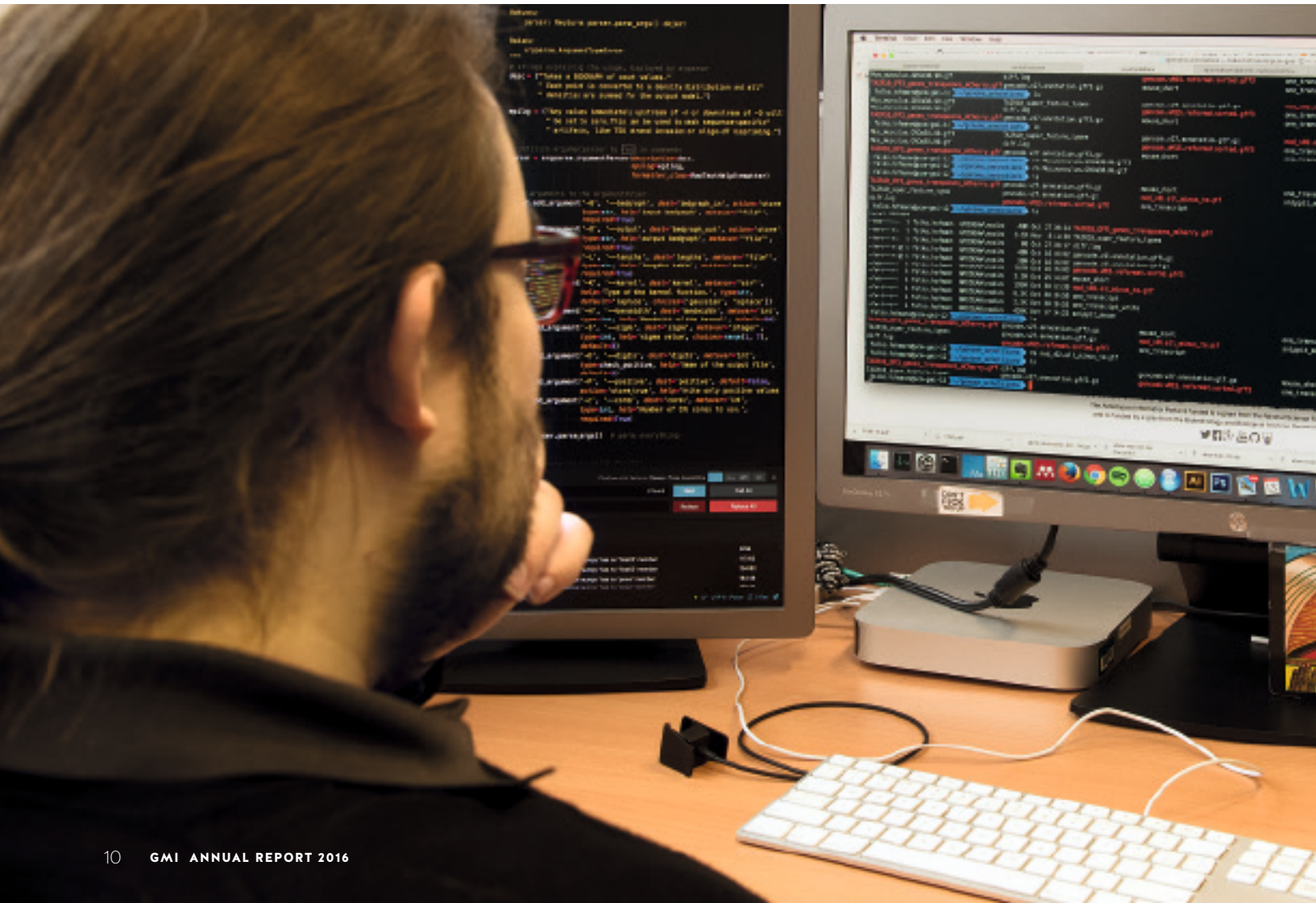


EDUCATION

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 GMI

The GMI provides a lively, international working environment with around 130 staff from over 35 countries. The working language is English. Research is complemented by scientific events, including a packed seminar series, an annual scientific retreat, GMI-organized conferences, and weekly social events.



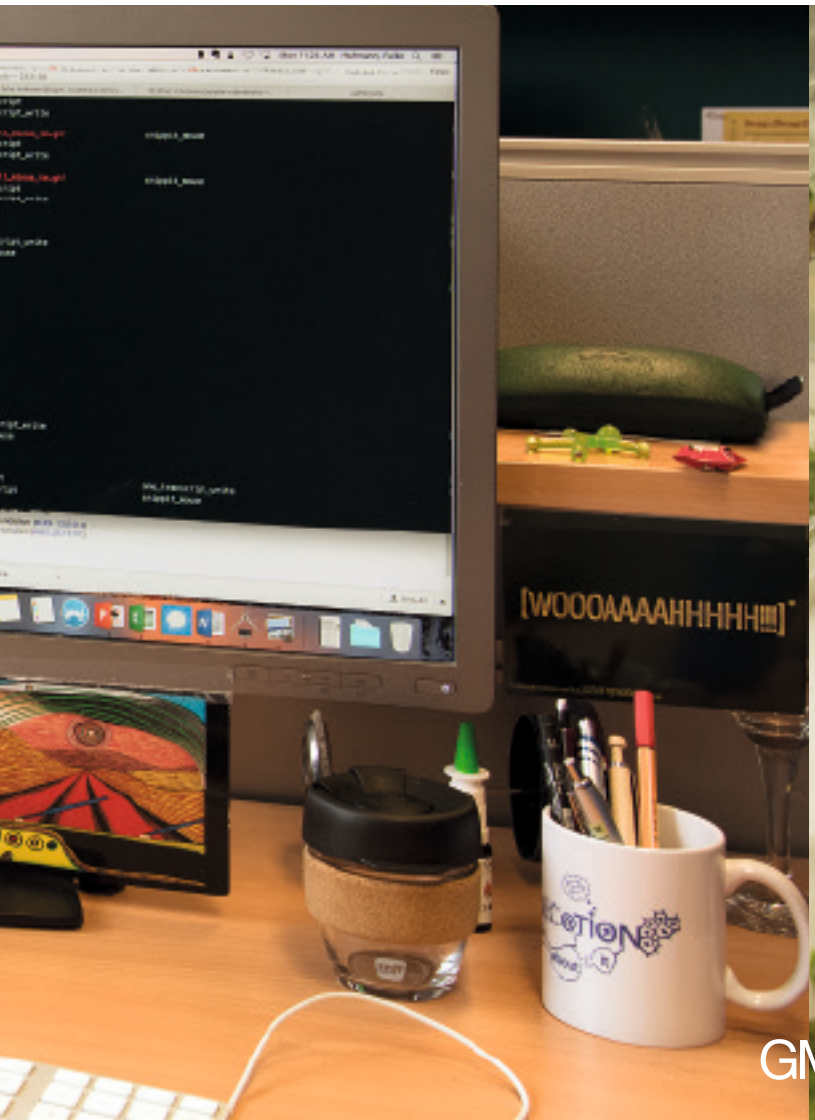
CAREER

The GMI focuses on providing a perfect environment for cutting-edge 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.

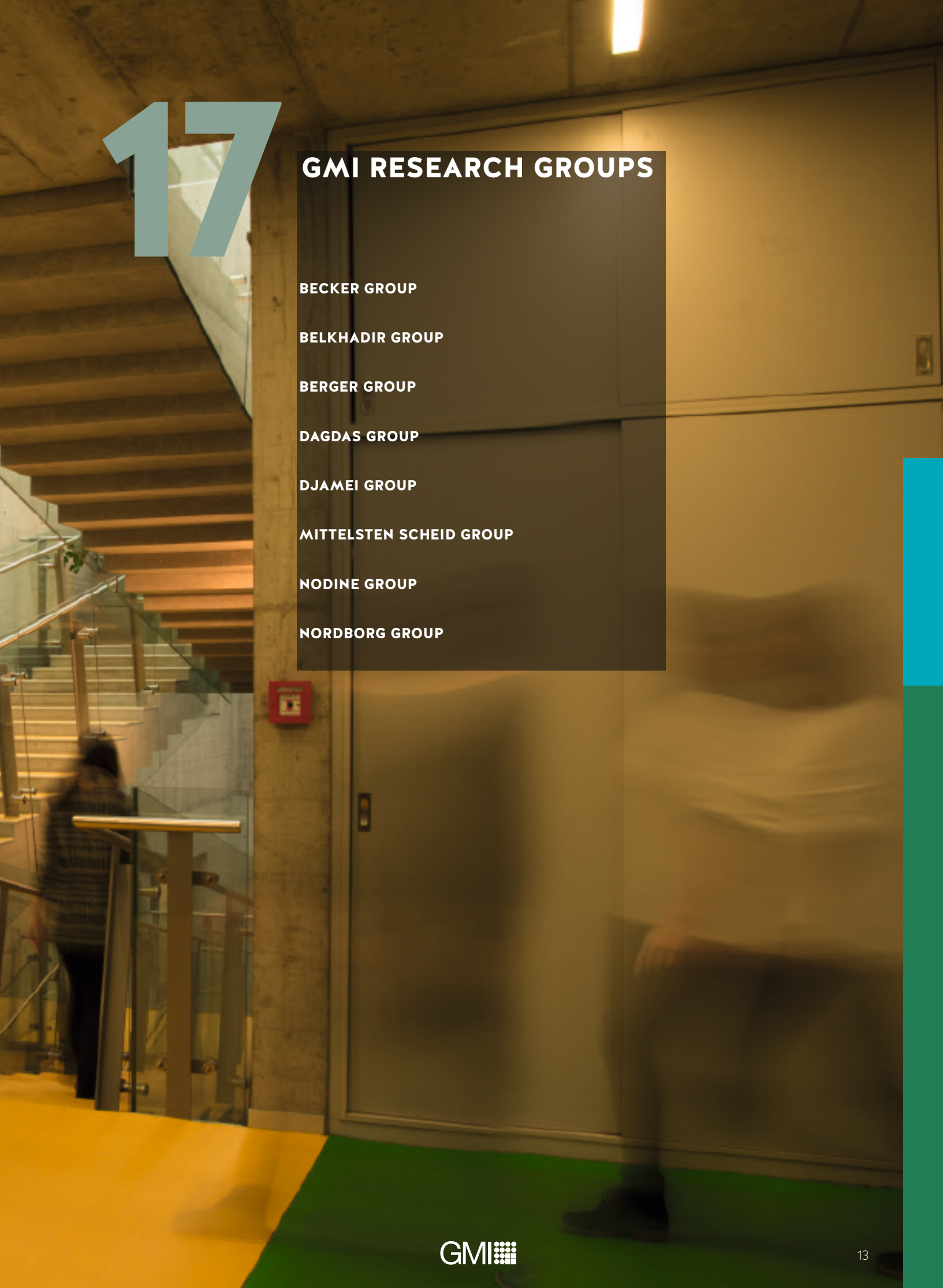
At the GMI we see the career development of our junior researchers as a priority. The faculty aims to provide effective mentoring to PhD students and postdocs in order for them to progress and be successful. While most of these mentoring efforts are involved in promoting a research career, we organize 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 leaving to become postdocs in academia as well as acquiring positions in industry.

> *Plants provide unique opportunities to explore the role of quality control pathways in adaptation. GMI and the VBC provide a stimulating environment and cutting edge infrastructure to tackle the role of autophagy mediated quality control mechanisms in plant stress tolerance.* (Yasin Dagdas)




3rd Floor
GMI



17 GMI RESEARCH GROUPS

BECKER GROUP

BELKHADIR GROUP

BERGER GROUP

DAGDAS GROUP

DJAMEI GROUP

MITTELSTEN SCHEID GROUP

NODINE GROUP

NORDBORG GROUP

BECKER GROUP

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PhD: Albert-Ludwigs-University, Freiburg, DE

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- Research Associate (2011-2016): Detlef Weigel Lab, Max Planck Institute for Developmental Biology, Tübingen, DE

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POSTDOCS

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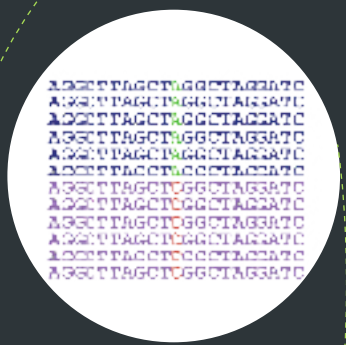
MECHANISMS OF INTERACTION BETWEEN ORGANISMS



Plants almost always grow in a community with other plants. They must therefore compete with their neighbours for limited resources such as nutrients, water, light, and space.

Our research group is interested in a very special competition strategy in which plants produce and release chemical compounds to prevent their neighbours from growing.

We want to understand how these chemicals act in the plant, how they influence the complex community of soil-dwelling bacteria and fungi, and how some species manage to tolerate the presence of these toxic compounds.

Plants rarely grow as solitary individuals but instead as a community of organisms. This can be a natural ecosystem with a diverse mixture of plant species, or an agricultural monoculture composed of many genetically similar individuals. Independent of the habitat, every plant strives to secure optimal access to resources by outcompeting others in direct proximity. During evolution, plants have developed diverse strategies to gain advantage over their neighbours. To secure access to light for example, bamboo grows faster than any other plant, while trees instead play the long game and grow slow but tall, eventually towering over the surrounding species.

Some plant species employ a quite different strategy: they engage in chemical warfare by producing chemical compounds that they release into the soil. Some species directly release these substances from their roots, while others store them in the above-ground tissues and release them when the leaves fall to the ground and decompose. In either case, these compounds enter the roots of nearby plants and interfere with molecular and cellular processes to prevent growth or development, leaving the 'donor' plant with a competitive advantage.

This process of chemical interference between organisms is called "allelopathy" and has been known to farmers and gardeners for centuries. Many species that use allelopathy to suppress their neighbours have been identified; they range from trees (e.g. walnut) to shrubs and grasses, and include many of today's major crops, including wheat, rye, and maize. Even though many of the chemicals involved ("allelochemicals") have been identified, it remains unclear how most of them act in the plant and why these chemicals are toxic to some plants and not to others.

Our laboratory focuses on allelochemicals that are produced in wheat and maize, amongst other species. Chemically, these compounds belong to the benzoxazinones. Upon release from the roots, they are only mildly toxic. However, because they are unstable in soil, they are quickly converted to more toxic aminophenoxazinones that can remain stable for weeks or even months (→ Fig. 1). We recently found that once these degradation products enter the cells of plants, they bind to and inhibit the activity of a particular class of enzymes called histone deacetylases (HDA). The role of HDAs is to remove acetyl groups from proteins, particularly from histones. Histones contribute to the organization of the DNA in the nucleus, and the addition and removal of acetyl groups regulates the level of compaction of this DNA-protein complex (also known as chromatin). HDAs thus ultimately contribute to regulating the "openness" of DNA and consequently the accessibility of the genes in a certain region of the genome (→ Fig. 1). We were able to show that by inhibiting HDA activity, aminophenoxazinones change the overall organization of the chromatin and thereby interfere with basic cellular functions.

Currently, our group is working on solving two questions. First, we want to understand the specificity of HDA inhibition. Plants have several genes encoding for HDAs that are slightly different from each other. For example, our model plant *Arabidopsis thaliana* has 18 HDA genes in its genome, each responsible for the removal of acetyl groups from a specific set of target proteins. Using a combination of molecular, biochemical, and genomic tools, we investigate which HDAs are particularly responsive to the allelochemical, and what types of histones are affected by it. In parallel, using high-resolution microscopy, we look for cellular defects in the root caused by the allelochemical to learn more about its physiological activity (→ Fig. 2).

The second question that we address originates from the evolutionary history of the HDAs. These enzymes have been highly conserved during evolution, which means that the catalytic centre of HDAs from different plant species are almost identical. It is therefore surprising that some plants are sensitive to allelochemicals and stop growing in their presence, while others – including those plants that produce and release the compounds – remain unaffected. Our hypothesis is that these plants have evolved resistance or tolerance to these chemicals independent of the primary molecular target, the HDAs. To test this hypothesis, we make use of the natural genetic variation in *A. thaliana*. Using a collection of more than 1,100 plants that were collected from across the Northern Hemisphere (1001genomes.org) and whose genomes have been fully sequenced, we look for differences in the response to allelochemicals (→ Fig. 3). Using statistical analysis, we search for associations between specific genetic variants and increased resistance to the allelochemical to identify genes that are responsible for providing resistance.

Our research is not limited just to the plants involved in allelopathy: because the soil space surrounding plant roots is populated by thousands of bacterial and fungal species, some of which are tightly associated with the plant, we furthermore ask if and to what extent the presence of allelochemicals affects – negatively or positively – the microbial community, and how microbes in turn might contribute to the chemical dynamics in the soil (→ Fig. 4).

Altogether, our research aims at resolving, at a molecular and genetic level, the intricate relationship between plants that grow in close proximity to each other. We hope that our work will contribute to a better understanding of the dynamics of natural ecosystems and agricultural plant communities, and that it will prepare the ground for the development of sustainable plant protection strategies.

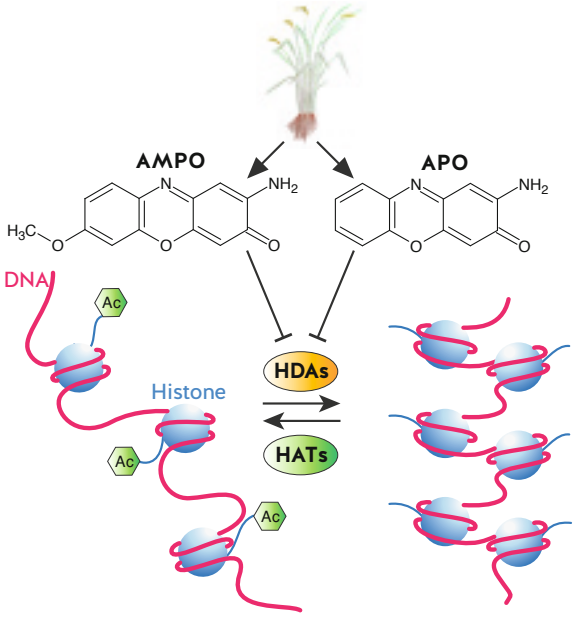


FIG.1

Model of aminophenoxazinone activity. Histone acetylation is added by histone acetyltransferases (HATs) and removed by histone deacetylases (HDAs). APO and AMPO are derived from chemical compounds released from the roots of donor plants. Once APO and AMPO enter the root cells of target plants, they bind to and inhibit HDAs. This increases histone acetylation levels, relaxes chromatin, and changes gene expression. Adapted from Venturelli et al., Plant Sig Behav 2016.

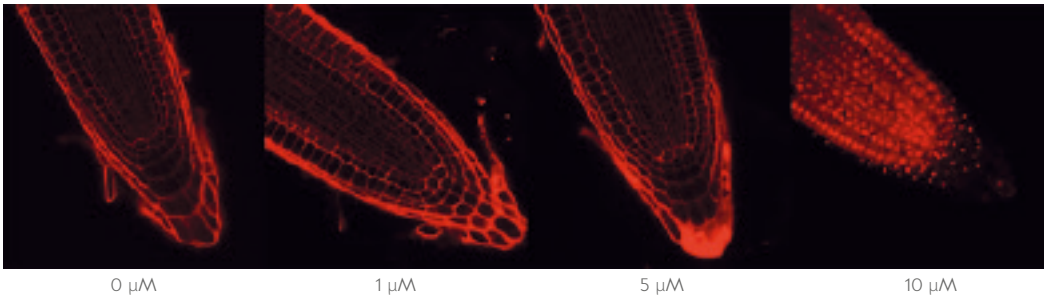


FIG.2

Arabidopsis thaliana roots after 24 h exposure to different concentrations of APO. Roots were stained with propidium iodide (PI, red). At higher concentrations (10 µM), cell integrity is lost, which is indicated by PI entering the cells and accumulating in the nucleus.

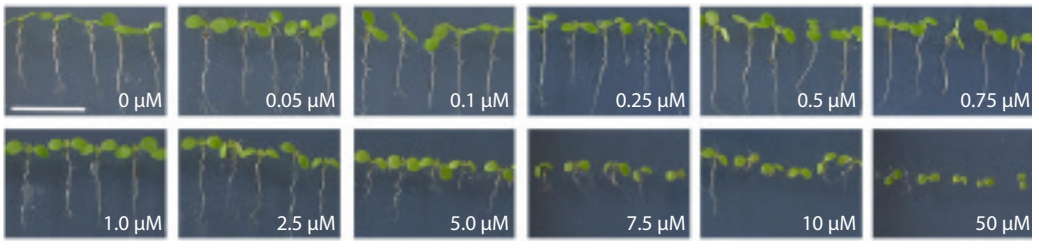


FIG.3

Arabidopsis thaliana seedlings show a concentration-dependent inhibition of root growth when exposed to the allelochemical APO. Scale bar = 10 mm; adapted from Venturelli et al., Plant Sig Behav 2016.

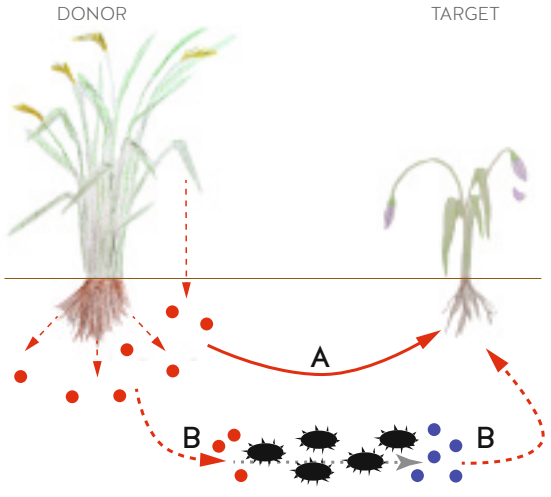


FIG.4

In allelopathy, the donor plant releases secondary metabolites (red) into the soil. In "true" allelopathy **A***) , these metabolites act as toxic allelochemicals and inhibit the growth of neighbouring plants. In contrast, "functional" allelopathy* **B***) requires microorganisms in the soil that convert non-toxic or mildly toxic metabolites into potent allelochemicals (blue). Conversely, allelochemicals can potentially influence the growth and proliferation of soil-dwelling microorganisms, thus generating a complex inter-dependence between plants, bacteria, and fungi.*

BELKHADIR GROUP

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Joined GMI in Jun 2014

PhD: University of North Carolina at Chapel Hill, NC, US

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- Chief Scientific Officer (2011-2013): Atlas Genomics, Casablanca, MA
- Postdoc (2006-2011): Joanne Chory Lab, SALK Institute for Biological Studies, La Jolla CA, US

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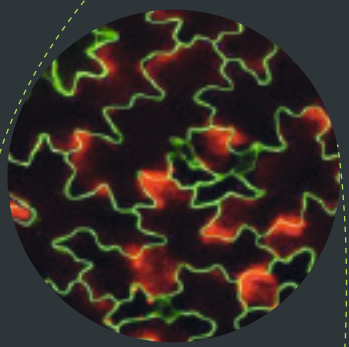
Elwira Smakowska

TECHNICIANS
Karin Grünwald

(*left the lab in 2017)

RECEPTOR CONTROL OF GROWTH AND DEFENSE IN ARABIDOPSIS



Plant receptor kinases (RKs) are central to the evolutionary success of plants in the colonization of their habitats. RKs function in a wide variety – perhaps even all – of plant developmental and defense-related processes, including pathogen sensing, stem cell maintenance, cell proliferation, cell expansion, stomata development, and symbiosis. Yet, despite considerable efforts, only a handful of plant RKs have been well-characterized with respect to their associated ligands and *in vivo* functions in the past two decades. While the principles governing RK signaling activation are emerging, the systems-level organization of this family of proteins is totally unexplored. To address this, my laboratory exploits frontier technologies to discover and explore the interaction properties of RKs with each other or with their putative ligands. Our central goal is to understand the mechanisms by which RKs exert their function at the system-level.

AIM1:

Extracellular interaction mapping of RKs to assign functions to previously uncharacterized RKs in *Arabidopsis*.

RATIONALE.

The size of the predicted RK proteomes in metazoans is at least an order of magnitude less than that of well-defined plant RK proteomes. In plants, heterotypic interactions of RKs with each other have profound effects on the downstream signaling pathways they control. Activation of plant RKs is thought to be initiated by the rapid formation of combinatorial extra-cellular domain (ECD) interactions, which most likely juxtapose the respective intracellular kinase domains for subsequent interaction, transphosphorylation, and signal transduction. However, the mechanisms that allow RK complexes to transition from a "resting state" to an "active state" remain unknown, because they involve transient interactions that are difficult to study by analytical proteomic approaches. Thus, there is a lack of reliable interaction data for RKs. As a consequence, ECD interactions are poorly mapped and understood, despite their importance for dissecting RK function and understanding the complicated circuitry and resulting network of RKs at the cell surface.

PROOF-OF-CONCEPT.

The leucine-rich repeat receptor kinase (LRR-RK) family is the largest sub-family of cell surface receptors in plants, with >220 members in the model plant *Arabidopsis thaliana.* LRR-RKs encompass a large number of signaling paradigms for ligand perception and receptor activation. In the past years, my group has focused on LRR-RKs from *Arabidopsis* to provide a proof of principle for undertaking a much larger network-function analysis of plant RKs. We combined our knowledge of protein polishing techniques with our expertise in analyzing protein modules to build tools suitable for a high-scale high-throughput interaction mapping assay involving pure and soluble extracellular LRR modules. To accomplish this, we built a library of bait and prey expression clones containing the ECDs of 200 LRR-RKs from *Arabidopsis* for secreted expression in Drosophila Schneider S2 cells. We then implemented an avidity-enhanced extracellular interaction assay and tested, in a reciprocal fashion, 40,000 ECD interactions. This has resulted in an experimentally determined LRR-based cell surface interactome map (CSILRR) containing 567 significant interactions (→ Fig. 1). We leveraged CSILRR with a suite of algorithms to build an LRR-RK network and to identify its most relevant players. We are currently investigating the mechanisms of action of these novel LRR-RKs. In summary, we used an unbiased system-level approach to assign a biological function to uncharacterized LRR-RKs that control both defenses and growth.

THE NEXT STEP.

An extracellular interactome of the entire RK family in *Arabidopsis* (AtCSIRKs).

We have expanded our library of bait and prey expression clones with the ECDs of 200 additional RLKs and 50 Receptor Like Proteins (RLPs) for a total of >800 complementary ECDs. I anticipate that my group will produce novel plant molecular networks of great importance, with potential for both high-impact research and high-level funding. Furthermore, my lab will generate resources that will allow the scientific community to better understand how cell surface receptors self-organize into networks to regulate various biological functions.

THE NEXT LEVEL.

Comparative extracellular interactome analysis of RK networks in European crops. With the motivation to bolster the European agricultural biotechnology industry, which depends on basic knowledge and research tools for continuous innovation, we will deploy the CSI interaction mapping pipeline to crops (e.g. tomato, pepper, potato). Our goal is to use the knowledge derived from crop RK networks to devise novel strategies for engineering disease immunity while also boosting yield. Although this goal is ambitious in scope and represents a considerable amount of work, our expertise and expanded network of collaborators places us in ideal position to achieve our goals.

AIM 2:

Use genome wide association (GWA) mapping to map biological function onto RKs network.

RATIONALE.

Natural variation through selection should have produced RK complexes that vary in interactions and stoichiometry to control immunity and developmental pathways.

RESULTS.

My group used genome-wide association (GWA) mapping to identify receptors that regulate well characterized LRR-RK signaling pathways. We performed >300 hundred GWA studies by monitoring the root responses of 570 natural *Arabidopsis* accessions to known LRR-RK ligands. For this, we used a set of plant defense peptides that are produced endogenously during pathogen attack. Our screens have successfully identified several genomic regions coding for RK genes that are significantly associated with the modulation of root development upon exogenous peptide treatments.

THE NEXT STEP.

My laboratory will greatly benefit from the more than 300 GWA studies we have in our database. All these resources will be ready to be mined by my group members. My lab will mainly focus on assigning causality to these RK-containing genomic regions and will in parallel use the RK interaction network generated in the frame of Aim1 to reconcile our quantitative genetics data with our biochemical results.

CONCLUDING REMARKS.

The research programs of my laboratory rely on high-risk/high-gain approaches that build on the expertise, resources, and tools my group has assembled over the last four years. Our approaches go beyond the current state of the art by taking full advantage of recent technological developments to perform large-scale receptor-receptor pairing studies as well as quantitative genetics studies. The first approach, a systems biology approach (Aim.1), relies on genome scale profiling of receptor interactions controlling development and immune responses. The power of the second approach (Aim.2) lies in its capacity to tackle a fundamental challenge in modern biology, which is achieving a better understanding of naturally occurring receptor control of growth-defense variation in the root, an organ that is central to plant development and constantly exposed to a wide variety of beneficial and detrimental microbes.

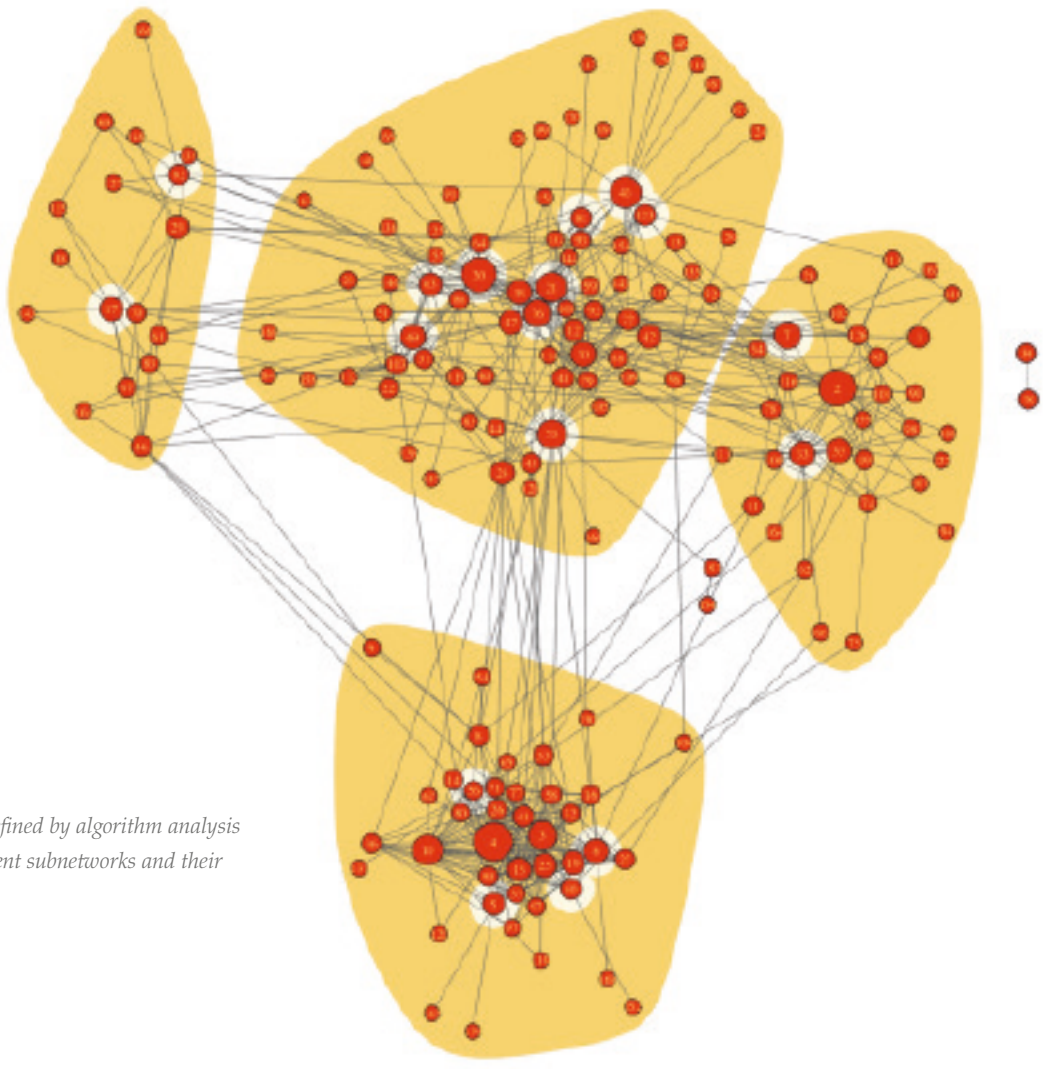
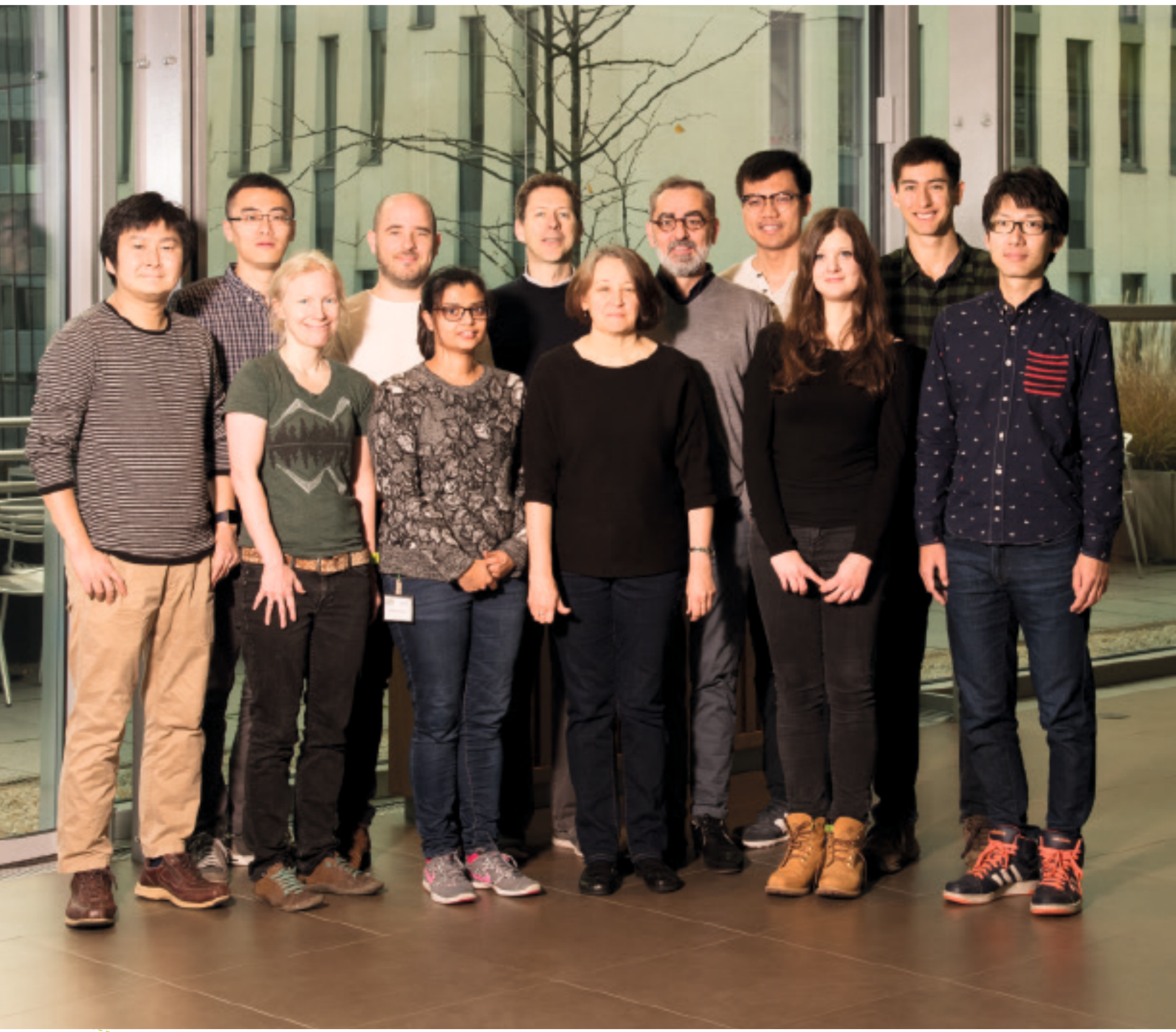


FIG.1

LRR-RK network defined by algorithm analysis detailing four different subnetworks and their connections.

BERGER GROUP



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Joined GMI in Jan 2014

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PREVIOUSLY

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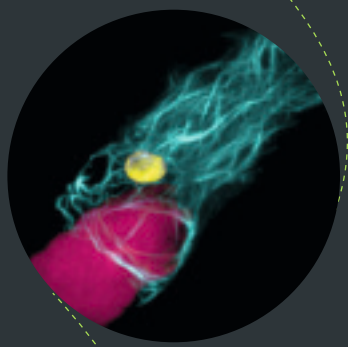
- Research assistant professor (1997–2004): Institut National de la Recherche Agronomique (INRA) Lyon, France

CHROMATIN ARCHITECTURE AND FUNCTION



The genetic information contained in DNA is organized into functional units that are assembled as domains within the nucleus. This organization is crucial for the correct expression of the genome and it becomes severely disrupted in cancer cells. We propose that variants of the core histone proteins that associate with DNA play a key role in genome organization. The core histone proteins H2A, H2B, H3, and H4 form an octamer called the nucleosome, which is the basic unit of the architecture supporting DNA. We focus our work on the roles of functionally-defined isoform variants of the core histones H3 and H2A. We use plants as models because they have evolved a remarkable diversity of histone variants.

This year, we made advances in understanding the roles played by H3 variants in maintaining and reprogramming the essential repressing modification H3K27me3 and we uncovered the unsuspected roles played by H2A variants in defining functional domains of the chromatin.

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STAFF SCIENTIST
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TECHNICIAN
Svetlana Akimcheva

TRAINEE
Valentina Stuchlik

(*left the lab in 2017)

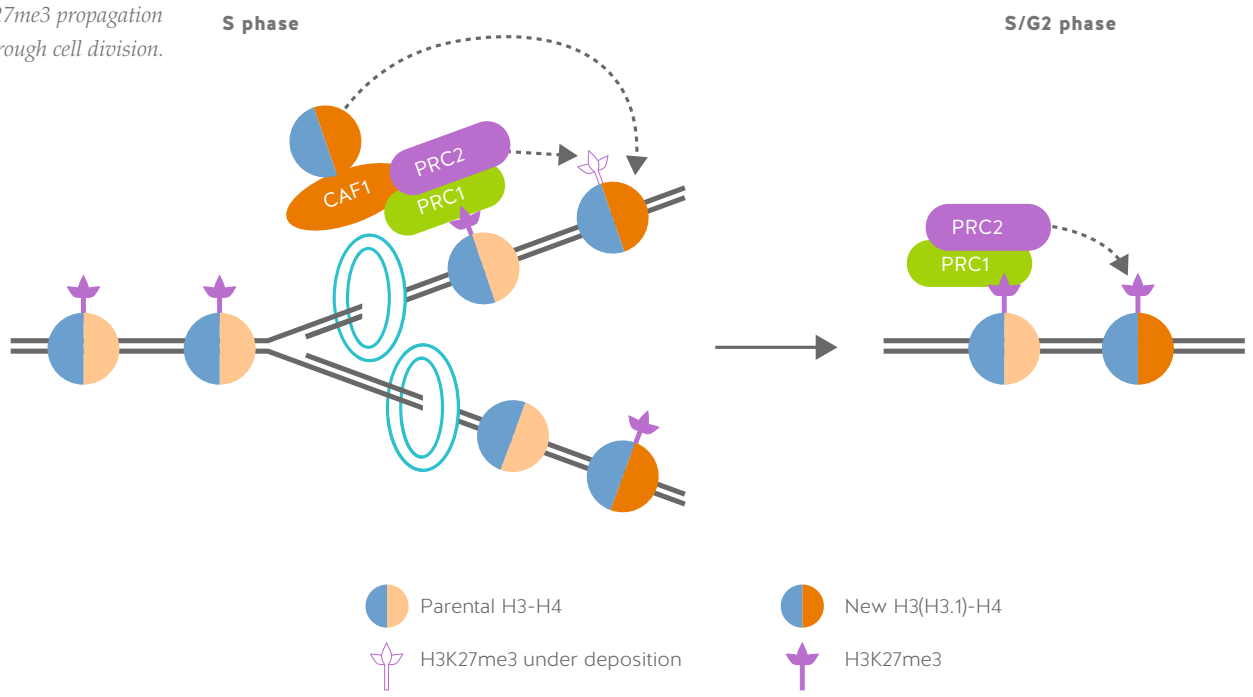
1. TRANSMISSION OF CHROMATIN MEMORY THROUGH CELL DIVISION

It has been proposed that modifications of histones constitute a code which influences gene expression. Notably, repressive H3K9 methylation was shown to be inherited through cell divisions, thus constituting a true memory of transcriptional inhibition in dividing cells. H3K27 trimethylation is deposited by the complex Polycomb Repressive Complex 2 (PRC2) and is also associated with repression, but there has been much debate if, and how, H3K27me3 is inherited through cell division. We have shown that this is the case in plants and elucidated the mechanism involved. Inheritance of H3K27me3 depends on the deposition of the variant H3.1 at the DNA replication fork. Only H3.1 can be monomethylated by the protein ATXR, which is tethered to the fork. PRC2 proteins localize at sites of ongoing DNA replication and directly interact with the H3.1 chaperone CAF1. PRC2 rapidly di- and trimethylates H3.1H27me1 to restore the levels of H3K27me3 following DNA replication (→ Fig. 1). **Our results have uncovered a mechanism that coordinates the incorporation of nucleosomes and inheritance of H3K27me3 during DNA replication, providing an explanation for the epigenetic memory associated with this chromatin mark.**

2. CHROMATIN REMODELLING AND ERASURE OF H3K27ME3 IN MALE GAMETES

The H3K27me3 mark inhibits expression of genes that control crucial events during development. For example, the gene FLC needs to be repressed during early vegetative growth and through the winter to ensure flowering in spring. Because H3K27me3 is epigenetically inherited, it is essential that this repressive marks is removed when it is no longer required. This reprogramming event has been subject to controversy. We have obtained direct evidence that H3K27me3 is completely erased during male gametogenesis in Arabidopsis. This reprogramming event depends on three major events: the suppression of PRC2 genes, the sperm-specific expression of H3K27 demethylases, and the replacement of H3.3 by the sperm-specific variant H3.10. We further showed that these events correspond to a complete reprogramming of chromatin accessibility in sperm cells, leading to the expression of a gene network responsible for sperm cell differentiation. The reprogramming of H3K27me3 during male gametogenesis is likely responsible for resetting expression of essential developmental genes controlling seed development, flowering, and floral development. **This new evidence for reprogramming of H3K27me3 is essential for understanding the plant life cycle.**

FIG.1
Impact of H3.1 on H3K27me3 propagation through cell division.



3. H2A VARIANTS STRUCTURE THE CHROMATIN LANDSCAPE

By combining 17 profiles of chromatin components we showed that H2A and H3 histone variants, together with the linker histone H1 and methylation of H3K27, are the foundations for a specific set of **chromatin states** in the model flowering plant *Arabidopsis thaliana* (→ Fig. 2). We found that the three recognized forms of chromatin, (constitutive heterochromatin, facultative heterochromatin, and euchromatin) can be further classified into several chromatin states. Constitutive heterochromatin comprises transposons and non-coding sequences, which are marked by DNA methylation and H3K9 methylation. These marks are found exclusively in states HC1 through HC4, which also mark genes with the lowest levels of transcription. Importantly, these four distinct states of constitutive heterochromatin are distinguished by the relative enrichment of the histone variants H2A.W.6, H2A.W.7, H3.1, and the linker histone H1. We found that, in a similar manner, H2A variants in combination with H1 and other histone modifications define states of facultative heterochromatin where genes are repressed (FC states) and euchromatin where genes are active (EC states). Our analysis suggests a hierarchical model in which H2A variants establish the major distinction between the three classes of chromatin states, which are then further sub-classified by their relative enrichment of histones H3.1, H1, and specific histone modifications. **These findings shed a new light on the function of histone variants in eukaryotes.**

4. OUTLOOK FOR 2018

We are pursuing analyses of H2A.W evolution, function, and properties using structural, biochemical, and molecular analyses. 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 and are investigating the function of these new domains. We are also closely investigating the interplay between H2A.Z and H3K27me3 in the definition of specific subdomains of chromatin.

The *Marchantia* genome was published in 2017 and we have obtained a much-improved version of this genome assembly per chromosome. With this new assembly, we are now able to obtain a comprehensive series of chromatin profiles of histone variants and modifications in *Marchantia*. 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.

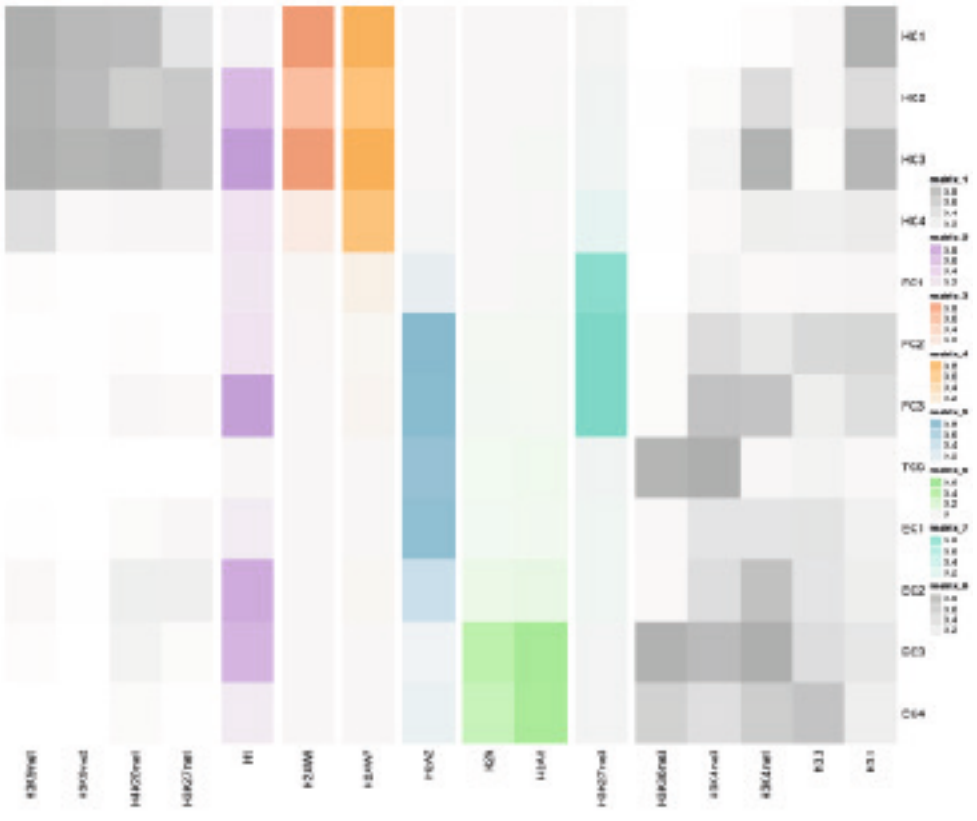
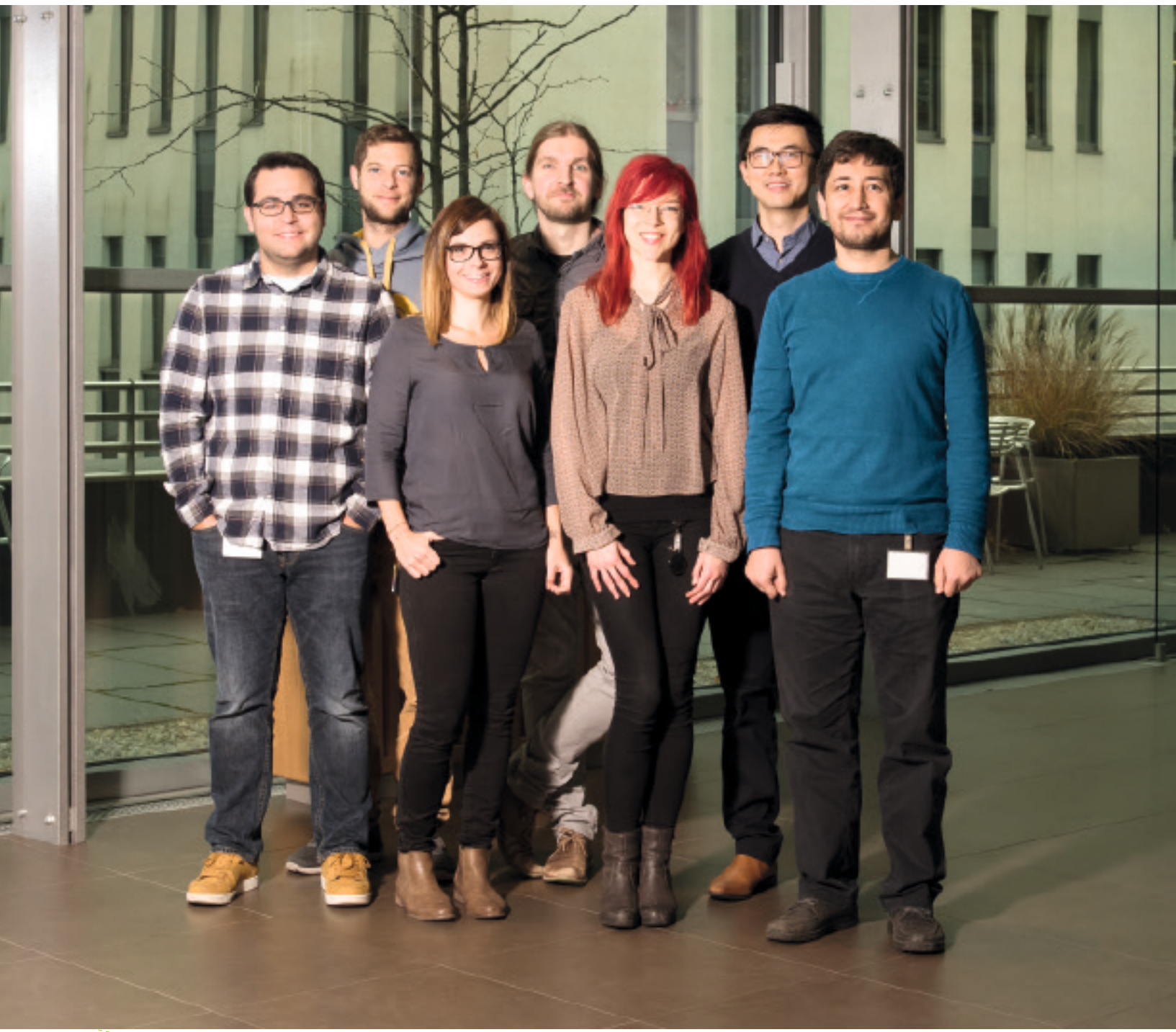


FIG. 2

Chromatin states and chromatin signatures in Arabidopsis. Hidden Markov Model applied to a set of 17 genomic profiles of chromatin marks led to the identification of 12 combinations referred to as chromatin states. Colors are used for chromatin components that appear to define the chromatin states.

DAGDAS GROUP



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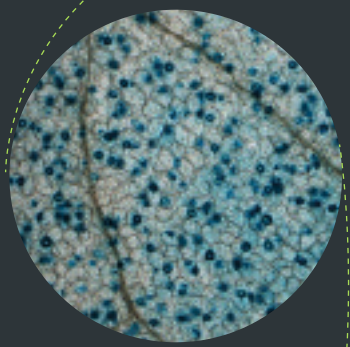
SELECTIVE AUTOPHAGY IN PHENOTYPIC PLASTICITY



Quality control pathways are essential for sustaining multicellular life. By promptly tailoring cellular contents in a cell-type specific manner, they maintain the ability to respond to external changes and thereby maximize fitness. Selective autophagy is a potent quality control pathway that recycles damaged or unnecessary macromolecules to keep cells healthy and in tune with the environment. Most of our knowledge of selective autophagy is derived from studies that utilized *in vitro* cell cultures. Addressing how selective autophagy contributes to cellular homeostasis in different cell types, and how this translates into overall performance of the organism, is extremely challenging and has therefore remained elusive.

Plants provide unique opportunities to tackle this question. For example, functional tools to investigate distinct cell lineages in a growing root, a highly phenotypically plastic organ, are readily available. Furthermore, plants rely on quality control mechanisms to adapt to changing conditions.

THE GOAL OF OUR LAB is to study how selective autophagy mediates cellular reprogramming and enables plasticity so that we can leverage this information to improve plant stress tolerance.

To achieve our goal, we are

1. Developing a comprehensive toolbox to monitor and manipulate autophagy in *Arabidopsis thaliana* and *Marchantia polymorpha*
2. Characterizing novel autophagy receptors that mediate the recycling of cellular organelles and protein complexes
3. Defining selective autophagy networks in *A. thaliana* and *M. polymorpha* to perform comparative evolutionary studies.

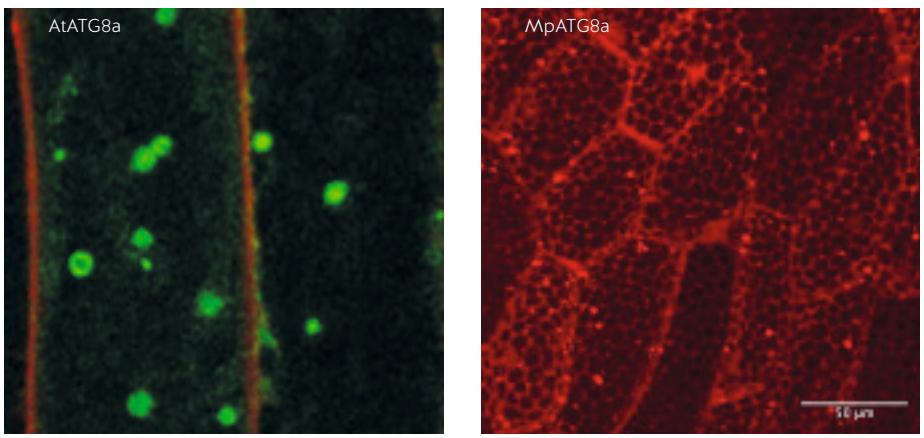
It is now well-established that autophagy is highly selective. Autophagic cargo sorting involves labelling cargo with non-self tags, such as polyubiquitin chains, followed by selective engulfment into the autophagosomes. Autophagic cargoes are rapidly quarantined from the rest of the cytoplasm within de novo formed vesicles, the autophagosomes (→ Fig. 1). There are three key players in selective autophagy: ATG8, selective autophagy receptors, and autophagic cargoes. ATG8 directly interacts with selective autophagy receptors and labels the autophagosomes for cargo recruitment and trafficking to the vacuole. Selective autophagy receptors or cargo receptors are modular proteins that contain cargo-binding domains and conserved ATG8 interacting motifs (AIMs). This modular architecture allows cargo receptors to bring autophagic cargo to the growing autophagosome and ensures selective cargo recruitment. The autophagic receptors and cargo are then carried to the vacuole for degradation (→ Fig. 2).

Even though the ATG8 gene family is expanded in plants – 9 in *Arabidopsis thaliana* compared to 1 in yeast and 2 in *C. elegans* – most studies have used a single ATG8 isoform. Functional specialization of the ATG8 gene family, which could contribute to selective autophagy, is currently neglected in the plant autophagy field. Our recent phylogenetic analyses revealed the presence of plant-specific ATG8 isoforms. (→ Fig. 3). This includes nine clades in Brassicales (a-i), four clades in Solanaceae (So-I to IV) and at least two clades in Poaceae (Po-I and Po-III).

Using biochemical and cell biology approaches, we are investigating whether these ATG8 clades are functionally specialized and contribute to selective autophagy responses. We are also using ATG8 expansion as a platform to explore selective autophagy networks in plants.

FIG. 1

ATG8 labels autophagosomes. AtATG8a: Arabidopsis thaliana GFP-ATG8a, MpATG8a: Marchantia polymorpha TagRFP-ATG8a



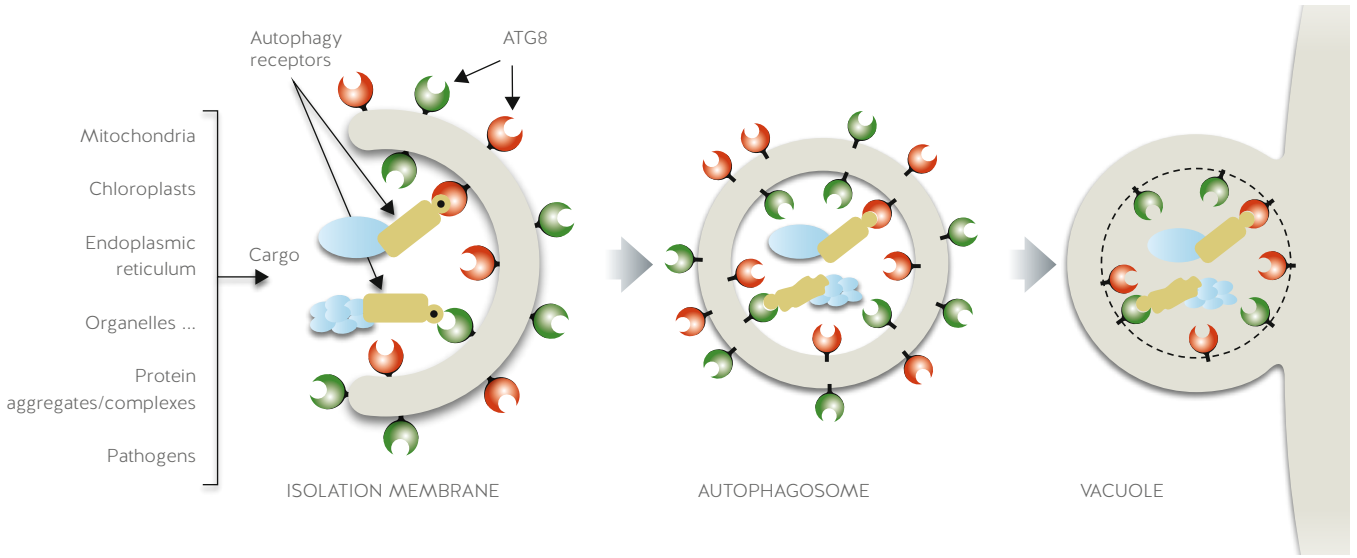
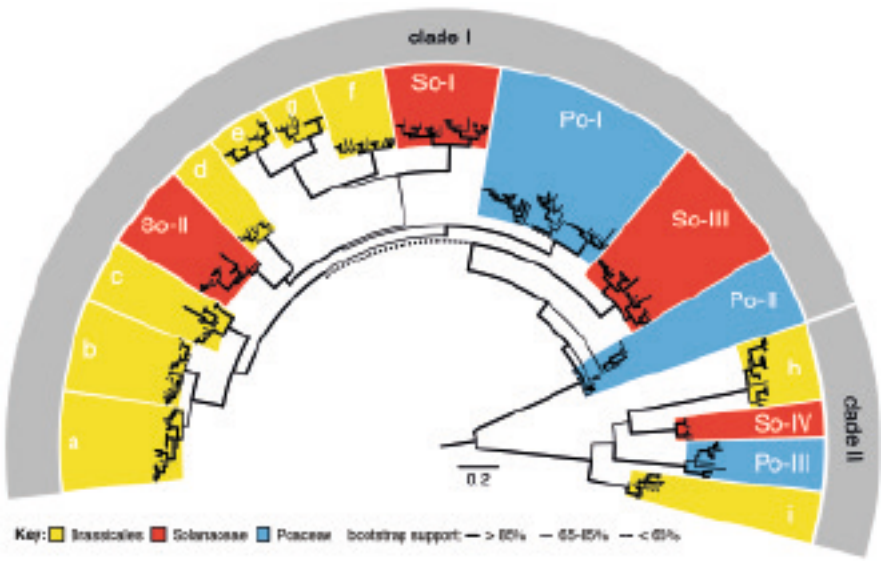


FIG. 2

Selective autophagy is mediated by the interaction of autophagy receptors with ATG8 on the growing phagophore/isolation membrane. Autophagy receptors recognize and recruit specific cargo into the growing phagophore for degradation in the vacuole (adapted from Stolz et al., 2014).

FIG. 3

Plants have family-specific ATG8 clades. Neighbour Joining analysis of ATG8 sequences from three plant lineages (Brassicales: a-i, Solanaceae: So-I/II/III/IV, Poaceae: PoI/II/III) showing monophyletic clades of higher taxonomic order.



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EFFECTOMICS – EXPLORING THE TOOLBOX OF BIOTROPHIC PLANT PATHOGENS

Plant pathogenic fungi are biotrophs that live and feed on their living host. They evolved a set of manipulative secreted molecules, termed 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*. Using 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 (→ Fig. 1).

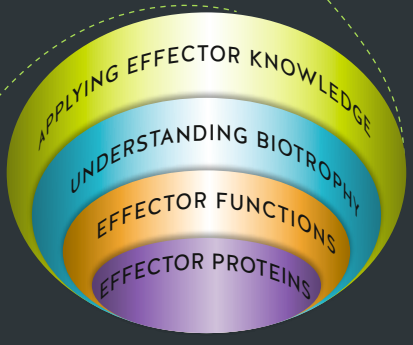


FIG. 1
Starting with a library of effector proteins, identifying their functions is the basis for mechanistically understanding biotrophy. This knowledge can then be applied for plant protection strategies and effectors can be used as tools to study plant biology.

Successful plant biotrophic pathogens must constantly sense and modulate the molecular manipulation of their host's metabolism to balance their interaction and keep the host alive. To suppress the highly evolved plant defence system and divert the host metabolism, plant pathogenic biotrophs coevolved fascinating strategies. The molecular basis for manipulation of the host plant is encoded in a versatile, secreted repertoire of effectors. Effectors are manipulative molecules employed by the pathogen to create favourable conditions for its reproductive success inside the living host. Functional characterization of effectors is challenging, as they mostly lack known motifs which could otherwise suggest a putative function. Nevertheless, characterisation of these effectors and their host target sites give fundamental insights into the requirements of the pathogen and point to key-nodes in the host metabolic network. Effector studies may thus prove rewarding for both pest control and plant breeding.

USTILAGO MAYDIS – MAIZE, AN ESTABLISHED MODEL PATHOSYSTEM

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

With its small genome size, ease of symptom recognition (*U. maydis* causes gall formation within a week of infection), amenability to molecular genetic manipulation, and relevance as a pathogen of an important crop plant, *U. maydis* is a fantastic pathogen to study biotrophic interactions.

As most effectors lack sequence similarity to known proteins, our group decided to follow a systematic approach by screening all ~300 putative effector genes of *U. maydis*. These screens will provide insights into:

1. The localisation and place of action of the putative effectors
2. Host interaction partners
3. Functional aspects / pathways the effector might interfere with

Integrating the results of several screens is the basis for functional studies of individual effectors. An important aspect of this characterization is to determine whether deletion of an individual effector influences virulence. Classically, hundreds of plants needed to be syringe infected with the mutant and control strain to identify differences in symptom development, where disease symptoms scoring is used as a proxy for virulence. This year, we finished the development of a novel Next Generation Sequencing based approach that dramatically increases the throughput of these experiments. As a proof of concept, using 200 mutant strains in a pooled infection we identified 19 novel and 5 previously known virulence factors of *U. maydis* (→ Fig. 2 and → Fig. 3) (manuscript under review).

Using this key-technology, we are preparing to generate a genome wide virulence map of *U. maydis* to identify unknown virulence factors.

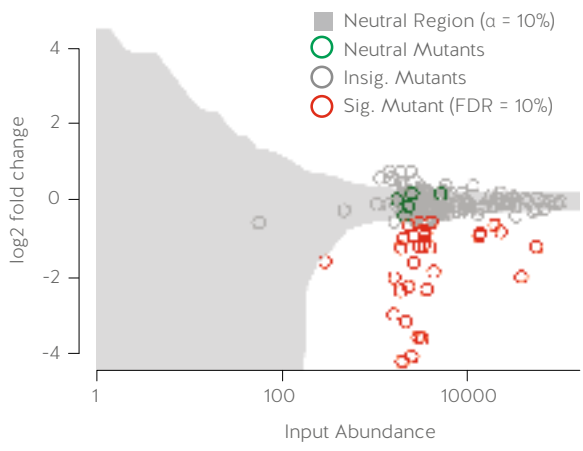


FIG. 2
iPool-Seq identifies significantly depleted mutants after pooled infection. Red circles indicate mutants with a significant virulence defect, green circles are internal neutral references.

NON-INVASIVE PHENOTYPING OF FUNGAL INFECTION IN *BRACHYPODIUM DISTACHYON*

Ustilago bromivora infects the model monocot *Brachypodium distachyon*. Whereas *U. maydis* causes qualitative symptoms on maize seedlings 7 days after infection, studying *U. bromivora* is more challenging as disease symptoms are not outwardly visible until the plant flowers. Over the past year, we showed that Brachypodium plants infected by *U. bromivora* display reduced growth phenotypes which can be exploited to predict whether the plants will develop spore filled spikelets weeks after infection. In an interdisciplinary effort, we designed the Phenobox, a photochamber with an automatized turntable to obtain pictures from different angles of infected plants (→ Fig. 4). The pictures are automatically transferred to a bioinformatic pipeline where features are extracted from the pictures. Based on a principal component analysis followed by K-means classification, we can almost perfectly predict, as early as 10 days after vernalisation, whether infected seedlings will develop spore filled sori in the spikelets ~6 weeks later. The Phenobox/Phenopipe system is open source and the paper is in revision.

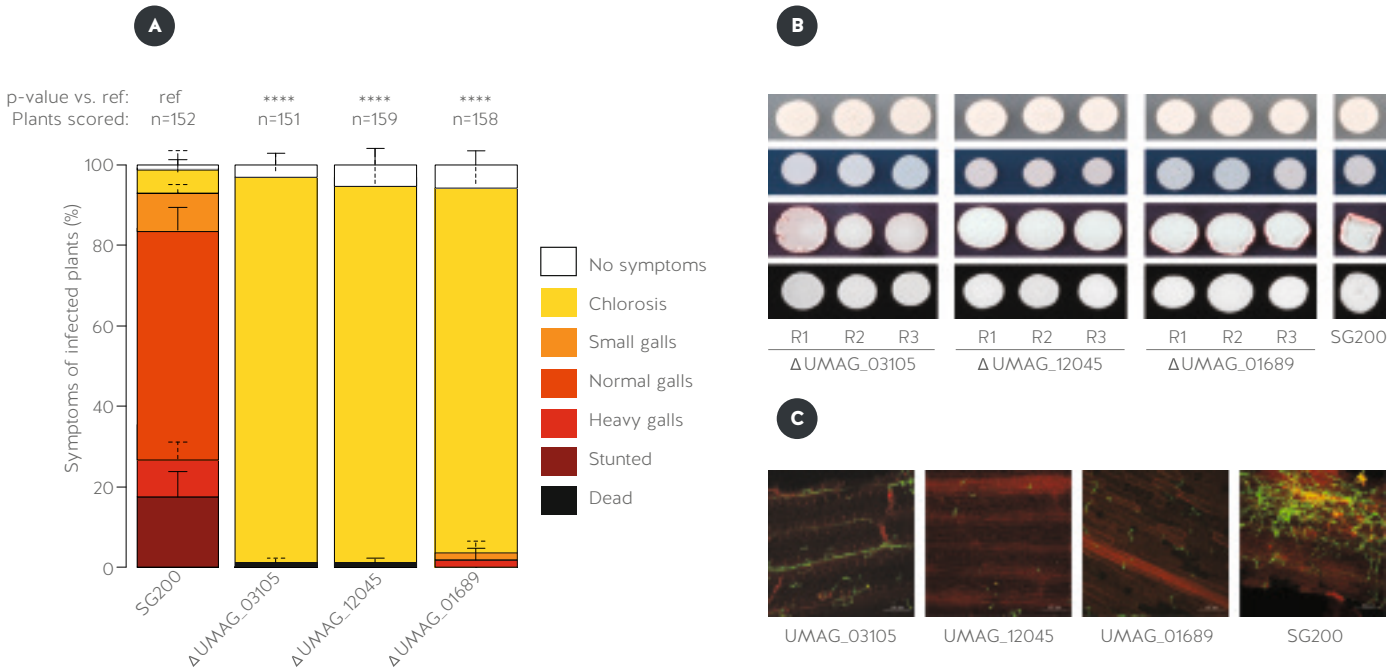


FIG. 3

Virulence factor mutants identified by iPool-Seq cause reduced disease symptoms on maize. **A***) Three effector mutants show significantly less virulence using standard assays.* **B***) The effector mutants specifically affect virulence, and not fungal growth even under stress.* **C***) Confocal microscopy confirms the absence of fungal infection in the virulence mutants.*

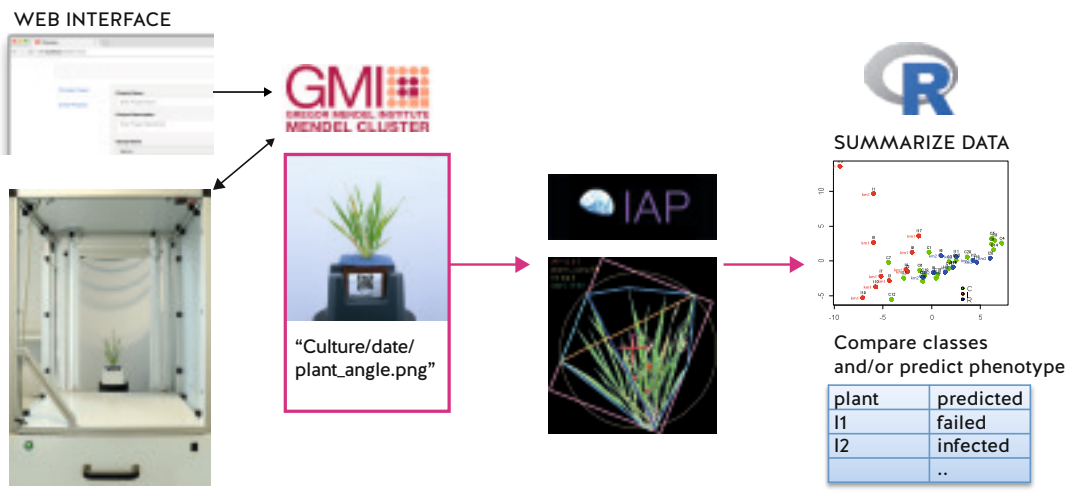
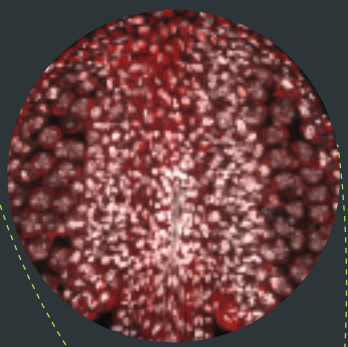


FIG. 4

„PhenoBox" and the processing pipeline „PhenoPipe": A picture of the Phenobox and a flow chart of the automated visual phenotyping pipeline „PhenoPipe". Pictures of the plant are taken automatically, the pictures are transferred to a network drive for analysis, and data is made available through a web interface.

MITTELSTEN SCHEID GROUP

GENETIC AND EPIGENETIC CHANGES IN PLANTS



The characteristics of organisms are influenced by two components of inheritance: genetic and epigenetic information. Our group is interested in their mutual influence on each other. We study epigenetic components of DNA repair and recombination and epigenetic information under abiotic stress, during differentiation, and in polyploids, using *Arabidopsis thaliana* as a model organism. With *Aethionema arabicum*, we study adaptive traits in seed formation and germination.

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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. It is involved in the regulation of development and morphology in response to internal and environmental stimuli, in defense against intruding DNA and RNA molecules, and in genome stabilization.

Faithful maintenance and transmission of genetic information is constantly challenged by DNA damage. Several damage repair pathways can restore DNA molecules, but the repair proteins must be able to access lesions even in densely packed chromatin. Access is provided by chromatin remodeling factors, and we study the role of the SWR1 complex that is required for efficient DNA damage repair by homologous recombination in *Arabidopsis thaliana*. We induce DNA breaks at a specific gene necessary for chlorophyll synthesis with the "gene scissor" CRISPR-Cas9 (→ Fig. 1) and follow the recruitment of proteins and RNA during the repair process.

The complex organization of the long chromosomal DNA molecules within the small nucleus is achieved by association with RNA and proteins, especially 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. Using molecular tools and microscopy of living root cells of Arabidopsis, we record gene expression and nuclear architecture under regular temperature or heat stress conditions. The stress causes a transient change in nuclear shape and heterochromatin condensation (→ Fig. 2), in addition to specific changes in gene expression and nucleosome occupancy.

FIG. 1

Induced expression of Cas9 produces a targeted DNA break in a gene necessary for chlorophyll biosynthesis, leading to white and growth-retarded plants (right), while seedlings without the transgene (left) are unaffected (Photos: Mattia Donà).

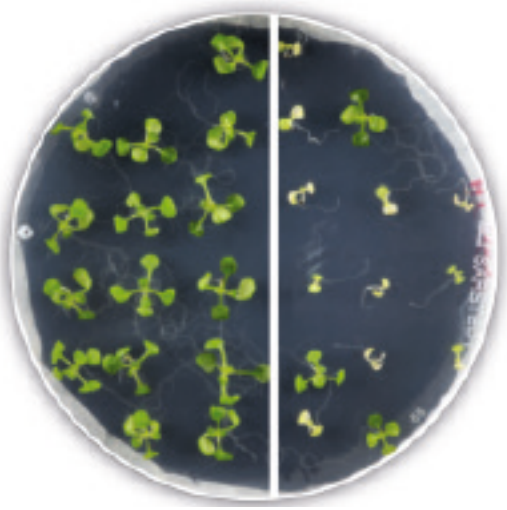
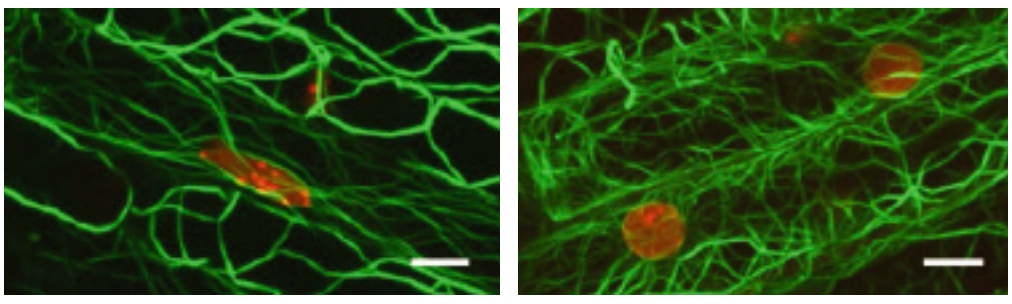


FIG. 2

Nuclear shape and heterochromatin organization within a living Arabidopsis root, under regular temperature (left) and after 37 h of heat stress (right). Nuclei are visualized with RFP-histone (red), while the actin filaments are labelled with Venus (green). Size bar: 10 µm (Photos: Tao Dumur).



To ask whether stress-induced epigenetic changes are transmitted to non-stressed plants in the next generation, we want to analyze the epigenetic configuration of Arabidopsis stem cells in the shoot apical meristem. To isolate the nuclei from these few cells, we specifically label one of the histones in these cells (→ Fig. 3) and apply fluorescence-activated nuclei sorting, followed by transcriptome and methylome analysis.

Only a few cases of heritable epigenetic changes, through which acquired gene expression states can be transmitted, are described. The most well-described example is paramutation, which refers to the inactivation of a paramutable allele of a gene when it encounters a paramutagenic allele of the same gene. The silent state remains even after segregation of both alleles. We study the molecular basis of paramutation and its connection with polyploidy in Arabidopsis, based on different alleles of a resistance marker gene.

Aethionema arabicum, a distant relative of Arabidopsis, developed natural variants in different geographical regions with striking differences in seed germination biology: while one accession can germinate equally well in light and darkness, the other is strongly inhibited by light and germinates only in darkness (→ Fig. 4). This light inhibition contrasts with the light requirement of Arabidopsis seed germination, and we found that expression of genes for some key enzymes undergo converse changes upon light compared to Arabidopsis. This illustrates that similar components of a pathway have been assembled by evolution to produce a divergent and alternative pathway.

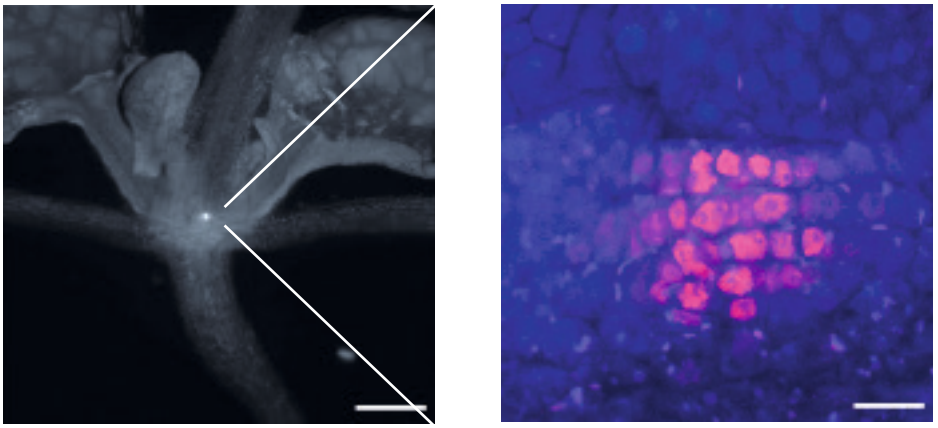


FIG. 3
Nuclei in the shoot apical meristem of an Arabidopsis seedling, labelled with mCherry-histone (white (left) and red (right)), counterstained with DNA dye (blue, right). Size bar 1 mm (left) and 5 µm (right) (Photos: Ruben Gutzat).

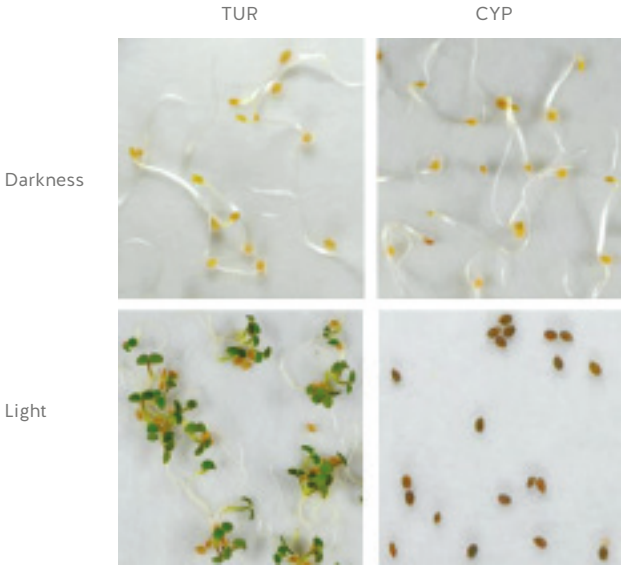


FIG. 4
An accession of Aethionema arabicum *from Turkey (left) germinates equally well in darkness (top) or light (bottom), while germination of the seeds from Cyprus (right) are inhibited by light. (Photos: Zsuzsanna Mérai).*

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GENE REGULATION DURING EARLY EMBRYOGENESIS

We study gene regulatory mechanisms required for pattern formation in early plant embryos. We use *Arabidopsis thaliana* (Arabidopsis) as a model system for several reasons including the abundance of genetic and genomic resources available. Moreover, Arabidopsis embryos undergo invariant division patterns to generate morphologically simple structures composed of diverse cell types. Their simplified morphology makes them ideal for investigating complex regulatory mechanisms that govern pattern formation.

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(*left the lab in 2017)

After fertilization of egg and sperm, the basic body plan is established during early embryogenesis (→ Fig. 1). Although decades of research have deciphered molecular mechanisms regulating these fundamental processes in animals, much less is known about them in plants. Rather than a lack of interest, this is primarily due to the difficulty in studying early plant embryos because they are small and deeply embedded within maternal tissues. To circumvent these limitations, we have developed molecular biology and bioinformatics approaches to characterize small regulatory RNA-mediated mechanisms controlling pattern formation during early plant embryogenesis. For instance, we developed exogenous small RNA spike-in oligonucleotides that allow for absolute normalization of small RNA sequencing (sRNA-Seq) data (→ Fig. 2). These sRNA spike-ins facilitate comparisons of small RNA levels across different tissue types and genotypes, as well as serve as internal controls for a low-input sRNA-Seq protocol that we have optimized (in preparation). Additionally, we produced a statistical tool that revealed the presence of substantial RNA contamination from maternal tissues in nearly all published Arabidopsis endosperm and early embryo transcriptomes (→ Fig. 3). Not only is this a useful tool for the community to ensure the generation of accurate datasets, but we also found that maternal RNA contamination in previously published datasets had been repeatedly misinterpreted as epigenetic phenomena including the magnitude and maternal bias of imprinted genes.

We are using these and additional enabling technologies to assess the regulatory roles of sRNAs in establishing the basic body plan of plant embryos. Plant sRNA populations consist of three main classes: 20-22 nt microRNAs (miRNAs) and trans-acting siRNAs (tasiRNAs) that generally post-transcriptionally regulate protein-coding genes, and 20-24 nt small interfering RNAs (siRNAs) that typically transcriptionally silence transposons. Previously we found that miRNAs are required to prevent

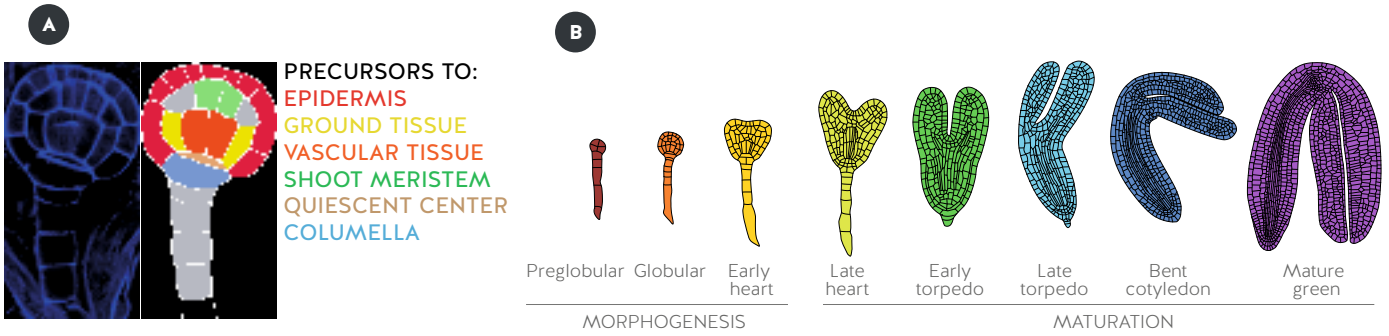


FIG. 1

Arabidopsis embryogenesis. **A***) Confocal laser scanning microscopy image of late globular embryo and tracing with precursors to the fundamental cell-types of the plant body.* **B***) different stages of embryo development.*

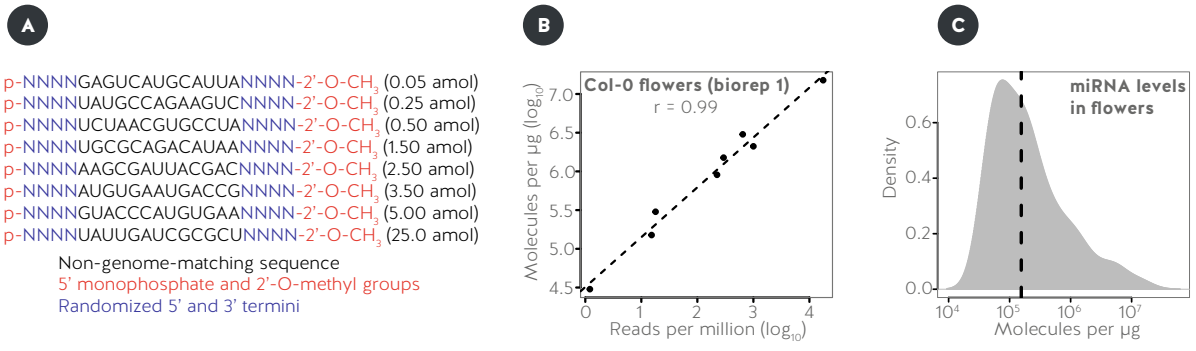
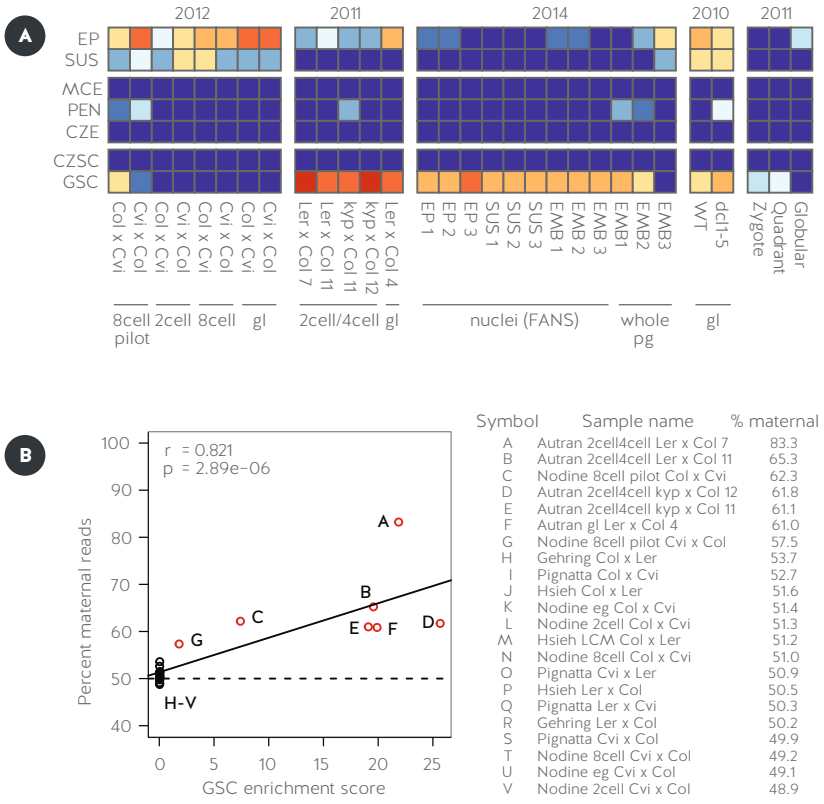


FIG. 2

Small RNA spike-in design and use as a tool to estimate absolute small RNA levels. **A***) Design features* **B***) Scatter plot of relative small RNA spike-in levels compared to absolute levels* **C***) Density plot of individual miRNA family levels in Col0 flowers; vertical dashed line indicates the median number of molecules per miRNA family.*

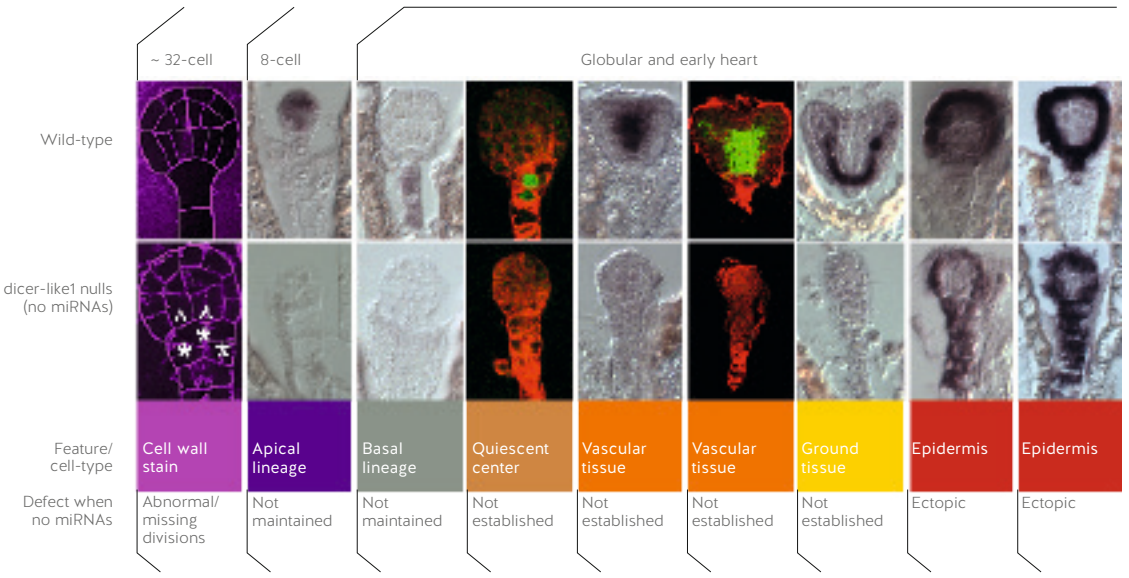
premature differentiation and enable pattern formation during embryogenesis (→ Fig. 4). However, the functions of individual embryonic miRNAs remain mostly uncharacterized. By using a combination of cutting-edge experimental and computational approaches, we have identified the molecular functions of dozens of miRNA families and have also discovered several miRNAs whose repression of transcripts encoding transcription factors is required for proper embryo morphogenesis. We are currently characterizing how the miRNA-mediated repression of transcription factors influences cellular differentiation and the establishment of the basic body plan during early embryogenesis.

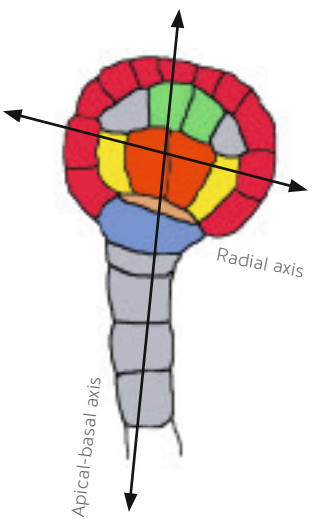


Symbol	Sample name	% maternal
A	Autran 2cell4cell Ler x Col 7	83.3
B	Autran 2cell4cell Ler x Col 11	65.3
C	Nodine 8cell pilot Col x Cvi	62.3
D	Autran 2cell4cell kyp x Col 12	61.8
E	Autran 2cell4cell kyp x Col 11	61.1
F	Autran gl Ler x Col 4	61.0
G	Nodine 8cell pilot Cvi x Col	57.5
H	Gehring Col x Ler	53.7
I	Pignatta Col x Cvi	52.7
J	Hsieh Col x Ler	51.6
K	Nodine eg Col x Cvi	51.4
L	Nodine 2cell Col x Cvi	51.3
M	Hsieh LCM Col x Ler	51.2
N	Nodine 8cell Col x Cvi	51.0
O	Pignatta Cvi x Ler	50.9
P	Hsieh Ler x Col	50.5
Q	Pignatta Ler x Cvi	50.3
R	Gehring Ler x Col	50.2
S	Pignatta Cvi x Col	49.9
T	Nodine 8cell Cvi x Col	49.2
U	Nodine eg Cvi x Col	49.1
V	Nodine 2cell Cvi x Col	48.9

FIG. 3

Widespread seed coat contamination in early embryo transcriptomes. **A***) Heatmaps of tissue-enrichment test results. Row labels indicate seed compartments: embryo proper (EP), suspensor (SUS), micropylar endosperm (MPE), peripheral endosperm (PEN), chalazal endosperm (CZE), chalazal seed coat (CZSC) and general seed coat (GSC). Colors indicate the level of tissue-enrichment.* **B***) Scatterplot depicting the relationship between the presence of seed coat-enriched transcripts in a dataset and the percentage of SNP-containing reads that map to the maternal genome. Red circles indicate samples with significant presence of seed coat-enriched transcripts.*



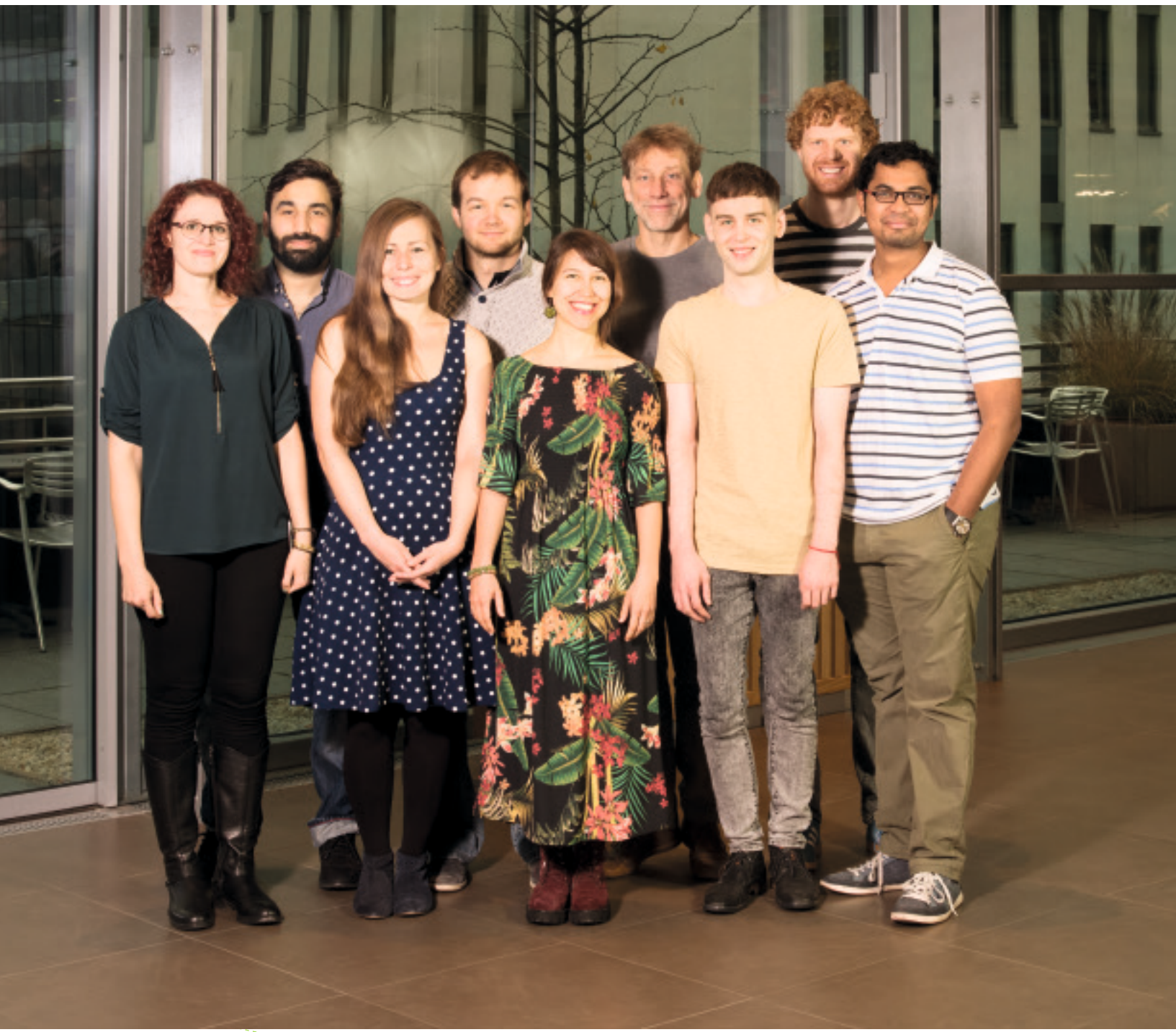


PRECURSORS TO:
EPIDERMIS
GROUND TISSUE
VASCULAR TISSUE
SHOOT MERISTEM
QUIESCENT CENTER
COLUMELLA

FIG. 4

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. Unpublished and adapted from Nodine and Bartel (2010) Genes & Development.*

NORDBORG GROUP



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PREVIOUSLY

- Associate Professor (2004-2015): University of Southern California, Los Angeles CA, US
- Assistant Professor (2000-2004): University of Southern California, Los Angeles CA, US
- Research Assistant Professor (1997-2000): Lund University, SE
- Postdoc (1994-1997): Joy Bergelson, Brian & Deborah Charlesworth Labs, University of Chicago, IL, US

POPULATION GENETICS

Our group studies 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.

GROUP MEMBERS

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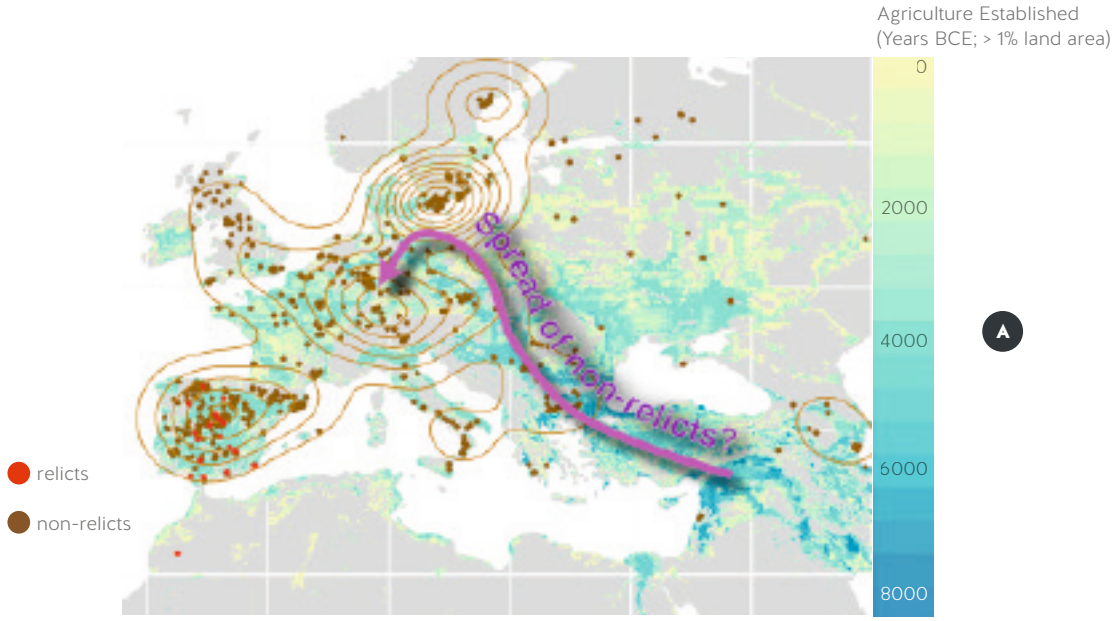
Eriko Sasaki

PROGRAMMER
Ümit Seren

TECHNICIANS
Jagoda Joanna
Viktoria Nizhynska

(*left the lab in 2017)



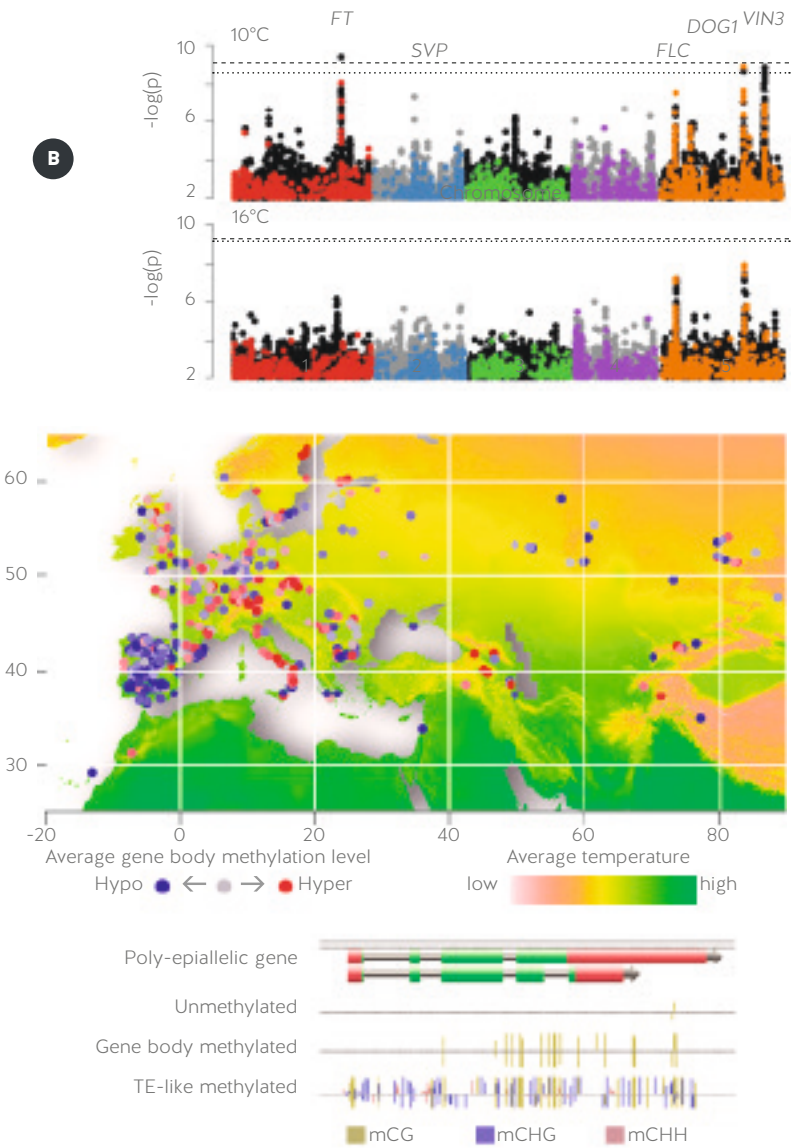


FIG. 1

A) *Genomic sequencing analysis of over 1,000 natural inbred lines of* Arabidopsis thaliana *reveals its global population structure, migration patterns, and evolutionary history.* **B**) *GWAS of flowering time variation at two different temperatures pinpoint major genes involved in climate adaptation.* **C**) *Methylomes and transcriptomes from the same inbred lines provide insights into how the epigenome is shaped by natural genomic variation and by the environment. (Kawakatsu et al. 2016)*

One of the most important challenges facing biology today is making sense of genetic variation — within and between species. 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. Our research is quantitative, with several group members doing exclusively computational work. The following is an overview of a few of our group's many projects.

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 because it naturally occurs as inbred lines which can be genotyped once and phenotyped repeatedly. For over 15 years, we have been spearheading an international effort to make genome-wide association in *A. thaliana* a reality, and we recently published the genomes, transcriptomes, and epigenomes of over 1000 natural inbred lines — a fantastic resource for the genetic community. We are also supporting public websites and databases that allow anyone to carry out GWAS and help coordinate as much phenotypic information (→ Fig. 1).

THE GENETICS OF ADAPTATION

We are carrying out large-scale GWAS 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. 2) 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.

FIG. 2 A) *Common garden experiment.*

FIG. 2 B) *Close-up of a dispersal experiment.*

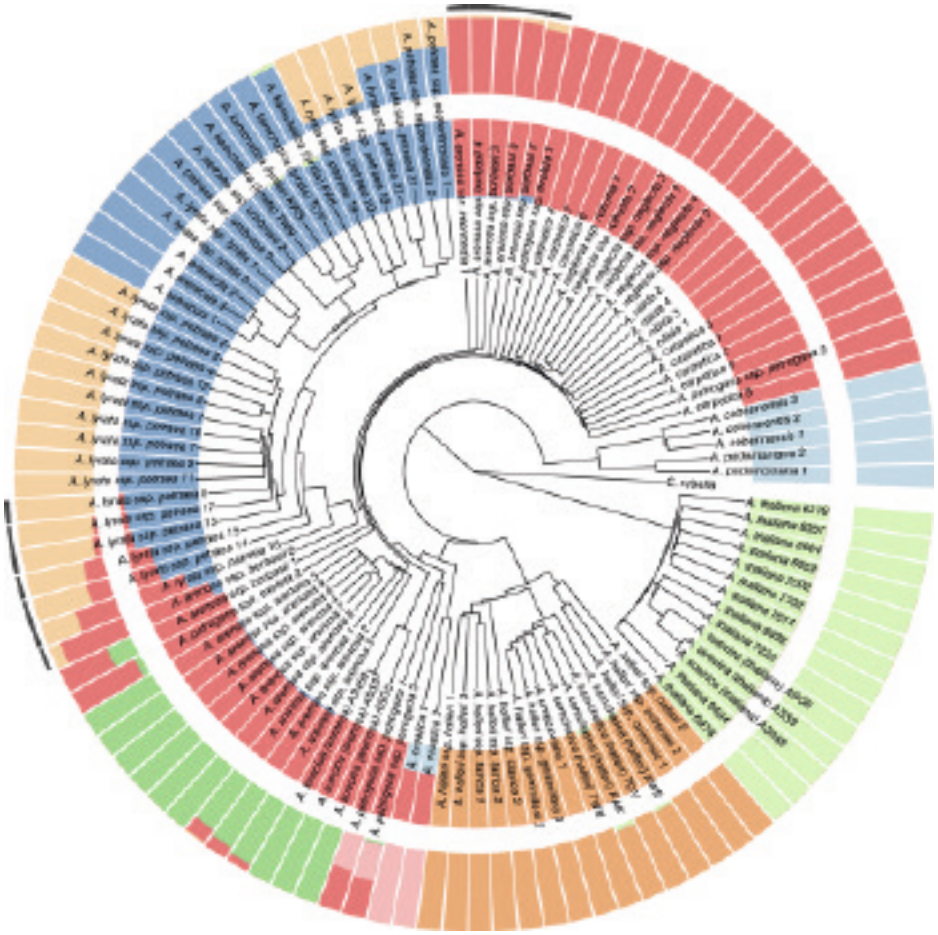


FIG. 3

Clustering of sequenced individuals on the basis of polymorphism data. (Novikova et al. Nat Genet 2016).

FIG. 4

Columbine species currently being sequenced by JGI. (Courtesy of Scott Hodges, UCSB)

EUROPE

Aquilegia aurea

Aquilegia vulgaris

NORTH AMERICA

Aquilegia chrysantha

Aquilegia pubescens

Aquilegia coerulea

Aquilegia jonesii

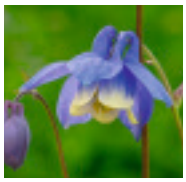
Aquilegia formosa

Aquilegia pinetorum

Aquilegia barnebyi

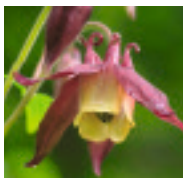
Aquilegia longissima

ASIA



Aquilegia sibirica

Aquilegia flabellata



Aquilegia oxysepala

Aquilegia ecalcarata

SISTER GROUP

Semiaquilegia adoxoides

SPECIATION IN THE GENUS ARABIDOPSIS

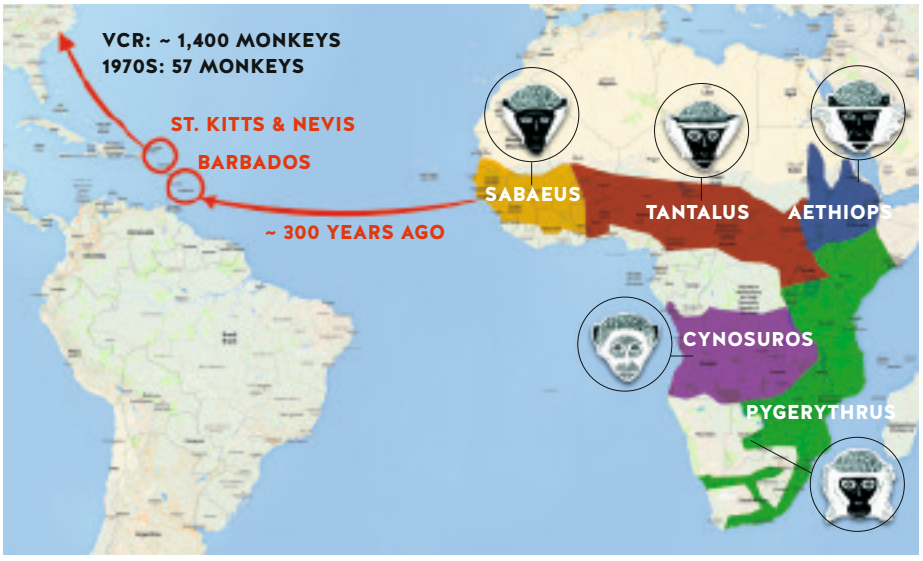
We seek to understand how diversity arises at the level of species, and have used the genus *Arabidopsis.* Long-term questions include the evolution of genome size, the effects of polyploidy, and the switch to self-fertilization, but our immediate goal is to understand how genetic variation is distributed across a diverse group of plant species. To this end, we sequenced over a hundred individuals from all taxa in the genus, and demonstrated that speciation in the genus is a messy (and ongoing) process involving long periods of partial reproductive isolation (→ Fig. 3).

THE GENETICS OF SPECIES DIFFERENCES IN AQUILEGIA

We are also studying the genetics of species differences in the columbine genus, *Aquilegia* (Ranunculaceae). The genus is a beautiful example of a recent, rapid, adaptive radiation, especially with respect to floral morphology and color (→ Fig. 4). We seek to understand the genetic basis for such striking differences, focusing particularly on two North American species, *A. formosa* and *A. pubescens,* the former of which is pollinated by hummingbirds, the latter of which is pollinated by hawkmoths, resulting in reproductive isolation. 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.

POPULATION GENETICS OF AFRICAN GREEN MONKEYS

The African green monkey *(Cercopithecus sp.)* is a common Old World monkey, spread throughout much of Africa, and introduced by humans to the Caribbean. It is also kept in large colonies for behavioral and biomedical research, in particular for understanding HIV resistance. As part of an international consortium to develop genomic resources for vervets, we have sequenced over 100 monkeys sampled across the African continent, covering all known species, and discovered dramatic footprints of selection at genes involved in response to viruses. (→ Fig. 5)



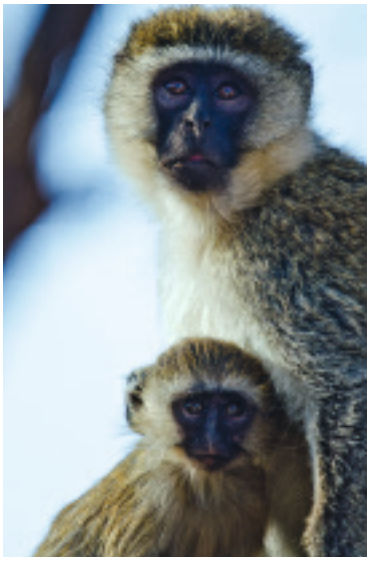
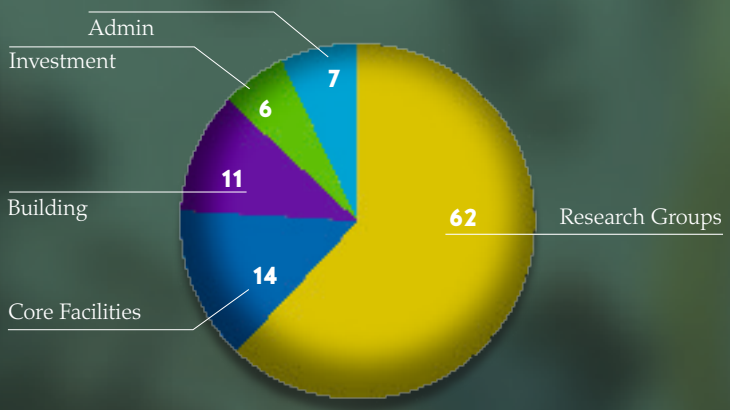


FIG. 5

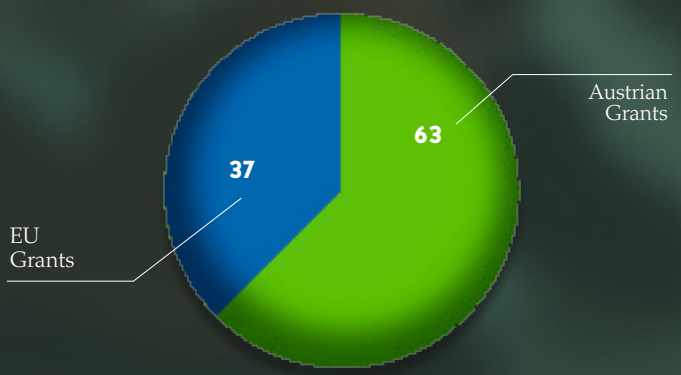
Distribution of vervet monkeys.

17 KEY FACTS *(as of Dec 31, 2017)*

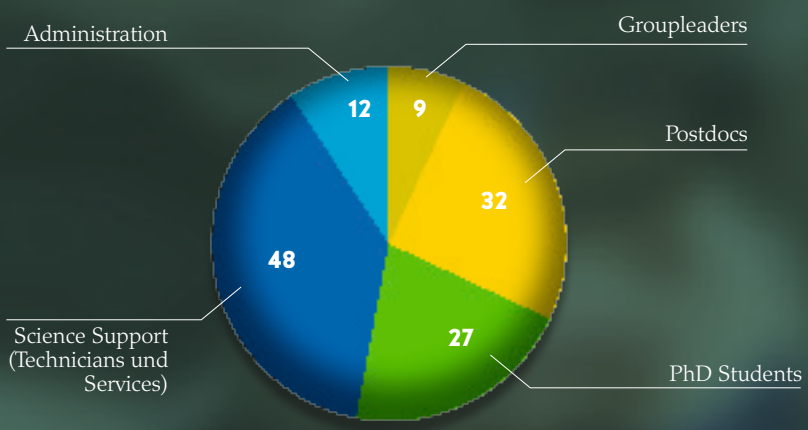
EXPENDITURES (%)



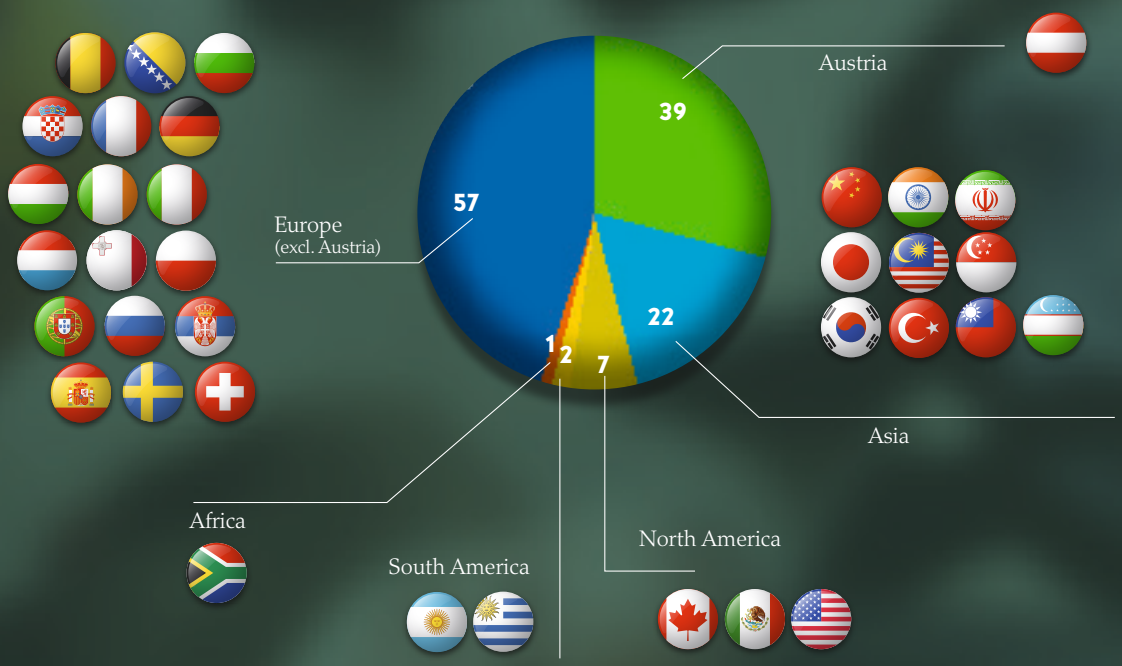
RESEARCH GRANTS (%)



STAFF BY FUNCTION (Head Count)



STAFF - NATIONALITIES (Head Count)



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Sasaki E, Frommlet F, Nordborg M *(2017)* **The genetic architecture of the network underlying flowering time variation in Arabidopsis thaliana.** *bioRxiv 175430.*

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Seren Ü, Korte P, Nizhynska V, et al. *(2017)* **Verification of Arabidopsis stock collections using SNPmatch - an algorithm for genotyping high-plexed samples.** *bioRxiv 109520.*

Svardal H, Jasinska A, Apetrei C, et al. *(2017)* **Ancient hybridization and strong adaptation to viruses across African vervet monkey populations.** *Nat Gen 49(12):1705-13.*

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Tsuchimatsu T, Goubet PM, Gallina S, et al. *(2017)* **Patterns of polymorphism at the self-incompatibility locus in 1,083 Arabidopsis thaliana genomes.** *Mol Biol Evol 34(8):1878-89.*

FORMER GROUPS

Valuchova S, Fulnecek J, Prokop Z, et al. *(2017)* **Protection of Arabidopsis blunt-ended telomeres is mediated by a physical association with the Ku heterodimer.** *Plant Cell 29(6):1533-45.*

Wallner ES, López-Salmerón V, Belevich I, et al. *(2017)* **Strigolactone- and Karrikin-independent SMXL proteins are central regulators of phloem formation.** *Curr Biol 27(8):1241-7.*

SERVICE GROUP

Osman K, Yang J, Roitinger E, et al. *(2017)* **Affinity proteomics reveals extensive phosphorylation of the Brassica chromosome axis protein ASY1 and a network of associated proteins at prophase I of meiosis.** *Plant J [epub].*

Rao S, Sigl V, Wimmer R, et al. *(2017)* **RANK rewires energy homeostasis in lung cancer cells and drives primary lung cancer.** *Genes Dev 31(20):2099-112.*

Stadlmann J, Taubenschmid J, Wenzel D, et al. *(2017)* **Comparative glycoproteomics of stem cells identifies new players in ricin toxicity.** *Nature 549(7673):538-42.*

17 GRANTS

BECKER GROUP

Epidiverse - epigenetic diversity in ecology
European Research Council (ERC), Life Sciences:
H2020-MSCA-ITN-2017
€ 255,374
September 2017 – August 2021

Function and evolution of attack and response strategies during allelopathy in plants
European Research Council (ERC), Life Sciences:
ERC Starting Grant: FEAR-SAP
€ 1,500,000
January 2018 – December 2022

BELKHADIR GROUP

An extracellular interactome map of plant receptor kinases (H. Firnberg fellowship Smakowska)
Austrian Science Fund: T947-B29
€ 230,010
August 2017 - July 2020

BERGER GROUP

Impact of the new histone H2a on chromatin structure and dynamics
Austrian Science Fund: P 26887 B21
€ 351,960
June 2014 – May 2019

Evolution of sexual reproduction in plants
Austrian Science Fund: I 2163-816 (ERA-CAPS)
€ 317,657
May 2015 – April 2018

Evolution of the chromatin organization in plants
Austrian Science Fund: P 28320-821
€ 334,237
January 2016 – December 2018

The histone variant H2A.W: a novel component that structures chromatin domains
Austrian Science Fund: I 2303-B25
€ 44,632
January 2016 – December 2017

Graduate program "Chromosome Dynamics" (Montgomery)
Austrian Science Fund: DK W1238-B20
€ 142,020
April 2016 – February 2020

BUSCH GROUP

Quantitative live imaging to determine the regulatory impact of chromatin dynamics
Vienna Science and Technology Fund: WWTF WB
€ 341,350
January 2014 – December 2017

EXO70 exocyst subunits in morphogenesis and adaptation
Austrian Science Fund: I 2377-B25
€ 344,539
November 2015 – December 2017

Root growth control and epistasis
Austrian Science Fund: P 27163-B22
€ 344,799
January 2015 – December 2017

The role of PLD1 in iron dependent root growth regulation (Lise Meitner fellowship LI)
Austrian Science Fund: M 1826-B16
€ 159,620
February 2016 – January 2018

MYCROPHOS"The genetic bases of MY-Corrhizal ROot responses to PHOSphate" (Giovannetti)
European Commission (Horizon 2020): H2020-MSCA MYCROPHOS
€ 166,156
March 2017 – February 2019

DJAMEI GROUP

ERC Starting Grant: Effectomics – elucidating the toolbox of plant pathogens
European Research Council (ERC)
€ 1,446,316
February 2014 – January 2019

Elucidating salicylic acid sensing in biotrophic smut fungi
Austrian Science Fund: P 27429-B22
€ 304,300
January 2015 – December 2017

Characterization of an essential virulence factor in the maize pathogen Ustilago maydis
Austrian Science Fund: P 27818-B22
€ 255,895
April 2015 – March 2018

Host jump enabling factors in a fungal/grass pathosystem
Austrian Science Fund: I 3033-822
€ 304,300
April 2017 – March 2020

L'ORÉAL Austria [Fellowships for Young Female Scientists in Basic Research]
(Czedik-Eysenberg)
€ 20,000

MITTELSTEN SCHEID GROUP

Dimorphic fruits, seeds and seedlings as adaptation mechanisms to abiotic stress in unpredictable environments
ERA-CAPS / Austrian Science Fund: I 1477-B16
€ 275,236
May 2014 – April 2017

Quantitative live imaging to determine the regulatory impact of chromatin dynamics
WWTF Life Sciences "New Ventures Beyond Established Frontiers" 2013
€ 682,700
(shared with co-applicant Wolfgang Busch)
November 2014 - December 2018

Graduate program "Chromosome Dynamics"
Austrian Science Fund: W1238
€ 324,820
March 2012 – February 2020

SINUDYN – Stress-induced nucleosome dynamics in plants
Austrian Science Fund: I 1107
€ 170,730
September 2013 – December 2016

Plant Stemness Genes
FEMTech / FFG 1237857
€ 3,040
August 2017 – September 2017

NODINE GROUP

Small RNA directed reprogramming of lineage-specific epigenomes in plant embryos
Austrian Science Fund: F 4324 (SFB-RNA-REG)
€ 360,360
February 2015 – January 2019

Small RNA regulation of the body plan and epigenome in Arabidopsis embryos
European Research Council (ERC), Life Sciences: ERC sRNA-EMB
€ 1,499,989
July 2015 – June 2020

Graduate program "RNA Biology"
Austrian Science Fund
€ ~150,000
January 2014 – December 2016

extended
Austrian Science Fund
€ ~170,000
January 2017 – December 2019

European Plant Embryology Consortium
Austrian Science Fund
€ 316,000
March 2014 – December 2017

NORDBORG GROUP

Integrated genetic and genomic resources for a model system
Laboratory of Molecular Genetics, National Institutes of Health, NIH Vervet
€ 240,000
May 2012 – April 2017

Starting from scratch: adaptation to variable environments after an extreme bottleneck
Deutsche Forschungsgemeinschaft: DFG-NO 942/1-1
€ 228,510
July 2011 - July 2017

17

VIENNA BIOCENTER INTERNATIONAL PHD PROGRAMME IN LIFE SCIENCES

EMPOWERING CURIOUS RESEARCHERS

The GMI offers PhD positions within the framework of the prestigious Vienna BioCenter (VBC) International PhD Programme in Life Sciences, providing students the opportunity to undertake research at the cutting edge of modern plant biology. The VBC programme has established itself as one of the premier programs in biology and life sciences in the heart of Europe. Modest group sizes ensure students receive excellent supervision, plenty of interaction with fellow students, and unhindered access to cutting-edge scientific equipment.

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. Many GMI faculty are involved in giving lectures, seminars, and practical courses in Molecular Plant Biology in the context of this program.

The Institute of Molecular Biotechnology (IMBA), the Max F. Perutz Laboratories (MFPL), and the Research Institute of Molecular Pathology (IMP) also participate in the programme. For detailed information and application procedures, please consult the programme's website www.training.vbc.ac.at/phd-programme/.

Several GMI PhD students are funded through Doctoral Programmes of the FWF in Chromosome Dynamics and RNA Biology.

vienna BIOCENTER | PhD Programme

17 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 aim to develop our employees' research performance, future employability, professionalism, and social engagement.

GENERAL TRAINING

- German language courses
- Introduction to intellectual property and patent law

TRAINING FOR PHD STUDENTS AND POSTDOCTORAL FELLOWS

- Career Development Workshop: "Career Planning"
- Career Symposium
- Methodologies/expertise
  (statistics, bioinformatics, microscopy, software)

SPECIAL TRAINING FOR PHD STUDENTS

- Introductory course for PhD Students: Priming your PhD
  Managing your PhD | Analyzing Primary Literature | Scientific Writing | Numbers in Biology | Responsible Research and Innovation | Presentation Skills
- Writing for publication
- Scientific presentations

SPECIAL TRAINING FOR POSTDOCTORAL FELLOWS

- Facing the challenge of effective writing
- Professional Development Course for Young Scientists (aka Lab management course)

SPECIAL LEADERSHIP AND MANAGEMENT TRAINING FOR GROUP LEADERS

- Leadership in science
- Using writing as a driving force for research
- Personal coaching
- Media training
- Negotiation skills

17 ALUMNI

The GMI 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. 2017 saw the departure of several PhD students and postdocs. We said „Auf Wiedersehen und viel Glück" in 2017 to:

WOLFGANG BUSCH
Assoc. Professor, Salk Institute, US

CLAUDIO CAPITÃO
Product Manager, Biomin, AT

ENVEL KERDAFFREC

JIXIANG KONG
Research Scientist, KWS Group, DE

ANNA MALOLEPSZY
Postdoc, Salk Institute, US

FERNANDO RABANAL
Post Doc, Max Planck Institute for Developmental Biology Tübingen, DE

SANTOSH SATBHAI
Research Associate, Salk Institute, US

RADKA SLOVAK
Postdoc, U. of Oxford, UK

DIVYA VASHISHT

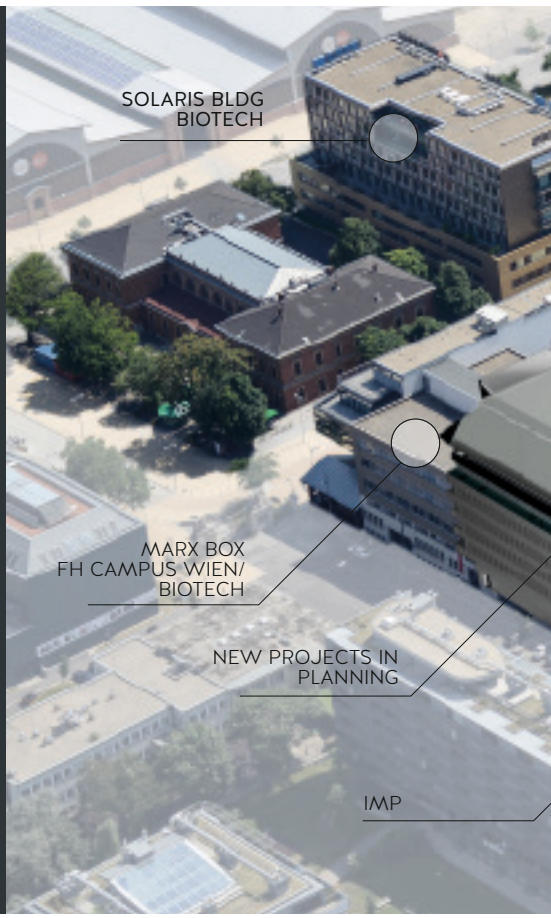
HAN WANG
PhD, U. of California San Diego, US

RUI ZHANG
Research Assistant, Research Institute for Subtropical Forestry CAF, CN

17 THE VIENNA BIOCENTER

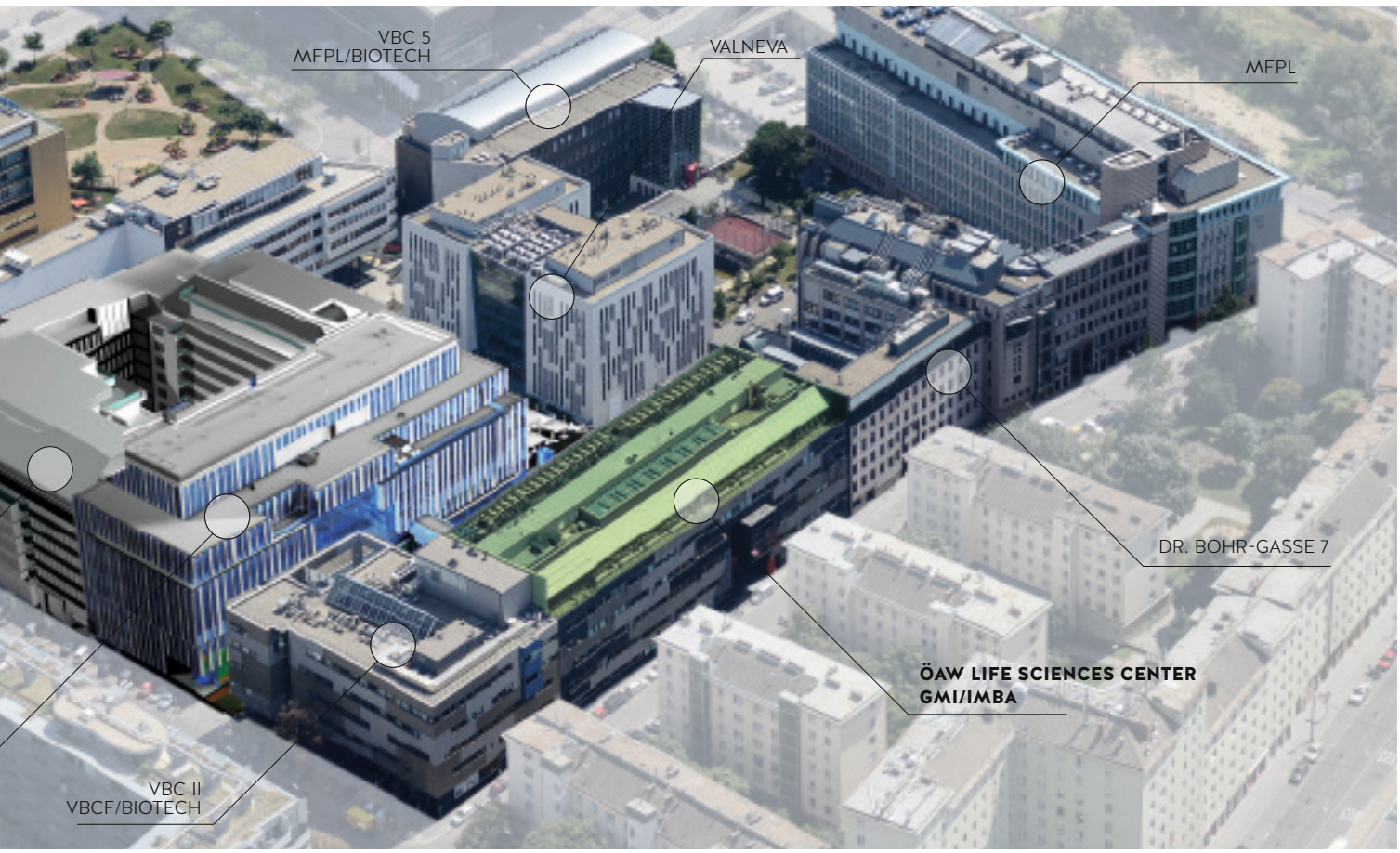
ONE OF EUROPE'S LEADING LIFE SCIENCE LOCATIONS

FOUR RESEARCH INSTITUTES, A UNIVERSITY OF APPLIED SCIENCES, 18 BIOTECH COMPANIES, A BUSINESS INCUBATOR, TWO SCIENTIFIC OUTREACH ORGANIZATIONS, AND THREE SERVICE COMPANIES, OPERATING IN 90,000 M² LAB AND OFFICE SPACE WITH 1,700 EMPLOYEES AND 1,300 BACHELOR AND MASTER STUDENTS FROM 69 COUNTRIES – THE VIENNA BIOCENTER IS ONE OF EUROPE'S LEADING LIFE SCIENCE LOCATIONS.



Vienna BioCenter

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 VBC 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 Sciences** 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.

Motivated and talented young students are offered two **international PhD programs:** the VBC PhD Programme and the MFPL PhD Program. During the selections that take place twice a year, applicants from all over the world compete for the attractive positions. Furthermore, the VBC summer school provides a unique opportunity for undergraduate students to work together with leading scientists at the VBC.

A growing number of biotech-companies complement the training and research activities at the Vienna BioCenter. Currently, eighteen **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 dialogue between 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 Sciences.

The passionate and creative scientists in **88 research groups** have acquired 41 ERC grants, 11 Wittgenstein Awards, and publish around 350 scientific papers per year. They are supported by the Vienna BioCenter Core Facilities (VBCF), providing first class scientific infrastructure. The successful cooperations, broad expertise of the researchers, and the established infrastructure offer unique working conditions that enable the members of the VBC to operate at the cutting edge of Life Science research.

17 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. They provide instrumentation, education, and expertise for flow cytometry experiments, manage more than twenty-five microscopy 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 and 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 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.

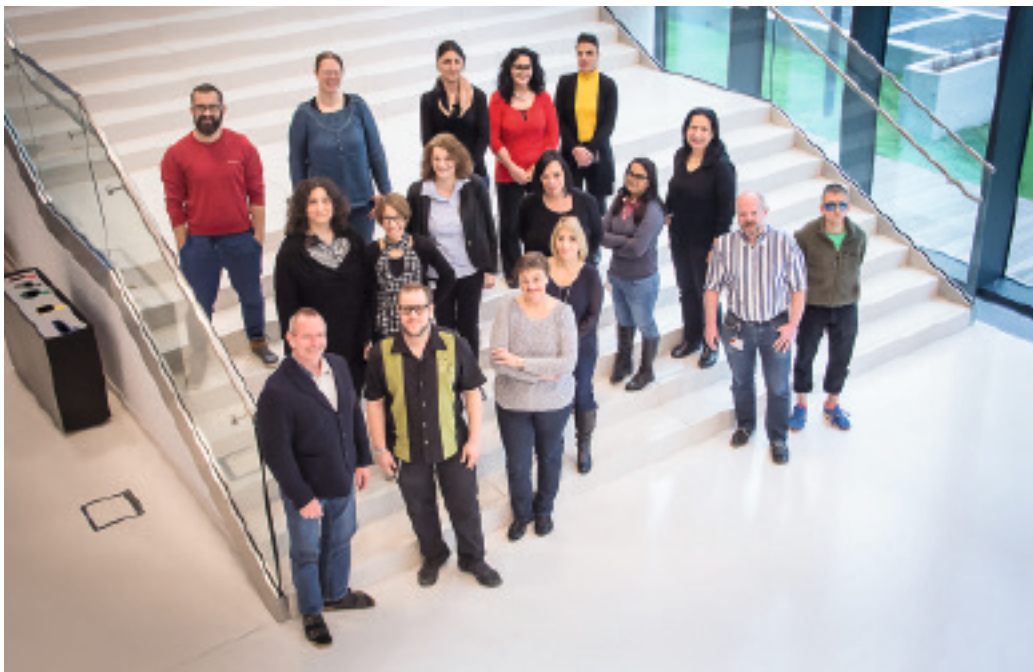
MOLECULAR BIOLOGY SERVICES

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, plasmid prep in 96 well format, and the production of more than 80 growth factors and enzymes. In addition, they 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. They assist with protein identification, characterization of posttranslational modifications, protein quantification, and data interpretation. Additionally, the facility provides peptide synthesis and affinity purification of antibodies. They operate several chromatography systems for both protein and peptide separations and a number of state-of-the-art mass spectrometers.

Molecular Biology Services Staff.



VIENNA BIOCENTER CORE FACILITIES (VBCF)

The VBCF provides advanced scientific services to the GMI and other members of the campus, and also runs the campus child care center. The VBCF is divided into separate units, some of the most important to the GMI are:

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. Together with Youssef Belkhadir, the Advanced Microscopy unit developed a new microscope for measuring the mechanical characteristics of plant cells through Fluorescent Brillouin Imaging (FBi).

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 their 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 two Illumina HiSeq2500s, a MiSeq, and a PacBio Sequel.

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 their chambers is equipped with a robotic plant phenotyping system linked to LemnaTec image analysis software.

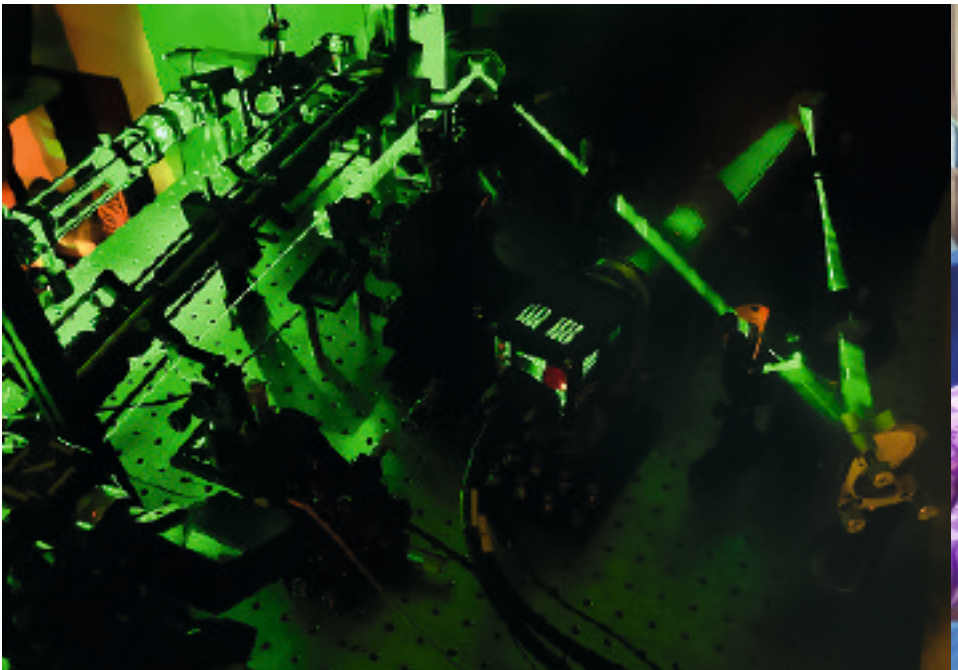
PROTECH

The mission of the Protein Technologies Facility (ProTech) is to help researchers at the VBC overcome two major experimental bottlenecks: protein production and purification. In addition, they 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. ProTech also provides consulting and reagent generation for CRISPR/Cas9 genome engineering through the 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 child's heart desires.

Advanced Microscopy : the Fluorescent Brillouin Imaging (FBi) Microscope.



The Child Care Center at the Vienna BioCenter.

Matthew Watson | Philipp Heinz | Martina Gsur | Barbara Weigel | Erich Birngruber | Johanna Ostah |

17 FINANCE & ADMINISTRATION

HEADS OF FINANCE & ADMINISTRATION

DR MARKUS KIESS
Business Director

DR BORRIES LUBERACKI
Head of Lab Services

DR J. MATTHEW WATSON
Head of Science Support

MIREIA VERDAGUER MSC
Head of Finance

MARIOLA GLAWISCHNIG
Human Resources Officer

ECKEHARD SIEGMANN
Head of IT Services
(CEO net4biz)

MARTINA GSUR
Assistant to the Directors

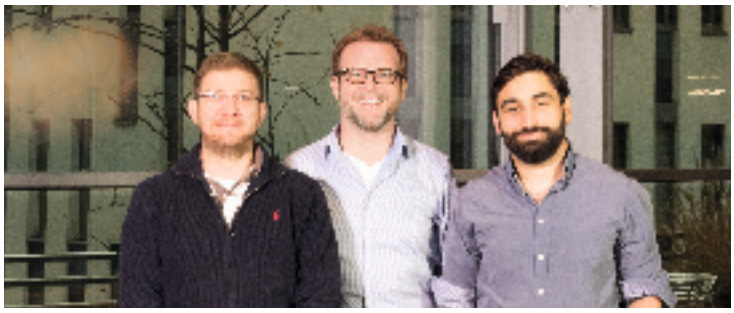
Mireia Verdaguer | Markus Kiess | Mariola Glawischnig | Jens Schaich | Ümit Seren | Borries Luberacki

LAB SERVICES

Jens Schaich
Anneliese Auer
Stefan Ferscha
Borries Luberacki

IT SERVICES (NET4BIZ)

Eckehard Siegmann
Gert Brünner
Thomas Ciganek
Danko Pranjic
Kurt Liebenberg



HPC OPERATIONS

Erich Birngruber
Borries Luberacki
Ümit Seren

17 GMI SCIENTIFIC ADVISORY BOARD

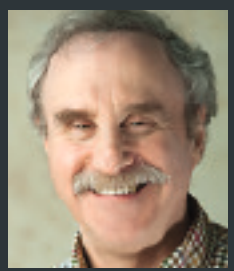
Research at the GMI is annually evaluated by the GMI Scientific Advisory Board (SAB). The SAB comprises independent international experts whose primary role is to provide the Institute's management, and the Austrian Academy of Sciences, with feedback on the quality of the science being undertaken. The 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 is one of the premier plant science institutes in the world and our visit in 2017 confirmed that this reputation is well deserved. We anticipate that several discoveries reported will change the ways the research community thinks about fundamental processes involved in gene regulation, evolution and ecological and environmental responses. New technological innovations we heard about will also change the way plant science is done in the future."

LEIF ANDERSSON
Uppsala University, Uppsala, SE

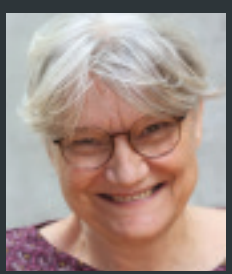
DOMINIQUE BERGMANN
Dept. of Biology, Stanford University, Stanford CA, US

GEORGE COUPLAND
Max Planck Institute for Plant Breeding Research, Cologne, DE



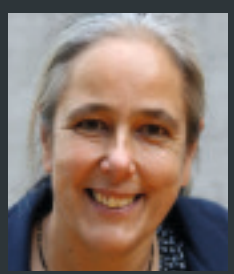
STEVEN HENIKOFF
Fred Hutchinson Cancer Research Center, Seattle WA, US

SOPHIEN KAMOUN
The Sainsbury Laboratory, Norwich, UK



CATHIE MARTIN
John Innes Centre, Norwich, UK

CRAIG PIKAARD
Indiana University, Bloomington IN, US



KARIN SCHUMACHER
Cell Biology, Centre for Organismal Studies Heidelberg, DE

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 770 members and 1,600 employees; it stands for the transdisciplinary exchange of knowledge, innovative basic research, and progress for society. Its headquarters are 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 fulfills two main functions. On the one hand, its 770 members form a scholarly society, advising decision-makers from politics, industry, and society and conveying scientific insights to the public. On the other, it is Austria's major supporter of research outside the university system, funding 28 research institutions in both the natural sciences and humanities. The Academy also organizes events and lecture series, and supports talented young and established scientists alike through its awards and scholarships programs.

ÖAW AUSTRIAN ACADEMY OF SCIENCES

17 PROMOTING THE IMPORTANCE OF PLANT SCIENCE

Our stylized Arabidopsis plant, named Gregor, helps personalize the website, and guides students through the different activities

At the GMI, we consider the public dissemination of our scientific research to be an important objective. In addition to taking part in the Fascination of Plants Day in a cooperation with the Vienna Open Lab, we have two projects aimed at providing a lasting opportunity to engage the public with plant science.

GMI4KIDS

In an effort to further our digital presence, we collaborated with Science Pool, a local organization aimed at bringing the world of science into the classroom, to develop an "edutainment" website that can be used by grade school teachers in Austria to accompany their teaching program by allowing children to explore concepts learned in class through web-based games.

www.gmi4kids.at

BOTANIC QUEST

In collaboration with the Botanical Gardens of the University of Vienna at Rennweg and with funding from the Vienna Business Agency, the GMI developed a mobile phone based scavenger hunt/quiz named Botanic Quest. Players must find plants with specific QR codes attached, read information about the plant or the research from the GMI related to the plant, and then receive points based on how quickly they answer questions associated to what they've read, or see, or smell. Over 1500 visitors played Botanic Quest in the first two months that it was available.

www.botanicquest.at

High school students playing Botanic Quest during our initial testing. The feedback was uniformly positive, "This was better than every museum trip we've taken with the class!"

17 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 eight years in a row (2010-2017)! 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 two 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

GREGOR MENDEL INSTITUTE OF MOLECULAR PLANT BIOLOGY
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OF MOLECULAR PLANT BIOLOGY

ÖAW
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ACADEMY OF
SCIENCES