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GREGOR MENDEL INSTITUTE
OF MOLECULAR PLANT BIOLOGY

ÖAW AUSTRIAN ACADEMY OF SCIENCES

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# ANNUAL REPORT 2018

GREGOR MENDEL INSTITUTE
OF MOLECULAR PLANT BIOLOGY

GMI
GREGOR MENDEL INSTITUTE
OF MOLECULAR PLANT BIOLOGY

# 18 ANNUAL REPORT

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



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# 18 DIRECTORS' STATEMENT

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.

Dr. Magnus Nordborg
*Scientific Director*

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, supported by an efficient administration and world-class services. Like the other institutes that are part of the Vienna BioCenter, 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. Thus, we congratulate one of our Junior Group Leaders, Armin Djamei, on becoming a Research Group Leader at IPK Gatersleben, and two of our postdocs, Danhua Jiang and Takeuchi Hidenori on becoming faculty at the Institute of Genetics and Developmental Biology of the Chinese Academy of Sciences in Beijing, and the University of Nagoya, respectively. The success of departing researchers is one of the most important indicators of our success as a research institute.

We also recruited two new Junior Group Leaders, Arturo Marí Ordóñez and Kelly Swarts, both of whom will start in January 2019. Importantly, Kelly was hired for a joint, tenure-track position with the Max F. Perutz Laboratories of the University of Vienna, the first position of its kind at the Vienna BioCenter.

Dr. Markus Kiess
*Business Director*

Our main indicator is, of course, scientific productivity, and on this front, we believe our publications speak for themselves.

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 Vienna BioCenter; and all our colleagues at the Vienna BioCenter for making this an amazing place to work.

*Magnus Nordborg, Markus Kiess*

# INTRODUCING THE GMI 18

## 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, and developmental biology. While *Arabidopsis thaliana* is the primary model organism in most groups, the focus is on basic biology and a wide range of organisms are studied. 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.

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 Vienna BioCenter Core Facilities. 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 for independant research positions in academia as well as 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)

# 18 GMI RESEARCH GROUPS

BECKER GROUP

BELKHADIR GROUP

BERGER GROUP

DAGDAS GROUP

DJAMEI GROUP

MITTELSTEN SCHEID GROUP

NODINE GROUP

NORDBORG GROUP

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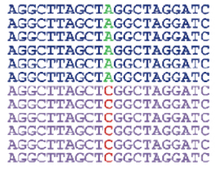



BECKER GROUP

# MECHANISMS OF INTERACTION BETWEEN ORGANISMS

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 an 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, e.g. 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.

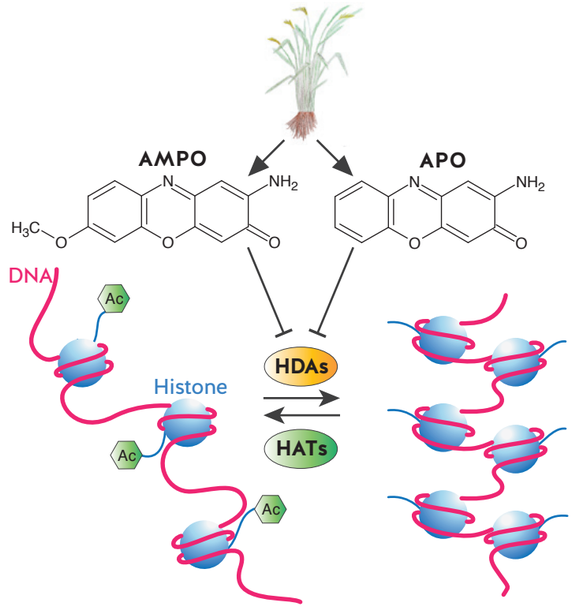
Our laboratory studies allelochemicals that are produced in horticultural and agricultural crops. Upon release from the roots, some of them, such as benzoxazinones, are only mildly toxic but are quickly converted to more toxic compounds in soil (→ Fig. 1). We recently found that once these degradation 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 showed 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 the enzymatic specificity of aminophenoxazinones and the mechanisms of allelochemicals from other plant species, including those of barley and rice. To this end, we analyse global changes over time at the protein and gene expression levels, coupled with biochemical assays using purified proteins. To determine the potency of allelochemicals, we use the model plant *Arabidopsis thaliana* as a readout. For example, aminophenoxazinones inhibit root growth of this species in a dose-dependent manner (→ Fig. 2).

We also use *A. thaliana* for another approach in which we want to identify genes that allow some plants to tolerate allelochemicals. More specifically, we make use of the vast genetic diversity that exists in this species: the GMI is home to a large collection of seeds from more than 1,100 *A. thaliana* plants that were collected from across the Northern Hemisphere (1001genomes.org) and whose genomes have been fully sequenced. We have screened approximately half of this collection and have identified a dozen genotypes that are resistant to aminophenoxazinones (→ Fig. 3). Using

**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.*



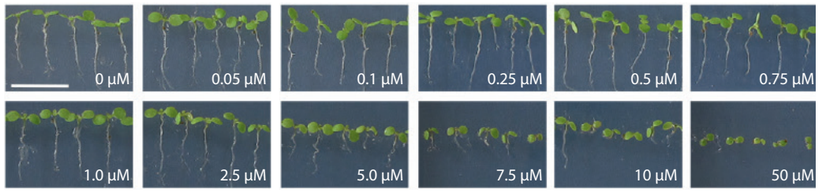
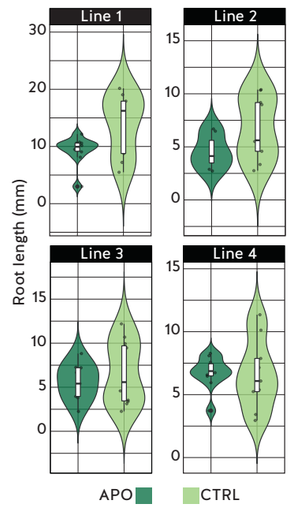




**FIG.2**

Arabidopsis thaliana *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.3**

*Different lines of* Arabidopsis thaliana *show different behaviour in response to allelochemicals. By screening >500 natural genotypes, we identified 10 that were fully resistant to the allelochemical aminophenoxazinone (APO). Each graph shows the root length (y-axis) of one genotype, measured individually for 20 seedlings. Seedlings were grown for 10 days on either APO-containing medium (dark green) or on control medium (CTRL, light green).*



statistical analysis, we are searching for associations between specific genetic variants and increased resistance to the allelochemical to identify genes that are responsible for the resistance.

Our analyses are 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 soil (→ Fig. 4). Using high-throughput, automated culture handling, we are screening approximately 200 bacterial strains, individually as well as in different combinations, for resistance to different allelochemicals (→ Fig. 5). Our goal is to identify bacteria that are able to metabolize and chemically convert the compounds, and that might play a role in detoxifying them in soil.

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.

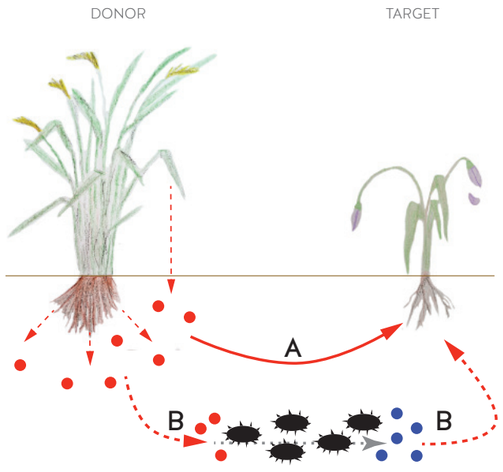



**FIG.4**

*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.*

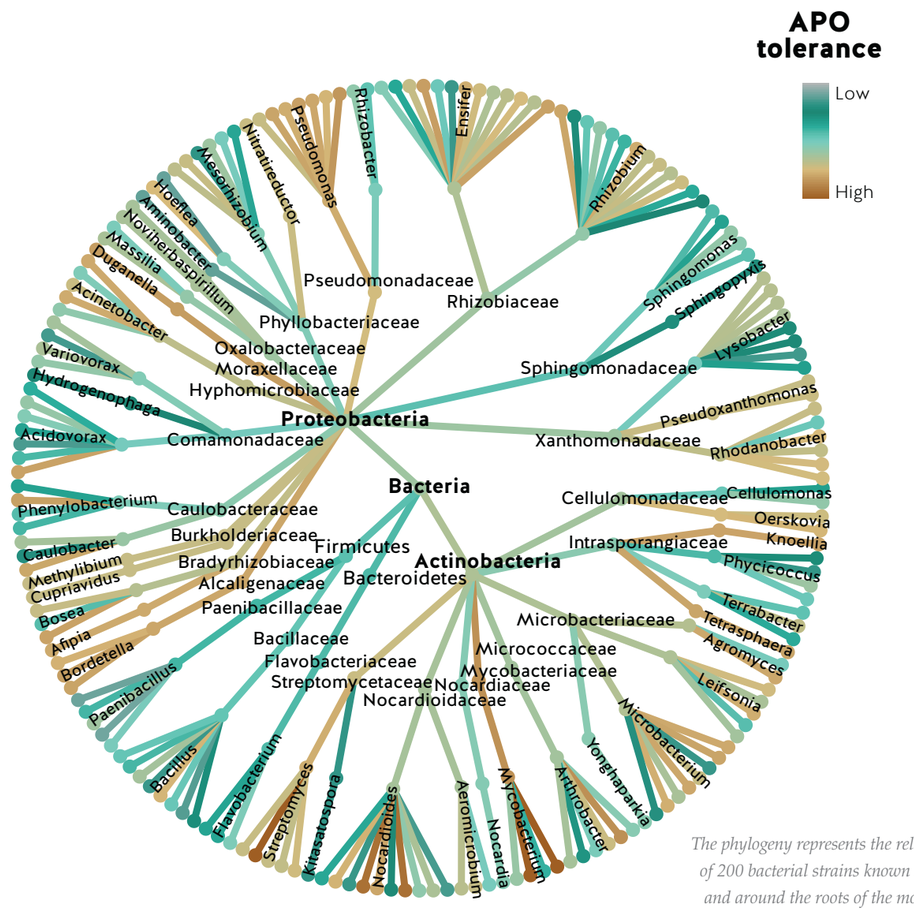



**FIG.5**

*The phylogeny represents the relationship of 200 bacterial strains known to live on and around the roots of the model plant* Arabidopsis thaliana; *each point in the outer circle represents one strain. The colour code indicates the tolerance of the strain to the allelochemical APO when grown in individual culture supplemented with 50 µM of the compound. While some genera do not show variation in terms of response and are either fully sensitive (e.g.* Sphingomonas*) or tolerant (e.g.* Pseudomonas*), other genera, such as* Rhizobium*, show noticeable diversity.*

**YOUSSEF BELKHADIR**

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Joined GMI in Jun 2014

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

**PREVIOUSLY**
- Chief Scientific Officer (2011-2013): Atlas Genomics, Casablanca, MA
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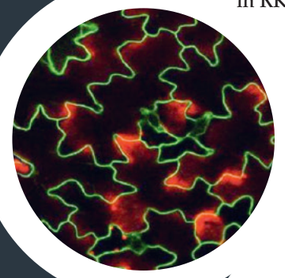
(*left the lab in 2018)

# RECEPTOR CONTROL OF GROWTH AND DEFENSES 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 – if not 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 cutting-edge technologies to discover and explore the interaction properties of RKs with each other or with their putative ligands. Our central goal is to understand how RKs exert their function at the system-level (Aim 1) and to define the role of downstream molecular players involved in RK pathway responses (Aim 2).



## AIM 1:

**System-level analysis of the RK families in *Arabidopsis thaliana*.**

### 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. 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.

### Progress

In the past 4 years, my group has focused on the LRR-RKs to establish a large-scale ECD interaction mapping pipeline. Using our knowledge of protein polishing techniques, we built a recombinant protein library of 400 LRR ECDs. We then implemented an avidity-enhanced interaction assay and tested 40,000 ECD interactions. This screen has resulted in an extracellular interaction map containing 567 interactions with strong predictive power. In the process, we have identified novel sets of molecular players that were missed in forward and reverse genetic screens and targeted proteomic approaches over the past 20 years. Most notably, our efforts surpassed the output of the whole research field over the past two decades by 10-fold. To take our work a step further, we are currently targeting a larger number of RKs with the aim of producing a network-function analysis of greater impact. We have expanded our recombinant protein library with the ECDs of >200 additional RKs and >50 Receptor Like Proteins (RLPs). We started an unbiased robotic screen that will interrogate >200,000 interactions in the coming year. Preliminary results from these new screens indicate that specific families of RKs physically interact with each other while others do not (→ Fig. 1).

## AIM 2:

**Identify and define the function of novel molecular players involved in RK pathway responses.**

### Rationale

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

### Progress

In collaboration with the group of Dr. Wolfgang Busch, we performed >300 GWA studies by monitoring the root responses of 554 natural Arabidopsis accessions to known LRR-RK ligands. For this, we used brassinosteroids (BRs), as well as a set of plant defense peptides that are endogenously produced during biotic stress defense. Our screens were successful, and we identified genomic regions that are associated with the modulation of 14 root traits upon exogenous treatments with these ligands. Using these approaches, we have identified several associations with genomic regions coding for LRR-RK genes. We have also mapped associations with genes coding for Receptor Like Proteins (RLPs). The laboratory is currently establishing causality by using molecular genetics, biochemistry, and cell biology approaches. In addition to these genomic associations involving sensory receptors, we have also identified a sugar influx transporter that acts downstream of RK activation. The activation of this sugar transporter in the reference accession Col-0 is radically different in some natural Arabidopsis accessions (→ Fig. 2). We are currently testing to what extent the activities of this sugar transporter are to restrict pathogen's access to plant sugars or to retrieve sugars to promote plant development.

### 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**

**ECD-based interaction map of RK families.** *Interaction map obtained from 50 x 50 pairwise interaction tests. The heatmap is organized by phylogenetically related families of RKs. (CRs: Cystein-Rich, LysM: Lysin Motif, MLDs: Malectin-like Di-glucose binding, RLPs: Receptor Like Proteins, WAKs: Wall Associated Kinases) Red pixels represent strong interactions.*

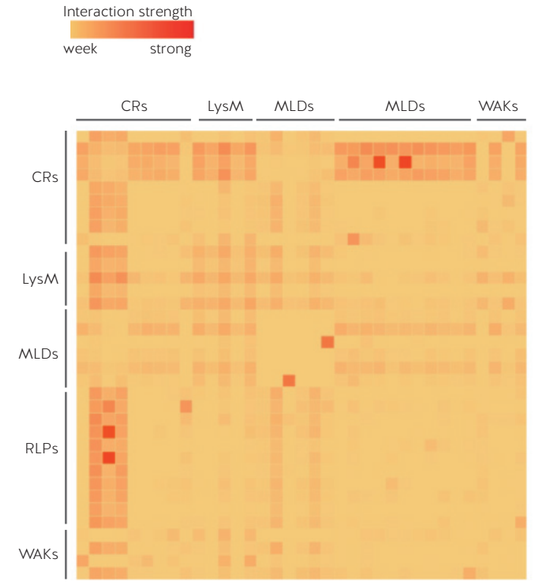
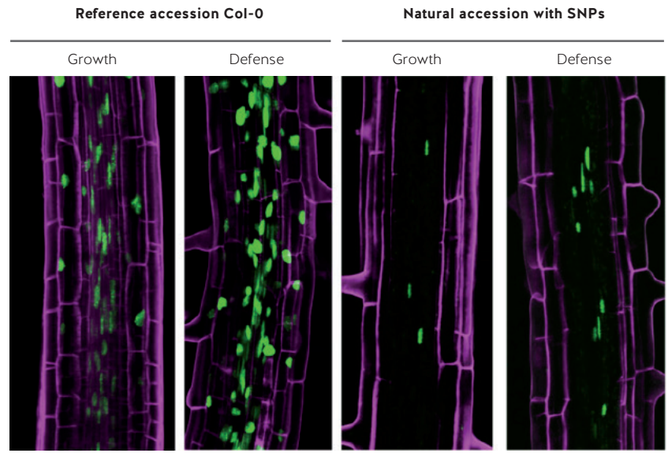
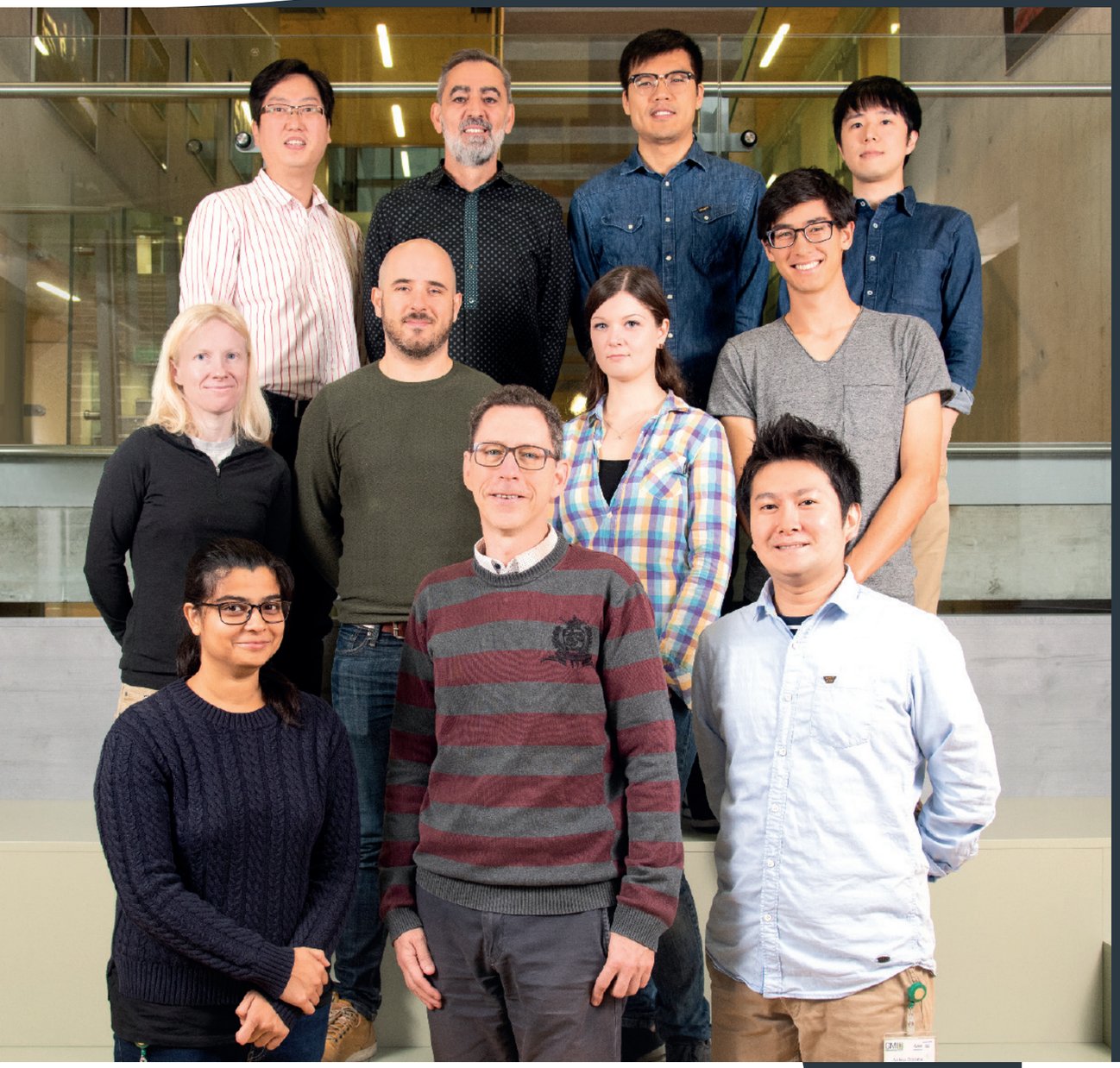



**FIG.2**

**Activation of sugar transport is distinctly wired in natural Arabidopsis accessions.** *Confocal microscopy images obtained by using transcriptional reporter lines that read-out the activity of sugar transport in Arabidopsis roots.*





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Joined GMI in Jan 2014

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

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

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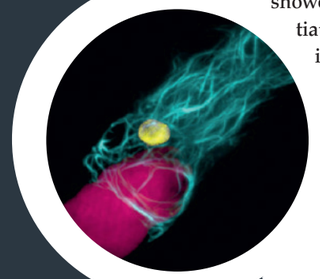
(*left the lab in 2018)

# CHROMATIN ARCHITECTURE AND FUNCTION

The genetic information contained in DNA is organized into functional units assembled in specific territories within the nucleus. This organization is crucial for a proper, balanced expression of the genome. DNA is wrapped around octamers of core histone proteins H2A, H2B, H3, and H4, which form the basic units of chromatin called nucleosomes. Variants of the core histone proteins confer specific properties to nucleosomes and we propose that they provide information that is crucial for genome organization. We focus our work on the roles of histone variants from the H3 and H2A core histones and 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 reprogramming the essential repressing modification H3K27me3. Reprogramming unleashes the pathway responsible for sperm differentiation; we uncovered the key transcription factor involved and showed how its evolution determined the sperm differentiation pathway in the land plant lineage. We are pursuing our investigations on the impact of H2A variants on properties of nucleosomes and their roles in defining functional domains in the genome.



## CHROMATIN REMODELLING AND ERASURE OF H3K27ME3 IN MALE GAMETES

The H3K27me3 mark is associated with prevention of expression of genes that control crucial events during development. For example, suppressors of flowering and flower development that are required to maintain vegetative development are repressed by H3K27me3 to ensure flowering in Spring. Because H3K27me3 is epigenetically inherited, it is essential that this repressive mark is removed after flowering when it is no longer required. The timing and mechanism of 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 several concurrent mechanisms (→ Fig. 1). The most remarkable of these is the sperm-specific expression of a histone H3 variant that is immune to methylation at the K27 residue. We further show a complete reprogramming of chromatin accessibility in sperm cells, leading to the expression of a gene network responsible for sperm cell differentiation under the control of the MYB transcription factor DUO1. The reprogramming of H3K27me3 during male gametogenesis is also responsible for resetting expression of essential developmental genes controlling seed development, flowering, and floral development. These findings unravel a new mechanism of epigenetic reprogramming and an unsuspected set of target pathways that undergo cyclical reprogramming during the plant life cycle.

## EVOLUTIONARY ORIGIN OF SPERM DIFFERENTIATION IN PLANTS

We used the MYB transcription factor DUO1 that drives expression of H3.10 to explore mechanisms underlying the evolution of sexuality. We have identified a substitution, which took place in the algal ancestors of land plants, leading to a new type of MYB transcription factor capable of binding a new cis-regulatory element. Orthologs of this transcription factor eventually formed the DUO1 clade, which is characterised by a specific DNA binding site and target recognition motif. Evolution of DUO1 led to the innovation of a gene network responsible for the differentiation of motile sperm circa 700 Mya. Conjugating green algae, a sister group of land plants, accumulated mutations in the DNA binding domain of DUO1 and lost sperm differentiation. In contrast, the common ancestor of early land plants conserved sperm differentiation and innovated sperm lineage-specific expression of the DUO1 transcription factors. Subsequently, the downstream network of DUO1 was rewired, leading to sperm with distinct morphologies in the diverse groups of land plants. Our findings suggest that the emergence of DUO1 was the defining event in the evolution of sperm differentiation and the varied modes of sexual reproduction in the land plant lineage (→ Fig. 2).

## H2A.W VARIANTS PREVENT EXPRESSION OF TRANSPOSONS

Nucleosomes contain two heterodimers of H2A and H2B. Since there are four main types of H2A variants in land plants, it is in theory possible that a nucleosome contains two types of H2A variants. Yet our biochemical analyses have shown that each plant nucleosome contains a single type of H2A variant. The mutual exclusion between H2A variants was confirmed using Super High Resolution microscopy and chromatin genomic profiling. Additionally, these H2A variants confer distinct properties to their nucleosomes. H2A.W confers the highest stability to nucleosomes while H2A.Z containing nucleosomes are the least stable. H2A.W is specifically associated with constitutive heterochromatin. The enrichment of heterochromatin in transposable elements led us to hypothesize that the highly stable H2A.W containing nucleosomes participate in supressing transposon expression. Indeed, we confirmed that H2A.W acts in synergy with pathways that methylate H3K9 to repress expression of at least half of the transposons that are able to be reactivated. This is a novel pathway, suggesting a direct role of the increased nucleosome stability conferred by H2A.W on chromatin accessibility to transcription factors.

## OUTLOOK FOR 2019

We are further studying the roles of H3 variants in reprogramming specific marks through collaborations.

We are pursuing analyses of H2A variants in dividing chromatin into distinct functional domains and are investigating the roles of specific combinations of H2A variants and H3 modifications in functional chromatins states. The *Marchantia polymorpha* genome was published in 2017 and we have obtained a full assembly per chromosome with defined centromeres and telomeres and profiles of the main chromatin marks. This will be released in January 2019 for the benefit of the research community and will be used by us to study the evolution of the role of H2A variants in the definition of chromatin states. This project represents 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.

Overall our team is focusing on functional studies of H2A variants, their evolutionary origins, their functions, and the mechanisms that regulate their dynamics.

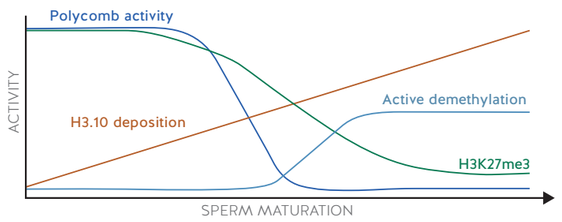



**FIG.1**

*A model of the specific reprogramming of H3K27me3 that takes place during sperm differentiation in flowering plants.*

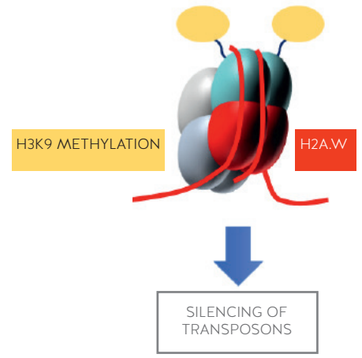



**FIG. 3**

*Joint action of H2A.W and H3K9 methylation on transposon silencing.*

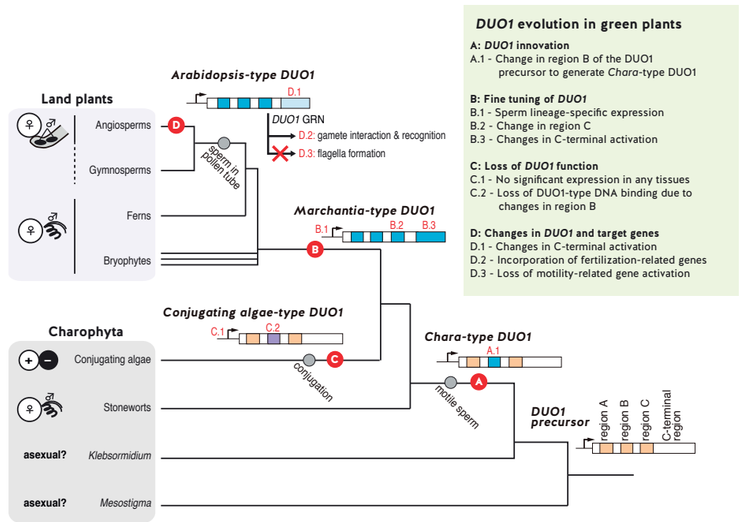
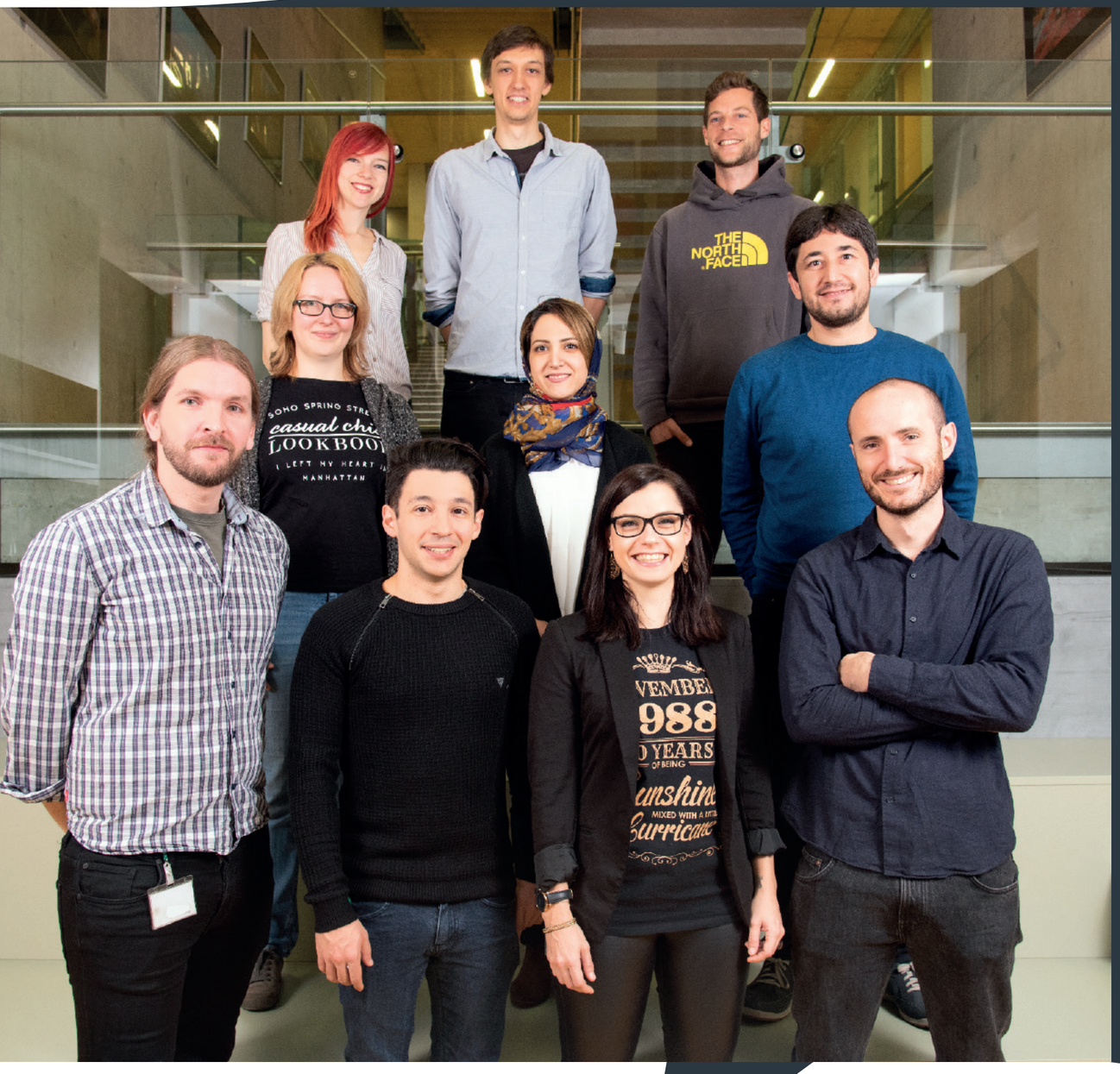



**FIG.2**

*A model of sperm evolution in the plant lineage. 700 Mya an ancestral MYB transcription factor acquired a specific mutation in the DNA binding region B that led to the neo-functionalised transcription factor DUO1 with a new set of gene targets, forming the sperm differentiation network. The model explains how new mutations and the acquisition of a sperm-specific expression pattern took place in ancestors of land plants, leading to the definition of transcription networks controlling the various morphological features of plant sperm.*

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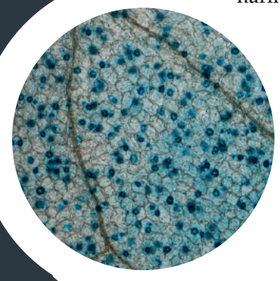
# QUALITY CONTROL MECHANISMS IN HEALTH AND DISEASE

Like us, plants have two types of disease states. The first one is inflicted by pathogens and fought off with the immune system. The second state, which is much less appreciated, manifests as a result of defects in the cellular proteome and organelle contents and is responded to by quality control pathways. Similar to the immune system, quality control pathways closely monitor the integrity of cellular contents and can initiate signaling cascades to either repair damaged components or remove them. In humans, shortcomings in these quality control pathways are associated with neurodegenerative diseases, such as Alzheimer's and Parkinson's, and aging. In plants, however, in contrast to immunity against pathogens, quality control mechanisms and their potential for improving plant productivity is mostly unexplored. Our long-term goal is to study quality control pathways at the single cell and organismal level and leverage this information to improve plant health. Currently, we are focusing on the role of selective autophagy in recycling harmful cytosolic aggregates and damaged organelles.



## SELECTIVE AUTOPHAGY

Macroautophagy (hereafter autophagy) is a conserved cellular quality control pathway that removes unwanted self- and non-self macromolecules to maintain homeostasis in the face of physiological and environmental fluctuations. There is a growing appreciation that autophagy is a highly selective process, with multiple layers of specificity defining the dynamics of uptake, sub-cellular trafficking, and turnover of autophagic substrates (→ Fig. 1). However, despite these advances, the molecular details of how various autophagy cargoes and components are recognized, recruited, and recycled remain to be fully elucidated. In particular, our understanding of the molecular codes that define selective autophagy in plants is limited.

Autophagic cargo sorting involves labeling cargo with non-self tags, such as polyubiquitin chains, followed by selective engulfment into the autophagosomes. 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. 1).

## OUR CURRENT RESEARCH TOPICS INCLUDE:

1) Exploring the contribution of ATG8 isoforms to the compartmentalization of selective autophagy responses
2) Searching for novel selective autophagy receptors, ergo novel autophagy cargoes and pathways
3) Searching for novel autophagy adaptors, ergo the mechanism of autophagosome trafficking and fusion with the vacuole
4) Studying the evolution of the autophagy pathway by comparative mechanistic approaches

## OUR APPROACH:

In *What Mad Pursuit* Francis Crick says: "Classical genetics is, after all, a black-box subject. The important thing was to combine it with biochemistry. In nature hybrid species are usually sterile, but in science the reverse is often true. Hybrid subjects are often astonishingly fertile, whereas if a scientific discipline remains too pure it usually wilts."

Following this invaluable advice, we are trying to combine genetics with biochemical, biophysical, and cell biological approaches to understand the molecular principles of quality control mechanisms, specifically autophagy mediated cellular homeostasis.

**To achieve our goal, through an evolutionary perspective, we are exploring three different scales of specificity:**

1) **Conditional specificity.** Quality control pathways will target different components under different developmental stages and stress conditions.
2) **Cell-type specificity.** As each cell-type has a unique response to intrinsic and extrinsic stress factors, quality control mechanisms will also be wired in a cell-type specific manner.
3) **Subcellular specificity.** Quality control pathways mostly share the same molecular players. To prevent cellular chaos, the cell must have evolved means for subcellular compartmentalization.

## MODEL SYSTEMS:

Although not limited to, we are currently using *Arabidopsis thaliana* and *Marchantia polymorpha* as comparative model systems.

The *Arabidopsis thaliana* root is an excellent model system to perform mechanistic studies at cell-type specific resolution. The genetic and cell biological tools are already established. We are complementing these tools with our autophagy toolbox to analyze spatiotemporal dynamics of autophagy at the three different scales described above (→ Fig. 2).

*Marchantia polymorpha* is an emerging model system that offers many exciting possibilities. It is easy to culture and amenable to genetic manipulation. Most importantly, compared to other model systems it has reduced genetic redundancy and an extended haploid stage in its life cycle. We are particularly interested in exploiting *M. polymorpha* for high-throughput cell biological screens to identify novel autophagy regulators (→ Fig. 3).

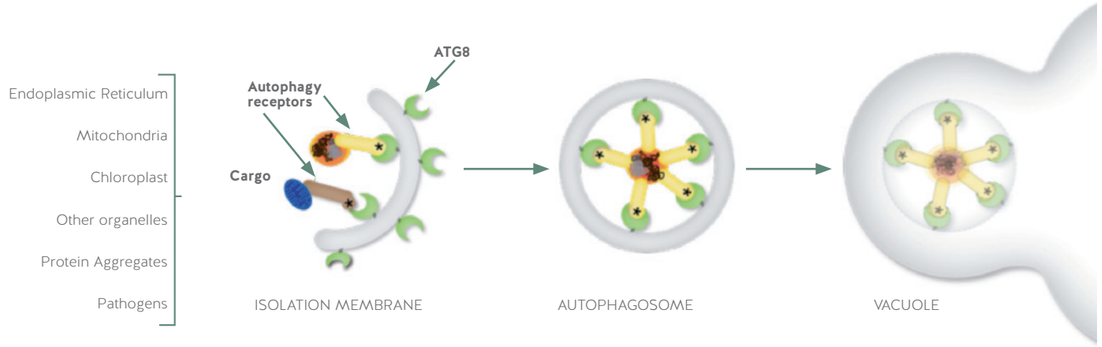



**FIG.1**
*Selective autophagy is mediated by the interaction of autophagy receptors with ATG8 on the growing phagophore. Autophagy receptors recognize and recruit specific cargo into the growing phagophore. Cargoes could be damaged organelles, protein complexes, or pathogens. Autophagy receptors interact with ATG8 via the ATG8 Interacting Motif (*). The contribution of multiple ATG8 isoforms to selective autophagy, the biochemical basis of cargo recognition, and the types of cargoes are poorly understood in plants.*

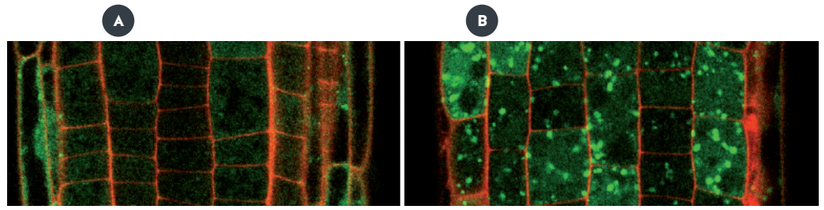



**FIG.2**
*Live cell images of transgenic GFP-ATG8a lines under (A) basal (B) induced conditions. The puncta represent the mature autophagosomes.*


**FIG.3**
Marchantia polymorpha *as a model system to study selective autophagy in plants. Similar to other plant species, autophagy mutants show early senescence phenotypes.*

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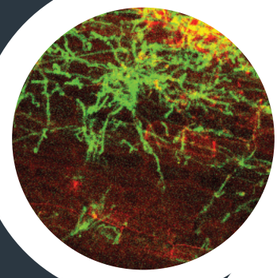

# EFFECTOMICS – EXPLORING THE TOOLBOX OF BIOTROPHIC PLANT PATHOGENS

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 (→ Fig. 1). 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. 2).

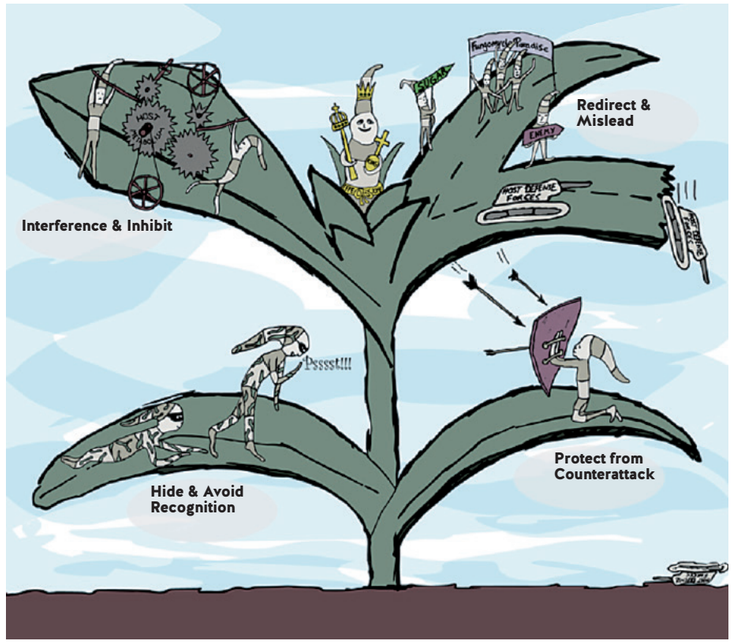


**FIG.1**

*Strategies for successful host invasion. Plant-colonizing microbes employ effectors fulfilling various functions during the host invasion, which are visualized symbolically in this cartoon. (taken from Uhse and Djamei, 2018)*

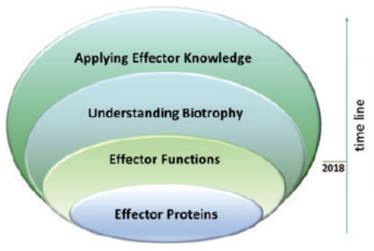


**FIG.2**

*iScheme: 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.*

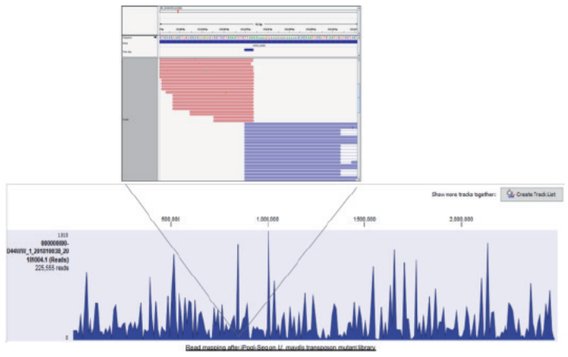

**FIG.3**

*Transposon mutant library covering the whole genome of* U. maydis. *Reads derived from the sequenced transposon mutant pool after performing iPool-seq. In the closeup, the left (red) and right border (blue) reads of the insertion cassette are shown while the sequence aligning with the insertion cassette has been removed bioinformatically.*

Plant biotrophic pathogens developed, over millions of years, fascinating strategies to overcome the host defense system as well as ways to divert the host metabolism (→ Fig. 1). 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. Due to constant co-evolution between the host immune system recognizing effectors and the evasion of recognition by the pathogen, effectors evolve quickly and do not show high sequence similarity among even relatively close species. Additionally, functional characterization of effectors is challenging, as they mostly lack known motifs which could otherwise suggest a putative function. Nevertheless, characterization of these effectors and their host target sites give fundamental insights into the requirements of the pathogen and point to key nodes in the host metabolic network. Effector studies may thus prove rewarding for both pest control and plant breeding.

## *USTILAGO MAYDIS* – MAIZE, AN ESTABLISHED MODEL PATHOSYSTEM

*U. maydis* is a basidiomycete and belongs to the large class of Ustilaginomycetes which comprises more than 1400 species infecting, as biotrophic specialists, a similar number of plant species.

The *Ustilago maydis* - *Zea mays* pathosystem is a versatile model for studying biotrophic grass - fungal interactions. 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* (→ Fig. 2). 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.
This year we published the sensitive method iPool-seq, developed to screen for virulence factors among hundreds of insertion mutants of *U. maydis* infected as a pool into maize plants. Although a technical breakthrough, mutant generation was performed classically by homologous recombination, a reliable but very time-consuming procedure which is not suitable for the generation of thousands of mutants.

A genome-wide virulence map with thousands of insertion mutants is the basis for a more detailed understanding of the factors important for pathogenicity of *U. maydis*. This is important as *U. maydis* serves as a reference for many other fungal genomes due to its relatively well annotated genome. Nevertheless, to date ~40% of all ORFs of *U. maydis* encode for "uncharacterized"proteins and an efficient way to reveal functional links on the genome-wide level will help reduce this number. Aiming to obtain a genome-wide virulence map, we developed an efficient transposon-based method to generate thousands of insertion mutants of *U. maydis* (→ Fig. 3, unpublished). With this key-technology in hand we will now aim to perform pooled infection assays on maize to identify novel virulence factors through negative selection screens.

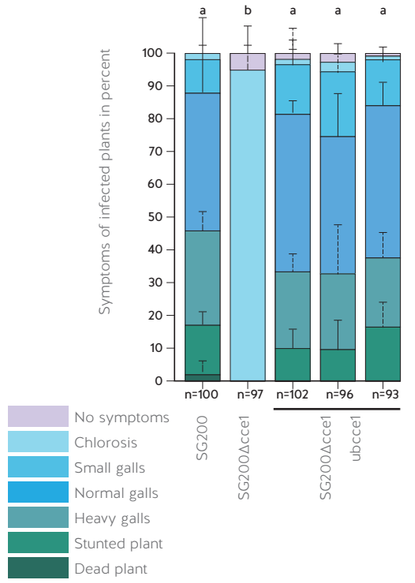


**FIG.4**

*Complementation of the* U. maydis *cce1 mutant with the* U. bromivora *ortholog. Symptom rating of infected maize plants were done 7 dpi. Mean and standard deviation of relative counts from three replicates are displayed. N = number of plants scored. Significant differences between the strains are indicated by a, b. p-values calculated by Fisher´s exact test, MTC by Benjamini-Hochberg algorithm α=0,05*

## CCE1 – A CYSTEINE RICH CORE EFFECTOR OF *U. MAYDIS*

Among the few identified effectors with a strong impact on virulence we identified Cce1. This effector is secreted into the apoplast and upon its deletion the fungus is no longer able to successfully establish biotrophy. We further demonstrated that the effector has orthologs in related smuts that can be used to complement the dramatic virulence defect (→ Fig. 4). The findings were published in Molecular Plant Pathology this year.

## THE PHENOBOX AND PHENOPIPE

In the past years, we have developed tools to study *Ustilago bromivora*, a smut fungus that infects the model grass Brachypodium. In our effort to develop a non-invasive method to quantify infection symptoms, we developed a half-automatized rotating photobox including a full analysis pipeline integrating the previously developed analysis software IAP. This whole system, comprising the so-called PhenoBox and PhenoPipe, is an open source tool published this year. This system enables us to predict infection of Brachypodium several weeks prior to the development of qualitative infection symptoms in the infected spikelets.


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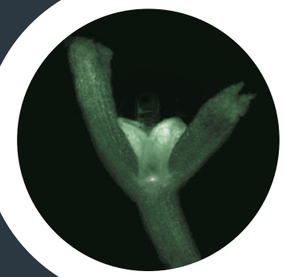

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# GENETIC AND EPIGENETIC CHANGES IN PLANTS

The characteristics of organisms are influenced by two components of inheritance: genetic and epigenetic information. While the DNA sequence of the genome provides the blueprint that is transmitted from one generation to the next, epigenetic factors determine the three-dimensional organization of the genome, transcriptional activity regulating differentiation, development, and adaptation, and stability and defense against intruding DNA and RNA molecules. Using the model plants *Arabidopsis thaliana* and *Aethionema arabicum,* we investigate how development, genome duplication, and environmental factors like heat, light, or genotoxic stress influence chromatin features, gene expression, and epigenetic inheritance, within plants and between generations.

## RESPONSE OF CHROMATIN TO HEAT STRESS

Most genomes contain large repetitive regions that are poorly transcribed. These are densely packed, visible by strong accumulation of DNA stain and therefore called heterochromatin, in contrast to less stained euchromatin that contains most of the active genes. During developmental transitions and in response to different environmental conditions, heterochromatin can decondense, allowing its content to contribute to a cell's RNA pool. Among transcripts from heterochromatin are many derived from transposons, opening a chance for amplification of these "jumping genes". We analyze changes in chromatin composition in response to heat stress, resulting in transient activation of heterochromatic genes, changes in the association of the DNA with histones, and in nuclear shape and organization (→ Fig. 1).

## ROLE OF CHROMATIN AND RNA DURING REPAIR OF DNA DAMAGE

While epigenetic changes are largely reversible, mutations at the level of the DNA sequence are often permanent and mostly deleterious. Plants have several efficient repair mechanisms to deal with DNA damage. Lesions embedded in chromatin need to be made accessible to the repair enzymes, which is achieved by chromatin remodeling complexes (→ Fig. 2). We investigate the role of one such complex during repair of random or induced and targeted DNA damage, the interplay between the protein components, as well as the role of specific RNAs.

## HERITABILITY OF EPIGENETIC CHANGES

Although epigenetic changes are often transient and reversible, there are several examples for the formation of epialleles that are stably inherited in either the silent or active state, even between generations, without being encoded in the DNA sequence. How these epialleles originate and what determines their stability is not clear. We investigate the nature of a pair of epialleles and their paramutation-like interaction in plants with a duplicated genome, a case of non-Mendelian inheritance. We also focus on the epigenetic configuration in the stem cells of the shoot (→ Fig. 3), as potentially heritable epigenetic changes must pass through them to the progeny.

## LIGHT INHIBITION OF SEED GERMINATION

Timing of seed germination is crucial for seed plants and coordinated by internal and external cues, reflecting adaptations to different habitats. Light is an important factor. In contrast to Arabidopsis that requires light for efficient germination, some accessions of the distantly related *Aethionema arabicum* germinate only in complete darkness (→ Fig. 4). We investigate the physiology, molecular biology, and a potential epigenetic basis of this light inhibition and ask whether this is an adaptive trait.

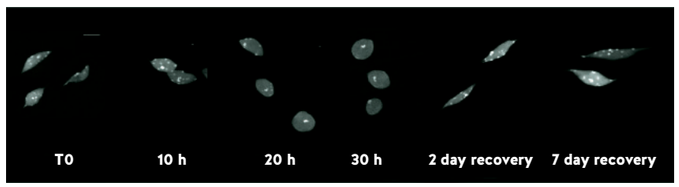



**FIG.1**
***Dynamic nuclear architecture during heat stress***
*Live imaging of nuclei in the root of young Arabidopsis seedlings expressing H2B-RFP, before (T0) and during heat stress (10/20/30 h) and after recovery at regular temperature (2/7 days later). Size bar 10 µm. Photos: Tao Dumur*

**FIG.2**
***Lack of chromatin remodelling impairs growth after DNA damage.***
*Repair-efficient young Arabidopsis seedlings can form true leaves (i) after exposure to DNA double strand break-inducing bleomycin, while repair-deficient plants cannot (ii, left). Mutants lacking components of the SWR1-C complex* (pie1, arp6, swc6) *are significantly impaired in their DNA damage repair, comparable to the repair-deficient* ku70 *mutant (right). Images: Rosa et al. 2013*

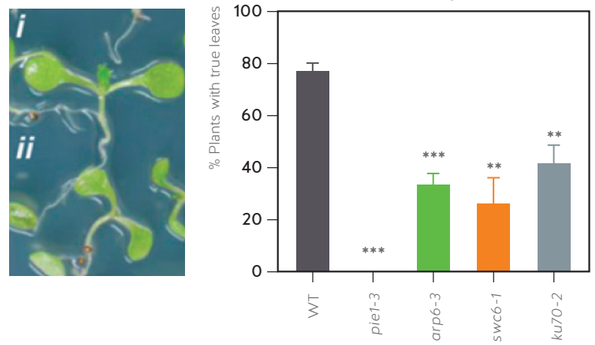



**FIG.3**
***Stem cells in the shoot apical meristem***
*Expression of H2B-mCherry under control of the CLV3 promoter in a young Arabidopsis seedling. Whole-mount immunostaining with mCherry antibodies and laser scanning microscopy. Size bar 10 µm.*
*Photos: Ruben Gutzat*

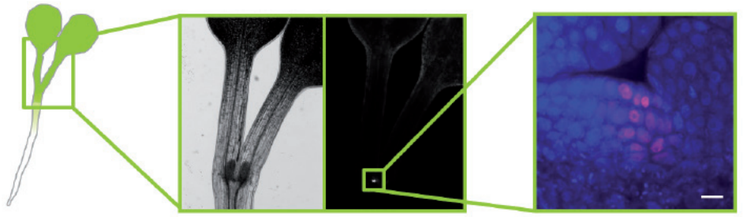
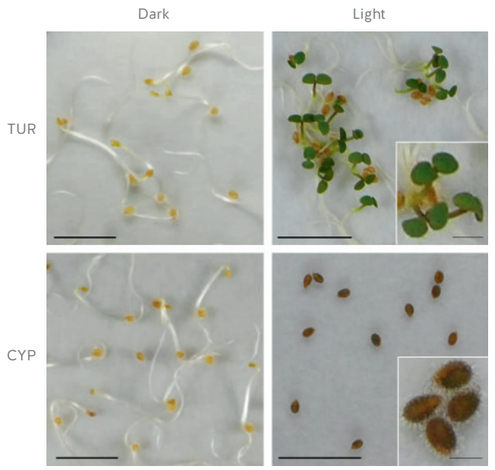
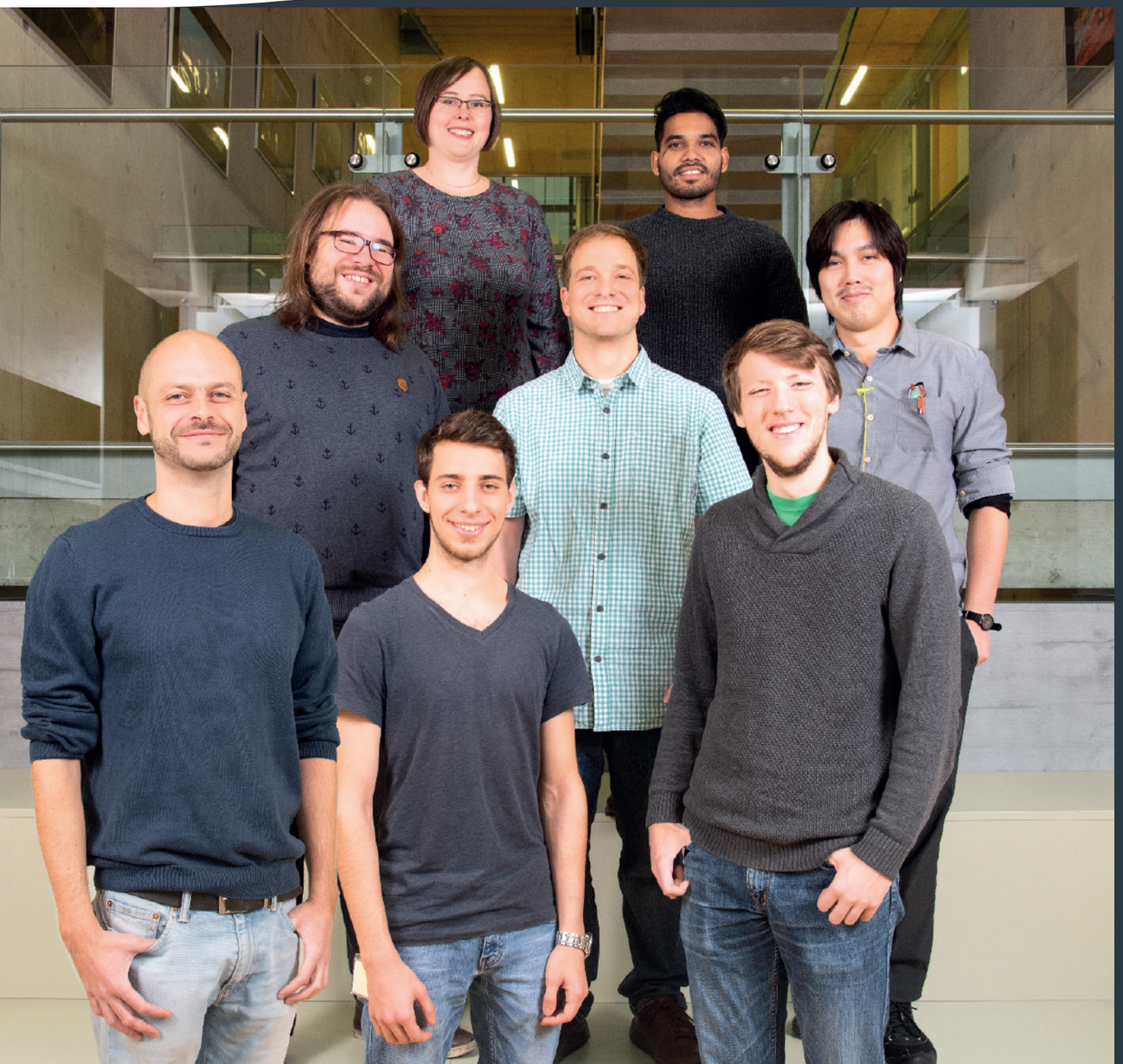



**FIG.4**
***Seed germination in response to light in* Aethionema arabicum.**
*The accession from Turkey (top) germinates equally well in light and darkness; the accession from Cyprus (bottom) is inhibited by light. Size bars 1 cm or 2 mm, respectively.*
*Photos: Zsuzsanna Mérai*



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**TRAINEES**
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Ralf Jansen*
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Anna Smolka
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(*left the lab in 2018)

# DEVELOPMENTAL GENOMICS

Soon after fertilization of the egg and sperm, the zygotic genome is transcriptionally active and drives a series of coordinated cell divisions and gene regulatory programs to establish the basic plant body plan. Although decades of research have deciphered the molecular mechanisms regulating these fundamental processes in animal embryos, 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, microscopy, and bioinformatics approaches to characterize the molecular basis of body plan formation at the beginning of plant life.

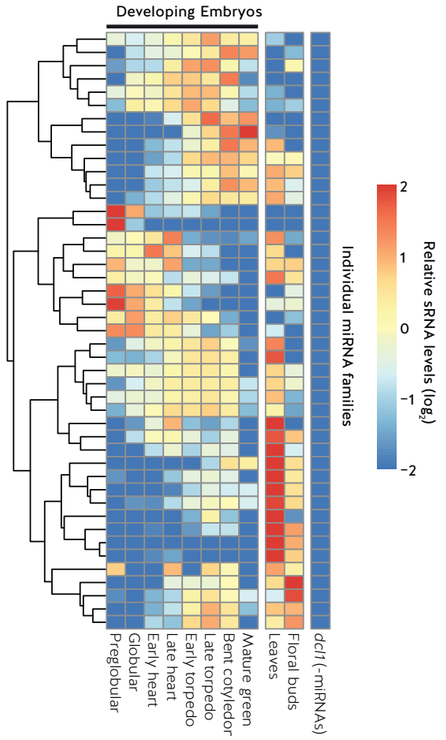



**FIG.1**

***MicroRNA dynamics during embryogenesis.*** *A heatmap illustrating individual miRNA family levels in developing wild-type embryos, leaves and flowers. Small RNA levels in miRNA-deficient* dcl1 *mutant embryos are shown for comparison. Only miRNA families with ≥10 reads per million genome-matching reads during the morphogenesis phase of embryogenesis are shown.*

MicroRNAs (miRNAs) are short non-coding RNAs that regulate gene expression in plants and animals. Although miRNAs are essential for proper differentiation, little is known regarding their embryonic functions, especially in plants. One of our main objectives is to assess the regulatory roles of miRNAs during the establishment of the basic body plan. Plant miRNAs are 20-22 nt long and typically post-transcriptionally regulate protein-coding genes. miRNAs are required to prevent premature differentiation and enable pattern formation during embryogenesis. However, the functions of individual embryonic miRNAs remain mostly uncharacterized. The first step towards systematically characterizing embryonic miRNAs was to identify the miRNAs present in early embryos. Therefore, we optimized a high-throughput sRNA sequencing (sRNA-seq) approach that requires 1,000-fold less starting total RNA than conventional approaches. We then used this method to profile sRNA populations across embryogenesis. We detected hundreds of miRNAs during embryogenesis, and initially focused on approximately 50 miRNA families that were abundant during early embryogenesis (→ Fig. 1).

Biological functions of miRNAs are defined by the genes they regulate. Because plant miRNAs guide endonucleolytic cleavage of their target RNAs, the resulting cleavage products can be detected on a genome-wide scale using methods referred to as Parallel Analysis of RNA Ends (PARE), or degradome, sequencing. Because PARE protocols require 10,000-fold more total RNA than what is obtainable from early embryos, we developed a next-generation sequencing-based method called nanoPARE and associated software, which can accurately detect sRNA-mediated cleavage sites from specific tissue-types (→ Fig. 2). Moreover, nanoPARE enables the identification of transcription start sites at single-nucleotide resolution from single-cell levels of total RNA and is applicable to poly(A) RNA from any species. We utilized nanoPARE to identify >50 miRNA/target interactions operating during embryogenesis. Based on transcriptome profiling, a novel sRNA *in situ* hybridization technique and a fluorescent protein-based reporter system, we found that most miRNAs cleave and repress transcripts encoding transcription factors and this often occurs in specific cell-types. Further genetic analyses revealed that such dynamic miRNA-mediated repression of transcription factors is required to define their spatiotemporal domains and ultimately contributes to the establishment of the body plan (→ Fig. 3).

Altogether, we have developed and implemented an array of methods for the generation of genome-wide molecular profiles and histological analyses of plant embryos. Such tool and resource development has provided a pathway for discoveries regarding sRNA functions and pattern formation. We are beginning to reap the benefits of our systematic efforts as exemplified by our discovery of miRNA-mediated regulation of pattern formation. Together with collaborators from Vienna, Europe, America, and China, we are also applying the next-generation sequencing based methods and software that we have developed on a variety of mutants and rare plant and animal cell-types to test hypotheses pertaining to RNA biology and organismal development.

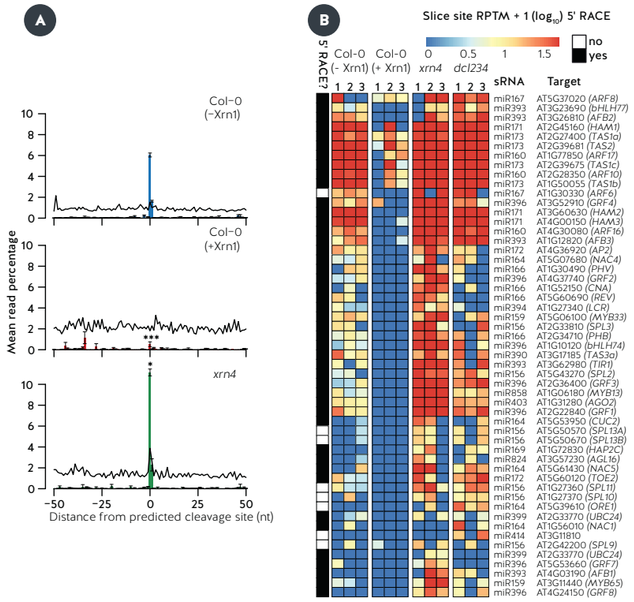



**FIG.2**

***Detection of sRNA-mediated cleavage sites with nanoPARE.*** **A**) *Number of nanoPARE read 5' ends mapping to detected cleavage sites in wild-type floral buds without (Col-0 -Xrn1) or with Xrn1 (Col-0 +Xrn1) exoribonuclease treatment, or in* xrn4 *mutants. As expected for bona fide miRNA-directed cleavage sites, those detected by nanoPARE were either significantly depleted or enriched upon Xrn1 incubation or in* xrn4 *mutant background, respectively.* **B**) *Heat map depicting the number of nanoPARE read 5' ends per 10 million transcriptome-mapping reads (RPTM; log10) mapping to miRNA targets detected by nanoPARE. Small RNA families and corresponding targets are indicated beside each row, and targets previously verified by 5' RACE are annotated. Figure was adapted from Schon et al. (2018) Genome Research*

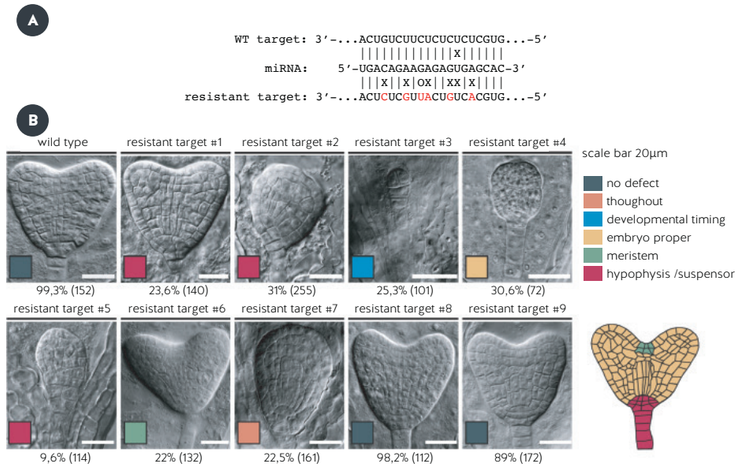
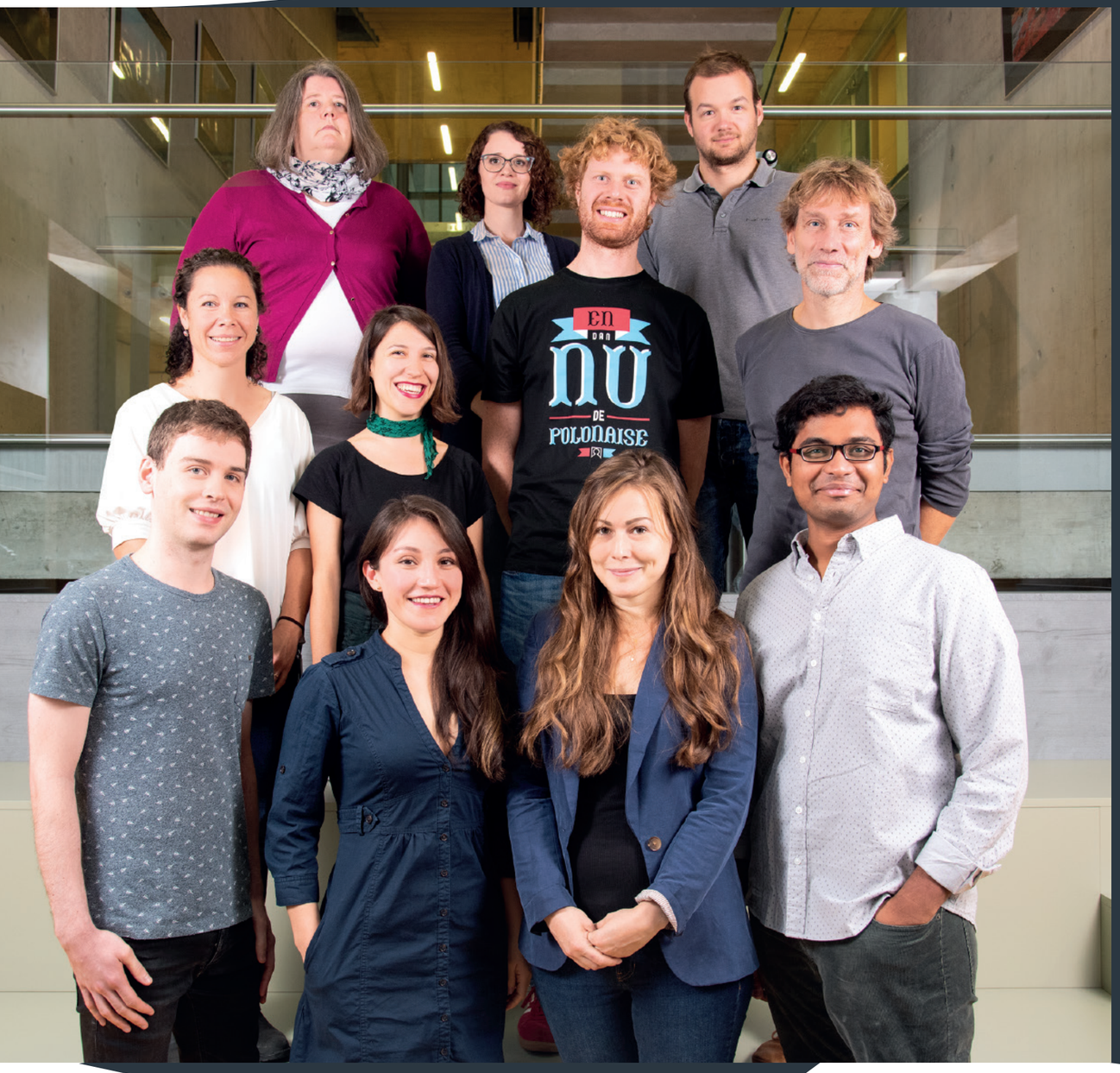



**FIG.3**

*miRNA-mediated repression of transcription factors is required for pattern formation.* **A**) *Diagram showing an example of base-pairing interactions between a miRNA and either its wild-type target (WT target; top) or a mutated version that is resistant to miRNA-mediated cleavage (resistant target; bottom).* **B**) *Representative microscopy images of embryo phenotypes that result from the expression of nine different miRNA-resistant targets. Percentages for the number of embryos exhibiting different phenotypes are shown, and numbers in parentheses indicate the total number of embryos examined. A cartoon of an embryo with different regions is shown and color-coordinated with the microscopy images.*

# POPULATION GENETICS

Our group studies the mechanisms of evolution and uses evolutionary principles to understand biology — from genes to species. We seek to understand variation: 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.

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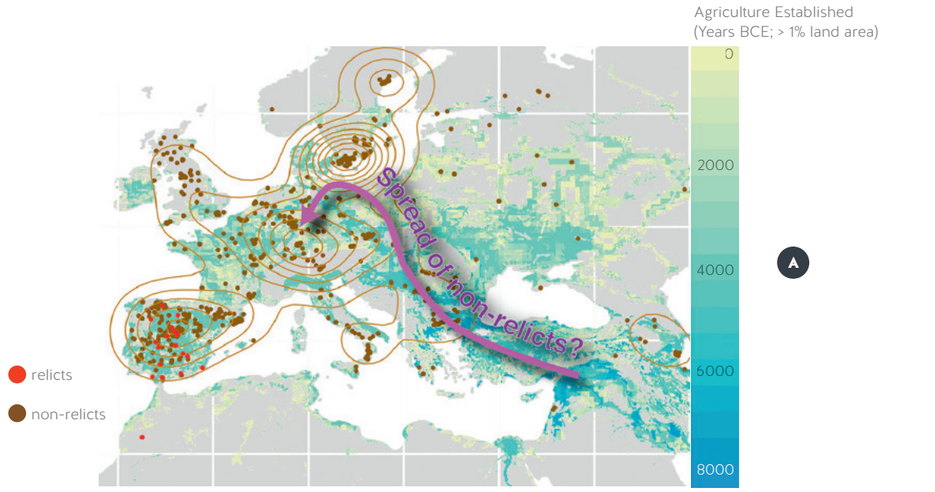
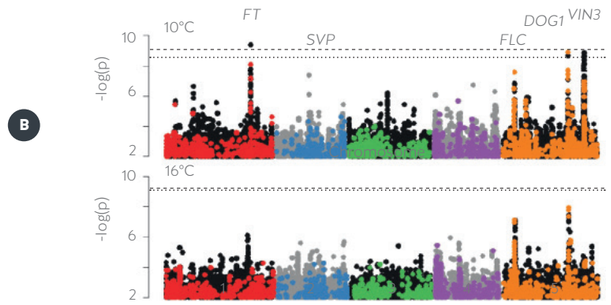
**TRAINEE**
Yalcin Ege Okyar*

**VISITING SCIENTIST**
Masaru Bamba*
Nikwan Shariatipour

(*left the lab in 2018)



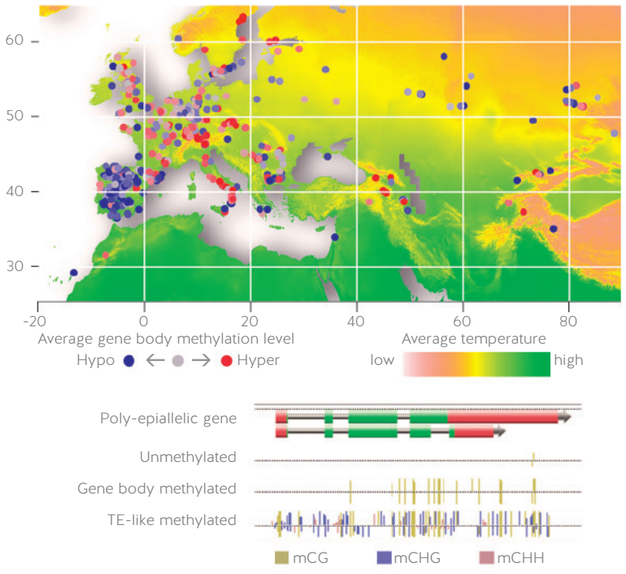




**FIG.1**

**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. It helps us understand how the genome works. 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, producing genomes, transcriptomes, and epigenomes of over 1000 natural inbred lines — a fantastic resource for the genetic community (→ Fig. 1). We are also supporting public websites and databases that allow anyone to carry out GWAS and help coordinate as much phenotypic information.

## THE GENETICS OF EPIGENETICS

Epigenetics continues to fascinate, especially the notion that it blurs the line between "nature and nurture" and could make Lamarckian adaptation via the inheritance of acquired characteristics possible. That this is in principle possible is clear: in *A. thaliana*, experimentally induced DNA methylation variation can be inherited and affect important traits. The question is whether this is important in nature. Our studies have revealed a pattern of correlation between levels of methylation and climate variables that strongly suggests that methylation is important in adaptation (→ Fig. 1c). However, somewhat paradoxically, genetic experiments also showed that much of the variation for this epigenetic trait appears to have a genetic rather than an epigenetic basis. This suggests that epigenetics may indeed be important for adaptation, but as part of a genetic mechanism that is currently not understood. We are trying to determine whether the global pattern of methylation has a genetic or an epigenetic basis, and to use this information to elucidate the ultimate basis for the global pattern of variation: natural selection.

## 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.*

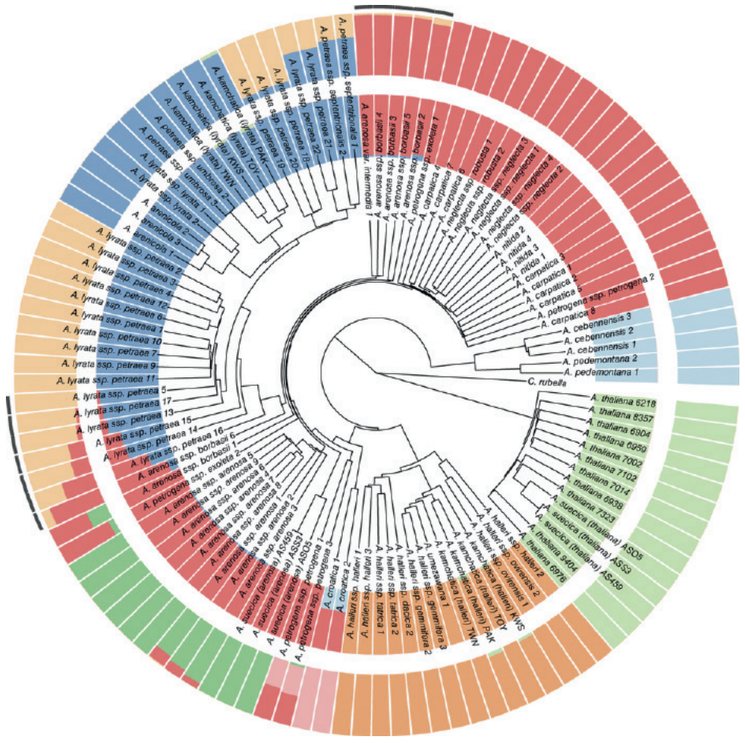


**FIG.3**
*Clustering of sequenced individuals on the basis of polymorphism data. (Novikova et al. Nat Genet 2016).*

**FIG.4**
*Columbine species currently being sequenced by JGI. (Courtesy of Scott Hodges, UCSB)*


## SPECIATION IN THE GENUS ARABIDOPSIS

Differences between individuals within species are micro-versions of differences between species. Understanding the nature of species differences, and the process by which they arise, is a long-standing question in biology — one that modern DNA sequencing methods allow us to tackle using brute force. We are doing this in several groups of organisms, one of them being the genus Arabidopsis, home of the model plant *A. thaliana.* Long-term questions include the evolution of genome size, the effects of polyploidy, and the switch to self-fertilization, but our immediate goal was to understand how genetic variation is distributed across a diverse group of plant species. To this end, we sequenced over one-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).

## SPECIATION 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 by sequencing genomes from multiple species to understand the history and nature of species differences in this genus. We are particularly interested in 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.

## SPECIATION IN AFRICAN GREEN MONKEYS

The African green monkey *(Cercopithecus* sp.*)* is a common Old World monkey, spread throughout much of Africa, and introduced by humans to the Caribbean (→ Fig. 5). 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 virus response.

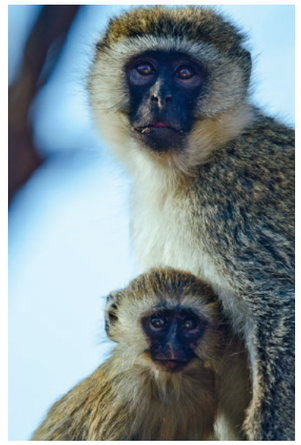
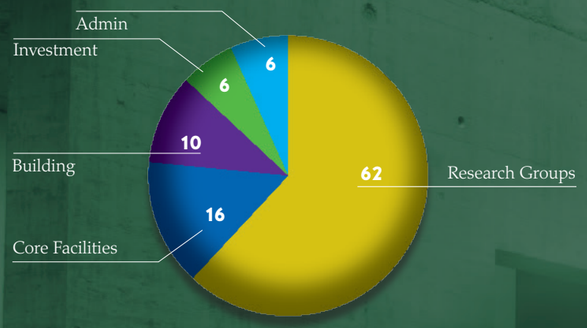



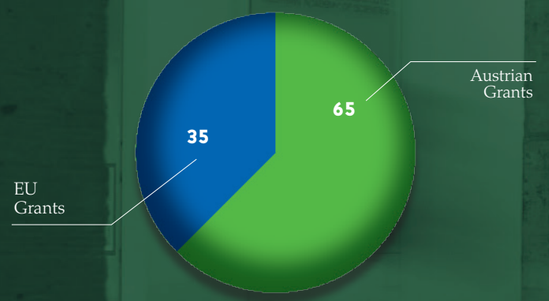
**FIG.5**
*Distribution of vervet monkeys.*

# 18 KEY FACTS *(as of Dec 31, 2018)*

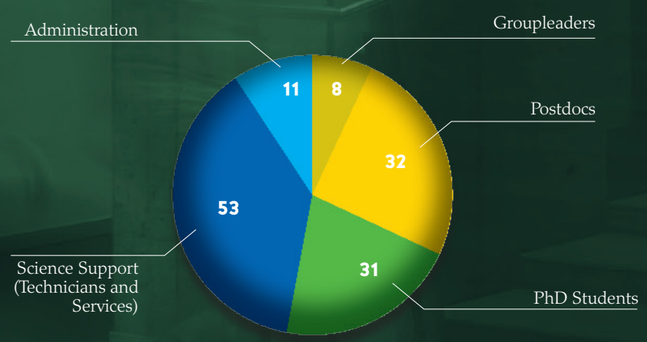
## EXPENDITURES (%)



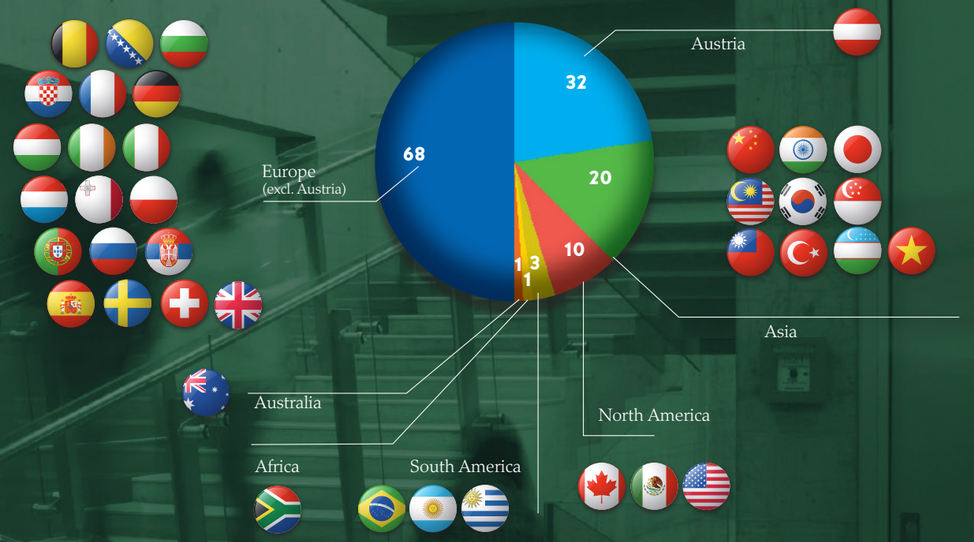

## RESEARCH GRANTS (%)




## STAFF BY FUNCTION (Head Count)




## STAFF - NATIONALITIES (Head Count)



# 18 PUBLICATIONS

## BECKER GROUP

Alonso C, Ramos-Cruz D, Becker C *(2018)* **The role of plant epigenetics in biotic interactions.** *New Phytol [epub].*

Dubin MJ, Mittelsten Scheid O, Becker C *(2018)* **Transposons: a blessing curse.** *Curr Opin Plant Biol 42:23-9.*

Exposito-Alonso M, Becker C, Schuenemann VJ, et al. *(2018)* **The rate and potential relevance of new mutations in a colonizing plant lineage.** *PLoS Genet 14(2):e1007155.*

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Tedeschi F, Rizzo P, Huong BTM et al. *(2018)* **EFFECTOR OF TRANSCRIPTION factors are novel plant-specific regulators associated with genomic DNA methylation in *Arabidopsis*.** *New Phytol 221(1):261-78.*

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## BELKHADIR GROUP

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Smakowska-Luzan E, G. Adam Mott, ..., Belkhadir Y *(2018)* **An extracellular network of *Arabidopsis* leucine-rich repeat receptor kinases.** *Nature 553(7688):342-6.*

## BERGER GROUP

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Wang H, Jiang D, Axelsson E, et al. *(2018)* **LHP1 interacts with ATRX through plant-specific domains at specific loci targeted by PRC2.** *Mol Plant 11(8):1038-52.*

## DAGDAS GROUP

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Gantner J, Ordon J, Ilse T, et al. *(2018)* **Peripheral infrastructure vectors and an extended set of plant parts for the Modular Cloning system.** *PLoS One 13(5):e0197185.*

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## DJAMEI GROUP

Bosch J *(2018)* **Four proposals for a more reliable scientific literature.** *SAJS 114(3):1-2.*

Czedik-Eysenberg A, Seitner S, Ulrich Güldener, et al. *(2018)* **The 'PhenoBox', a flexible, automated, open-source plantphenotyping solution.** *New Phytol [epub].*

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## MITTELSTEN SCHEID GROUP

Capitao C, Shukla N, Wandrolova A, et al. *(2018)* **Functional Characterization of SMG7 Paralogs in *Arabidopsis thaliana*.** *Front Plant Sci 9:1602.*

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Gutzat R, Rembart K., Nussbaumer T. et al. *(2018)* **Stage-specific transcriptomes and DNA methylomes indicate an early and transient loss of transposon control in *Arabidopsis* shoot stem cells.** *BioRxiv:430447.*

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## NODINE GROUP

Gutzat R, Rembart K., Nussbaumer T. et al. *(2018)* **Stage-specific transcriptomes and DNA methylomes indicate an early and transient loss of transposon control in Arabidopsis shoot stem cells.** *BioRxiv:430447.*

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Bouain N, Satbhai SB, Korte A, et al. *(2018)* **Natural allelic variation of the AZI1 gene controls root growth under zinc-limiting condition.** *PLoS Genet 14(4):e1007304.*

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Shibata M, Breuer C, Kawamura A, et al. *(2018)* **GTL1 and DF1 regulate root hair growth through transcriptional repression of ROOT HAIR DEFECTIVE 6-LIKE 4 in Arabidopsis.** *Development 145(3): dev159707.*

Toal TW, Ron M, Gibson D, et al. *(2018)* **Regulation of Root Angle and Gravitropism.** *G3 (Bethesda) [epub].*

Velicky P, Meinhardt G, Plessl K, et al. *(2018)* **Genome amplification and cellular senescence are hallmarks of human placenta development.** *PLoS Genet 14(10):e1007698.*

# 18 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*

**EPPN Transnational Access proposal** (ID 180): in-kind contribution (service and instrument time @ IPK Gatersleben);
*January 2018 – December 2020*

Bacterial activation and degradation of allelochemicals (Lise Meitner fellowship Eva Knoch)
**Austrian Science Fund: M 2482-B21**
€ 169,260
*November 2018 – November 2020*

EMBO Long-Term Fellowship
(Zane Duxbury)
**European Molecular Biology Organization: ALTF 875-2017**
€ 93,667
*April 2018 – April 2020*

## BELKHADIR GROUP

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

Manipulation of plant innate immune responses by small molecules probes
**Vienna Science and Technology Fund: LS17-047**
€ 324,800
*January 2018 – December 2021*

Regulation of growth defense tradeoffs by temperature
**Austrian Science Fund: I 3654-B29**
€ 299,533
*January 2018 - December 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"
**Austrian Science Fund: DK W1238-B20**
€ 142,020
*April 2016 – February 2020*

A mechanism of histone exchange involved in heterochromatin (Lise Meitner fellowship Akihisa Osakabe)
**Austrian Science Fund: M 2539-B21**
€ 169,260
*August 2018 – July 2020*

## DAGDAS GROUP

Manipulation of plant innate immune responses by small molecules probes
**Vienna Science and Technology Fund: LS17-047**
€ 324,800
*January 2018 – December 2021*

## DJAMEI GROUP

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

Characterization of an essential virulence factor in the maize pathogen *Ustilago maydis*
**Austrian Science Fund: P 27818-B22**
€ 255,895
*April 2015 – March 2020*

Host Jump Enabling Factors in a Fungal/Grass Pathosystem
**Austrian Science Fund: I 3033-822**
€ 304,300
*April 2017 – March 2021*

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

## MITTELSTEN SCHEID GROUP

Quantitative live imaging to determine the regulatory impact of chromatin dynamics
**WWTF Life Sciences "New Ventures Beyond Established Frontiers" 2013**
€ 331,350
*Nov. 2014 – Dec. 2018*

Graduate program "Chromosome Dynamics"
**Austrian Science Fund: W1238**
€ 182,800 + € 142,020 (prolongation)
*March 2012 – February 2020*

AUgmented REsilience After Transmission of Epimutations (Ruben Gutzat)
**Austrian Science Fund: I 3687-B25**
€ 302,719
*January 2018 – December 2020*

The role of long ncRNAs during DNA repair in Arabidopsis (Lise Meitner fellowship Nathalie Durut)
**Austrian Science Fund: M 2410-821**
€ 156,140
*May 2018 – April 2020*

The role of temperature for paramutation in Arabidopsis
**FFG FemTech stipend for internship Helene Fasching**
€ 4,200
*August 2018 – October 2018*

**"Indepth" (Impact of Nuclear Domains on Gene Expression and Plant Traits)**
COST action (European Cooperation in Science and Technology)
24 members
*November 2017 – November 2021*

## 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**
€ 339,980
*January 2014 – December 2019*

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

## NORDBORG GROUP

1001 Genomes Plus
**Austrian Science Fund: I 3684-B25**
€ 355,541
*January 2018 – December 2020*

ERC Advanced Grant: Elucidating the causes and consequences of the global pattern of epigenetic variation in *Arabidopsis thaliana*
**European Research Council (ERC): EPICLINES**
€ 2,498,468
*June 2018 – May 2023*

Role of long non-coding RNA variation in *A. thaliana* (Hertha Firnberg Aleksandra Kornienko)
**Austrian Science Fund: T 1018-B29**
€ 234,210
*September 2018 – August 2021*

# 18 VIENNA BIOCENTER INTERNATIONAL PHD PROGRAMME IN LIFE SCIENCES

## EMPOWERING CURIOUS RESEARCHERS

The GMI offers PhD positions within the framework of the prestigious Vienna BioCenter International PhD Programme in Life Sciences, providing students the opportunity to undertake research at the cutting edge of modern plant biology. The Vienna BioCenter PhD 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.

**NEW STUDENTS IN 2018**
Gabriele Bradamante
Dejan Dukic
Vu Nguyen
Lorenzo Picchianti
Isaac Rodriguez
Nuria Serra
Reshi Shanmuganathan
Emiliya Taskova
Marieke Trasser

**GRADUATES IN 2018**
Agnes Eder
Atil Saydere

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 PhD students are funded through Doctoral Programs of the FWF in Chromosome Dynamics and RNA Biology as well as Marie Curie International Training Networks.

Vienna BioCenter PhD PROGRAMME

# 18 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 POSTDOCS (https://www.training.vbc.ac.at)

- Career development workshop
- Career day
- 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 POSTDOCS

- Facing the challenge of effective writing
- Professional development course for young scientists (aka Lab management course)
- Entrepreneurship

## 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








# 18 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. 2018 saw the departure of several PhD students and postdocs. We said „Auf Wiedersehen und viel Glück" in 2018 to:

**JASMIN BASSLER**
*Management Training Program, Shire, AT*

**JANOS BINDICS**
*Senior Research Assistant, IMBA, AT*

**ANGELIKA CZEDIK-EYSENBERG**

**HIDENORI TAKEUCHI**
*Assistant Professor, University of Nagoya, JP*

**DANHUA JIANG**
*Group Leader, Institute of Genetics and Developmental Biology of the Chinese Academy of Sciences, CN*

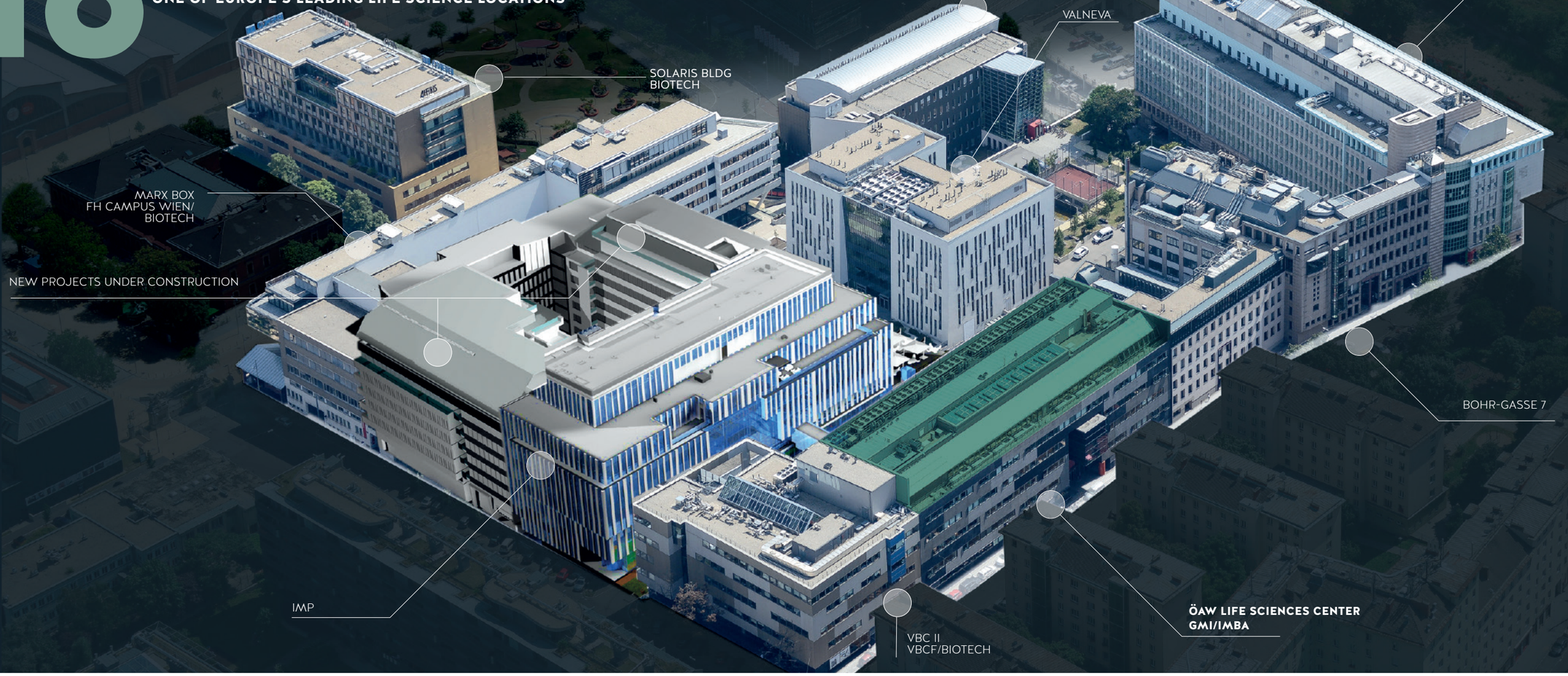
**STEFAN LUTZMAYER**

**ALEXANDER PLOTNIKOVA**

**HAIFENG WANG**
*Business Development Manager, Zeevhan, AT*

# 18 THE VIENNA BIOCENTER

## ONE OF EUROPE'S LEADING LIFE SCIENCE LOCATIONS




Vienna BioCenter

**VIENNA BIOCENTER IS A LEADING LIFE SCIENCES LOCATION IN EUROPE, OFFERING A UNIQUE COMBINATION OF RESEARCH, EDUCATION AND COMPANIES ON A SINGLE CAMPUS: 1700 EMPLOYEES, 1300 STUDENTS, 90 RESEARCH GROUPS, AND 21 BIOTECH COMPANIES. SCIENTISTS FROM 70 COUNTRIES CREATE A HIGHLY DYNAMIC ENVIRONMENT OF INTERNATIONAL STANDARDS.**

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

A growing number of biotech-companies complement the training and research activities and offer important collaborative opportunities to bridge academic and applied research. Moreover, the Vienna BioCenter hosts institutes and companies dedicated to science communication. The publicly funded organization **Open Science** aims at fostering dialogue between science and the public; it runs the **Vienna Open Lab,** which has already provided 45,000 visitors with an interactive glimpse into the Life Sciences.

The passionate and creative **scientists in 90 research groups** have acquired 45 ERC grants, 11 Wittgenstein Awards, and **publish around 350 scientific papers per year.** They are supported by the Vienna BioCenter Core Facilities, which provides access to cutting-edge scientific infrastructure. The successful cooperations, broad expertise of the researchers, and the established infrastructure offer unique working conditions that enable scientists here to operate at the forefront of Life Science research.

# 18 CORE SERVICES

Vienna BioCenter CORE FACILITIES

**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 quantitation, 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.

**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.

*Molecular Biology Services Staff.*

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

*The Child Care Center at the Vienna BioCenter.*

# 18 FINANCE & ADMINISTRATION

## HEADS OF FINANCE & ADMINISTRATION

**DR MARKUS KIESS**
*Business Director*

**DR BORRIES LUBERACKI**
*Head of Lab Services*

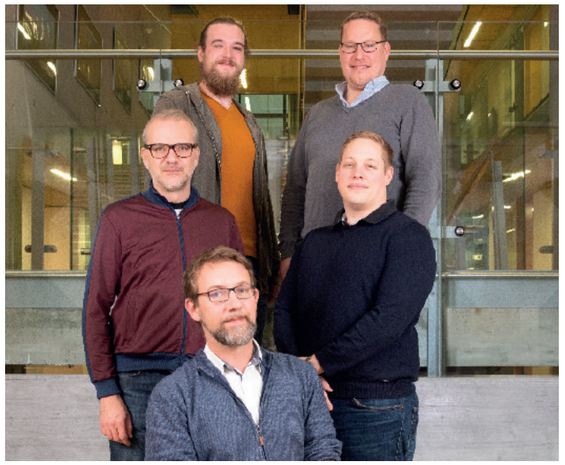
**DR J. MATTHEW WATSON**
*Head of Science Support*

**MIREIA VERDAGUER MSC**
*Head of Finance*

**MAG MARIOLA GLAWISCHNIG**
*Human Resources Officer*

**ECKEHARD SIEGMANN**
*Head of IT Services*
*(CEO net4biz)*

**MARTINA GSUR**
*Assistant to the Directors*



## IT SERVICES (NET4BIZ)

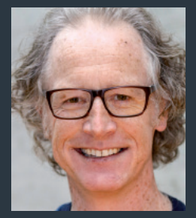
# 18 GMI SCIENTIFIC ADVISORY BOARD

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.

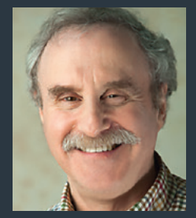
> The long-term investment that the Austrian Academy of Sciences has made in GMI is paying off in spectacular ways. There are few institutions in the world that fund scientists to pursue fundamental research in plant biology at the level of the GMI. Over the years, GMI has developed a great reputation as a center of excellence in plant sciences with contributions ranging from genome-scale analyses to detailed mechanistic research. But most importantly, the GMI has and continues to launch the independent careers of young plant scientists, with many Junior Group Leaders moving on to highly competitive positions in institutions throughout the world.

**LEIF ANDERSSON**
*Uppsala University, Uppsala, SE*

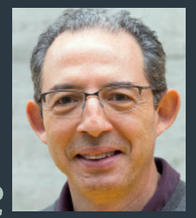
**DOMINIQUE BERGMANN**
*Dept. of Biology, Stanford University, Stanford CA, US*



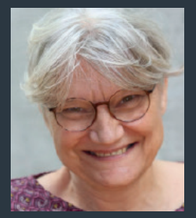
**LIAM DOLAN**
*Dept. of Plant Sciences, Oxford University, UK*



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

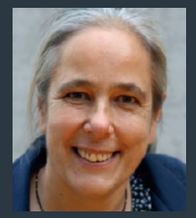


**SOPHIEN KAMOUN**
*The Sainsbury Laboratory, Norwich, UK*



**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

# 18 PROMOTING THE IMPORTANCE OF PLANT SCIENCE

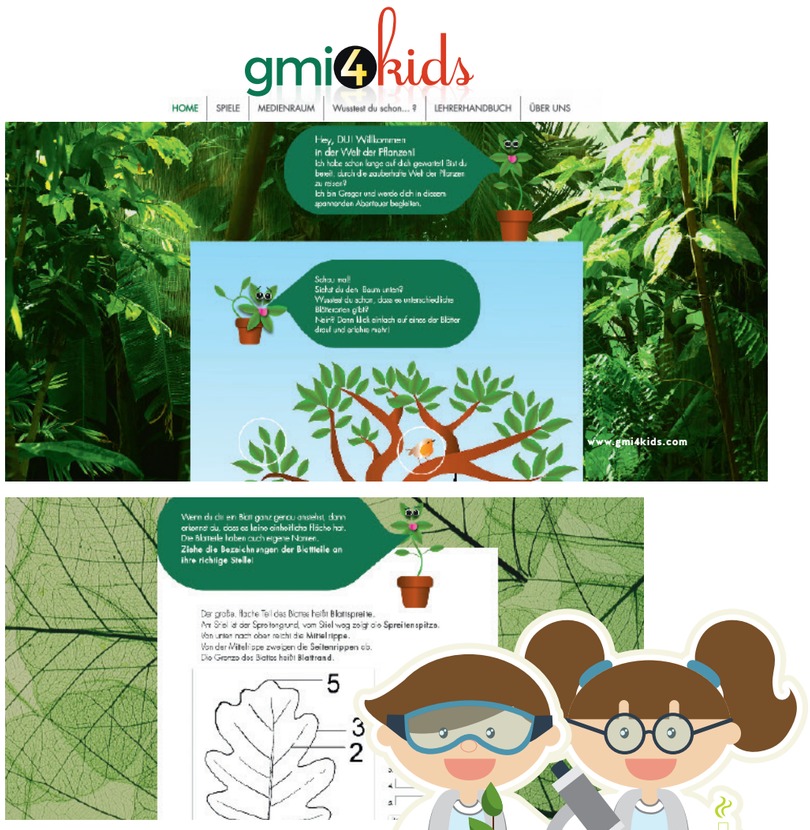
*Our stylized Arabidopsis plant, named Gregor, helps personalize the website, and guides students through the different activities*

**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.com




## 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!"*

# 18 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 nine years in a row (2010-2018)! 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 is a dynamic, multicultural, and cosmopolitan city.




# 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