ÖAW

AUSTRIAN ACADEMY OF SCIENCES

ANNUAL REPORT 2019

GMI

GREGOR MENDEL INSTITUTE OF MOLECULAR PLANT BIOLOGY

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

GMI
GREGOR MENDEL INSTITUTE
OF MOLECULAR PLANT BIOLOGY

19 ANNUAL REPORT

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19 DIRECTORS' STATEMENT

We are proud to be one of very few research institutions worldwide devoted to basic plant biology. The decision to establish such an institute over 15 years ago is looking increasingly visionary given 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. As **plant biology is important to everyone**, we've adapted the format of our annual report this year to make our research more accessible to a broad audience. We've also chosen to highlight some of the many people carrying out this important research.

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. This year we congratulate our two group leaders Youssef Belkhadir, who won the prestigious Science Award Weihenstephan of the City of Freising and Claude Becker on becoming Professor at the Technical University in Munich. Two postdocs also moved on to independent academic positions, Eriko Sasaki who will start as Associate Professor at Kyushu University and Elwira Smakowska who is now an Assistant Professor at Wageningen University. It is worth noting the continued success of those who recently left. For example, Wolfgang Busch (Junior Group Leader until 2017, now Associate Professor at the Salk Institute) helped secure a $35 million grant to fight climate change, and Hannes Svardal (postdoc until 2015) became Research Professor at the University of Antwerp. The success of departing researchers is one of the most important indicators of our success as a research institute.

Our main indicator is, of course, our publications, and on this front, we believe our work speaks for itself.

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.

Dr. Magnus Nordborg
Scientific Director

Dr. Markus Kiess
Business Director

INTRODUCING THE GMI 19

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. The Vienna BioCenter includes three other research institutes: Research Institute of Molecular Pathology (IMP), Institute of Molecular Biotechnology (IMBA), and the Max Perutz Laboratories, 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 epigenetics, transposon biology, population genetics, chromosome biology, developmental biology, stress signal transduction, autophagy, and defense. During the last 20 years, the model plant *Arabidopsis thaliana* has emerged as the primary experimental system for plant molecular biology. While it remains the main model organism at the GMI, we work on plants ranging from the liverwort Marchantia through crops such as maize and wheat to trees. 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.

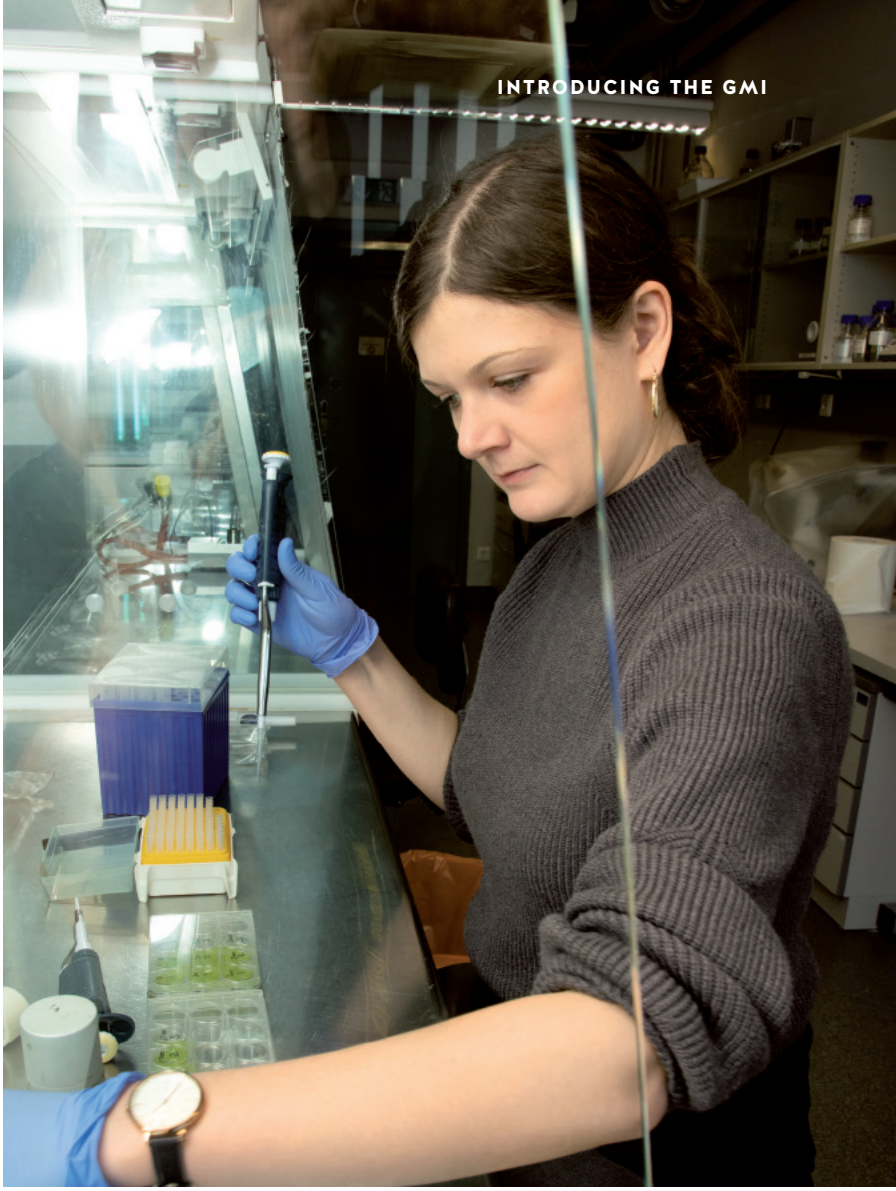
The GMI's research activities are supported by an efficient administration and a world-class scientific infrastructure consisting of the GMI's own services, including state-of-the-art plant growth facilities and a high-performance computing cluster, joint services with the IMP and IMBA, and other core 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, European Union, 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 discov-



ery 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 how histones and their modifications define genomic regions. 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.

> *Plants are not only beautiful and the basis of life as we know it but they are indeed our mysterious distant cousins and the journey towards understanding them is almost like a spiritual quest.* (Ruben Gutzat)

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 40 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.

The GMI strives to achieve a healthy work-life balance, offering flexible working hours and on-site day care facilities.

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.

> *Plants are critical ecosystem components, provide humans with food, medicine, timber and generate the necessary oxygen to sustain most animal life on earth.* (Kelly Swarts)

19 GMI RESEARCH GROUPS

BECKER GROUP
BELKHADIR GROUP
BERGER GROUP
DAGDAS GROUP
DJAMEI GROUP
MARÍ-ORDÓÑEZ GROUP
MITTELSTEN SCHEID GROUP
NODINE GROUP
NORDBORG GROUP
SWARTS GROUP

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Joined GMI in Dec 2016

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CHEMICAL WARFARE BETWEEN PLANTS

Plants almost always grow in a community with other plants and must therefore compete with their neighbors for limited resources such as nutrients, water, light, and space. During evolution, plants have developed diverse strategies to gain advantage over their neighbors. 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 different strategy; they engage in chemical warfare by producing chemical compounds that enter the roots of nearby plants and interfere with 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. Even though many of the chemicals involved 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.

The Becker lab is interested in identifying how these chemicals inhibit the growth of neighboring plants, how the donor plants protect themselves from the toxic chemicals they produce, and whether and how microbes within the soil are involved in processing these chemicals. The knowledge they gain may lead to novel forms of weed prevention which could reduce our reliance on herbicides.

ADVANCES IN 2019

One major theme of the lab is the allelopathic potential of benzoxazinoids, compounds that are produced in many grass species, including major crops such as maize, rye, and wheat. While the actual substances that are produced in these plants are only mildly toxic to other plants, they are rapidly converted in soil to more potent derivatives. The soil microbiome, i.e. the community of microorganisms living on and around the plant roots as well as freely in soil, plays a double role in this process: on the one hand, some of these microorganisms are essential for these conversions to take place, on the other hand these compounds can affect the well-being of these microorganisms and the configuration of the microbial community as a whole. Recently, we have investigated – in collaboration with partners in Bern, Switzerland – how the production of benzoxazinoids affects members of the soil microbiome, and how in turn such an affected microbiome might influence plants growing in the same soil. For example, by testing the growth of nearly 200 culturable bacterial strains isolated from plant roots, we observed that they respond markedly differently to treatments with benzoxazinoids and their derivatives: while some seem ignorant to the presence of the chemicals, others are substantially arrested in their growth. This indicates that part of the root microbiome is sensitive to these plant-derived chemicals, and that in turn these chemicals can potentially disrupt the microbiome of neighbouring plant species. To test whether the chemicals alter the soil microbiome in a way that influences plant growth, we first condition the soil by growing either wild-type, benzoxazinoid-producing maize, or a mutant deficient in benzoxazinoid production. By growing several hundred genetically distinct strains of the model plant *Arabidopsis thaliana* in these same soil conditions and closely monitoring their growth over time, we noticed substantial genotype-by-environment effects: while some genotypes grow equally well in both soil types, others show obvious differences (→ Fig.). In a next step, we will use this information to identify genetic variants that are causal for this differential growth behaviour dependent on the benzoxazinoid-conditioned microbiome.

Barley is yet another crop able to biochemically defend its territory by deploying a whole arsenal of secondary metabolites. Interestingly however, it seems that during barley domestication, the plants' capacity to produce some allelochemicals was lost, while the synthesis pathways of others were retained. The main allelopathic compound produced at considerable levels in many (but not all) modern barley cultivars is gramine. By using a historic crossing population of old barley landraces, we investigate if and how barley is able to tolerate its own toxin. By exposing the roots of barley plants from the different landraces to gramine, we measured a wide range of responses, ranging from complete growth arrest to growth promotion. Next, using genome sequence information from the different landraces and the crosses thereof, we will investigate if gramine tolerance can be linked to levels of gramine production, and search for the genetic components of autotoxicity tolerance.

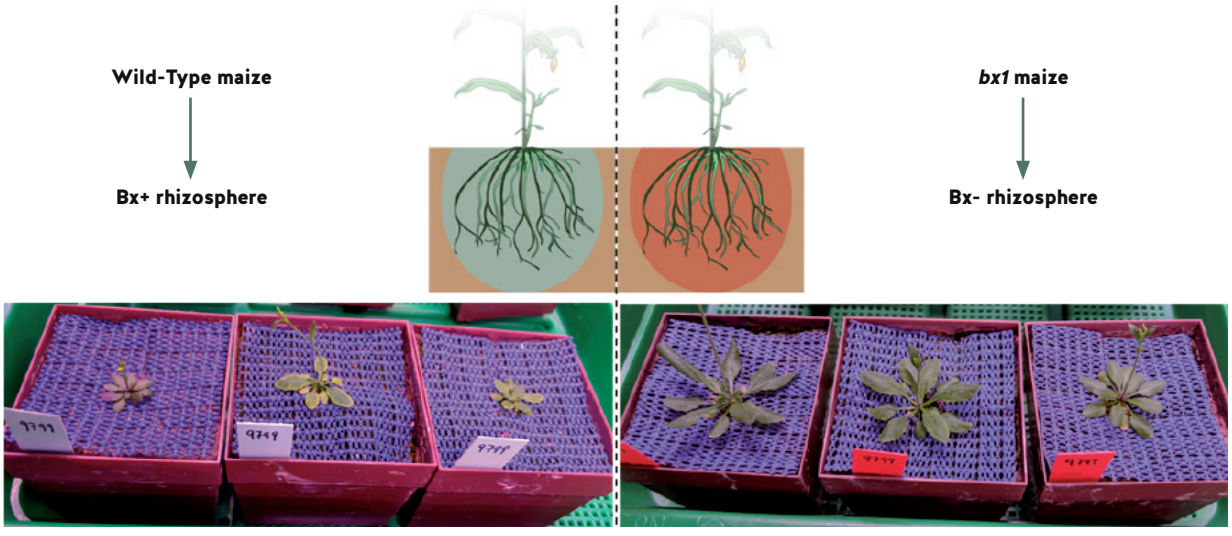

FIG. Response to BX. Arabidopsis thaliana *natural accessions were grown in soil conditioned with either wild-type or benzoxazinoids (Bx) deficient* bx1 *maize, which results in a Bx+ and Bx- rhizospheric microbial community, respectively. Shown here are individuals of the same genotype displaying substantial morphological differences, depending on soil type.*

INSIGHTS

Daniela Ramos, PhD Student
Born in Querétaro, Qro. México, 1988
Studied at Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional (CINVESTAV-IPN), México

How did you come to the GMI?

I heard about the GMI from a postdoc in my previous lab in Mexico who had come to the GMI before. I knew I wanted to do PhD in plant biology in a top-tier institution, so I searched for open positions at the GMI. A lot of groups attracted my attention and matched my interests, but I was especially interested in the group of Claude Becker.

What project are you working on?

In plant communities, plants are exposed to recurrent stresses, such as competition for resources. In competitive environments, some plants release chemical toxins (allelochemicals) to inhibit growth of competitors. I am studying how repeated exposure to allelochemicals can induce a memory of this stress that allows the plant to overcome later exposure. Specifically, I am studying plant memory in response to the allelochemical 2-aminophenoxazin-3-one (APO) in two model plant species; *Arabidopsis thaliana* and *Thlaspi arvense.*

What do you especially like about working at the GMI?

The scientific community at the GMI is very open and friendly. People are always willing to collaborate, help, and discuss ideas.

Where do you want to go next?

I would like to pursue a career in science communication or continue learning and discovering about plant-environment interactions by following an academic path.

YOUSSEF BELKHADIR

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Joined GMI in Jun 2014

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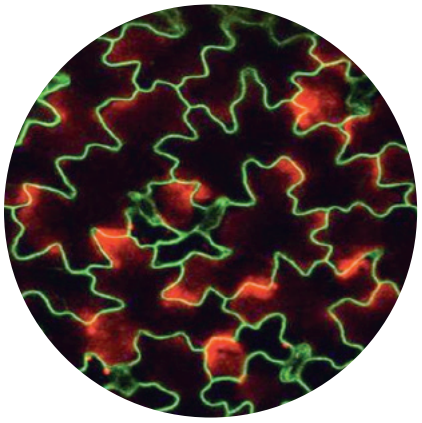
(*left the lab in 2019)

DECISION MAKING THROUGH RECEPTOR KINASES



To grow as efficiently as possible, plants must be able to sense and then respond to their environment. Instead of using sensory organs like animals, our eyes and ears for example, they rely on specialized proteins located on the surface of their cells called receptor kinases. These proteins recognize chemical signals from the environment and then, somehow, help the cell decide how to respond. With more than 600 in Arabidopsis, 10 times more than in animals, these proteins are involved in regulating nearly all aspects of plant development as well as defense against pathogens.

The Belkhadir lab wants to identify which chemicals these proteins recognize, how these hundreds of proteins process the chemical information they receive to decide on an optimal growth strategy for their current environment, and how this strategy is then carried out at the cellular and organismal level. They are especially focused on understanding how plants choose to allocate resources between growth and pathogen defense. The knowledge they gain will help us understand how plants make developmental decisions and could be used to develop plants that grow more robustly and are more resistant to pathogens.

ADVANCES IN 2019

Ligand-receptor pairs in plants have been established either through lengthy genetic studies or by tedious, direct biochemical approaches. These approaches have yielded a very limited number of ligands whose cognate receptors were later identified by genetic approaches. In the past year, we started identifying ligands of plant RKs by using a library of RK extracellular domains (ECDs) to interrogate a massive number of potential ligands, and then assign biological functions to the receptor-ligand pairs we identify. Our approach relies on the interrogation of high-density peptide, chemical, and glycan microarrays.

Pairing receptors with ligands by high density glycan arrays.
Specific RK families have been implicated in binding to various carbohydrate moieties, including plant and microbial cell-wall (CWs) components. Microarrays displaying hundreds of different glycan structures are versatile tools for rapidly analyzing interactions between RKs and CW molecules. Here (→ Fig.), the team has interrogated microarrays displaying synthetic glycans with the ECDs of a subset of RKs and has so far identified 2 glycan ligands.

Pairing receptors with ligands by high density peptide arrays.
To provide a proof-of-principle for the feasibility of our large-scale receptor-ligand pairing approach, the group is currently focusing on a major ligand-receptor pair involved in immunity. Our new experimental and computational analysis revealed that the ECD of the immune receptor has a clear preference for bacterial peptide epitope variants displaying negatively charged amino acids at very precise positions. The group is trying to understand what evolutionary forces are at play in this arms race between plants and bacteria.

Engineering ligands to rationally control RK-signaling and modulate plant cell behaviors.
In conventional chemical genetic screens, small chemicals are used to perturb a biological system to then explore the molecular outcome. Here the laboratory is proceeding in the opposite direction by interrogating molecular interactions of all the RK ECDs included in our library with a comprehensive compound screening deck of thousands of small molecules. Last year, we interrogated the molecular interactions between the ECD of an immune receptor and >20,000 small molecule ligands. We identified 83 chemicals for their ability to interact with the ECD of this receptor of which 14 are able to induce an immune response when exogenously applied to a plant. The systematic understanding of receptor interactions with non-natural ligands has important implications for engineering disease resistance in crops.

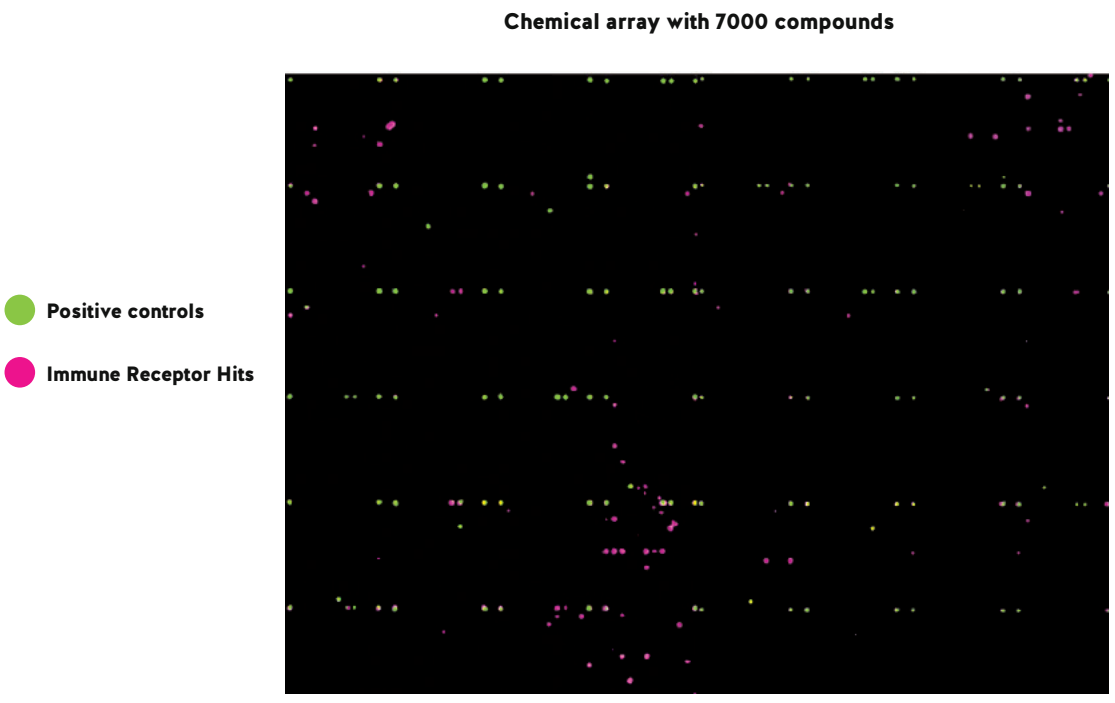
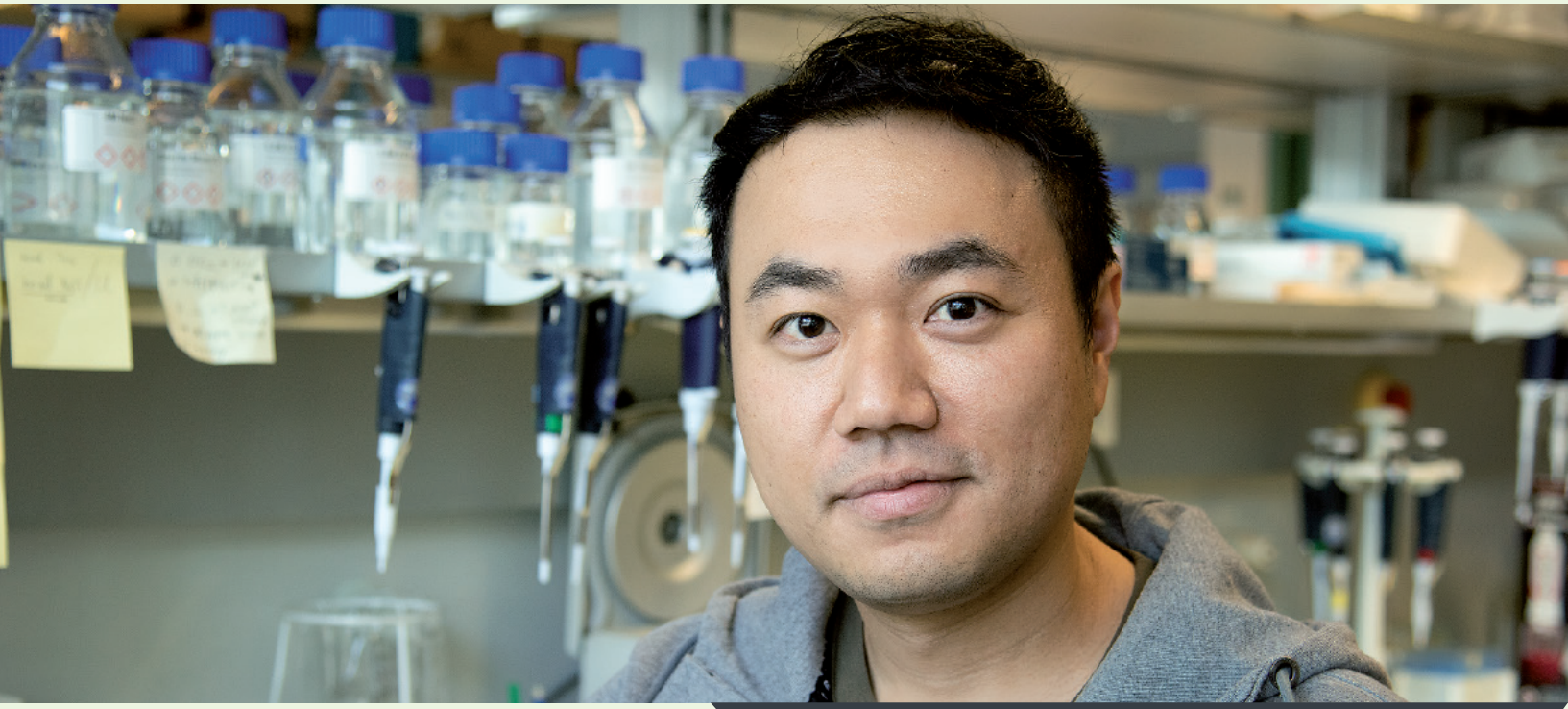


FIG. Interrogation of a chemical array with the extracellular domain of a plant immune receptor.



INSIGHTS

Ho-Seok Lee, Postdoc
Born in Seoul, S. Korea, 1985
PhD from Yonsei University, Seoul, S. Korea

How did you come to the GMI?

I was looking for a postdoc overseas that offered me a topic which could be a promising subject for the future. Also, at the time, I was working on the plant hormone brassinosteroid (BR). The Belkhadir lab was one of the best options due to Youssef's specialization in BR signaling and the role of receptor kinases in plant immunity. Thus, it seemed like a very bright topic for a future career in plant science. In addition, I found that the GMI has incredible support through services such as the media kitchen, Biooptics, Protein Technologies, etc. The large number of scientific support staff was very attractive to me.

What project are you working on?

Understanding how plants make the "decision" to allocate resources between defense and growth is crucial to our quest for an abundant food supply and cheap, dependable sources of energy. To balance this fine-tuned decision between growth and defense, plants perceive their constantly changing environment through Receptor-Like Kinases (RLKs) and Receptor-Like Proteins (RLPs) to relay environmental changes to the cell. These phylogenetically related protein families are involved in multiple aspects of defense and plant development. At the cell surface, brassinosteroid pathways and immune responses triggered by pathogen-associated or damage-associated molecular patterns are presumed to create crosstalk between each other.

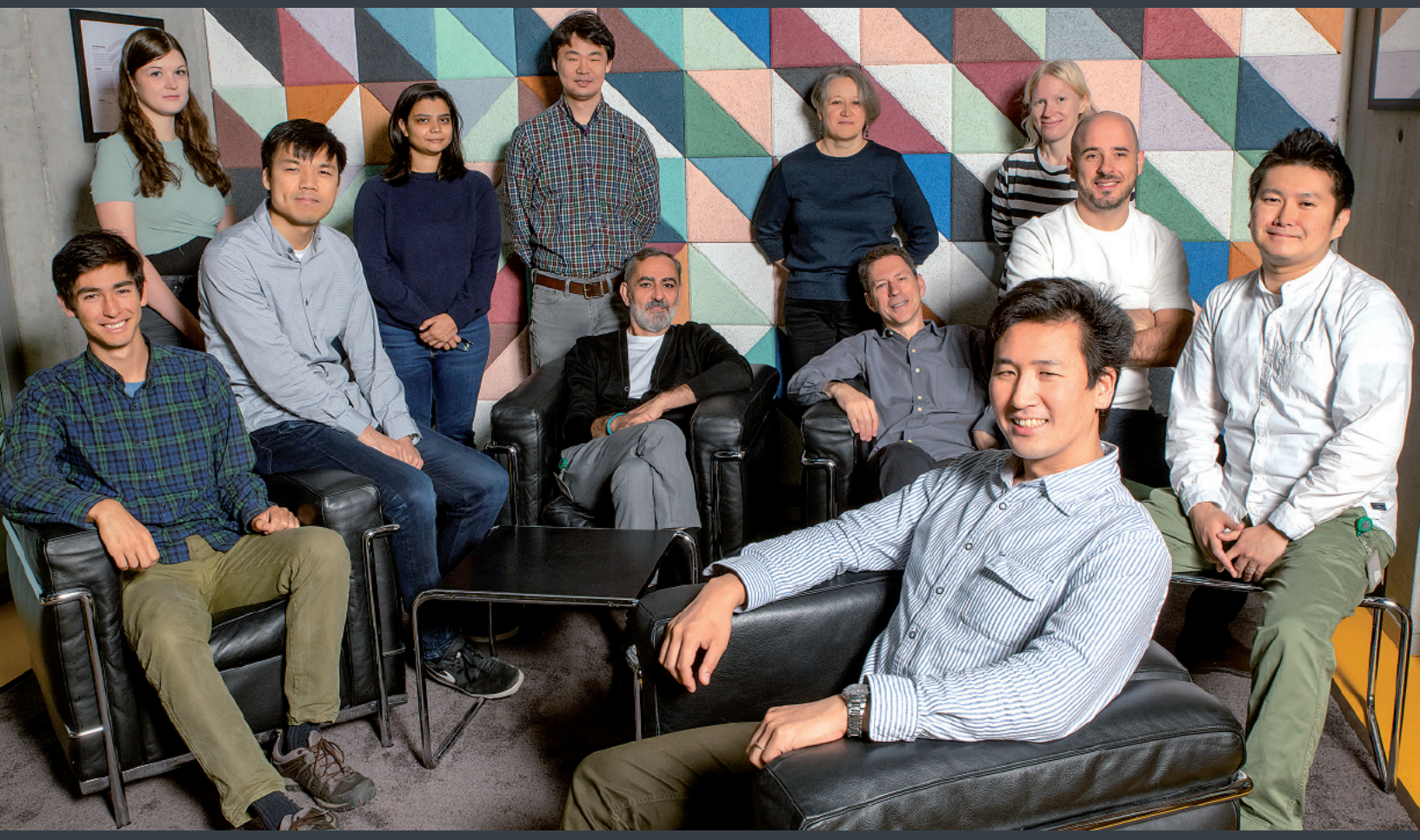
With a Genome-wide association study, we found that a pair of RLPs fine-tune growth and immune signaling.

What do you especially like about working at the GMI?

The massive support from the VBCF and the institute's internal services. Usually, plant institutes have small budgets compared with animal or medical science, limiting our use of the latest machines or technology which are needed for cutting-edge science. This often leads to frustration for many plant scientists. The GMI's access to these services is an amazing benefit.

Where do you want to go next?

My goal is to obtain a position as a principal investigator. There are a lot of a good opportunities for plant science in Europe, but I would like to return to Korea for its people and culture. I am sure that the support I receive from Youssef and the GMI will help me towards this goal.



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Joined GMI in Jan 2014

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

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

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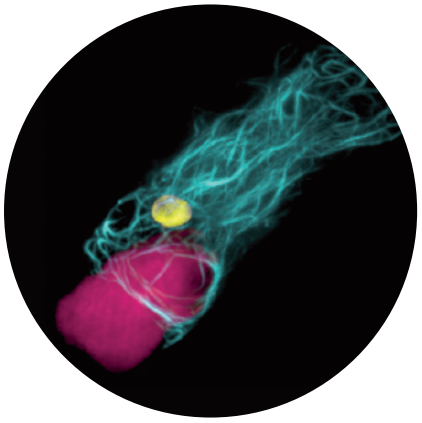
(*left the lab in 2019)

CHROMATIN ARCHITECTURE AND FUNCTION



In both plants and animals, DNA is wrapped around nucleosomes which consist of proteins called histones. Nucleosomes help organize DNA into functional units and are critical for all cellular processes that affect DNA, from copying it when cells divide, repairing it when it becomes damaged, and for enabling access to genes. Several different variants of histone proteins exist and they may modify the structural properties of the nucleosome. Some variants are found only in specific cells, some mark specific DNA sequences, while still others are involved in DNA repair. In addition to these variants, histones can be "decorated" with chemical modifications that can further alter their structural properties, resulting in an almost unlimited number of possible combinations.

The Berger lab is trying to understand the role that different histone variants and modifications play in organizing DNA and how their ability to regulate which genes are turned on and off contributes to development.

ADVANCES IN 2019

Histone H3 variants have distinct expression profiles during the cell cycle and in different tissues, suggesting a functional diversification. In Arabidopsis, H3.3 is expressed and incorporated into chromatin throughout the cell cycle whereas H3.1 is incorporated during DNA replication. H3.1 is essential for the transmission of the chromatin modification H3K27me3 that is deposited by the Polycomb group repressive complex and involved in maintenance of transcriptional repressed states. Surprisingly, H3.1 is excluded from the sperm lineage and instead, a sperm specific H3 variant accumulates in sperm cell chromatin. We have shown that this sperm-specific histone is immune to K27 methylation. Together with the activity of specific JMJ demethylases, the deposition of sperm-specific H3 variants contributes to the global resetting of H3K27me3 but no other histone modifications. Epigenetic resetting of H3K27me3 enables expression of genes responsible for sperm differentiation and licenses transcriptional priming of genes required in the next generation. This novel form of epigenetic reprograming is likely more general in plants that express other still unstudied H3 variants potentially immune to H3K27me3. Hence, we propose that plants evolved H3 variants expressed in specific cell types or in response to specific stimuli with remarkable properties and capacities to reprogram chromatin.

In addition to its primary function in packaging the genome, during eukaryotic evolution, chromatin has acquired regulatory roles including the control of gene expression and selfish genetic elements. The earliest diverging lineages of land plants, the bryophytes represented by liverworts, mosses, and hornworts, diverged from land plants circa 550 Mya. We have obtained a full chromosome assembly of the genome of the liverwort *Marchantia polymorpha.* This revealed that deep changes arose during land plant evolution. In flowering plants, transposons represent 10-90% of the genomes but invariably tend to cluster; most transposons in Arabidopsis are clustered in pericentromeric heterochromatin, clearly delimiting regions of condensed chromatin around the centromeres. In contrast, transposons and genes are spread relatively evenly across chromosomes in Marchantia(→ Fig.). A large number of transposons are associated with H3K9 methylation as shown in flowering plants. However, a quarter of Marchantia transposons are associated with H3K27me3 marked chromatin, which also represents the major component of repressive heterochromatin as defined per HiC analysis, suggesting that heterochromatin in Marchantia is defined by H3K27me3. Recently, H3K27me3 was also associated with transposons in ciliates, which separated from plants and animals more than 1 billion years ago. These findings suggest that H3K27me3 was involved in silencing transposons in early eukaryotes, leading us to reconsider the role of Polycomb marks in repressing developmental genes and the mechanisms that control transposon mobility and their dynamic role in the evolution of eukaryotic genomes.

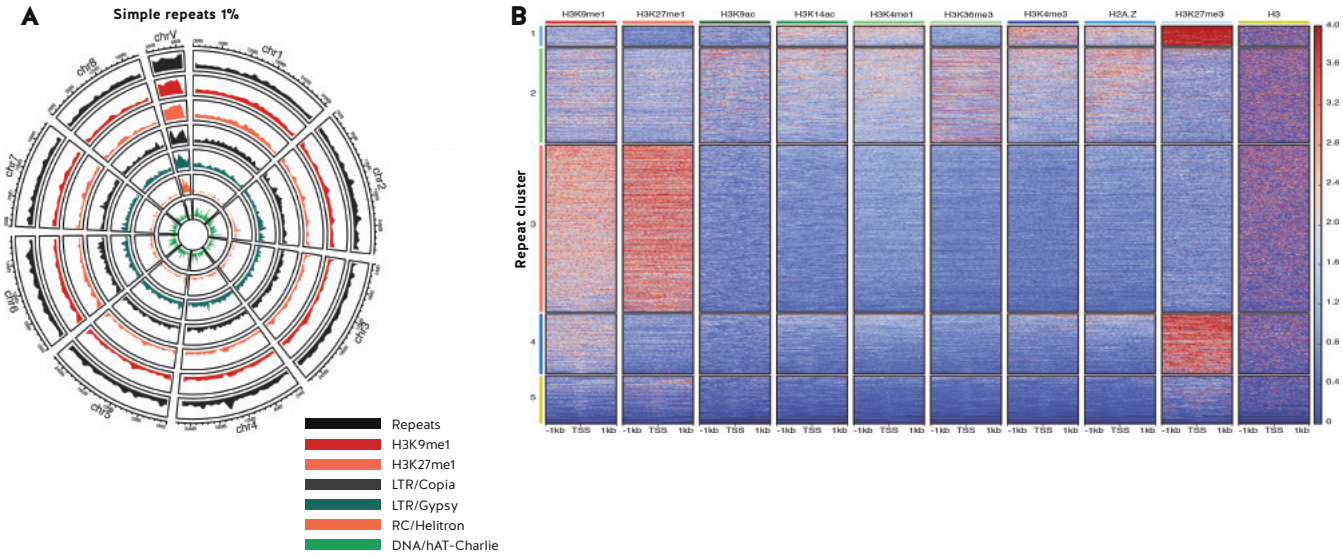


FIG. Organization of transposons and associated chromatin marks in Marchantia.
A *Circos plot of transposons and repressive PTM in Marchantia.* **B** *Association between histone modifications, H2A.Z, and transposon clusters.*

INSIGHTS

Sean Montgomery, PhD Student
Born in Vancouver, Canada, 1993
Studied at University of British Columbia, Canada

How did you come to the GMI?

I went on Google Scholar to search for articles on plant epigenetics to find who the main people in the field were. One of those persons was Ortrun and through her I found out about the VBC PhD Programme and applied to it. During the interview process, I met Fred and he told me he had a project looking at chromatin and epigenetics in Marchantia. I had a long interest in early land plants and evolution, thus the project was and is a perfect fit for me.

What project are you working on?

I am looking into the chromatin organization of *Marchantia polymorpha,* specifically the dynamics between stages in its life cycle.

What do you especially like about working at the GMI?

I enjoy the collaborative atmosphere at the GMI the most. Everybody is quite helpful whenever one needs advice or training or reagents. It expands the network of people you can rely on instead of getting stuck on a problem when the person in the neighboring lab has the solution. Being part of the VBC campus further expands this network and it can be especially useful to discuss and gain insights from people in a diverse array of fields.

Where do you want to go next?

I would like to do a postdoc somewhere else in Europe, though I think I still have some time before that needs to be decided for certain.

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Victor Sanchez De Medina*
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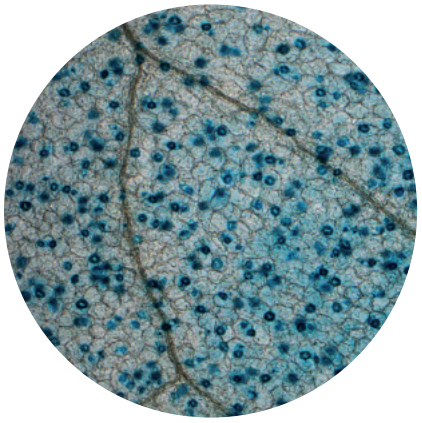
(* left the lab in 2019)

ADAPTATION THROUGH AUTOPHAGY



To respond to environmental changes and pathogen attack, plants have to rapdily modify the protein content of their cells. In both plants and animals, proteins that are no longer needed, as well as those that have been damaged and are potentially dangerous to the cell, can be recycled through a process called autophagy. Autophagy is a critical process for keeping cells healthy and in tune with their current environment. Defects in autophagy have been linked to neurodegenerative and metabolic diseases in humans and a wide range of stress responses in plants.

The Dagdas lab is studying the details of how autophagy works in plants and the role it plays in plant development, stress responses, and immunity. They hope that their findings will contribute to developing plants with improved yield that are more tolerant to environmental stress and pathogens.

ADVANCES IN 2019

In our lab, we combine a variety of mechanistic tools to understand how plants employ selective autophagy to maintain cellular homeostasis. Using Marchantia and Arabidopsis as comparative model systems, we are using a three-layered approach to explore (i) organelle recycling mechanisms, (ii) cross-talk between selective autophagy and other quality control pathways, and (iii) stimulus and cell-type specificity of selective autophagy mediated cellular quality control (→ Fig.).

Over the last year, we have made significant progress on the stimulus specificity and subcellular compartmentalization aspects of our model. Together with the Petersen group in Copenhagen, we found that autophagy functions in many types of cellular reprogramming. Stimuli as diverse as phytohormones, danger signals, and microbial elicitors all trigger rapid and robust activation of autophagy. Using quantitative proteomics, we show that autophagy mediates the switch between somatic cell programs by removing unnecessary cellular components. At the same time, autophagic mechanisms ensure the controlled execution of the newly established programs. Accordingly, autophagic dysfunction leads to defects in organismal fitness, dedifferentiation of somatic cells into pluripotency, and redifferentiation of pluripotent cells into other cell types.

We have also shown that diversification of ATG8 isoforms in plants underlies functional specialization. We used quantitative biochemistry and proteomics to explore the molecular basis of ATG8 specialization. First, we used IP-Mass Spec to determine that the six ATG8 isoforms in potato bind distinct sets of proteins with varying degrees of overlap. Domain swaps and structure-guided mutagenesis experiments revealed that a recently derived polymorphism within the N-terminal β-strand of ATG8-4 underpins weak binding affinity towards the well characterized autophagy receptor mimic PexRD54 and contributes to enhanced selectivity towards AIM-containing proteins. Our findings are a first step towards decoding the molecular signatures that define selective autophagy in plants. We propose that ATG8 specialization is an important specificity layer that determines the recruitment of cellular proteins to modulate selective autophagy pathways.

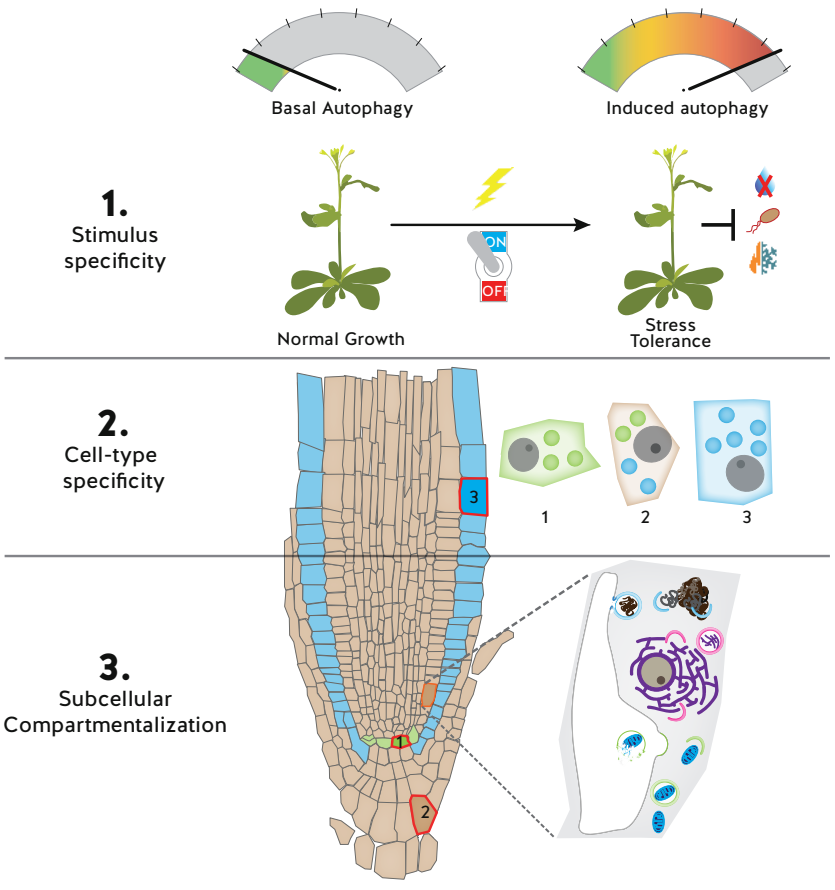


FIG.

A three layered approach to study selective autophagy.

1 *Stimulus specificity. Selective autophagy functions as a toggle switch between different growth and stress conditions. During these switches the degradome is determined by the stimulus, and highly specific.*

2 *Cell-type specificity. Each cell type has a different need for autophagy, as they have distinct physiological and metabolic conditions. Here depicted with different colored autophagosomes are quiescent center (1), lateral root cap (2), and epidermal (3) cells..*

3 *Subcellular compartmentalization. Various selective autophagy processes happen concurrently in a cell. ATG8 isoforms could facilitate compartmentalization of these responses by differential binding to different selective autophagy receptors and accumulating at different cellular compartments. The root cartoon was adapted from http://www.ens-lyon.fr/RDP/SiCE/Resources.html.*

INSIGHTS

Madlen Stephani, PhD Student
Born in Halle, Germany, 1991
Studied at Martin-Luther University Halle-Wittenberg, Germany

How did you come to the GMI?

Vienna was ranked the most liveable city in the world for several years in a row and its reputation for top research, especially at the Vienna BioCenter, was recommended to me by fellow students and a professor at my former university.

After starting my PhD, I realized that my project did not really suit me. With the great support of the VBC's PhD coordinator, I undertook rotations in different labs. When I started at the GMI in Yasin's group, I felt warmly welcomed and was totally inspired by the new project. This convinced me to stay here.

What project are you working on?

My project is concerned with a recycling pathway, named autophagy, which helps the endoplasmic reticulum cope with stress. This pathway is highly conserved and its malfunction leads to low stress resilience in plants and fatal diseases such as colon cancer in humans. This lethal phenotype makes investigations in human cells difficult. In plants however, we can easily dissect and probe the whole machinery. In this way, we are currently making rapid progress and found that the pathway seems to be regulated by a novel post-translational modification.

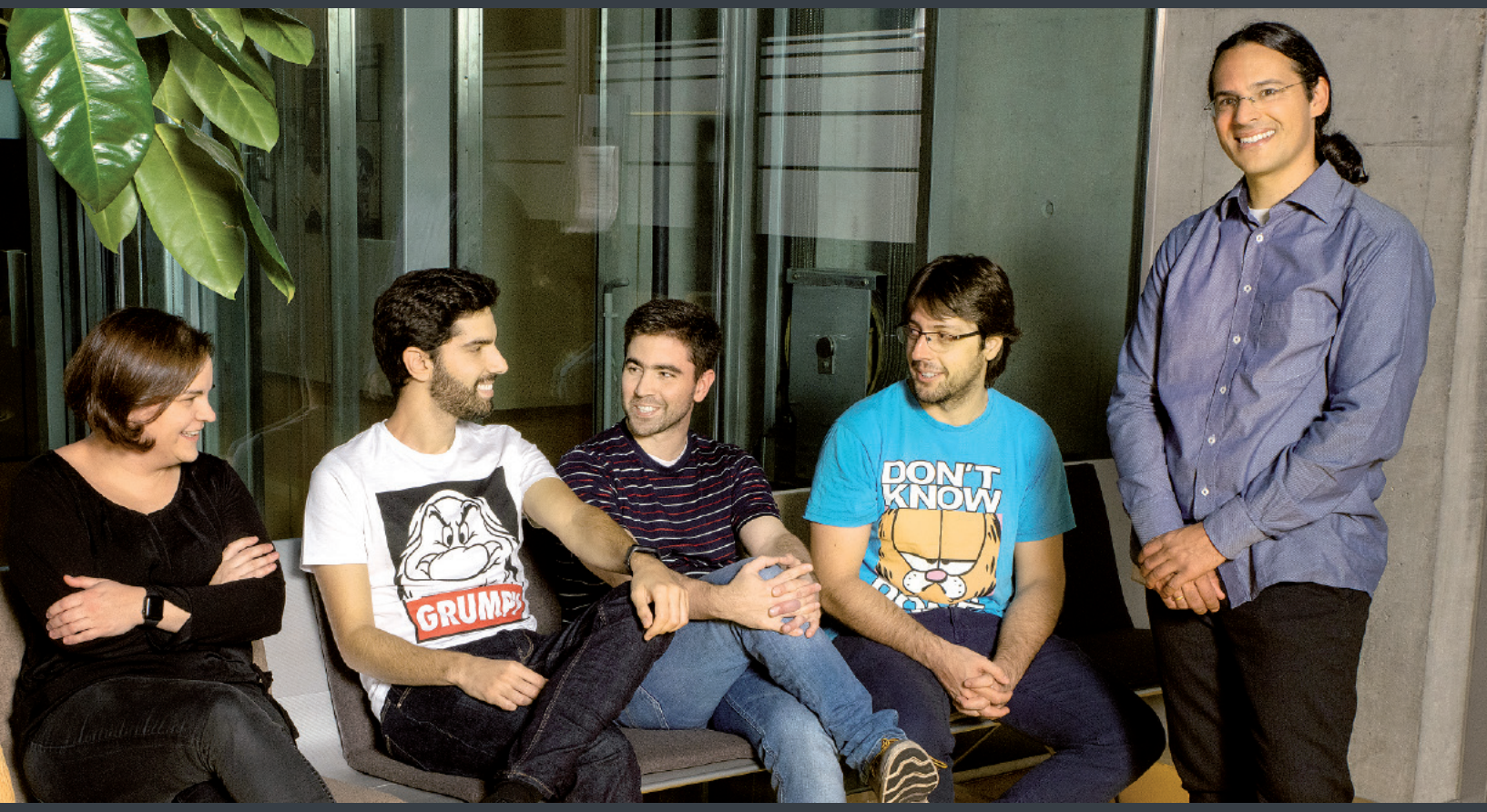
What do you especially like about working at the GMI?

The GMI has a family atmosphere that makes you feel that you belong and are acknowledged. People care about your feelings. Improvements and complaints are quickly approached and openly discussed. Nearly every day, you can join talks given by top international scientists. We have weekly social events and annually an organized retreat of the whole institute into the mountains.

The work in general is enhanced by the state-of-the-art equipment in the labs, the strong networking of different groups on the campus, and the very efficient core facilities.

Where do you want to go next?

My main focus lies on finalizing my first publication. I could imagine extending my time at the GMI by doing a Postdoc, but have not yet made any further plans.



ARMIN DJAMEI

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TECHNICIANS
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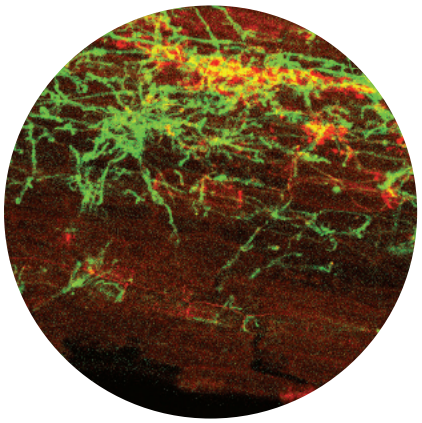
(*left the lab in 2019)

EFFECTORS – A PLANT PATHOGEN'S TOOLBOX



To succesfully infect plants, pathogens have to overcome the plant's sophisticated immune system. While the pathogen establishes its interaction with the host, it needs to manipulate the plant's metabolism to create an optimized environment for its own growth. To achieve these goals, pathogens use a set of proteins called effectors that they release into the host plant. While a single pathogen can have hundreds of different effectors, and there are many different plant pathogens, we know the function of relatively few effectors from all plant pathogens.

The goal of the Djamei lab is to characterize the whole complement of effectors from the pathogen *Ustilago maydis,* which causes corn smut disease. Since effectors often target core processes in plants, they expect to learn more about how plants function in addition to learning how to better protect them from pathogens.

ADVANCES IN 2019

One major finding published by our group this year was the discovery of an effector network. Using a systematic yeast-two-hybrid approach, we selected 63 putative effectors for one-on-one matings with a library of nearly 300 effector candidates. We found that 126 of these effector candidates interacted either with themselves or other predicted effectors. Although the functional relevance of the observed interactions remains elusive, we propose that the observed abundance in complex formation between effectors adds an additional level of complexity to effector research and should be taken into consideration when studying effector evolution and function.

While many putative effector genes are clustered in the *Ustilago maydis* genome, a functional link between clustered effectors was never shown. This year we also finalized our study on a cluster of ten effectors. Nearly all members of this cluster, the Pleiades, share the ability to suppress pathogen associated molecular pattern (PAMP)-triggered ROS-burst upon transient expression in plants. Upon deletion of the cluster, we observe strongly impaired virulence and accumulation of reactive oxygen species (ROS) in infected tissue. Although genetically redundant, the Pleiades target different host components. The paralogs Taygeta1 and Merope1 suppress ROS production in the cytoplasm or nucleus, respectively. Merope1 targets and promotes the autoubiquitination activity of RFI2, a conserved family of E3 ligases that regulates the production of PAMP-triggered ROS burst and influences flowering time in plants.

We have also studied host specificity using a hybrid fungus formed by mating two closely related fungi: *Ustilago bromivora,* which normally infects *Brachypodium spp.,* and *U. hordei,* which normally infects barley. Although *U. hordei* was unable to infect *Brachypodium spp.,* the hybrid could. By analyzing the genomic composition of 109 hybrid strains backcrossed with *U. hordei* over four generations, we identified three regions associated with *Brachypodium spp.* infection and 75 potential virulence candidates. The most strongly associated region was located on chromosome 8, where seven genes encoding predicted secreted proteins were identified. The fact that we identified several regions relevant for pathogenicity on *Brachypodium spp.* but that none were essential suggests that host specificity, in the case of *U. bromivora,* is a multifactorial trait which can be achieved through different subsets of virulence factors.

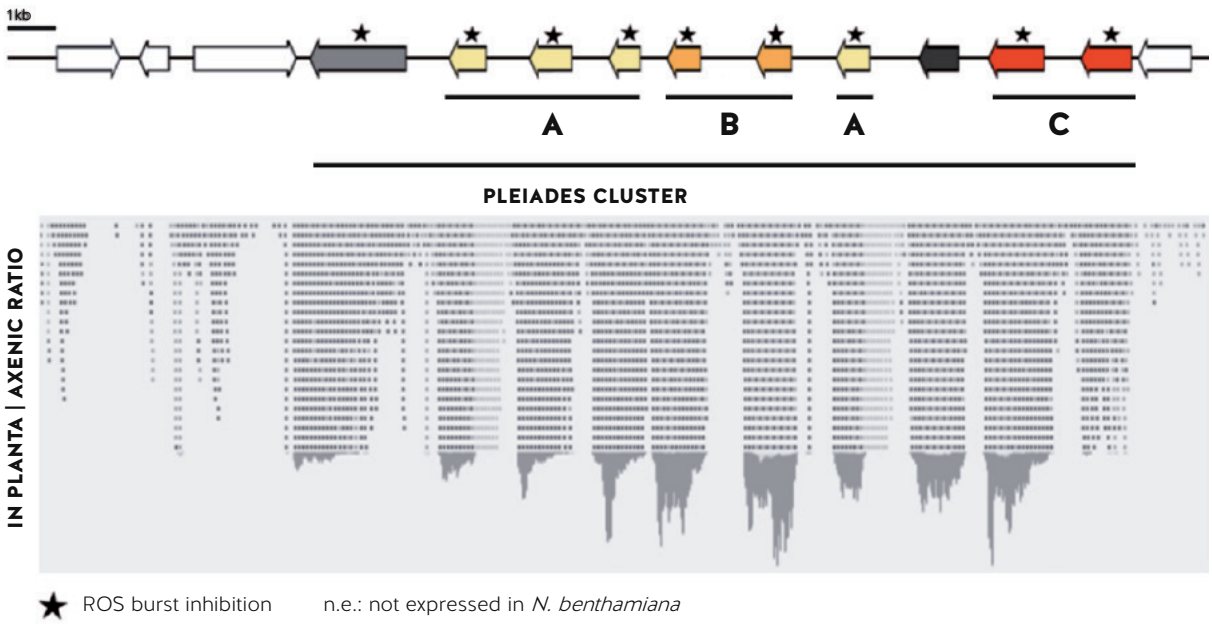
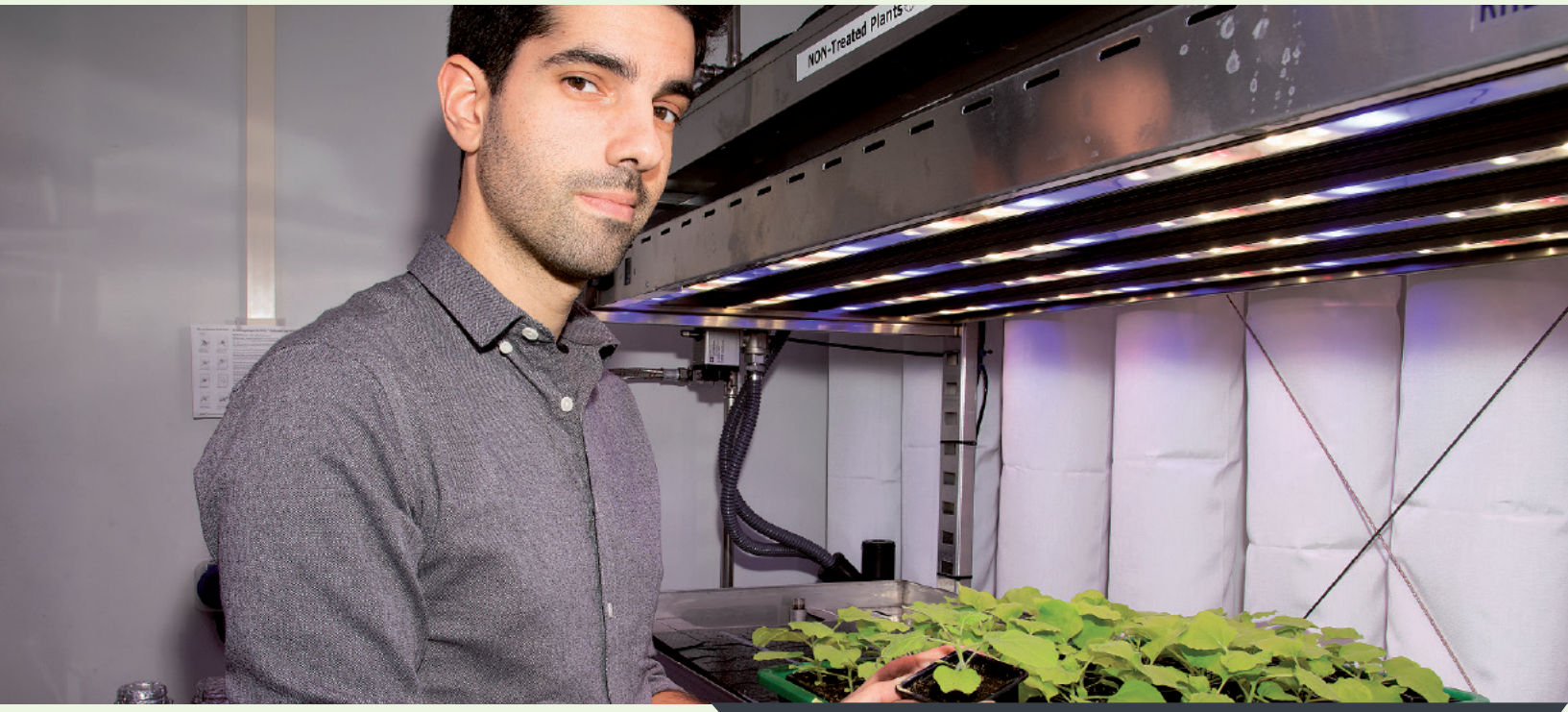


FIG. The Pleiades cluster. Top *Schematic of the Pleiades cluster. Differently colored arrows indicate paralogs, * indicate genes which inhibit ROS-burst.* **Bottom** *Pleiades genes are upregulated during infection.*



INSIGHTS

Andre Alcantara, PhD Student
Born in Solothurn, Switzerland in 1987
Studied at University of Lisbon, Portugal

How did you come to the GMI?

When I applied here, I was looking for PhD programmes where I didn't have to apply to a specific project. That way I could meet a number of potential supervisors and discuss several projects before making my decision. The VBC PhD programme offered just that and after passing the initial interview I was impressed with the facilities and the people at the VBC.

What project are you working on?

My PhD focuses on dissecting the molecular interactions between plants and their pathogens. Using *Ustilago maydis* as a model organism, I developed a method to identify which secreted molecules interfere with plant immunity through a conserved mechanism called the unfolded protein response.

What do you especially like about working at the GMI?

I think that what distinguishes the GMI from many other institutes is the access to the great facilities at the VBC that enables us to do cutting edge science. Additionally, the campus has scientists from many different areas who are very approachable and open to cooperation.

The social hours are also great.

Where do you want to go next?

Ideally, I would like to go to the agronomical industry sector so that I can have a greater impact in improving crops and help achieving food security.

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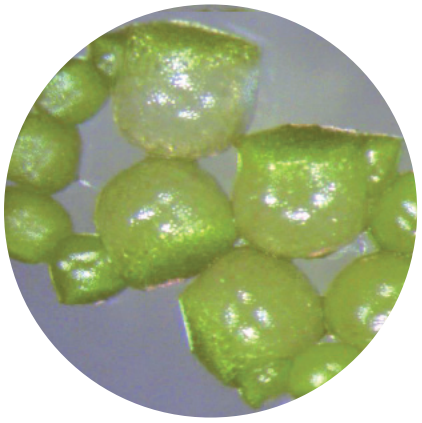
HOW TO RECOGNIZE A TRANSPOSON



Transposons, commonly called jumping genes, are DNA sequences in plants and animals that can copy themselves and then move around the genome. Because they are able to move throughout the genome, they are important drivers of evolution. This same ability, however, can result in them disrupting genes and causing disease. Because they copy themselves before moving, they can expand exponentially; they make up more than 40% of all the DNA in humans and as much as 90% in maize. For these reasons, transposons are thought of as genetic parasites and both plants and animals have evolved complex machinery to recognize transposons and stop them from moving. While we understand many of the details involved in keeping them still, it remains unclear how they are initially recognized.

The Marí-Ordóñez lab is investigating this first step, how cells recognize new transposons, which will help us understand how they affect genomes. As part of this goal, they are developing a new group of plants that have not been traditionally been used in science, called Duckweeds. Duckweeds are rapdily growing aquatic plants gaining attention as a new source of fuel and food. The tools developed in the lab will facilitate research throughout the world.

ADVANCES IN 2019

Organisms have evolved an array of mechanisms to identify and suppress the activity of transposable elements (TEs). In plants, animals, and fungi, a common strategy is the use of small RNA molecules to guide, in a sequence specific fashion, silencing complexes that abrogate transposon expression. A major goal of the lab is to investigate how such mechanisms allow plants to rapidly identify new invading transposons. We use the well-established *Arabidopsis thaliana* model to gain a better understanding of the molecular mechanisms that permit cells to identify, target, and propagate to the progeny the silencing of transposons. By reactivating a transposon in the genome, we are able to recapitulate all the steps during *de novo* silencing. We have recently identified translation as the mechanism by which active transposons are recognized by the host to initiate a small RNA silencing response similar to antiviral defense in plants. Although the exact molecular mechanisms await further detailed investigation, our data suggests that, in contrast to gene coding mRNAs, transposon mRNAs trigger ribosome stalling during translation. To resolve such stalling events and recycle ribosomes, a mechanism known as ribothripsis "cuts" the RNA between stalled ribosomes. The resulting RNA fragments are, in principle, bona fide substrates for the cellular machinery responsible for small RNA biogenesis in plants. We are currently investigating the precise nature of the ribothripsis RNA products and their association with the silencing machinery.

Our other line of research focuses on investigating alternative silencing mechanisms in plants. To do so we have chosen Duckweeds. Duckweeds represent the smallest and fastest growing flowering plants (→ Fig.). Duckweeds are aquatic plants that mostly reproduce asexually through clonal propagation. Although genomic resources are still scarce, a closer look at the ancestral *Spirodela polyrrhiza* genome has revealed that many of the factors involved in TE silencing are absent. Hence, duckweeds represent a unique opportunity to investigate non-canonical silencing pathways to elucidate the basis of silencing in plants as well as the complex evolutionary interplay between TEs and their hosts. During this first year, we have implemented duckweed culture at the GMI and have started optimizing techniques for genetic manipulation and genome sequencing projects to investigate the evolution of this fascinating family of plants.

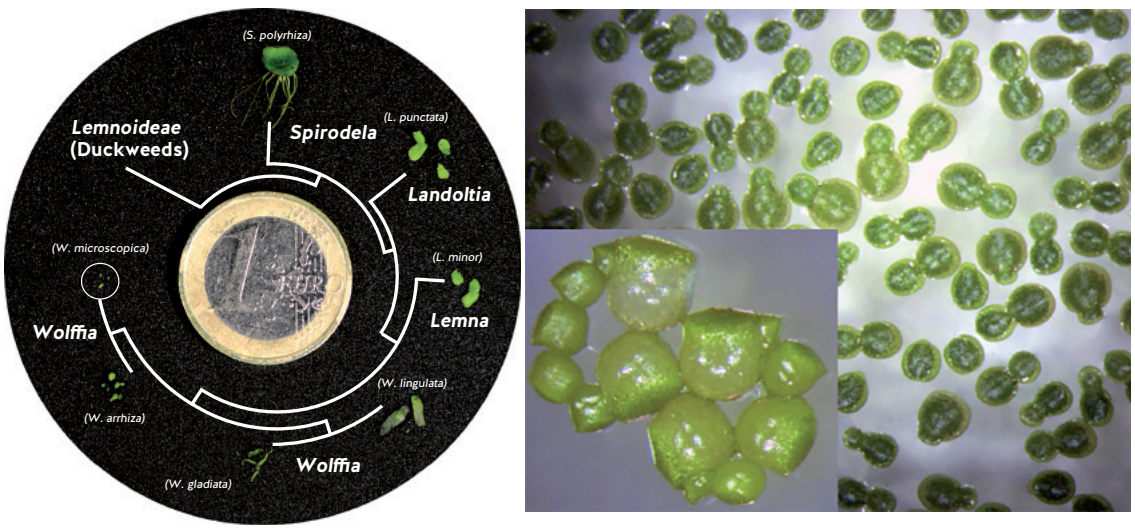


FIG. Duckweeds *(Lemnoideae)*, the smallest flowering plant.
Left *Phylogeny of the five* Lemnoideae *genera. Individual fronds and/or clusters of seven representative species currently growing in the group are pictured next to a 1€ coin as a size reference.* **Right** Wolffia arrhiza *fronds multiplying in liquid media. Insert:* W. arrhiza *initiating colony formation on solid media.*

INSIGHTS

Verónica Barragán Borrero, Lab Manager
Born in Huelva, Spain, 1977
PhD from Sevilla University, Spain

How did you come to the GMI?
I was working at the ETH in Zurich and, after 5 years, I felt that I needed a change. Fortunately, a former member of my lab in Zurich had just got a position as a junior PI when I was starting to look for a new lab and invited me to the GMI for an interview so I could be impressed with the facilities... In conclusion, he really convinced me with the place, the people, and his amazing and novel projects.

What project are you working on?
My more exciting project is the establishment of duckweeds as a new plant model organism. Duckweeds are aquatic monocots that reproduce sexually and asexually by producing clones, thus duplicating the population in several days. This makes them very attractive as a model. We are setting up the culture, carrying out the molecular characterization, studying their ploidy, analyzing their genomes, and developing molecular tools in order to achieve our goal.

On the other hand, the lab is interested in transposon silencing mechanisms, using the retrotransposon EVADE as a model. I am involved in the characterization of ribosomal stalling during EVADE translation and its consequences in siRNA production and subsequent silencing.

What do you especially like about working at the GMI?
There are many facilities on campus supporting the labs, which makes the day-to-day work much easier. Furthermore, there is frequent interaction among the different groups, creating a really people-friendly working environment.

Where do you want to go next?
I started working at the GMI less than one year ago, so I haven't thought about my next destination yet. However, if I could choose, maybe somewhere in Spain…

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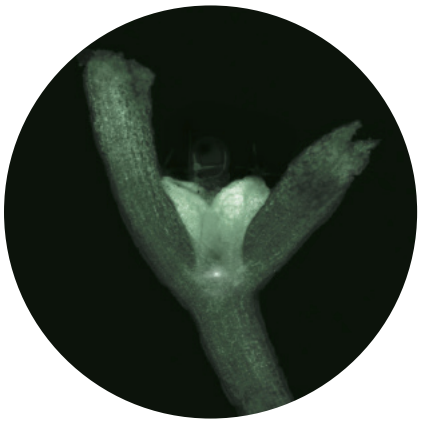
EPIGENETICS



The offspring of plants and animals resemble their parents. The inherited information that shapes the appearance and other features of the next generation is primarily made up of two components. The first, genetic information, is encoded in the DNA sequence of the genes. The second component, called epigenetic information, instructs a cell whether genes are turned on or off and is determined by the way the DNA is packaged inside the cell. It includes modifications to the DNA (without changing the sequence), variants of DNA-binding proteins, and several types of RNA molecules.

The Mittelsten Scheid group is interested in how genetic and epigenetic information interact with each other. They study how epigenetic information is inherited between generations, how it changes during stress, and how it is involved in DNA repair.

ADVANCES IN 2019

Genetic and epigenetic changes in plants

Inheritance refers to passing on traits to progeny. Genetic inheritance is primarily based on continuity of genome information laid down in DNA sequence, but epigenetic inheritance adds another layer, encoded by the way in which the long linear DNA molecules are organized within the nuclei. Plants are often exposed to DNA-damaging conditions that endanger the correct transmission of genetic information to daughter cells. Multiple proteins repair DNA lesions efficiently, while there is growing evidence for the additional involvement of non-protein-coding RNAs in DNA repair (reviewed in *Durut and Mittelsten Scheid 2019*). Studying the nature and function of these RNAs, and their interaction with specific repair complexes and broken DNA in the context of densely packed chromatin is one of the research topics in the group.

Adverse conditions, like heat stress, can cause transient changes in the chromatin organisation *(Dumur et al. 2019)*. While the conservation of DNA sequences by replication and repair is quite well understood, the maintenance of epigenetic information during cell division is less clear, especially upon formation of the germ cells. How far environmentally induced epigenetic changes are inherited, and how relevant this is for the phenotype of the progeny, is a much-debated topic. In plants, such directed and heritable changes would need to pass the bottleneck of the stem cells in the shoot apical meristem (SAM), from which all postembryonic aerial organs are continuously formed. The group has applied fluorescent activated nuclear sorting (FANS) *(Gutzat and Mittelsten Scheid 2019)* to investigate gene expression and DNA methylation, one of the epigenetic hallmarks, in plants of different age. Transient activation of some transposable elements and early epigenetic reprogramming indicate dynamic changes in the stem cells during the life span of the plants *(Gutzat et al. 2018)*, and the experiments will now be extended along the germ line to the next generation.

Light is one of the most important regulatory factors for plants, including for developmental decisions. The light-dependent seed germination of the model plant Arabidopsis is one well-investigated example. In this case, the signalling pathway is composed of light receptors, transcription factors, and hormone biosynthesis, connected by transcriptional control with negative and positive feedback loops. Much less is known in plants in which seed germination is inhibited by light, likely securing that this process occurs only underground. Taking advantage of natural variation between light response in seed germination in different *Aethionema arabicum* accessions, the group uncovered that key regulators corresponding to those in Arabidopsis are involved but undergo converse changes upon illumination, resulting in antipodal hormone regulation (→ Fig.). This is an example how the same modular components were differentially connected during evolution to produce divergent pathways, likely as adaptive traits *(Mérai et al 2019)*.

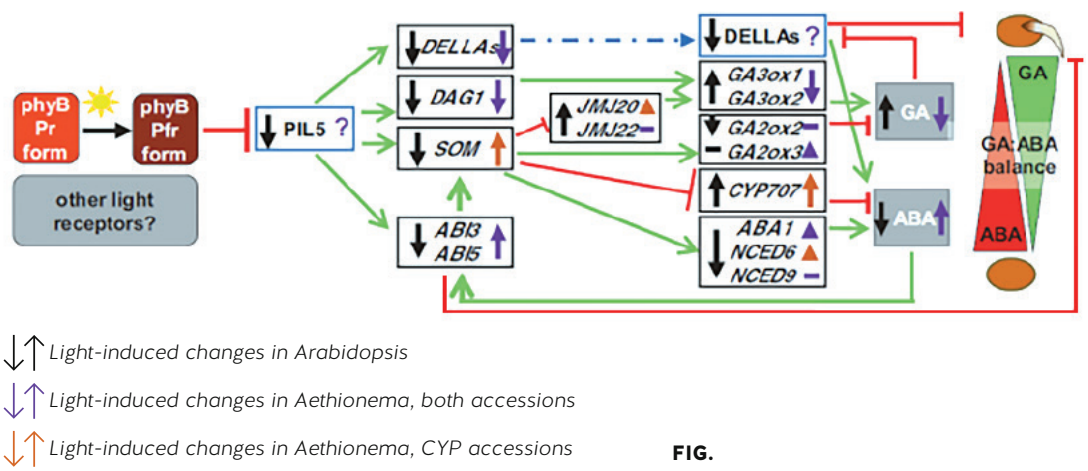
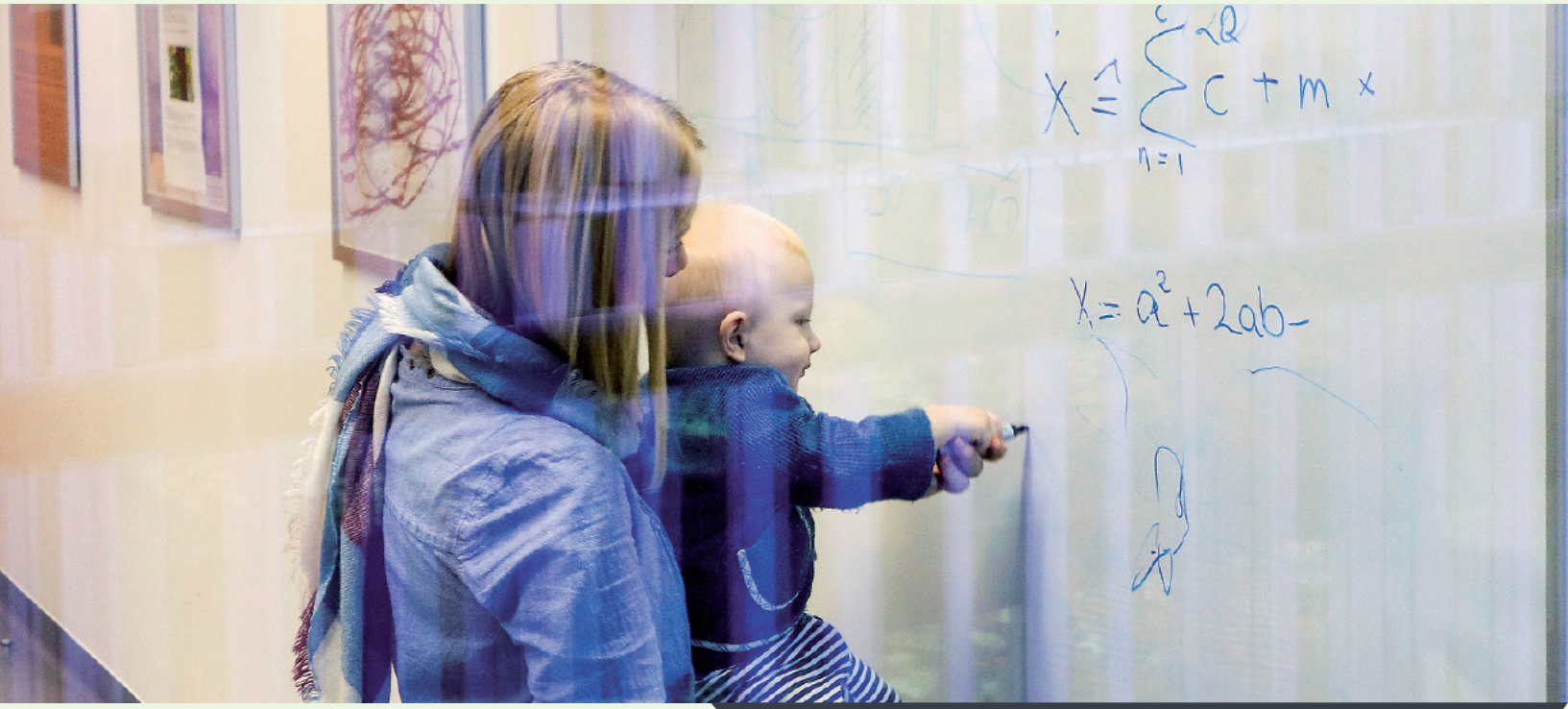


FIG.
Antipodal transcriptional changes in *Arabidopsis thaliana* and *Aethionema arabicum* of key hormone regulatory genes.
Black boxes indicate genes whose expression is light-regulated. Changes in expression upon light exposure are indicated by black (Arabidopsis), purple (Aethionema, light-neutral and light-inhibited accessions), and orange (Aethionema, light-inhibited accession only) arrows (Mérai et al. 2019, Arabidopsis scheme after Stawska and Oracz 2015).



INSIGHTS

Zsuzsanna Mérai, Postdoc
Born in Budapest, Hungary
PhD from Eötvös Loránd University, Budapest, Hungary

How did you come to the GMI?

I got the chance to join the GMI in 2012 after applying for a post-doc position in Hisashi Tamaru's group investigating the epigenetic aspects of male gametophytes. After the group finished, I joined Ortrun Mittelsten Scheid's lab and started studying an interesting, novel plant called *Aethionema arabicum.*

What project are you working on?

Over the last years, I have had the very exciting, and sometimes challenging, endeavor to obtain insight into many different aspects of a non-model plant - including ecology, plant physiology, genetics, molecular biology, and many others. The advantage of a 'new' plant is that there are phenotypic variations which cannot be observed in a classical model plant like Arabidopsis. I'm particularly interested in the light regulation of seed germination, which is not just fundamentally different from Arabidopsis, but also shows remarkable natural variation among Aethionema ecotypes. I believe my work contributes to a more comprehensive picture of the molecular regulation of germination, which was rather one-sided over the past decades because all we knew was based on Arabidopsis studies. The disadvantage of using a novel plant model is that we faced several difficulties in the beginning to set up a not-established system, from plant growth through analysis of genomic data.

What do you especially like about working at the GMI?

My work would not be possible without the great support I get from the GMI as an institute, with many experts from different fields. Lab Support and the VBCF Facilities make the work efficient and professional. Everyone, including colleagues within and outside of the group, are very friendly and ready to help. The only negative side is that I need at least 2 minutes at the end of my presentations to acknowledge everyone who has helped! Finally, an unusual point to mention; the GMI is an absolutely politically-free institute. We tend to forget that it is not always the case in other institutes in Europe, and I really appreciate it here.

Where do you want to go next?

All of the reasons listed above make it hard to leave, the GMI has set a high bar for what I'm looking for in my next position.

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(*left the lab in 2019)

DEVELOPMENTAL GENOMICS

Soon after fertilization of the egg and sperm, genes in the zygote are turned on, beginning a precisely coordinated developmental program. Already during very early stages of development, this program has established the basic blueprint of the plant body, including the root, shoot, and first leaves. Specialized cell types within these organs are also established at this time, and each of these cell types has to turn on only a specific set of genes. Although decades of research in animals have found how many of these processes are regulated in animals, little is known in plants because the developing embryos are deeply embedded in maternal tissues, making them difficult to study.

The Nodine lab is interested in learning more about how these very early stages of development are regulated. They are developing new tools to help study early plant embryos and are especially interested in how a special type of RNA, called microRNAs, regulate these processes.

ADVANCES IN 2019

We continue to develop molecular biology, microscopy, and bioinformatic approaches to characterize zygotic genome activation, establishment of the nascent epigenome, and body plan formation at the beginning of plant life using Arabidopsis as a model system. Below, I have highlighted two projects that we published in 2019, and which revealed the molecular basis for the initiation and modulation of gene expression programs during Arabidopsis embryogenesis.

The timing and parental genomic contributions to early zygotic transcriptomes in plants had been controversial for almost 20 years. Our model proposed that maternal and paternal genomes contribute equally to the early embryonic transcriptome, while a previous model proposed that the paternal genome is transcriptionally silenced by maternal epigenetic pathways during early embryogenesis. To visualize transcriptional activities in zygotes, we optimized an expansion microscopy technique for robust immunostaining in ovules and seeds. Our results indicated that RNA polymerase 2 (RNAPII) transcriptional activities increase during the egg-to-zygote transition. To investigate when RNAPII activities are initially required for embryogenesis, we performed live-cell confocal imaging of developing embryos within seeds cultured with RNAPII inhibitors and found that transcription was necessary for the initial cell divisions (→ Fig.). Our results demonstrated that zygotic genome activation occurs before the first cell division in Arabidopsis and complement recently published results including those indicating that the zygotic genome is transcriptionally activated shortly after fertilization throughout flowering plants as we had previously proposed.

MicroRNAs (miRNAs) are short non-coding RNAs that regulate gene expression in plants and animals. Although miRNAs are essential for proper development in plants, relatively little is known regarding their embryonic functions. To systematically assess the regulatory roles of embryonic miRNAs, we first developed a small RNA sequencing method to profile miRNA populations of developing Arabidopsis embryos. Then we developed next-generation sequencing based methods to identify miRNA targets genome-wide from the low amount of RNA obtainable from early embryos. Based on these technology-enabled resources, we discovered dozens of miRNAs that dynamically cleave and repress target transcripts, including 30 that encode transcription factors. Transcriptome analyses indicated that these miRNA:target interactions have a profound effect on embryonic gene expression programs, and we further demonstrated that the miRNA-mediated repression of seven transcription factors were individually required for embryo morphogenesis. These data indicate that the miRNA-directed repression of multiple transcription factors is critically important for the establishment of the plant body plan and provide a foundation to further investigate how miRNAs contribute to these initial cellular differentiation events.

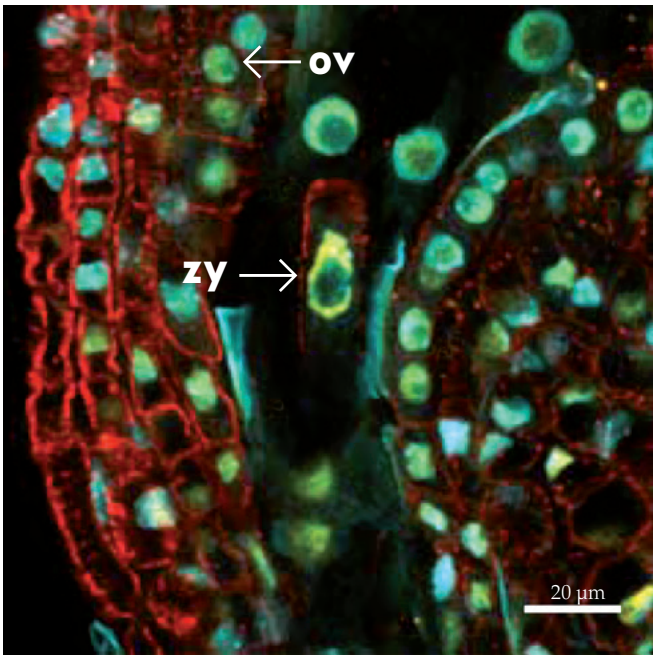


FIG.
Visualization of transcription in zygotes with expansion microscopy
Representative expansion microscopy images of RNAPII Ser2P (yellow; indicates elongating RNAPII) with tubulin (red) and DAPI-stained nuclei (cyan). ov, ovule/seed tissue; zy, zygote. Scale bar represents 20 µm.

INSIGHTS

Balaji Enugutti, Postdoc
Born in Mangalam Kandriga, India, 1980
PhD from TU Munich, Germany

How did you come to the GMI?

I graduated from the Technical University in Munich, Germany, where I cloned and characterized a gene that suppresses ectopic growth during ovule integument pattern formation. After a short research stint at the neighboring IMBA, I realized I wanted to follow my interest in understanding the molecular underpinnings of formative divisions during organogenesis and stem cell biology and therefore joined the Nodine lab at the GMI.

Tell me about your project?

Multicellularity was one of the most significant innovations in the history of life, bringing new capabilities to organisms. My research interest pertains to understanding the role of small non-coding RNAs (sRNAs) that act as guides to sculpt the gene expression program during polarity establishment, cell fate specification, and stem cell maintenance, all of which are fundamental for organogenesis and growth in multicellular organisms. Establishment of the main body axis is the first pivotal patterning step in developing an organism from a unicellular zygote. In the Nodine Lab, one of my projects addresses how a specific sRNA orchestrates body axis formation by promoting zygote elongation and establishing polarity for the first asymmetric cell division in Arabidopsis embryogenesis.

Ultimately, plant embryogenesis results in a miniature seedling with only a few basic cell types and tissues. The final body architecture is determined by post embryonic activation and maintenance of pluripotent stem cells, which continuously generate new organs. Stem cell maintenance is an active process that requires constant communication between different regions of the meristem and the environment. This communication is mediated by signaling molecules and sRNAs among others and I am studying the role of sRNAs in this communication process.

What do you especially like about working at the GMI?

The research atmosphere at the GMI is extremely stimulating. I like the scientific freedom, first-class research, and state-of-the-art scientific services at the GMI and across the whole VBC. Additionally, the subsidized campus child care center is a boon to working parents, which both my child and I cherish.

Where do you want to go next?

I want to continue to focus on the field of cell fate specification and stem cell biology and am keen on testing out ideas that combine this focus with entrepreneurship.

MAGNUS NORDBORG

magnus.nordborg@gmi.oeaw.ac.at

@magnusnordborg

Joined GMI in Feb 2009

PhD: Stanford University, US

PREVIOUSLY

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

GROUP MEMBERS

LAB MANAGER
Almudena Mollá Morales

PHD STUDENTS
Gökce Aköz
Robin Burns
Dejan Đukić
Rahul Pisupati
Luz Mayela Soto Jiménez

POSTDOCS
Pieter Clauw
Thomas Ellis
Danièle Filiault
Benjamin Jaegle
Aleksandra Kornienko
Haijun Liu
Eriko Sasaki

TECHNICIANS
Joanna Jagoda
Viktoria Nizhynska

TRAINEE
Sonia Celestini
Sanjay Narayanaswamy*
Yalçın Ege Okyar

(*left the lab in 2019)

EXPLORING GENOMIC VARIATION

Differences in the DNA sequence between individuals lead to differences in appearance or behavior. Sometimes differences in a single gene can have a dramatic effect, the classic example being round and wrinkled peas, which Gregor Mendel used to discover the laws of genetics. More commonly, hundreds to thousands of DNA differences each contribute only a very small amount to the differences we see, as is the case for human height.

The Nordborg lab wants to understand how and which DNA differences are responsible for differences between individuals. How has evolution selected these differences, and which differences were selected for, to make some plants grow well in Sweden while others grow well in Spain? The lab uses a combination of computational biology together with lab and field work to address these questions. The knowledge they gain will help us better understand evolution and adaptation in plants, knowledge which will be useful for understanding how plants will react to our changing climate.

ADVANCES IN 2019

Whole-genome polymorphism data

The first eukaryotic genomes were sequenced almost two decades ago, and the last decade has seen an explosion in polymorphism studies, especially in humans, and primarily due to cheap "next-generation" or "short-read" sequencing that makes it economically feasible to genotype lots of individuals with respect to millions of single-nucleotide polymorphisms (SNPs). However, these methods rely on comparison with the reference genome (and thus only work for certain regions of the genome) and can only identify SNPs and very short (ca. 10 bp) length polymorphisms. As a result, we only have a poor understanding of the role played by other kinds of structural variants, and all polymorphism data sets suffer from "reference bias" because the polymorphisms are identified by comparison to the reference genome.

To investigate the seriousness of this problem, we are sequencing large numbers of *Arabidopsis thaliana* genomes *de novo* in order to identify polymorphisms by comparing multiple genomes directly. This year has been a breakthrough one in that we have established methods and workflows to make this happen. Using PacBio long-read technology, we can now routinely sequence and assemble nearly complete *A. thaliana* genomes, leaving gaps only for highly repetitive regions such as centromeres that will require better technology. A paper describing the first 30 genomes is in preparation.

The "Dark Matter" of the genome

A major reason for looking at whole-genome polymorphism data is "parasitic" transposable elements, which constitute huge portions of the genome of most higher organisms. Over 40% of the human genome is derived from transposable elements, for example. Generally speaking, most of the variation in genome size between organisms is due to transposable elements. The *A. thaliana* genome is relatively small and is only about 20% transposable elements. Until recently, it was believed that these were all "dead" in the sense that they no longer actively proliferate, but this conjecture was based on little data as short-read sequencing technologies are incapable of sequencing highly repetitive transposable elements.

Our new data clearly reveal a very different picture. About half of all annotated transposable elements in the *A. thaliana* reference genome are polymorphic, and most insertions are rare. In other words, a very large fraction of the known transposable element insertions will be missing from a given genome — which will instead have different insertions, many of which will be unique. Even more surprisingly, we see a strong geographic pattern in the distributions of transposable elements, with plants from the north carrying many more elements (→ Fig.).

What about "epigenetics"?

There is currently much excitement about the heritable "epigenetic" DNA modifications as a source of adaptive mutation. There is essentially no data to support such notions, but there is little doubt that they play a major role in controlling transposable elements. A major focus of the lab is on understanding variation in DNA methylation, and we have made several exciting discoveries. First, much of this variation appears to be genetic, with major trans-acting loci controlling much of the variation. Second, there are again strong geographic patterns, suggesting an adaptive role for methylation.

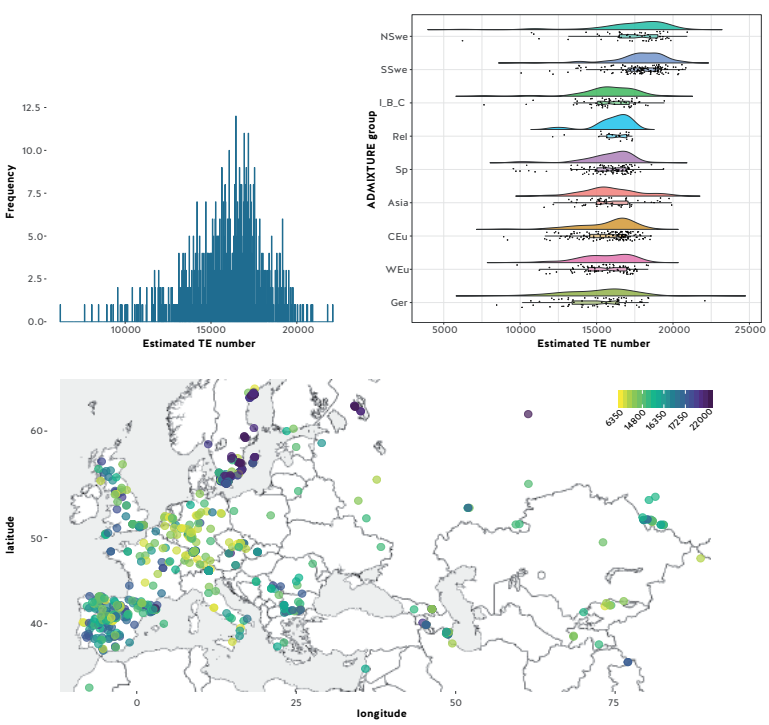


FIG.
Variation in transposon load.
There exists and almost three-fold variation in the number of transposons between Arabidopsis genomes **(top left),** *and this variation is geographically structured.*

INSIGHTS

Eriko Sasaki, Postdoc
Born in Mie Prefecture, Japan
PhD from the University of Tokyo, Japan

How did you come to the GMI?

I joined GMI seven years ago after my partner started working at the GMI as a postdoc. As we are both plant researchers, the GMI was the best institute for us because the diversity of research groups provide many opportunities to find a fitting position. With the support of a Lise Meitner Fellowship from the Austrian Science Fund, I joined Magnus Nordborg's group, a leading lab in the study of natural variation in Arabidopsis.

What project are you working on?

I'm working on natural variation in *Arabidopsis thaliana* using quantitative genetics approaches. *A. thaliana* lines that were collected from different regions show large variation in traits such as flowering time and responses to cold temperatures. My main scientific goal is to understand how morphological and physiological traits are regulated by genetic and environmental factors in plants and how natural selection shapes these traits and variation.

What do you especially like about working at the GMI?

I like the friendly and supportive atmosphere of GMI. Especially, the administrative staff and senior PIs are in much closer contact to Postdocs and PhD Students than at any other institute I know of.

Where do you want to go next?

I'm starting my next position in Japan as a tenure track PI. I want to develop my research field and also help young researchers as much as I have been supported at the GMI.

KELLY SWARTS

kelly.swarts@gmi.oeaw.ac.at

@dendrogenomics

Joined GMI in Jan 2019

PhD: Cornell University, US

PREVIOUSLY

- Postdoc (2017-2018): Hernan Burbano Lab, Max-Planck Institute for Developmental Biology, Tübingen, DE

GROUP MEMBERS

PHD STUDENT
Mehrta Shirzadian

POSTDOC
Miguel Vallebueno

TECHNICIANS
Alexis Arizpe
Miroslav Poláček
Julia Riefler

TRAINEES
Laura Manerus
Daniel Pleyer*
Sonja Steindl
Clemens Wager*
Lisa Weidlich

(*left the lab in 2019)

TREE RING GENOMICS

Forests around the world are succumbing to drought, disease, and fire as a result of climate change. Long lived trees are especially susceptible, as the rate of climate change outpaces the speed with which they can adapt. If, however, we can understand how individual trees respond to different environments that exist now, we can predict which seeds will be best adapted to future environments.

The Swarts lab is addressing this problem with a novel approach focused on Norway spruce, one of the most economically important trees in Europe. They are collecting core samples from thousands of living trees, a process which does not harm the tree, from different locations across Europe. Using these samples, they can then measure the rings a tree produces every year to determine how well an individual tree grew over every year of its life.

Comparing an individual tree's growth to historical weather data, they can then determine which trees performed best in different environmental conditions. By sequencing the trees' genomes, they will then determine which genes are important in different environments. Using this information, they hope to help foresters determine which seeds will be best suited for the local environments that are predicted in the future, thereby improving the health of Europe's forests.

ADVANCES IN 2019

We focus on the economically and ecologically important conifer Norway spruce *(Picea abies)* to 1) develop models and infrastructure to understand the fraction of annual growth that can be attributed to genotype, environment, and genotype-by-environment interactions (GxE), 2) map the genetic basis of adaptive response using estimates for GxE as a response in genome-wide association studies (GWAS), and 3) predict genetic responses to novel environments. This approach will enable estimation of the genetic basis of adaptive responses in any population — cultivated, experimental, or natural — providing the means to evaluate any given tree as a possible parent for reforestation under changing climate.

The data generated for this project – images from core data, spatial information, field collected metadata, genotype information, publicly available weather and satellite information – is diverse, complex, and must be updated and accessed quickly and in parallel. We designed and implemented a PostgreSQL database housed on the Azure cloud platform to organize and integrate field-collected data with publicly available environmental data, measured annual growth metrics, and genotype information. For field data collection, we developed an open source android application that interfaces with the database remotely to minimize data loss and errors. To automate phenotyping of the 3,000 core samples collected from 25 plots in Austria, Czech Republic, Slovakia, and Romania over the summer, we worked with engineers at the VBC to develop an automated digitization platform using a Zeiss broad spectrum light microscope and a custom robotic stage that allows us to digitize microtome-prepared increment cores in reusable aluminum core mounts in a single run (up to 650 cm of cores/run). This provides robust, high quality images that we are currently implementing Convolutional Neural Nets (CNNs), a deep learning approach to identify annual ring boundaries and other wood anatomical traits.

Efficiently genotyping large numbers of trees is critical to the project. Over the past year we have tested and optimized DNA extraction protocols, generating a low-cost CTAB, high-throughput plate-based protocol that produces DNA with a median fragment length of 25 kb, even after 10 days of field storage conditions. We chose to focus on cambial tissue because it is easily collected during the active growing season from small punches through the tree trunk. The resulting high-quality DNA is suitable for both short and long-read sequencing technologies, and we are developing Genotyping-by-Sequencing (GBS) library protocols and developing genotyping imputation approaches to reduce the cost of sequencing a genome 6X the size of a human genome.

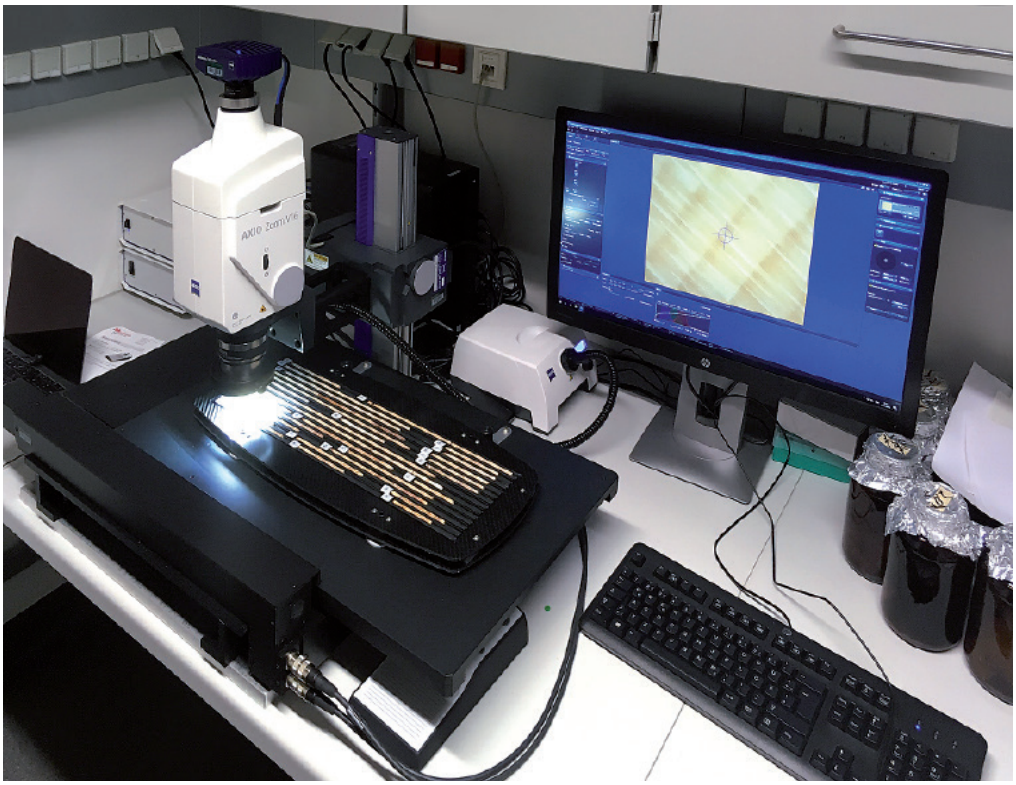


FIG.
Automated microscopy system for digitizing tree rings.

INSIGHTS

Julia Riefler, Technician
Born in Vienna, Austria, 1973
PhD from the BOKU, Vienna, Austria

How did you come to the GMI?

A former working colleague asked me to apply for an open position in the lab of Thomas Greb. She thought I might fit into the team and she was right! Already from the very evening after my interview, I knew that I would enjoy working at the GMI and with Thomas. This was almost 11 years ago, in early 2009.

What project are you working on?

I was part of the Greb group working on secondary growth until my maternal leave in 2012. For the last 6 years I worked with Armin Djamei, mostly establishing and maintaining cell cultures of monocotyledons. Since February this year, I joined Kelly Swarts' team in a collaboration on the topic of tree-ring genomics and will start as a full member in 2020.

What do you especially like about working at the GMI?

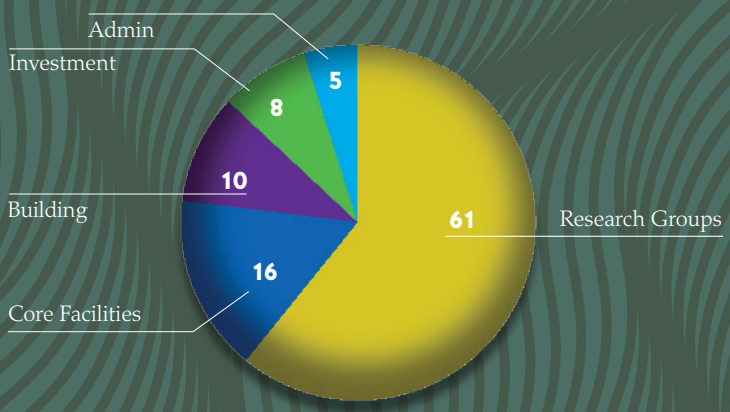
Since I was born and raised in Vienna, I especially enjoy the international atmposphere at GMI within my own hometown.

Where do you want to go next?

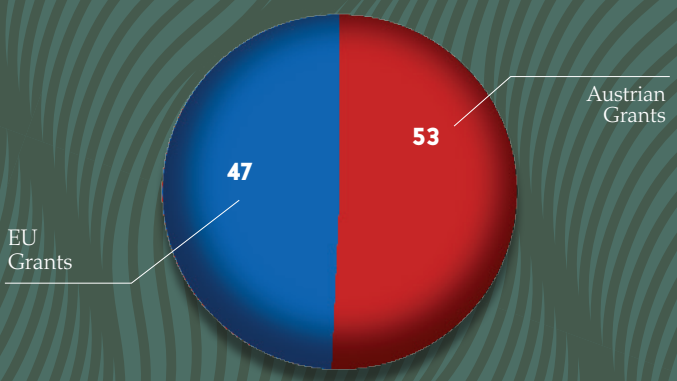
GMI already makes me go to different places through its international atmosphere. So why not stay in Vienna?

19 KEY FACTS *(as of Dec 31, 2019)*

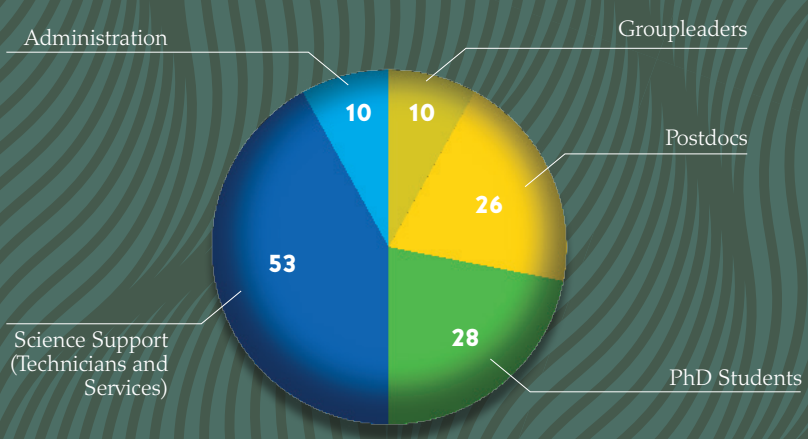
EXPENDITURES (%)



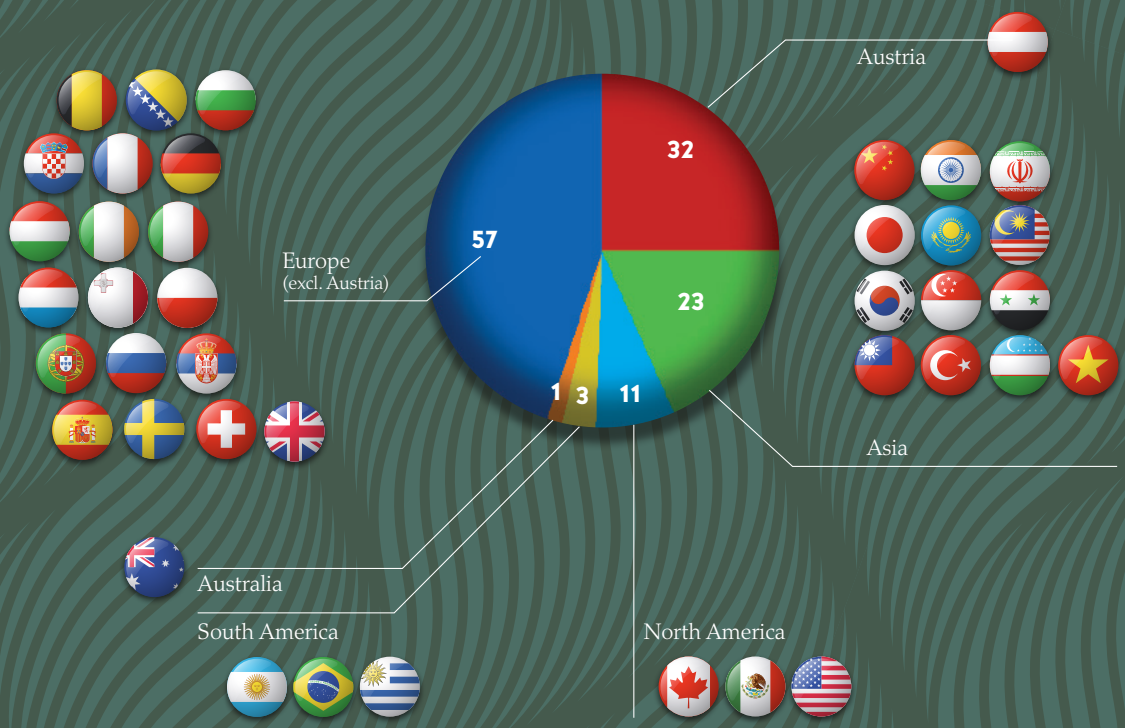
RESEARCH GRANTS (%)



STAFF BY FUNCTION (Head Count)



STAFF - NATIONALITIES (Head Count)



19 PUBLICATIONS

BECKER GROUP

Schandry N and Becker C (2019) **Allelopathic Plants: Models for Studying Plant–Interkingdom Interactions.** *Trends Plant Sci [epub].*

BELKHADIR GROUP

Kutschera A, Dawid C, Gisch N, et al. (2019) **Bacterial medium chain 3-hydroxy fatty acid metabolites trigger immunity in Arabidopsis plants.** *Science 364(6436):178-81.*

Luu DD, Joe A, Chen Y, et al. (2019) **Biosynthesis and secretion of the microbial sulfated peptide RaxX and binding to the rice XA21 immune receptor.** *Proc Natl Acad Sci USA 116(17):8525-34.*

Mott GA, Smakowska-Luzan E, Pasha A, et al. (2019) **Map of physical interactions between extracellular domains of Arabidopsis leucine-rich repeat receptor kinases.** *Sci Data 6:190025.*

Xiao Y, Stegmann M, Han Z, et al. (2019) **Mechanisms of RALF peptide perception by a heterotypic receptor complex.** *Nature 572(7768):270-4.*

BERGER GROUP

Berger F (2019) **An ancient antisense-driven RNA switch drives plant sex determination.** *EMBO J 38(6).*

Berger F (2019) **Emil Heitz, a true epigenetics pioneer.** *Nat Rev Mol Cell Biol 20(10):572.*

Borg M, Buendía D, Berger F (2019) **A simple and robust protocol for immunostaining Arabidopsis pollen nuclei.** *Plant Reprod 32(1):39-43.*

Drinnenberg IA, Berger F, Elsässer SJ, et al. (2019) **EvoChromo: towards a synthesis of chromatin biology and evolution.** *Development 146(19).*

Hisanaga T, Yamaoka S, Kawashima T, et al. (2019) **Building new insights in plant gametogenesis from an evolutionary perspective.** *Nat Plants 5:663-9.*

Nie WF, Lei M, Zhang M, et al. (2019) **Histone acetylation recruits the SWR1 complex to regulate active DNA demethylation in *Arabidopsis*.** *Proc Natl Acad Sci USA 116(33):16641-50.*

DAGDAS GROUP

Rodriguez E, Chevalier J, Olsen J, et al. (2019) **Autophagy mediates temporary reprogramming and dedifferentiation in plant somatic cells.** *bioRxiv:747410.*

Ryder L, Dagdas Y, Kershaw M, et al. (2019) **A sensor kinase controls turgor-driven plant infection by the rice blast fungus**. *Nature 574(7778):423-7.*

Stephani M and Dagdas Y (2019) **Plant Selective Autophagy - Still an uncharted territory with a lot of hidden gems.** *J Mol Biol [epub].*

Zess EK, Jensen C, ... Dagdas Y (2019) **N-terminal β-strand underpins biochemical specialization of an ATG8 isoform.** *PLoS Biol:3000373.*

Zuo Z, Edna M, Rodriguez E, et al. (2019) **mRNA decapping machinery targets transcripts of the LBD3/ASL9 transcription factor to authorize formation of apical hook and lateral roots in Arabidopsis.** *bioRxiv:834465.*

DJAMEI GROUP

Alcantara A, Bosch J, ..., Djamei A (2019) **Systematic Y2H screening reveals extensive effector-complex formation.** *Front Plant Sci 10:1437.*

Bosch J, Czedik-Eysenberg A, ..., Djamei A (2019) **Two Is Better Than One: Studying Ustilago bromivora-Brachypodium Compatibility by Using a Hybrid Pathogen.** *Mol Plant Microbe Interact 31(12):1623-34.*

Han X, Altegoer F, Steinchen W, et al. (2019) **A kiwellin disarms the metabolic activity of a secreted fungal virulence factor.** *Nature 565(7741):650-3.*

Uhse S, Pflug FG, ... Djamei A (2019) **Insertion Pool Sequencing for Insertional Mutant Analysis in Complex Host-Microbe Interactions.** *Curr Protoc Plant Biol 4(3):e20097.*

MITTELSTEN SCHEID GROUP

Dumur T, Duncan S, Graumann K, et al. (2019) **Probing the 3D architecture of the plant nucleus with microscopy approaches: challenges and solutions.** *Nucleus 10(1):181-212.*

Durut N and Mittelsten Scheid O (2019) **The Role of Noncoding RNAs in Double-Strand Break Repair.** *Front Plant Sci 10:1155.*

Mérai Z, Graeber K, Wilhelmsson P, et al. (2019) ***Aethionema arabicum:* a novel model plant to study the light control of seed germination.** *J Exp Bot 70(12): 3313-28.*

Mittelsten Scheid O (2019) **Illuminating (White and) Purple Patches.** *Plant Cell 31(6):1208-9.*

Omony J, Nussbaumer T, Gutzat R (2019) **DNA methylation analysis in plants: review of computational tools and future perspectives.** *Brief Bioinform [epub].*

NODINE GROUP

Kao P and Nodine MD (2019) **Transcriptional Activation of Arabidopsis Zygotes Is Required for Their Initial Division.** *Sci Rep 9(1):17159.*

Plotnikova A, Kellner MJ, ..., Nodine MD (2019) **MicroRNA Dynamics and Functions During Arabidopsis Embryogenesis.** *Plant Cell [epub].*

NORDBORG GROUP

Aköz G and Nordborg M (2019) **The Aquilegia genome reveals a hybrid origin of core eudicots.** *Genome Biol 20(1):256.*

Barton N, Hermisson J, Nordborg M (2019) **Why structure matters.** *eLife:45380.*

Duszynska D, Vilhjalmsson B, Castillo Bravo R, et al. (2019) **Transgenerational effects of inter-ploidy cross direction on reproduction and F2 seed development of *Arabidopsis thaliana* F1 hybrid triploids.** *Plant Reprod 32(3):275-89.*

Marbach F, Rustad CF, Riess A, et al. (2019) **The Discovery of a LEMD2-Associated Nuclear Envelopathy with Early Progeroid Appearance Suggests Advanced Applications for AI-Driven Facial Phenotyping.** *Am J Hum Genet 104(4):749-57.*

Sasaki E, Kawakatsu T, Ecker J, et al. (2019) **Common alleles of CMT2 and NRPE1 are major determinants of de novo DNA methylation variation in *Arabidopsis thaliana*.** *bioRxiv:819516.*

Togninalli M, Seren Ü, Freudenthal J, et al. (2019) **AraPheno and the AraGWAS Catalog 2020: a major database update including RNA-Seq and knockout mutation data for *Arabidopsis thaliana*.** *Nucleic Acid Res [epub].*

FORMER GROUPS

Bouain N, Korte A, Satbhai SB, et al. (2019) **Systems genomics approaches provide new insights into Arabidopsis thaliana root growth regulation under combinatorial mineral nutrient limitation.** *PLoS Genet:e1008392.*

Le Goff S, Nur Keçeli B, Jerabkova H, et al. (2019) **The H3 histone chaperone NASPSIM 3 escorts CenH3 in Arabidopsis.** *Plant J [epub].*

Li B, Sun L, Huang J, et al. (2019) **GSNOR provides plant tolerance to iron toxicity via preventing iron-dependent nitrosative and oxidative cytotoxicity.** *Nat Commun 10(1):3896.*

Ma Y, Miotk A, Šutiković Z, et al. (2019) **WUSCHEL acts as an auxin response rheostat to maintain apical stem cells in Arabidopsis.** *Nat Commun 10(1):5093.*

Ogura T, Goeschl C, ... Busch W (2019) **Root system depth in Arabidopsis is shaped by EXOCYST70A3 via the dynamic modulation of auxin transport.** *Cell 178(2):400-12.*

Shi D, Lebovka I, López-Salmerón V, et al. (2019) **Bifacial cambium stem cells generate xylem and phloem during radial plant growth.** *Development 146:e0103.*

Slovak R, Setzer C, Roiuk M, et al. (2019) **Ribosome assembly factor Adenylate Kinase 6 maintains cell proliferation and cell size homeostasis during root growth.** *New Phytol [epub].*

Stieger CE, Doppler P, Mechtler K (2019) **Optimized Fragmentation Improves the Identification of Peptides Cross-Linked by MS-Cleavable Reagents.** *J Proteome Res 18(3):1363-70.*

Watson JM, Trieb J, Troestl M, et al. (2019) **A hypomorphic allele of telomerase reverse transcriptase uncovers the minimal functional length of telomeres in Arabidopsis.** *bioRxiv:520163.*

19 GRANTS

BECKER GROUP

Epidiverse – Epigenetic Diversity in Ecology
European Research Council: Marie Skllodowska-Cure International Training Network No. 764965
€ 255,374
September 2017 – August 2021

Function and evolution of attack and response strategies during allelopathy in plants
European Research Council: Starting Grant No. 716823
€ 1,500,000
January 2018 – December 2022

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

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

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

The role of histone variants in chromatin organization
Austrian Science Fund: P32054-B21
€ 397,745
May 2019 – April 2023

Tracing the origins of male germline specification in plants
Austrian Science Fund: I 4258-B21
€ 306,589.00
May 2019 – April 2022

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

Role of ATG8 specialization in plant selective autophagy
Austrian Science Fund: P32355-B
€ 304,300
May 2019 – April 2022

DJAMEI GROUP

ERC Starting Grant: Effectomics – elucidating the toolbox of plant pathogens
European Research Council: Starting Grant No. 335691
€ 1,446,316
February 2014 – December 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 – October 2021

MITTELSTEN SCHEID GROUP

Graduate program "Chromosome Dynamics"
Austrian Science Fund: DK 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

A novel model to study light-regulated seed germination (Zsuzsanna Merai)
Austrian Science Fund: I 3979-825
€ 382,032.00
February 2019 – January 2021

NODINE GROUP

Graduate program "RNA Biology"
Austrian Science Fund: DK W1207-B09
€ 339,980
January 2014 – December 2019

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: Starting Grant No. 637888
€ 1,499,989
July 2015 – June 2020

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: Advanced Grant No. 789037
€ 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

19 VIENNA BIOCENTER INTERNATIONAL PHD PROGRAMME IN LIFE SCIENCES

EMPOWERING CURIOUS RESEARCHERS

NEW STUDENTS IN 2019
Rodolphe Dombey
Reshi Shanmuganathan
Mehrta Shirzadian
Jierui Zhao

GRADUATES IN 2019
Jason Bosch
Tao Dumur
Simon Uhse

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.

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 Perutz Labs, 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, Population Genetics, and RNA Biology as well as Marie Curie International Training Networks.

Vienna BioCenter PhD PROGRAMME

19 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

19 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. 2019 saw the departure of several PhD students and postdocs moving to various academic and industry positions. We said „Auf Wiedersehen und viel Glück" in 2019 to:

RUBEN BETZ
Postdoc, IPK Gatersleben, Germany

JASON BOSCH
Postdoc, University of Pretoria, South Africa

TAO DUMUR

MARCO GIOVANETTI

FABIAN KÜNZL
Customer support scientist, GENEWIZ, Leipzig, Germany

CHRISTIAN LÖFKE
Research & product development, BioBloom, Apetlon, Austria

CHULMIN PARK
Postdoc, University of Freiburg, Germany

ELWIRA SMAKOWSKA
Assistant professor, Wageningen University, The Netherlands

SIMON UHSE
Deputy Head of Microbiology, Octapharma, Vienna, Austria

19 THE VIENNA BIOCENTER

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:
1,800 employees, 1,300 students, 90 research groups, and 27 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),** a basic research institute funded by Boehringer Ingelheim. Following the relocation of five university departments – that are now under the umbrella of the **Max Perutz Labs** – 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 for 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 **96 research groups** have acquired **49 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.

19 CORE SERVICES

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

BIOOPTICS

The services offered by the BioOptics facility cover analytical flow cytometry and cell sorting, as well as a large variety of microscopy techniques, image processing, and analysis. Looking at the fine detail of cells and cellular structures can provide valuable insights into their function and interaction with other cells and molecules. With state-of-the-art equipment and skilled experts, the BioOptics Facility supports research groups by helping them analyze and visualize cells. The lab has ten flow cytometers and more than 25 microscope systems that are specialized in imaging a variety of subjects.

MAX PERUTZ LIBRARY

The Max Perutz Library is a specialized reference library. It maintains and develops literature collections and information services in support of present and future research and teaching needs. Furthermore, it provides a quiet and well-equipped study environment with a modern and secluded reading room.

MOLECULAR BIOLOGY SERVICES

The Molecular Biology Service offers a wide variety of services and materials. The most important ones include Sanger Sequencing, a "Speed Congenics" service, preparation of competent cells of various *E. coli* strains, production of recombinant proteins and enzymes, monoclonal antibodies, a routine mycoplasma testing service for tissue culture cells, and plasmid prep in 96 well format. In addition, the Molecular Biology Service provides instrumentation and expertise for lab automation and high-throughput methods. Over the last few years, the protein production service has grown substantially. As a routine service, it now produces more than 80 growth factors and enzymes to support research groups with high quality proteins. The Molecular Biology Service uses Gene Expression Microarrays and CGH Microarrays from Agilent. As an extra service, it also provides clones from its RIKEN clone repository where researchers have the possibility to search a database and order a specific clone.

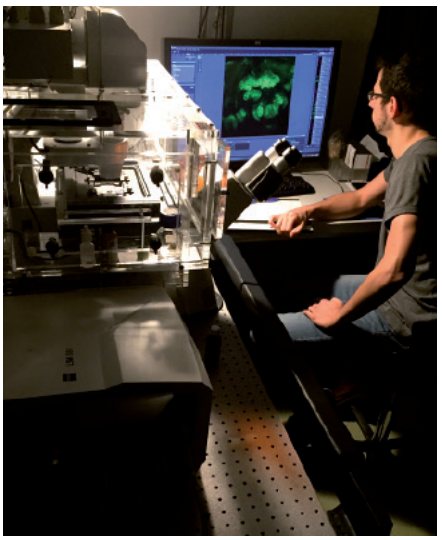
PROTEIN CHEMISTRY FACILITY

The Protein Chemistry facility offers protein analyses. Their services include protein identification, characterization of posttranslational modifications, protein quantification, and the respective data interpretation. Additionally, the Protein Chemistry facility provides peptide synthesis and affinity purification of antibodies. It operates several chromatography systems for both protein and peptide separations and several state-of-the-art mass spectrometers. To keep its technology platforms competitive, the facility constantly establishes and develops new protocols. Currently, it focuses on methods for improving the sensitivity of protein identification, protein quantification, and cross-linking technology. It also develops bioinformatics tools for data interpretation.

SCIENTIFIC WORKSHOP

The scientific workshop assists scientists in any hardware challenge: designing and building prototypes, robotics, or any custom-made experimental setup that requires expert skills and professional tools to translate ideas into custom-made products in the service of discovery.

BioOptics.



Vienna BioCenter
CORE FACILITIES

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:

NEXT GENERATION 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, NextSeq, and NovSeq, an ONT MinIon, and a PacBio Sequel.

PLANT SCIENCES

The Plant Sciences facility (PlantS) operates 22 state-of-the-art and highly specialized plant growth chambers along with professional support. 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. They offer several different phenotyping platforms, including the PHENOTron, a chamber equipped with an automated imaging system powered by LemnaTec and were recently awarded a €2.2 Mio FFG grant to develop a new automated phenotyping platform for mid-sized crop plants, PHENOPlant, which should come online in 2021.

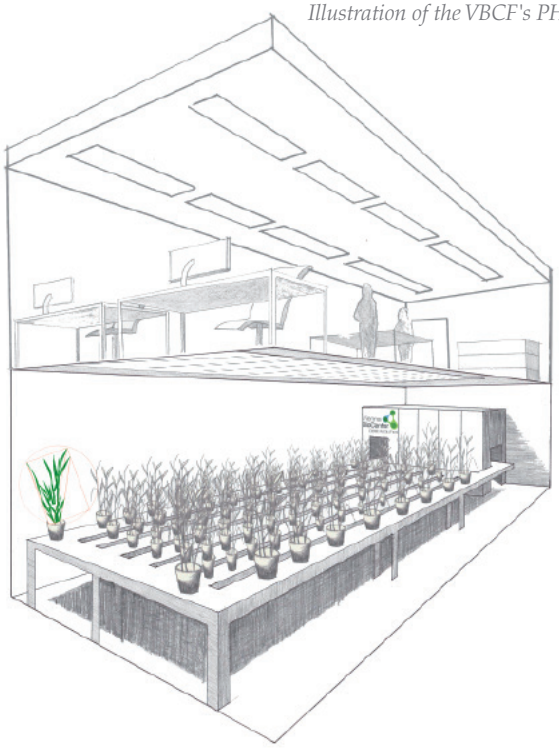
PROTEIN TECHNOLOGIES

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 theater, grow vegetables, go ice skating, and do everything else a children's heart desires.

Illustration of the VBCF's PHENOPlant.



The Child Care Center at the Vienna BioCenter.

19 FINANCE & ADMINISTRATION

Hansjörg Stampfl | Martina Gsur | J.Matthew Watson | Mariola Glawischnig | Mireia Verdaguer | Johanna Ostah | Jens Schaich
Anneliese Auer | Markus Kiess | Simona Wójcik | Borries Luberacki

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

MARTINA GSUR
Assistant to the Directors

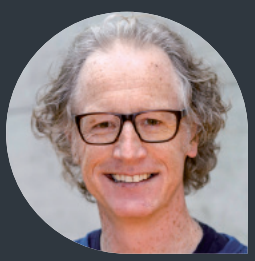
19 GMI SCIENTIFIC ADVISORY BOARD

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

> The GMI continues to hold its place among the top tier institutes for plant science world-wide. There is palpable excitement about the science being done at the GMI and this intellectual environment, coupled with exceptional infrastructure supported by the continued support of the Austrian Academy, have enabled the GMI to attract exceptionally high caliber group leaders at both senior and junior levels. These groups are making significant progress towards understanding fundamental processes involved in gene regulation, evolution and ecological and environmental responses in plants, while also building connections between the GMI and the VBC writ large.

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

Section of the ceiling fresco in the meeting room of the Austrian Academy of Sciences
© Klaus Pichler / ÖAW

THE AUSTRIAN ACADEMY OF SCIENCES

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

ÖAW 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.

19 PROMOTING THE IMPORTANCE OF PLANT SCIENCE

At the GMI, we consider the public dissemination of our scientific research to be an important objective. We are involved in several projects aimed at providing a lasting opportunity to engage the public with plant science.

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!"

ÖAW COMICS

This year, the ÖAW produced four comic books aimed at showcasing science for a younger audience. As part of their presentation, we presented our work and the importance of plant biology to school classes from around the country.

www.oeaw.ac.at/akademics

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

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

19 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 ten years in a row (2010-2019)! 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:

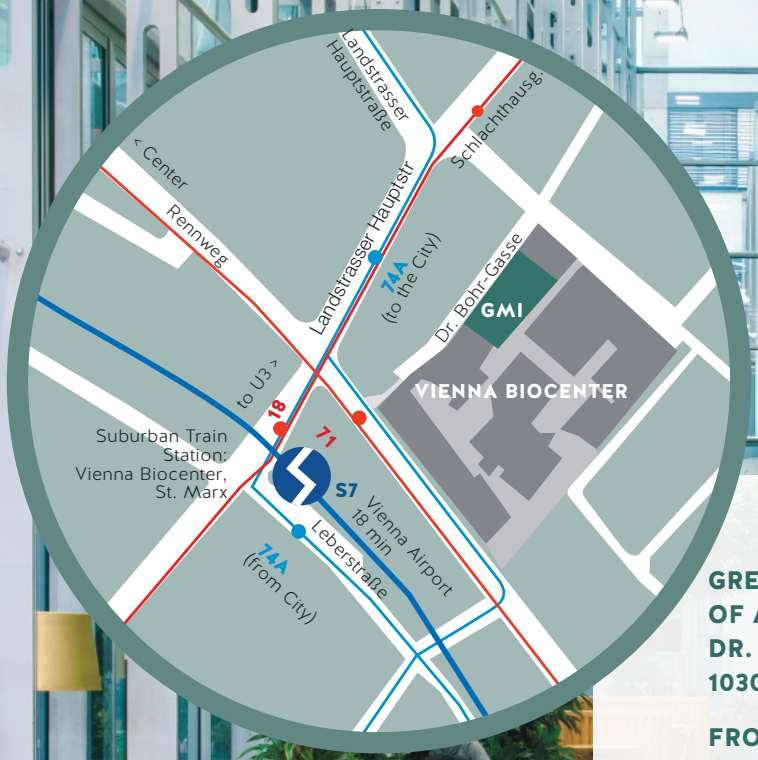
ITS LOCATION – in the heart of Europe, with easy connections in all directions, whether to go home or on a weekend excursion to another European capital.

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 and a number of other international corporations and organizations, Vienna has become a dynamic, multicultural, and cosmopolitan city in the last two decades.

LOCATION AND TRAVEL DIRECTIONS



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

FROM THE AIRPORT:
by city train (S-Bahn):
S7 to Sankt Marx-Vienna Biocenter

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

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

Vienna BioCenter

GMI

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SCIENCES