

WHERE
KNOWLEDGE
GROWS

WHERE
KNOWLEDGE
GROWS

CONTENTS

IMPRINT

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Front page: The theme of this year’s annual report is “Where Knowledge Grows”. The cover takes on this idea quite literally, when some of the model plants used at the GMI grow out of the GMI brand mark.

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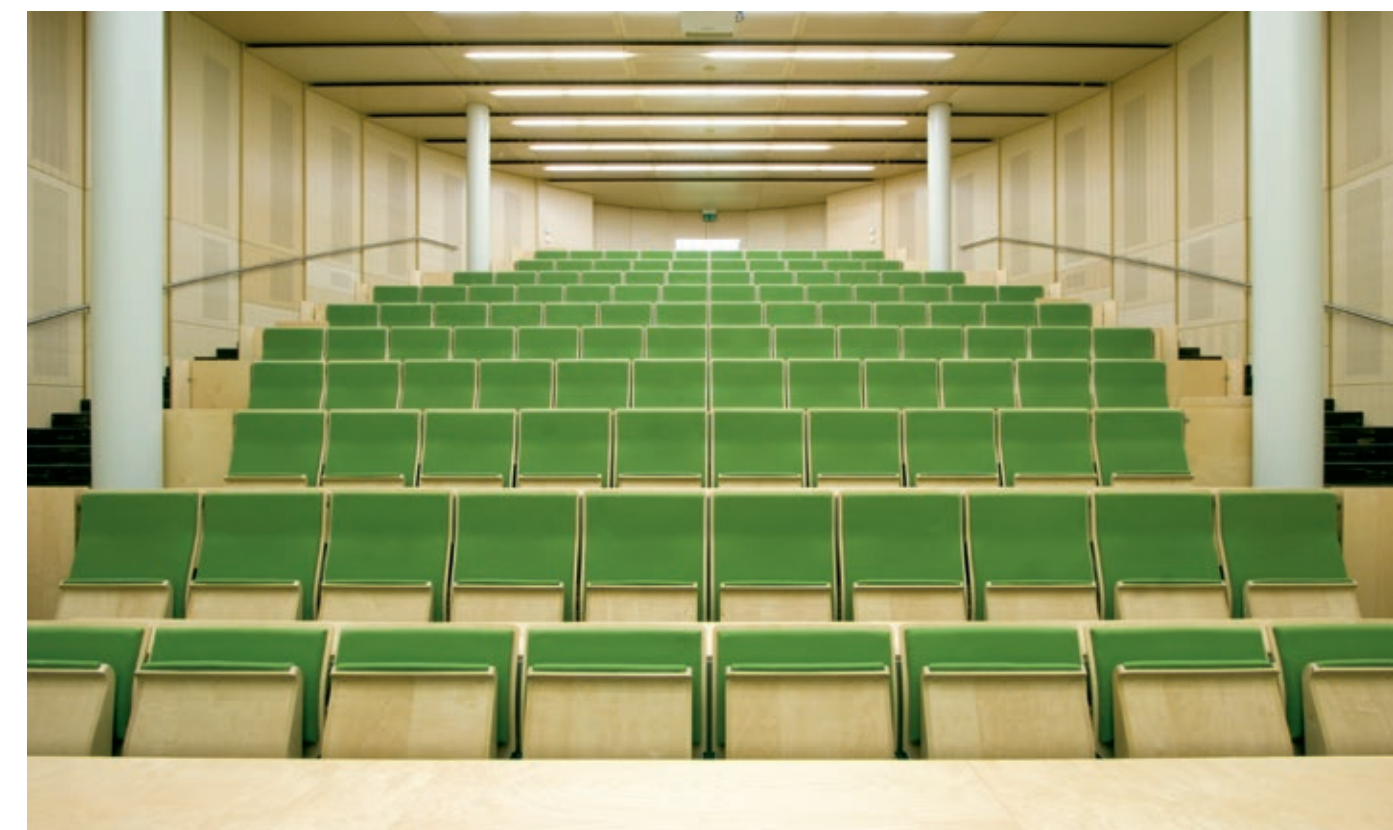
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01 —

INTRODUCTION



**DR. MAGNUS NORDBORG**

Scientific Director

DR. MARKUS KIESS

Business Director

DIRECTORS' STATEMENT

We are proud to be part of one of the very few research institutions worldwide devoted to basic plant biology. The vision of the GMI is to contribute to our understanding of biology, in particular plant biology, by carrying out excellent research and asking fundamental questions. Crucial aspects of how plants function are still unknown, from cell biology and development to evolution and ecology.

The centrality of plants to life on Earth is obvious: through millions of years of photosynthesis, plants created our atmosphere as well as our reserves of fossil fuel — a process humanity is currently partly reversing on a timescale of a few generations.

As directors, our main task is to create the research environment that makes realizing this vision possible,

through efficient administration, world-class services, and financial support for independent research groups. We create the sandbox: the rest is up to our researchers, as nothing about our research is top-down. We know that we have succeeded when students and postdocs collaborate across groups, follow their own ideas, and ultimately move on to other positions.

The world is starting to realize that humanity is facing its greatest challenge and is counting on science to help. Our work is only possible thanks to the continued support of the Austrian Academy of Sciences and the Federal Ministry of Education, Science and Research. We also wish to thank the Ministry as well as the City of Vienna for their general support of the Vienna BioCenter — and all our colleagues for making this an amazing place to work.



INTRODUCING THE GMI

PROFILE

The Gregor Mendel Institute of Molecular Plant Biology (GMI) was founded by the Austrian Academy of Sciences (ÖAW) in 2000 to promote research excellence in molecular plant biology. It is the only international center for basic plant research in Austria and one of the very few throughout the world. Our goal is to make fundamental discoveries that help us understand how plants function — discoveries that may be essential to address global challenges like climate change.

The GMI is located in the Vienna BioCenter, a leading life science cluster near Vienna's city center. The Vienna BioCenter includes biotech companies and five other research institutes: the Institute of Molecular Biotechnology (IMBA), the Research Institute of Molecular Pathology (IMP), the Max Perutz Labs, the Faculty of Life Sciences and the Centre for Microbiology and Environmental Systems Sciences (both University of Vienna). Together with the biotech companies located at the Vienna BioCenter, this life science cluster creates a forward-looking and fast-growing environment for GMI scientists to pursue their research and make fundamental discoveries.

RESEARCH

Research at the GMI covers many aspects of molecular plant genetics, including basic mechanisms of epigenetics, cell biology, plant-pathogen interactions, developmental biology, and population genetics. During the last 20 years, the model plant *Arabidopsis thaliana* has emerged as the primary experimental system for plant molecular biology. While *Arabidopsis* remains the main model organism at the GMI, scientists at the GMI 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.

Research activities at the GMI are supported by a streamlined administration, world-class scientific infrastructure, and a diverse set of core facilities and services which provide access to state-of-the-art equipment. Core funding is received from the Austrian Academy of Sciences, and scientists at the GMI are highly successful in acquiring third-party funds from a variety of Austrian, European Union, and international funding agencies.



Liam
DOLAN



“

GMI is a great place to work and play because the diversity of the research leads to exciting collaborations at the interface between traditional disciplines. Our lab has been able to make discoveries that would have been impossible without the input and skills of other scientists at GMI and the outstanding support of the VBC facilities.

INTRODUCING THE GMI

IMPORTANCE OF EXPERIMENTAL PLANT RESEARCH

Plants are the primary producers of the world’s ecosystem and thus essential for all life on earth. This basic fact is receiving new attention due to rising food prices, diminishing fossil fuel reserves, and a changing climate. To guarantee sustainable food and energy production in the 21st century, major innovations will be required. Some of these innovations 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 medicine.

Gregor Mendel’s discovery of the basic principles of genetics, Barbara McClintock’s discovery of transposons, and the recent work on epigenetics and RNA silencing are only a few of the dozens of examples.

What critical discoveries will plant research bring in the future? These are exciting times, for there is still much to learn, from the network interactions of receptor kinases, chloroplast biogenesis, and protein quality control, to how histones and their modifications define genomic regions. The possibility of fundamental discoveries in these and other areas is high, and everyone at the GMI is excited to push the limits of what we know about plant biology.

EDUCATION

The Gregor Mendel Institute offers many of its PhD positions through the international Vienna BioCenter PhD Program, and is also part of several externally funded doctoral programs. PhD candidate education plays a major role at the GMI, which offers a flexible and rigorous training program that is aimed at developing essential skills and competencies. Transferable skills courses and career development resources are provided by the Vienna BioCenter Training Unit.

Every summer, GMI research labs host undergraduate students as part of the Vienna BioCenter Summer School. In 2021, the GMI launched the International Internship Program I²P, which provides opportunities to perform cutting-edge plant research and guidance for embarking on scientific careers.

The GMI is committed to communicating the societal values of plant science research and accomplishes this, amongst other measures, through outreach events in collaboration with cultural and educational institutions in Austria and all over Europe.

WORKING AT THE GMI

The GMI provides a lively, international working environment with around 130 staff from over 30 countries. The working language is English.

The GMI is an excellent place to develop a scientific career. All researchers have access to superb infrastructure and generous funding, allowing for enormous intellectual freedom. We offer minimal hierarchy and bureaucracy, a subsidized cafeteria, flexible working hours, and on-site day care facilities.

Research is complemented by scientific events, including a packed schedule of seminars, an annual scientific retreat, GMI-organized conferences, and weekly social gatherings. Events are intentionally designed so students form important social and professional relationships and connect with career paths. Group leaders are mentors first and foremost, and actively create a space for students to openly discuss ideas.

Scientists at the GMI are driven by their curiosity to discover how plants function. Researchers pursue big questions, from the adaptation to climate change to the structure of chromatin, in an intellectually stimulating and collaborative environment.

CURIOUS

Lemna minor
DUCKWEED

02 —

RESEARCH GROUPS



BELKHADIR GROUP

BERGER GROUP

DAGDAS GROUP

DOLAN GROUP

MARÍ-ORDÓÑEZ GROUP

MITTELSTEN SCHEID GROUP

NORDBORG GROUP

RAMUNDO GROUP

SWARTS GROUP



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Chief Scientific Officer (2011-2013):
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Duhwa LEE

TECHNICIAN
Natalie EDELBACHER

INTERNS
Geon HEO*

(*left the lab in 2022)

BELKHADIR GROUP

DECISION-MAKING THROUGH RECEPTOR KINASES

To grow as efficiently as possible, plants must be able to sense and then respond to their environment. Unlike animals, which rely on sensory organs, plants sense using specialized proteins located on the surface of their cells called receptor kinases (RKs). Receptor kinases recognize chemical signals from the environment and then help the cell decide how to respond.

With more than 600 in *Arabidopsis*, 10 times more than in animals, RKs are involved in regulating nearly all aspects of plant development as well as defense against pathogens.

The Belkhadir lab aims to identify which chemicals the RKs recognize, how these hundreds of receptor proteins process the chemical information to decide on an optimal growth strategy for the plant's environment, and how this strategy is carried out at the cellular and organismal level. The group especially focuses on understanding how plants choose to allocate resources between growth and pathogen defense. The knowledge they gain will help the Belkhadir lab understand how plants make developmental decisions.

This understanding could be used to develop plants that grow more robustly and are more resistant to pathogens.

ADVANCES
IN 2022

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

BELKHADIR
GROUP

PAIRING RECEPTORS WITH LIGANDS BY
HIGH-DENSITY GLYCAN ARRAYS

Specific RK families have been implicated in binding to various carbohydrate moieties, including components of the plant and microbial cell wall (CW). Microarrays displaying hundreds of different glycan structures are versatile tools for rapidly analyzing interactions between RKs and CW molecules. We systematically tested RK ECDs on these arrays and revealed novel RK-glycan pairs. We have so far determined that one of these RK-glycan pairs is involved in plant immune responses to glycan ligands. In 2022, we have mainly focused on understanding the biological relevance of these receptor-ligand interactions.

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, we are currently focusing on a major ligand-receptor pair involved in plant immunity and bacterial motility. We decoded the immunogenic and motility profiles of the bacterial epitope and determined the spectrum of amino-acid mutations that drive antagonistic pleiotropy. In the process, we discovered two synthetic mutational tracks that undermine the detection of a bacterial epitope by the cognate immune receptor. These tracks generate epitopes with either weaker agonist or antagonist activities. Finally, we found that the output of these synthetic tracks occurs naturally in bacteria that co-exist with plants.



DUHWA LEE

POSTDOCTORAL FELLOW

Seoul, South Korea
PhD: Yonsei University, Seoul, South Korea

HOW DID YOU COME TO THE GMI?

When I finished my PhD course in 2019, I met Youssef at a seminar in Korea. I was impressed by his fascinating research style and efforts to answer fundamental questions in the plant immunity field. At the end of the seminar, he announced that he was hiring a new postdoc, which prompted me to reach out to him immediately. After meeting with him to discuss my motivation, he directly offered me a postdoc position. The quick decision was such an unforgettable experience.

WHAT PROJECT ARE YOU WORKING ON?

During the last two years, I have been working on developing small agonist ligands for plant immune receptors. We established high-throughput screening pipelines to identify novel agonists for a target receptor and obtained two strong agonist candidates. I am convinced that these novel agonist molecules will be effective in crops beyond model plants.

WHAT DO YOU ESPECIALLY LIKE ABOUT
WORKING AT THE GMI?

The support we receive at the GMI enables us to focus entirely on science. Cutting-edge scientific facilities and services help to accelerate our research. Moreover, I would emphasize the positive mentality of GMI researchers – people here are not afraid of change and are keen on exploring new perspectives.

WHERE DO YOU WANT TO GO NEXT?

I will be moving to BOKU (University of Natural Resources and Life Sciences) for another postdoc position in 2023. There, I intend to broaden my research field to studying glycans and glycan receptors using my experience at GMI. I will continue my project started at GMI to reveal novel glycan-receptor pairs.



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Tatsuo KANNO

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(*left the lab in 2022)

BERGER GROUP



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JOINED GMI

in January 2014

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Group Leader (2004-2014):
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EVOLUTION OF CHROMATIN

In both plants and animals, DNA is wrapped around nucleosomes. Nucleosomes consist of proteins called histones and help organize DNA into functional units, they are thus critical for all cellular processes that affect DNA.

Several different variants of histone proteins evolved. These variants either modify the structural properties of the nucleosome or confer specific properties to chromatin. Some variants exist in all eukaryotes while others are found only in specific groups of species. In addition, chemical modifications of histones regulate nucleosome properties.

The Berger lab investigates the evolution of histone variants and their roles in organizing the genetic information encoded by DNA into units that are readable by the transcription and translation machinery. Genetics, genomics, and biochemical analyses are combined with synthetic strategies to study chromatin in *Arabidopsis*, *Marchantia*, unicellular red algae, and fission yeast.

BERGER GROUP

A NEW TYPE OF
GENOMIC IMPRINTING

Parental genomic imprinting was reported so far only in flowering plants and mammals and causes preferential expression of one parental allele in a few hundred genes. This intriguing epigenetic regulation was thought to be determined by predominantly maternal nutrition of the embryo via extra-embryonic tissues, which connect the embryo and its mother.

Plants developed the capacity to produce embryos when ancestors of plants conquered the land around 500 million years ago. An early lineage of land plants is represented by the model liverwort *Marchantia* which produces male and female plants. The *Marchantia* embryo develops on the mother plant but nevertheless is devoid of extra-embryonic tissues. In 2022, we demonstrated that the embryo primarily expresses all genes inherited from the mother. In fact, the paternal chromosomes are repressed globally, a phenomenon that is mediated by the histone H3 modification through the Polycomb Repressive Complex 2. Furthermore, we demonstrated that this repression of paternal chromosomes is essential for the liverwort embryo’s survival (Montgomery et al., eLife 2022). We, therefore, propose that the innovation of imprinting does not rely on extra-embryonic tissues, suggesting that this epigenetic control could evolve in a much broader range of species that provide unique parental care to the embryo.

THE RELATIONSHIPS BETWEEN
CHROMATIN AND TRANSCRIPTION

Transcription factors and transcriptional activity recruit chromatin modifiers. To what extent chromatin instructs transcriptional activity is still a matter of debate. In *Arabidopsis*, we have shown that histone variants and their modifications assemble only in a surprisingly small number of stereotypic chromatin landscapes. The differentiation of the chromatin landscape depends equally on histone variants and histone modifications. We defined six chromatin landscapes occupied by specific families of transposons, which share a specific mode of transcriptional repression. In areas occupied by coding genes, ten chromatin landscapes were distinguished by the mode of transcriptional regulation and the type of gene function. We further showed that the nature of each chromatin landscape strongly influences the recruitment of transcription factors. Overall, our results suggest that the genome sequence provides cues for the organization of chromatin landscapes that can instruct transcriptional activity.



INSIGHTS

ZACHARY HARVEY

POSTDOCTORAL FELLOW
Cincinnati, Ohio, US
PhD: Stanford University, Stanford, US

HOW DID YOU COME TO THE GMI?
During my PhD, I had the fortune/frustration to work out the molecular mechanism of an unusual protein-based form of epigenetics, which through nearly a dozen factors changed the structure of heterochromatin. For my postdoc, I wanted to find a place where I could dig deeper into how such complexity evolved. By chance I met Fred at a conference, and after some discussions I thought that coming to his lab at the GMI would be an excellent opportunity to investigate these questions.

WHAT PROJECT ARE YOU WORKING ON?
Eukaryotes have evolved a staggering diversity of mechanisms to regulate their genomes. My focus is on understanding how one of those mechanisms – histone variants – arose, and what the molecular drivers of their divergence were. Using molecular phylogenetics and synthetic biology, I have uncovered

co-evolution between the histone H2A.Z and transcription, providing insight into both H2A.Z’s function in gene regulation, and highlighting one mechanism constraining the evolution of chromatin.

WHAT DO YOU ESPECIALLY LIKE ABOUT WORKING AT THE GMI?
GMI is a curiosity-minded, collegial, and diverse place to work. Compared to other places I have been, I find that there’s an unparalleled free and active exchange of ideas here. My colleagues genuinely want to hear what I’m working on during a coffee break. They are more than willing to share their thoughts and expertise to help me work better and dig deeper. I don’t think I would have the same confidence to pursue new and complex questions in a different environment.

WHERE DO YOU WANT TO GO NEXT?
That’s always a tricky question for a postdoc to answer. I’ve just had the fortune to secure another 3 years of funding from the Austrian Science Fund (FWF) ESPRIT program, which is designed to support postdocs in establishing an independent research program. I hope in the coming years to use this opportunity to do just that and will probably start looking for independent positions in due course.



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DAGDAS GROUP



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JOINED GMI

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PhD: University of Exeter,
UK

PREVIOUSLY

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ADAPTATION THROUGH AUTOPHAGY

To respond to environmental changes and pathogen attacks, plants must rapidly 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 studies the details of how autophagy works in plants and the role it plays in plant development, stress responses, and immunity. The group hopes that their findings will contribute to developing plants with improved yields that are more tolerant to environmental stress and pathogens.

DAGDAS GROUP

Comparative approaches have led to major scientific breakthroughs since the early days of molecular biology. Studies in “exotic” species resulted in the discoveries of green fluorescent protein (GFP, jelly-fish), action potential (squid), as well as learning and memory (*Aplysia*), just to name a few. In recent years, however, “model” organisms have become increasingly entrenched and comparative approaches have largely been neglected in mechanistic research. On the other hand, evolutionary biologists mostly focused on genes and proteins and largely neglected the cell. Since evolutionary change happens at the cellular level, understanding how cellular features arise and diversify should be a central question in evolutionary biology. Recent transformative technological advances in sequencing, genome editing, and transformation now make it feasible to bridge this gap.

Our lab employs a comparative mechanistic approach to understand how plants use selective autophagy to maintain cellular homeostasis. Using *Marchantia* and *Arabidopsis* as comparative model systems, we follow a three-layered approach to explore (i) organelle recycling mechanisms, (ii) crosstalk between selective autophagy and other quality control pathways, and (iii) stimulus and cell-type specificity of selective autophagy-mediated cellular quality control.

Over the last year, we have made significant progress on the crosstalk between autophagy and other quality control pathways. By characterizing an autophagy adaptor, we defined a hybrid compartment called the amphisome. The amphisome is formed when an autophagosome fuses with multivesicular bodies. We propose that these compartments function as sorting hubs that facilitate the coordination of various vacuolar trafficking pathways (Zhao et al., J Cell Biol 2022).

To further understand quality control, we studied the evolution of the C53 autophagy receptor, using a combination of phylogenetic profiling, cellular biochemistry, and Nuclear Magnetic Resonance spectroscopy. We have shown that C53 evolved non-canonical short linear motifs to coordinate autophagy and UFMylation, an enigmatic posttranslational modification system activated by ribosome stalling at the endoplasmic reticulum (Picchianti et al., bioRxiv).

Finally, we have contributed to a project in which cell type-specific autophagy responses were shown to be crucial for cell corpse clearance during programmed cell death in *Arabidopsis* root cells (Feng et al., Curr Biol 2022).



INSIGHTS

NI ZHAN

POSTDOCTORAL FELLOW

Beijing, China
PhD: Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China

HOW DID YOU COME TO THE GMI?

I am fascinated by the mechanism of plant autophagy. When I began to search for outstanding plant autophagy labs, I found that the Dagdas lab is systematically working on plant autophagy pathways using very interesting and diverse approaches. Without any hesitation, I contacted Yasin and he offered me the postdoc position at the GMI. With Yasin’s help, I successfully applied for the Marie Skłodowska-Curie Individual Fellowship, which allowed me to join the GMI.

WHAT PROJECT ARE YOU WORKING ON?

Currently, I am working on the regulation of the ER-phagy receptor C53 through a form of post-translational modification called UFMylation. ER-phagy defines the degradation of portions of the endoplasmic reticulum (ER) within lysosomes or

vacuoles. I am now cooperating with my colleagues, PhD students Lorenzo Picchianti and Victor Sánchez De Medina on uncovering the regulation mode of the C53 protein during ER stress and its physiological significance in plants.

WHAT DO YOU ESPECIALLY LIKE ABOUT WORKING AT THE GMI?

The GMI is a world-class plant biology institute, it provides an excellent research environment supported by cutting-edge core facilities. The experienced technicians, lab managers, and plant facilities at the GMI and our group greatly helped me accelerate the pace of my research project. Not to forget the excellent administration that has been helping me since the first day I arrived in Austria. I really appreciate the fantastic atmosphere here at the GMI and our supportive and friendly colleagues.

WHERE DO YOU WANT TO GO NEXT?

I do not have concrete plans for my next career step yet. However, I hope to be able to continue my academic research at a university or research institute.



JOINED GMI
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DOLAN GROUP

DEVELOPMENT AND EVOLUTION OF LAND PLANTS

The Dolan group uses the liverwort, *Marchantia polymorpha*, to discover mechanisms of plant development that are specific to bryophytes or are difficult to research in other model organisms.

By identifying genes that regulate the development of the rooting structure in *M. polymorpha* and comparing it to the mechanisms that control rooting structure in other land plants, the lab discovered the mechanism that controlled the development of the earliest land plant rooting structures.

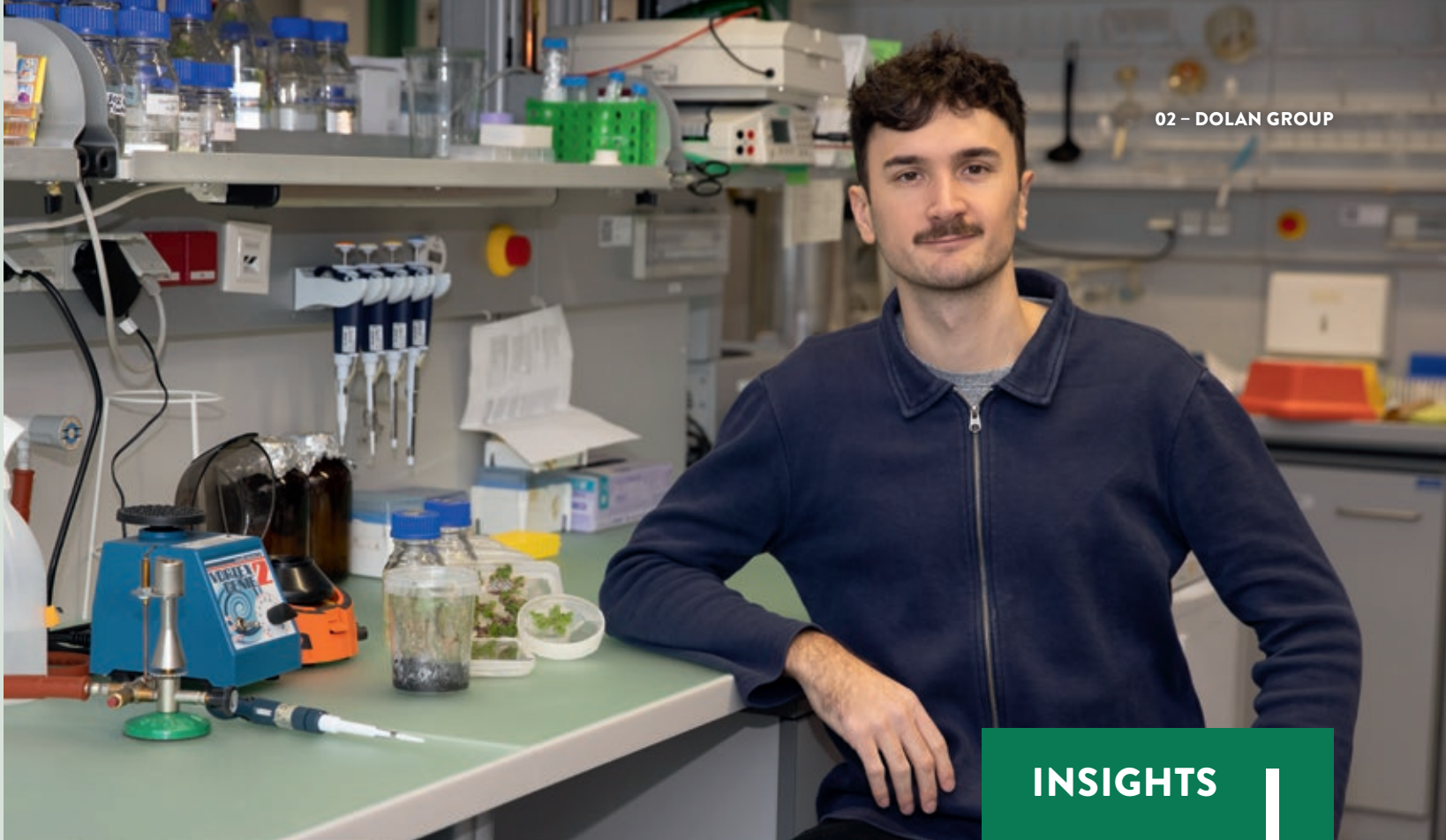
Currently, the lab investigates how cells develop polarity *de novo* – how a cell transitions from a non-polar state to a polar state. To study this question, the Dolan group uses unique characteristics of the *M. polymorpha* model and will investigate how these mechanisms operate in other land plants. These studies will define the mechanism that operated in the common ancestors of the land plants and demonstrate how these mechanisms have changed over the course of land plant evolution.

DOLAN GROUP

THE *DE NOVO* GENERATION OF CELL POLARITY IN PLANT CELLS

Land plants develop multicellular haploid and multicellular diploid phases in their life cycles. The multicellular diploid phase is derived from the polarized zygote. The zygote inherits its polarity from the polarized egg and this polarity defines the first apical-basal body axis. On the other hand, the multicellular haploid phase of the land plant life cycle is derived from a spore cell. The mature spore cell lacks polarity – it is spherical – and polarity develops *de novo* soon after germination. This polarity guides the development of the first apical-basal body axis. Nothing is known to date about the mechanisms of polarization in the spore and how this cellular polarity directs the formation of the apical-basal body axis.

We are currently investigating how different processes interact in spore cell polarization. The nucleus is located in the center of the cell, the cell core. The earliest visible evidence of polarization is the basal movement of the nucleus from the cell center to the cell cortex at the basal pole. This movement takes approximately 45 minutes. Soon after arriving at the cortex, the nuclear envelope breaks down, and a mitotic spindle forms near the basal pole. Cytokinesis results in an asymmetric cell division forming a relatively small basal cell that immediately differentiates as a rhizoid and an apical cell that functions as a regenerative stem cell. Therefore, the basal movement of the nucleus before cell division accounts for cellular asymmetry, which is an expression of cell polarity.



INSIGHTS

JOHANNES RÖTZER

PHD STUDENT

Vienna, Austria
MSc: Department of Botany and Biodiversity
Research, University of Vienna, Austria

HOW DID YOU COME TO THE GMI?

Although I studied botany in Vienna, I heard about the GMI only during my Master’s studies. During my botany studies, I focused mainly on palynology (the study of pollen grains), including melissopalynology (the study of pollen from honey samples) and forensic palynology. Shortly before deciding on a project for my Master’s thesis, I wanted to try something completely new. A few days after this decision, my application for a Master’s thesis position in Ortrun’s lab was already out. In Ortrun’s lab, I worked on RDR3/4/5 in *Arabidopsis*.

Since I really enjoyed the molecular biology work and it was challenging, I applied for a PhD position and luckily landed in Liam’s lab.

WHAT PROJECT ARE YOU WORKING ON?

Back to the roots – as in my work with pollen during my studies, I am again working with a very small model system. Using *Marchantia* spores, I am investigating the role of blue light receptors (e.g., MpPHOT, MpCRY, MpFKF) in the establishment of cell polarity in my main project.

WHAT DO YOU ESPECIALLY LIKE ABOUT WORKING AT THE GMI?

I am happy to work at the GMI because of the three Ps:
- Plants
- People
- Pcience (P=S)

WHERE DO YOU WANT TO GO NEXT?

I am in the second year of my PhD and fully focused on my projects. Depending on how this journey turns out and where it takes me, I can very well imagine pursuing a career in science. But I could also imagine a future in knowledge transfer or teaching. An unlikely scenario but sitting in the back of my mind is my Plan C, which is agriculture. Yes, I am a farmer’s son.

To do research means to be creative: finding new approaches to address questions that have not been asked before. At the GMI, scientists enjoy and embrace the intellectual freedom provided by the institute to push the boundaries of knowledge.



CREATIVE



Marchantia polymorpha
LIVERWORT

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(*left the lab in 2022)

MARÍ- ORDÓÑEZ GROUP

DEFENDING THE GENOME AGAINST TRANSPOSONS

Transposons are DNA sequences in plants and animals that can copy themselves and move around the genome. Because transposons are able to move throughout the genome – hence their nickname “jumping genes” – they are important drivers of evolution.

This same ability, however, can result in transposons disrupting genes and causing disease. Because they can copy themselves before moving, transposons can expand rapidly: Transposons make up more than

40% of all the DNA in humans and as much as 80% 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 investigates how plant cells recognize and silence transposons. This knowledge will help the research group understand how these selfish genetic elements affect genomes. As part of this research, the Marí-Ordóñez lab is investigating a group of plants that have not been traditionally used in science, called duckweeds. Duckweeds are rapidly growing aquatic plants gaining attention as a new source of fuel and food. Hence, the tools developed in the lab could have wide-ranging applications and help advance research in the field.



**ARTURO
MARÍ-ORDÓÑEZ**

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JOINED GMI

in January 2019

PhD: ETH Zurich, CH

PREVIOUSLY

Postdoc (2017-2018): Julius
Brennecke Lab, IMBA, Vienna, AT

Postdoc (2014-2016): Olivier Voinnet
Lab, ETH Zurich, CH

MARÍ-ORDÓÑEZ GROUP

Organisms have evolved mechanisms to identify and suppress the activity of transposable elements (TEs) through the formation of heterochromatin at TE insertions, which abrogates their expression. Once heterochromatin is established, small RNA molecules (18-30 nt long) produced from silenced TEs continuously guide silencing complexes to reinforce the heterochromatic state. Although the mechanisms that maintain TEs silenced are well described in the model plant *Arabidopsis thaliana*, the question of how silencing is initiated remains elusive, as heterochromatic small RNA pathways act on already silenced TEs. Furthermore, not all TEs are regulated by small RNAs, suggesting that other mechanisms might initiate the silencing of transposable elements.

We use duckweeds as a model system. Duckweeds are aquatic plants that mostly reproduce asexually. Some of the factors involved in TE silencing are missing or not expressed during duckweed clonal (asexual) reproduction. Hence, duckweeds represent a unique opportunity to investigate the molecular basis of silencing as well as the complex evolutionary interplay between TEs and their hosts. We have sequenced the genomes and epigenomes of three species: *Spirodela polyrrhiza*, *Lemna minor*, and *Wolffia brasiliensis* confirming that they display distinctive epigenetic landscapes compared to the epigenetic landscape of *Arabidopsis*. However, the landscapes also differ between species albeit sharing similar silencing machinery. Whereas one might expect that low TE silencing is associated with higher TE load, we have observed that the higher the TE content in the genome, the more silencing marks are deposited on TEs.

Interestingly, duckweeds have experienced a different TE activity in the “recent” past (on the evolutionary timescale). TEs have mobilized of late in *Lemna* (and especially in *Wolffia*) compared to *Spirodela*, where TEs are mostly degenerated and presumably non-functional. Hence, relaxed silencing in *Spirodela* might not pose a threat to genome integrity. In *Lemna*, on the other hand, strict TE silencing must be maintained to prevent the deleterious effects of recent and potentially functional TEs.

These observations raise very interesting questions. Which genes are responsible for TE silencing? Where/when are those genes expressed? Does silencing operate differently when organisms reproduce sexually?... To answer these questions, we are setting up genetic transformation, a challenging task in non-model organisms. Nonetheless, we have started to obtain positive results in transient and stable transformations in all three species. Hence, we are one step closer to exploring what duckweeds can teach us about controlling and dealing with TEs.



INSIGHTS

DANIEL BUENDÍA

PHD STUDENT

Madrid, Spain
MSc: Universidad Complutense de Madrid, Spain

HOW DID YOU COME TO THE GMI?

In 2017, I joined the GMI as a VBC Summer School student and immediately fell in love with the science done here and the great atmosphere. After that, I promised myself to come back at some point during my career. After meeting Arturo at a later VBC Summer School anniversary symposium and being captivated by his project, I decided to apply right away for a short internship in his lab, and for the VBC PhD program.

WHAT PROJECT ARE YOU WORKING ON?

In the lab, we are working with a very peculiar family of flowering plants: duckweeds. Duckweeds are unique not only due to their morphology and physiological traits, but also because they have lost a pathway (RdDM) that plays a key role in the silencing of transposable elements (TE). My project is trying to

understand, using genomic approaches, how duckweeds have adapted to silence TEs in the absence of this pathway.

WHAT DO YOU ESPECIALLY LIKE ABOUT WORKING AT THE GMI?

I especially enjoy how stimulating this institute is. The scientific discussions, the work atmosphere, and the people always willing to help are very enriching, both scientifically and on a personal level. In addition, the world-class facilities that support research on campus and the vibrant scientific community at the VBC make the GMI an outstanding place to do research. Not to forget that our institute is also located in the lovely city of Vienna!

WHERE DO YOU WANT TO GO NEXT?

Tough question... I have not yet decided what to do or where to go. Although I am more inclined on doing a postdoc and continuing in academia, I cannot exclude moving to industry or exploring other career paths. Only time will tell. At present, I am focusing on my project to get the most out of it.

**POSTDOCS**

Mattia DONÀ
Nathalie DURUT*
Ruben GUTZAT
Marco INCARBONE
Zsuzsanna MÉRAI

PHD STUDENTS

Gabriele BRADAMANTE
Vu NGUYEN

STUDENT HELPERS & INTERNS

Zorana BOGOJEVIC*
Marta SALAS GOMEZ*
Denise SCHRATT*
Tobias WEGSCHEIDER*
Philip WOLFF

(*left the lab in 2022)

MITTELSTEN SCHEID GROUP



ORTRUN MITTELSTEN SCHEID

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JOINED GMI
in January 2004

PhD: University of Hamburg, DE

PREVIOUSLY

Research Associate (1992-2003):
Jerzy Paszkowski Lab, Friedrich
Miescher Institute for Biomedical
Research, Basel, CH

Postdoc (1988-1992): Ingo Potrykus
Lab, Institute for Plant Sciences at the
Federal Institute of Technology (ETH),
Zurich, CH

Postdoc (1985-1987): Hans-Georg
Schweiger Lab, Max Planck Institute
for Cell Biology, Ladenburg, DE

EPIGENETIC CONTROL OF GENETIC PARASITES AND RE- SPONSE TO LIGHT

Two heritable components determine the properties
of plants: genetic and epigenetic information.

While genetic information is encoded in the DNA
sequence of the genome, epigenetic information is
encoded in how the DNA is organized and determines

whether genes are turned on or off. While the genome
is common to nearly all cells in an individual, the
epigenetic state differs between cell types, tissues,
organs, and developmental states and is also
responsive to environmental cues and pathogens.
Epigenetic determinants include modifications of the
DNA (without changing the sequence), variants and
modifications of DNA-binding proteins, and several
types of RNA molecules that act on transcription and /
or translation.

The Mittelsten Scheid group studies the mechanisms
of epigenetic inheritance within cell lineages and
between generations, how epigenetic inheritance
changes during stress or virus infection, and how it
keeps a memory of light exposure.

ADVANCES
IN 2022

MITTELSTEN
SCHEID
GROUP

In contrast to animals, where all organs are formed during embryogenesis, plants generate new organs lifelong. New leaves and flowers originate from stem cells in the shoot apical meristem (SAM). Therefore, these cells are part of the germline connecting generations and responsible for the faithful transmission of genetic and epigenetic information. However, how many and which stem cells are included in the germline still needs clarification. We address this question with a lineage tracing system that labels the nuclei of individual cells and all progenitors with a fluorescent marker.

Stem cells must be protected against mutations, but also against genetic parasites like transposons and viruses. We investigate whether stem cells have specialized defense systems to maintain genome integrity across generations. We isolated stem cells from the SAM of *Arabidopsis thaliana* and found two members of the ARGONAUTE protein family strongly and specifically expressed. Both proteins are also present throughout the plant life cycle in other cells that potentially contribute to the germline. Furthermore, they are associated with transposon-derived small RNA (sRNA) molecules. As sRNAs provide the sequence specificity for gene silencing mechanisms installing DNA methylation, this points to an enforced epigenetic control of transposons in stem cells (Bradamante, Nguyen, et al., bioRxiv).

Stem cells are also protected against invasion by viruses, as many viruses are excluded from the SAM even in otherwise systemically infected plants. Although this was observed long ago and exploited to amplify virus-free plant material, the mechanisms

of this antiviral defense are not known. Combining mutants lacking RNA silencing components, different fluorescence-labeled viruses, and several microscopy techniques, including long-term live imaging, we could capture the dynamics of virus infection in the meristem and assign a role of small RNAs also in this defense.

Epigenetic regulation is also vital in the developmental context. Seeds of some variants of *Aethionema arabicum* do not germinate in the light, in contrast to *Arabidopsis* seeds, and the *Aethionema* seeds “remember” light exposure even after they have been transferred to darkness. This could prevent germination during the hot and bright season. Among seeds from mutagenized plants, we screened for those plants that ignore the light or have lost their light memory. Characterizing the gene defects in the mutants, we identified several factors in the light signaling pathways and could connect these factors to the hormonal regulation of seed germination (Mérai et al., in print).



INSIGHTS

RUBEN GUTZAT

POSTDOCTORAL FELLOW
Germany and Australia
PhD: ETH Zurich, Switzerland

HOW DID YOU COME TO THE GMI?
During my PhD I became interested in epigenetics, also known as cellular memory. Ortrun had just opened a position investigating epigenetic mechanisms in the context of ecology and evolution, so it was a perfect match.

WHAT PROJECT ARE YOU WORKING ON?
I aim to understand “epigenetic memory” in plant stem cells, which produce all above-ground plant organs. In addition to their capacity to drive developmental decisions, we found that stem cells must keep intrinsic

parasitic sequences in check. Hence, stem cells are the stage of a genomic combat, and I want to understand every aspect of this phenomenon.

WHAT DO YOU ESPECIALLY LIKE ABOUT WORKING AT THE GMI?
There is fantastic expertise at the campus, and people at all levels are helpful and cooperative.

WHERE DO YOU WANT TO GO NEXT?
I don’t know! There are too many possibilities, not only in academia and industry but also beyond.



POSTDOCS

Pieter CLAUW
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Anna IGOLKINA
Benjamin JAEGLE*
Tatsuo KANNO
Alexandra KORNIENKO
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Gregoire BOHL VIALLEFOND
Elizaveta GRIGOREVA
Rahul PISUPATI*

LAB MANAGER

Almudena MOLLA MORALES

TECHNICIANS

Joanna GUNIS
Viktoria NIZHYNSKA

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Bohdana HURIEVA*
Anna Jasmine KOKINO*
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Matin SAEIDI*

(*left the lab in 2022)

NORDBORG GROUP



MAGNUS NORDBORG

magnus.nordborg@gmi.oeaw.ac.at

JOINED GMI
in February 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

EXPLORING GENOMIC VARIATION

Differences in the DNA sequence between individuals lead to differences in appearance or behavior. Sometimes differences in just 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 seeks to understand the nature of the differences that give rise to phenotypic variation. How has natural selection molded this variation? How can we use our understanding of evolution to make sense of what we see in the genome? The lab uses a combination of computational biology together with lab and field work to address these questions. The knowledge the lab gains will lead to a better understanding of evolution and adaptation, knowledge which will be useful for understanding how organisms will react to our changing climate.

NORDBORG GROUP

WHAT IS GENETIC VARIATION?

The first human genome, published in 2003, cost an estimated 1 billion dollars to sequence. By 2014, the cost of additional human genomes had dropped to \$1000. These genome sequences are produced by comparing millions of short DNA fragments to the 2003 reference genome to identify differences, in particular Single Nucleotide Polymorphisms (SNPs). However, only small differences can reliably be found this way: larger structural variants such as gene duplications are often missed.

To capture all the variation, we need to compare complete, independently assembled genomes. A major effort of our group is to complement the previous “1001 *Arabidopsis* Genomes Project” with many independently assembled genomes. By the end of 2022, we have generated several hundred such genomes. Comparison of these genomes will grant us new insights into the nature and mechanisms of genetic variation. We are particularly interested in the role of mobile genetic elements, which can create additional copies of themselves throughout the genome. With our new genomes, we can catch them in the act, identifying mobile sequences that have been moving in the recent past.

HOW IS TRANSCRIPTION REGULATED?

High-throughput methods for measuring transcription by sequencing RNA are a standard tool in genomics. We use such methods to look for non-coding transcription and to find long intergenic non-coding RNA in the model plant *Arabidopsis*. By looking in multiple tissues in large numbers of individuals, we discovered almost an order of magnitude more loci producing long non-coding RNA than was previously known. We could trace this phenomenon to expression-variability between both tissues and individuals. Indeed, most of these loci are usually silenced, either due to structural variation in the genome or due to epigenetic silencing mechanisms. Much of this silencing appears to be related to transposon activity, either in generating structural variation or in creating targets for epigenetic silencing. This work provides new information about the factors governing transcription.

EPIGENETICS

For several years, we have been trying to understand what causes natural variation in DNA methylation. We hypothesize that epigenetic variation is mostly caused by genetic and environmental factors. We recently described the genetic basis for variation in a particular type of methylation on transposable elements (Sasaki et al., PLoS Genetics 2022), and have just submitted a paper that examines CG methylation on gene bodies. CG methylation can be directly inherited, meaning that the observed variation may reflect past influences. Using genetic crosses, we have demonstrated that trans-acting genetic variants affecting CG methylation exist and can interact with the environment. These kinds of mechanisms may underlie the natural genetic variation we observe.



INSIGHTS

RAHUL PISUPATI

PHD STUDENT (graduated in 2022)
Hyderabad, India
MSc: Indian Institute of Technology,
Kharagpur, India

HOW DID YOU COME TO THE GMI?

During my Master's at IIT Kharagpur, I was quite interested in evolutionary theory and population genetics. Vienna is one of the few places where many experts work on population genetics. I initially joined Magnus' group as a research intern to gather research experience. Eventually, I started my PhD through PopGen and the VBC PhD Program.

WHAT PROJECT ARE YOU WORKING ON?

During my PhD, I mainly worked on understanding the epigenetic variation in natural lines of *Arabidopsis*. Epigenetics in plants is a fascinating field, as it blurs the line between “nature and nurture” by mediating the inheritance of acquired epigenetic marks. Gregor Mendel made seminal discoveries on the laws of inheritance by working with pea plants. We are following a similar approach by aiming to understand

the laws of epigenetic inheritance in plants and the role of genetics by analyzing pedigrees.

WHAT DO YOU ESPECIALLY LIKE ABOUT WORKING AT THE GMI?

GMI and the VBC are excellent places to work for multiple reasons. Being centered in the most livable city Vienna, the institutes are highly international. There is much emphasis on collaboration between research groups and the institutes provide many opportunities for social interactions. The facilities and resources are commendable. It is a privilege to be here.

WHERE DO YOU WANT TO GO NEXT?

Post pandemic, I aim to work on applied problems. Food systems are especially fragile with increasing temperatures and industries have an important role to play. I have secured a research scientist position at Yara International, Germany and am keen on applying my research expertise and skills in agritech.

**PHD STUDENT**

Pamela VETRANO

TECHNICIAN

Nicole LETTNER*

STUDENT HELPERS & INTERNS

Marco BELLIN*

Julia KOBER

Cheuk-Ling WUN

(*left the lab in 2022)

RAMUNDO GROUP

Chloroplasts are a crucial component of our planet's life-support system: they sequester carbon dioxide and release oxygen while transforming solar energy into chemical energy during photosynthesis.

Chloroplasts have a fascinating evolutionary history and are a marvelous example of the relationship between structure and function. They contain a highly organized system of membranes where chemical reactions occur with remarkable precision. These reactions are orchestrated by multiprotein complexes. Their subunits are often encoded by the physically separated genomes of the chloroplasts and the nucleus.

The Ramundo lab aims to investigate the core machines and the signaling pathways involved in chloroplast protein biogenesis and quality control. The team employs two complementary model organisms: *Chlamydomonas reinhardtii*, a tiny, single-celled, photosynthetic eukaryote, and *Arabidopsis thaliana*, a land plant widely used as a model organism in plant biology. With their work, the research team envisions answering fundamental questions in organelle biology while developing or applying innovative research tools.



**SILVIA
RAMUNDO**

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JOINED GMI

in October 2021

PhD: University of Geneva, CH

PREVIOUSLY

HHMI Research Specialist, Peter Walter Lab,
University of California, San Francisco, US
(2018-2021)

EMBO and SNF Postdoc, Peter Walter Lab,
University of California, San Francisco, US
(2013-2015)

RAMUNDO GROUP

Launching our laboratory at the Gregor Mendel Institute during the past year has been a very constructive experience. We benefited from the excellent quality of the infrastructure, the generosity of the core funding, the efficient services provided by the lab support team, the friendly atmosphere of the human resource office, and the slim bureaucracy.

All lab members are actively contributing to making scientific findings. In addition, we are fortunate that several colleagues (inside and outside the institute) expressed genuine enthusiasm for our research program. With their support, we achieved far more than expected during the past months, and therefore we are motivated to continue working together.

The scientific highlights of this year include the isolation of novel and highly promising mutants, which are defective in the activation of the chloroplast unfolded protein response. In addition, we identified and are characterizing two highly conserved proteins that appear to be crucial for photoprotection. We also purified an essential chloroplast multi-protein complex that is now being investigated via single-particle cryo-electron microscopy.

This year, the lab successfully contributed ideas and experiments that led to two preprints. In the first preprint, we worked with the Dagdas lab at the GMI to demonstrate that the UFMylation machinery is functionally conserved in *Chlamydomonas* (Picchianti et al., bioRxiv). In the second preprint, we worked with Claire McWhite and the Onishi lab to show that a Notch-like signaling process is operating in *Chlamydomonas* (McWhite et al., bioRxiv). These findings are important because *Chlamydomonas* is a unicellular organism, while both UFMylation and Notch signaling were previously thought to be biological innovations linked to the emergence of multicellular organisms.



INSIGHTS

PAMELA VETRANO

PHD STUDENT

Lecce, Italy
MSc: University of Pisa, Italy

HOW DID YOU COME TO THE GMI?

I heard about the GMI from a former colleague of mine. She came to the GMI for the VBC Summer School, three years ago. Since I was looking for a place to do an internship after my Master's degree, I applied here and started as an intern in Silvia Ramundo's group. Six months later, at the end of my internship, I applied for the VBC PhD Program.

WHAT PROJECT ARE YOU WORKING ON?

I am investigating the molecular machinery responsible for chloroplast membrane quality control. In particular, I am focusing on two conserved proteins of unknown function that seem implicated in preserving the thylakoid structure in response to photooxidative stress.

WHAT DO YOU ESPECIALLY LIKE ABOUT WORKING AT THE GMI?

I like the exciting and challenging environment at the GMI. But, of course, also the many research facilities and the possibility to be trained in so many techniques.

WHERE DO YOU WANT TO GO NEXT?

I still do not know. My PhD just started, but I would consider moving to a company afterwards in order to have a broader view of my future career possibilities.

**POSTDOC**

Miguel VALLEBUENO

PHD STUDENT

Vasilina AKULOVA

TECHNICIANS

Alexis ARIZPE
 Julia RIEFLER*
 Lucyna SLUSARZ

STUDENT HELPERS & INTERNS

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 Anna GSTEU
 Paige GUEVARRA
 Krisztian NEMETH*
 Anni NURMISTO
 Lisa WEIDLICH
 Nora WITTMANN*
 Chun Chieh YEN

(*left the lab in 2022)

SWARTS GROUP

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.

JOINED GMI
 in January 2019

PhD: Cornell University,
 Ithaca, US

PREVIOUSLY

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



**KELLY
SWARTS**

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The Swarts lab addresses this problem with a novel approach focused on Norway spruce, one of the most economically important trees in Europe. The researchers 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, the researchers 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, the Swarts lab hopes 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 2022

SWARTS
GROUP

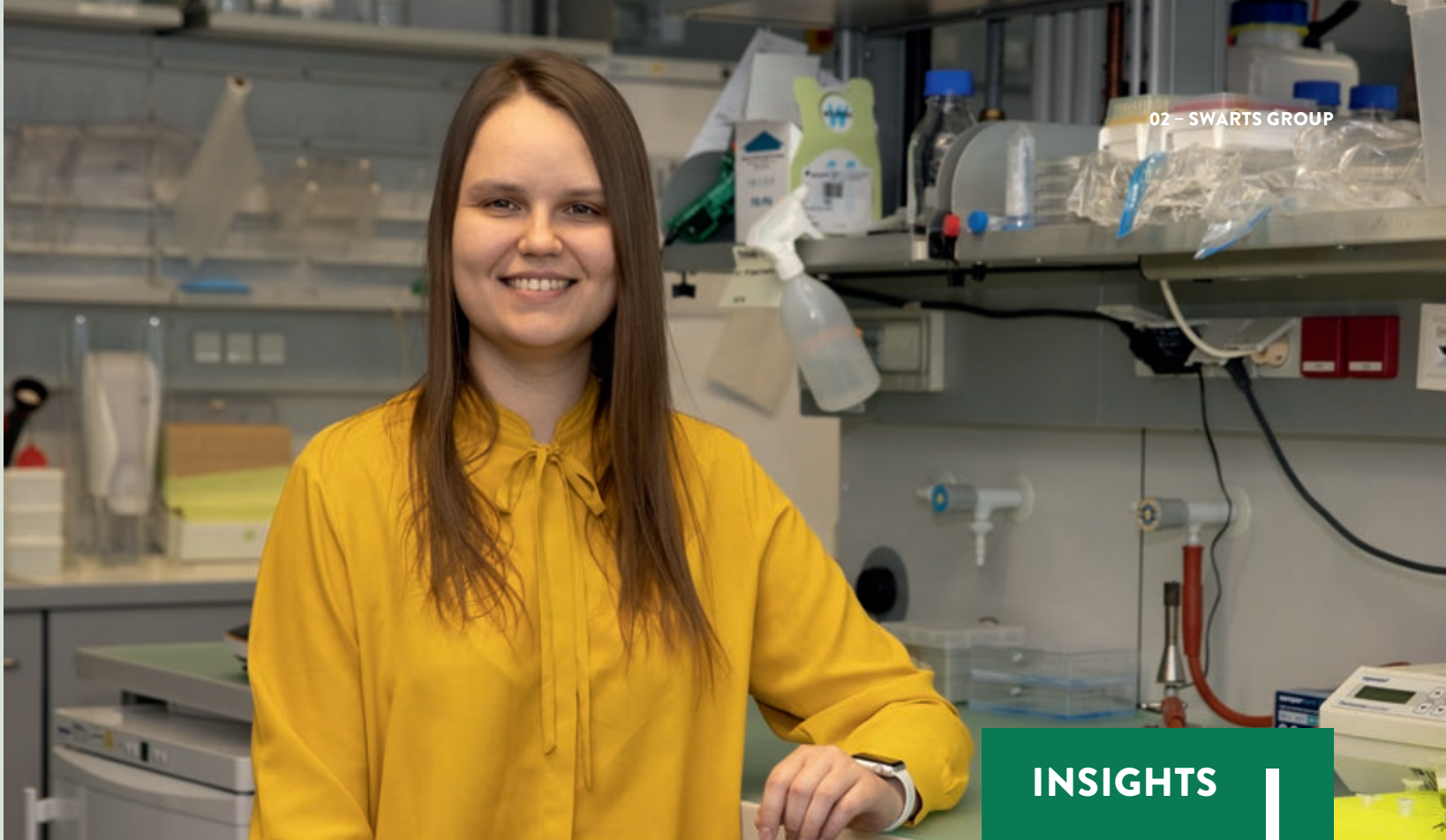
The 20-gigabase-pair genome of the Norway spruce makes whole-genome sequencing cost-prohibitive. However, Miguel Vallebuena developed a reduced representation, massively multiplexable Genotyping-by-Sequencing (GBS) restriction digest library protocol. In a small population, we discovered over 5 million variants and directly covered over 70% of coding regions, comparable to the current standard (Bernhardsson et al., Mol. Ecol. Resour., 2020), for less than one Euro per sample (Vallebuena-Estrada et al., bioRxiv). Because this approach samples a small fraction of the total genomic space, we are currently sequencing sampled haploid megagametophytes from managed and unmanaged plots across Europe. We can use these to estimate the power this variant set provides for the climate.

Hand measurement of annual growth is not only unfeasible but would be error-prone. With the GMI Core Services, we successfully developed an automated phenotyping platform. The platform relies on high-quality images generated from 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.

As of this summer, we have sampled 4,271 genotypes from 86 plots across 13 locations in the Alps, Bohemian and Carpathian regions and are currently working to genotype and phenotype at scale. Plots are placed across various slopes, altitudes, and aspects within a location to capture regional environmental variation. Each 26m-radius plot is georeferenced and mapped from a center point with 10cm accuracy to model microsite variation. Up to 79 trees are sampled for DNA and two increment cores, and tree metrics (height, diameter) are recorded. In the past year, we collected 3 cores per plot for power studies.

The resulting images are then automatically processed, and a Convolutional Neural Net (CNN) is applied for automated ring detection. After post-processing, the CNN has a precision (the proportion of called rings that are true) of 0.97 and a recall (the proportion of true rings that are called) of 0.99 (Poláček et al., bioRxiv). This pipeline allows for the fast and accurate generation of millions of ring-width measurements.

We are now able to combine genotypic variants with measurements of annual growth to understand the genetic basis of adaptation to environmental variation. I am very happy to report that the effect of the measured environment on annual growth is highly heritable (with a mean of 0.65 for over 70 environmental metrics, with many approaching 1) between locations as diverse as Romania, Slovakia, and Germany as measured using genotypic relatedness. This ensures that, with more samples, we can identify genetic variation underlying environmental adaptation and identify better-adapted trees for healthy future forests.



INSIGHTS

VASILINA AKULOVA

PHD STUDENT

Krasnoyarsk, Russia
MSc: Siberian Federal University,
Krasnoyarsk, Russia

HOW DID YOU COME TO THE GMI?

In 2020, I obtained an internship financed by the ÖAW for 4 months. I was really interested in the tree genomics projects, so I went to work in Kelly’s laboratory. Having enjoyed the project and experience, I decided to apply to the VBC PhD Program. Now I am here and happy about it!

WHAT PROJECT ARE YOU WORKING ON?

My main project is examining the mugo pine population structure and growth habits. In the mountains of the Berchtesgaden National Park, the mugo population includes trees with different growth forms, from up-right trees to ones crawling on the ground. We want to find out what stands behind this diversity: what

is the genetic structure of the observed growth form and whether the genetic or the environmental factor contributes more to this diversity.

WHAT DO YOU ESPECIALLY LIKE ABOUT WORKING AT THE GMI?

I really enjoy the environment that we have and all the support from the institute and our facilities. It is possible to get help on almost any matter. Also, the level of communication is amazing: we have frequent seminars and I know about multiple collaborations within the institute.

WHERE DO YOU WANT TO GO NEXT?

Currently I am aiming on continuing my path in academic research, but I do not have concrete plans yet. I would say that for now I am captivated by our current projects and the topics on plant natural populations and adaptation processes. Hence, I will be looking for a next position based on these factors.

03

2022 IN REVIEW



As a member of the Dolan group, postdoc Susanna Streubel explores how the bodies of land plants form.

Solanum lycopersicum
TOMATO



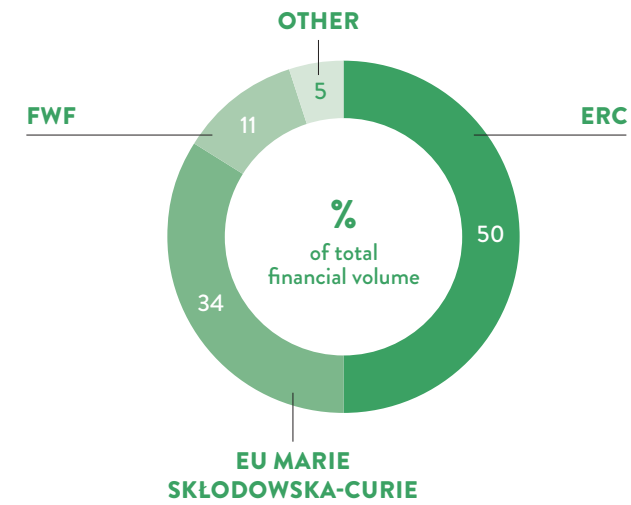
RESPONSIBLE



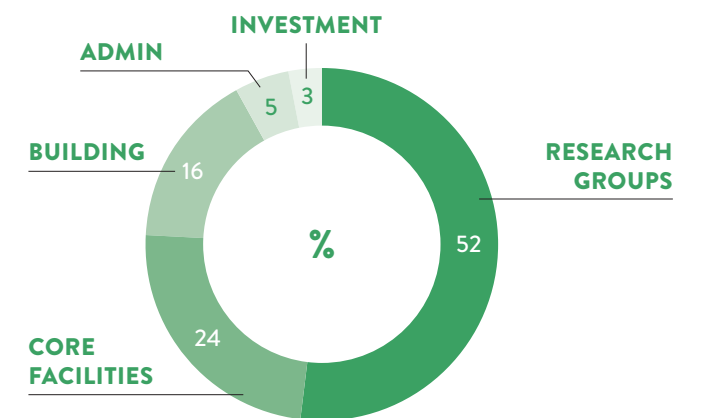
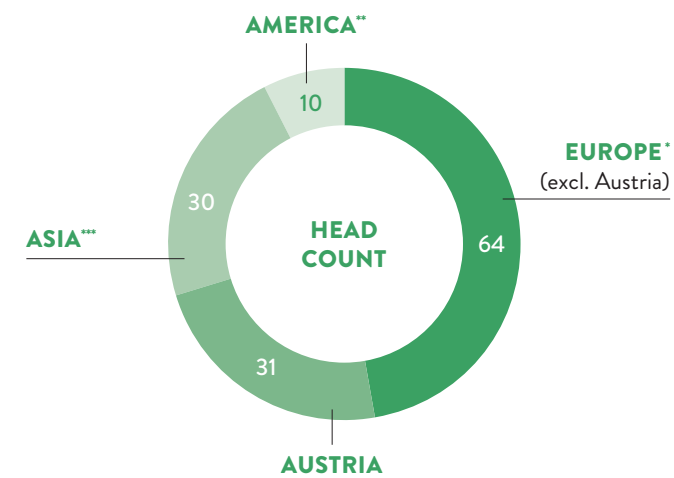
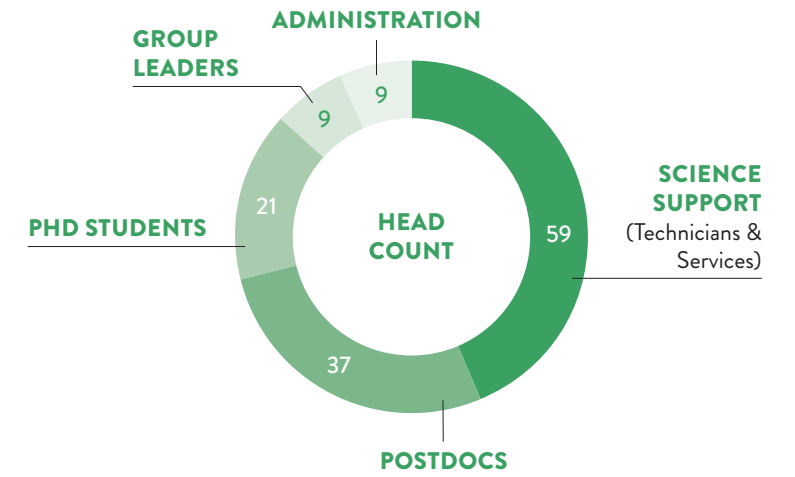
Photosynthesis in plants and bacteria created our atmosphere and sustain life on earth. Research at the Gregor Mendel Institute aims to discover molecular and genetic mechanisms that govern plant life. Fundamental knowledge of how plants function has the potential to contribute to the solutions we need to address global challenges like climate change and food security.

KEY FACTS 2022

RESEARCH GRANTS



STAFF BY FUNCTION



STAFF BY NATIONALITY

EXPENDITURES

as of December 31, 2022

* Belgium, Bulgaria, Croatia, Finland, France, Germany, Hungary, Ireland, Italy, Poland, Portugal, Russia, Serbia, Slovenia, Spain, Sweden, Switzerland, Ukraine, UK

** Canada, Mexico, US | *** China, India, Iran, Israel, Japan, Kazakhstan, Malaysia, South Korea, Syria, Turkey, Vietnam

PUBLICATIONS & PREPRINTS

BELKHADIR GROUP

Platre M, Satbhai S, Brent L, Gleason M, Cao M, Grison M, Glavier M, Zhang L, Gaillochet C, Goeschl C, Giovannetti M, Enugutti B, Neveu J, von Reth M, Alcázar R, Parker J, Vert G, Bayer E, Busch W (Epub: 2022) The receptor kinase SRF3 coordinates iron-level and flagellin dependent defense and growth responses in plants. *Nat Commun* 13(1):4445.

Chaube MA, Trattnig N, Lee D, Belkhadir Y, Pfrengle F (2022) Synthesis of Fungal Cell Wall Oligosaccharides and Their Ability to Trigger Plant Immune Responses. *European J Org Chem* 2022(27).

Lee D, Choi I, Park S, Kim S, Choi M, Lee H, Pai H (2022) Three consecutive glycolysis enzymes are involved in autophagic flux regulation through monitoring nutrient availability. *bioRxiv*: 2022.07.12.499818.

Gobinath R, Parasuraman S, Sreeramanan S, Enugutti B, Chinni S (Epub: 2022) Antidiabetic and Antihyperlipidemic Effects of Methanolic Extract of Leaves of *Spondias mombin* in Streptozotocin-Induced Diabetic Rats. *Front Physiol* 13:870399.

Clasen S, Bell M, Lee D, Henseler Z, Borbon A, de la Cuesta-Zuluaga J, Parys K, Zou J, Youngblut N, Gewirtz A, Belkhadir Y, Ley R (2022) Silent recognition of flagellins from human gut commensal bacteria by Toll-like receptor 5. *bioRxiv*: 2022.04.12.488020.

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BERGER GROUP

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DOLAN GROUP

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MITTELSTEN SCHEID GROUP

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FORMER GROUPS AND SERVICES

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2022 GRANTS

BELKHADIR GROUP

Regulation of growth defense tradeoffs by temperature
FWF (Austrian Science Fund): I 3654-B29
€ 299,533
January 2018 – January 2022

BERGER GROUP

EMBO Postdoctoral Fellowship (Arie Fridrich)
EMBO (European Molecular Biology Organization): ALTF914-2021
€ 138,600
January 2022 – December 2023

A new paradigm for genomic imprinting
FWF (Austrian Science Fund): P 36231-B
€ 399,540.75
September 2022 – August 2026

VIP² Fellowship (Pierre Bourguet)
H2020-MSCA-COFUND-2018: 847548
€ 98,640
January 2020 – December 2022

VIP² Fellowship (Tetsuya Hisanaga)
H2020-MSCA-COFUND-2018: 847548
€ 98,640
January 2020 – December 2022

The role of histone variants in chromatin organization
FWF (Austrian Science Fund): P 32054-B21
€ 397,745
May 2019 – April 2023

Tracing the origins of male germline specification in plants
FWF (Austrian Science Fund): I 4258-B21
€ 306,589
May 2019 – April 2022

Impact of dynamics of H2A variants on transcription
FWF (Austrian Science Fund): P 33380-B
€ 406,518
May 2020 – April 2024

A novel code to interpret genetic information
FWF (Austrian Science Fund): TAI 304-B
€ 152,382
June 2021 – May 2023

EMBO Long-Term Fellowship (Zachary Harvey)
EMBO (European Molecular Biology Organization): ALTF169-2020
€ 136,000
July 2020 – September 2022

Evolutionärer Einblick in H2A.Zs Genregulationsfunktion
(Zachary Harvey)
FWF (Austrian Science Fund): ESP-213
€ 324,015
December 2022 – November 2025

DAGDAS GROUP

Decrypting ufmylation through chemical biology
WWTF (Vienna Science and Technology Fund): LS21-009
€ 241,690
June 2022 – May 2026

How does autophagy rescue stalled ribosomes?
ERC (European Research Council) Consolidator Grant: 101043370
€ 1,999,006
October 2022 – September 2027

Illuminating the journey of autophagosomes in plants
FWF (Austrian Science Fund): P 34944-B
€ 404,586
January 2022 – December 2025

C53 and Ufmylation Regulation in Endoplasmic Reticulum-Autophagy (ER-phagy) (Ni Zhan)
H2020-MSCA-IF-2020: 101028611
€ 186,167.04
May 2021 – April 2023

VIP² Fellowship (Marion Clavel)
H2020-MSCA-COFUND-2018: 847548
€ 98,640
January 2020 – December 2022

VIP² Fellowship (Juan Carlos de la Concepcion)
H2020-MSCA-COFUND-2018: 847548
€ 98,640
March 2021 – February 2024

Targeted protein degradation – from small molecules to complex organelles
FWF (Austrian Science Fund): F 7912-B
€ 399,530
March 2020 – February 2024

Functional evolutionary analysis of a novel autophagy adaptor in plants (Jierui Zhao)
ÖAW (Austrian Academy of Sciences) Doc Fellowship: 25966
€ 38,000
August 2021 – July 2023

Role of ATG8 specialization in plant selective autophagy
FWF (Austrian Science Fund): P 32355-B
€ 304,300
May 2019 – April 2022

DOLAN GROUP

De novo Development of Polarity in Plant Cells
ERC (European Research Council) Advanced Grant: 787613
€ 1,959,500
October 2018 – September 2023

VIP² Fellowship (Shuangyang Wu)
H2020-MSCA-COFUND-2018: 847548
€ 98,640
January 2022 – December 2024

VIP² Fellowship (Pin Guo)
H2020-MSCA-COFUND-2018: 847548
€ 98,640
May 2021 – July 2022

Untersuchung von Mechanismen der Zellpolarität in Bezug auf Zellschicksal und Musterbildung während der Entwicklung von Vaskulatur und Spaltöffnungen in Arabidopsis (Eva-Sophie Wallner)
DFG (German Research Foundation): WA4709/1-1
€ 51,652
April 2021 – October 2022

MITTELSTEN SCHEID GROUP

A novel model to study light-regulated seed germination
(Zsuzsanna Mériai)
FWF (Austrian Science Fund): I 3979-B25
€ 382,032
February 2019 – October 2023

Transgenerational antiviral barriers in plants (Marco Incarbone)
FWF (Austrian Science Fund): M 2921
€ 169,260
June 2020 – May 2022

NORDBORG GROUP

Elucidating the causes and consequences of the global pattern of epigenetic variation in Arabidopsis thaliana
ERC (European Research Council) Advanced Grant: 789037
€ 2,498,468
June 2018 – May 2024

VIP² Fellowship (Yoav Voichek)
H2020-MSCA-COFUND-2018: 847548
€ 98,640
January 2021 – February 2022

Climate adaptation in Arabidopsis thaliana through evolution of transcription regulation (Yoav Voichek)
H2020-MSCA-IF-2020: 101028014
€ 186,167.04
March 2022 – February 2024

VIP² Fellowship (Hajjun Liu)
H2020-MSCA-COFUND-2018: 847548
€ 98,640
January 2021 – December 2023

SWARTS GROUP

VIP² Fellowship (Miguel Vallebueno)
H2020-MSCA-COFUND-2018: 847548
€ 98,640
January 2020 – December 2022

GMI scientists from more than 30 countries carry out discovery research on a wide variety of plants, from algae to pine trees and cress. The diversity of people with complementary world views and skills generates a vibrant culture that enables unexpected synergies and the generation of new knowledge. This knowledge is critical for our understanding of the roles that plants play on our planet and can be used by humanity to improve human wellbeing.

VIBRANT

Arabidopsis thaliana
THALE CRESS

GMI @ THE VIENNA BIOCENTER

GMI is located at the Vienna BioCenter, a leading life sciences location in Europe. The Vienna BioCenter offers a unique combination of research, education and companies on a single campus, creating an attractive environment for scientists at the GMI.

In addition to the GMI, five research institutes are located at the Vienna BioCenter: the Institute of Molecular Biotechnology (IMBA), the Research Institute of Molecular Pathology (IMP), the Max Perutz Labs, Centre for Microbiology and Environmental Systems Science (CMES) and the Faculty of Life Sciences of the University of Vienna. Currently, the Vienna BioCenter hosts 1,850 scientists (including 386 PhD students) coming from 78 countries.

Researchers at the Vienna BioCenter are supported by the Vienna BioCenter Core Facilities (VBCF), which provide exclusive access to cutting-edge scientific infrastructure. Complementary expertise and a high level of scientific and administrative services enable scientists to be early adopters and developers of new techniques. Together with the high-quality infrastructure, this offers unique working conditions that enable scientists at the Vienna BioCenter to operate at the forefront of Life Science research. A growing

Part of
Vienna
BioCenter



number of biotech-companies and space for start-up labs complement the training and research activities and offer important collaborative opportunities to bridge academic and applied research. Profiting from the assets offered at the location, the GMI has rapidly developed into one of the most renowned European research institutes in plant biology.

The competitiveness of research at the Vienna BioCenter is reflected by numerous grants and awards received by scientists at the Vienna BioCenter: 83 ERC research grants, 13 Wittgenstein Awards (the most highly endowed science award in Austria) and 3 Breakthrough Prizes have been awarded to scientists with ties to the Vienna BioCenter.



MEMBERS OF THE VBC PHD PROGRAM AT GMI IN 2022

Alibek ABDRAKHMANOV
 Vasilina AKULOVA
 Gabriele BRADAMANTE
 Daniel BUENDIA
 Sebastian DEIBER
 Alessia DEL CHIARO
 Rodolphe DOMBEY
 Roan GROH
 Bhagyshree JAMGE
 Jian Yi KOK
 Sean MONTGOMERY
 Marintia NAVA
 Vu NGUYEN
 Lorenzo PICCHIANTI
 Rahul PISUPATI
 Johannes RÖTZER
 Victor SANCHEZ DE MEDINA
 Anna SCHMÜCKER
 Vikas SHUKLA
 Marieke TRASSER
 Pamela VETRANO
 Jierui ZHAO

EDUCATION & TRAINING

Education is core to the mission of the Gregor Mendel Institute. A comprehensive scientific training program makes the GMI a destination for researchers at all stages of their careers, from interns to postdocs. Researchers at all levels have access to the GMI's core research facilities and scientific training program.

Marieke Trasser, a PhD student in the Mari-Ordóñez group, investigates the ability of *Arabidopsis thaliana* to identify and deactivate transposons. Also known as 'jumping genes', transposons are DNA sequences that can change location within DNA. [▶](#)



VIENNA BIOCENTER SUMMER SCHOOL

The VBC Summer School, sponsored by the Max Birnstiel Foundation, welcomes undergraduate students to work alongside staff scientists at one of the Vienna BioCenter's leading life science research institutes, including the GMI. Scholars form important professional interactions and get a head start in establishing their research profile.

I²P INTERNATIONAL INTERNSHIP PROGRAM

The International Internship Program – short, I²P – is a full-immersion internship program for predoctoral students. For three to six months, interns join a research group at the GMI. Participants assume ownership of a research project, work alongside a dedicated mentor, and earn a salary. The experience opens new ways of thinking about scientific research and scientific careers.

VIENNA BIOCENTER PHD PROGRAM

The Vienna BioCenter PhD program is one of Europe's leading PhD programs in the life sciences and is a Doctoral school of the University of Vienna and the

Medical University of Vienna, in collaboration with the GMI, IMBA, IMP and the Max Perutz Labs. The mission of the Vienna BioCenter PhD Program is to promote interdisciplinary research in the Life Sciences at the highest level. The program is designed to help excellent PhD students develop into tomorrow's leading scientists; a comprehensive training program supports them in their first steps in a scientific career. PhD students at the GMI are recruited twice a year in March and September through the Vienna BioCenter PhD Program.

VIENNA INTERNATIONAL POSTDOCTORAL (VIP²) FELLOWSHIP PROGRAM

The GMI is a member of the Vienna International Postdoctoral (VIP²) Fellowship Program, a 3-year postdoctoral fellowship program. The VIP² program is designed as an attractive career opportunity for researchers who hold a PhD in life sciences (or a related discipline) and who have projects that may lead to distinct research lines. The fellowship is fully funded and offers prime research conditions, exposure to different sectors, and a two-mentor scheme. Fellows are advised and supported by an inter-sectoral advisory board.

Eva-Sophie Wallner, a post-doctoral fellow, gives guests a hands-on look at the process of crossbreeding.



Under the guidance of PhD student Anna Schmücker, visitors extract plant embryos from seeds of *Arabidopsis*.



OUTREACH

Outreach at the Gregor Mendel Institute is part of its mission to establish long-term cooperations, create spaces for scientific exchange, and expand on recruitment pathways. Through public engagements, group leaders and students convey the work of the institute and its significance in a simple, concise, and interesting way to a non-scientific and global audience.

HIGHLIGHTS OF THE 2022 OUTREACH YEAR



2022 was a banner year for the namesake of our institute, Gregor Mendel. The GMI joined institutions across Europe in celebrating Mendel's 200th birthday anniversary with a festival of activities that strengthened public engagement with our research. Highlights included a lecture by Nobel prize winner Sir Paul Nurse, outreach engagements, an art competition, an exhibition at the Vienna BioCenter, and the development of an anniversary website.

OUTREACH THAT CAPTURES THE IMAGINATION

Reaching out to a young audience, Johannes Rötzer and Sebastian Deiber, PhD students at GMI, explained basic Mendelian genetics at Vienna Children's University (KinderuniWien). The event brought over 600 students to the Austrian Academy of Sciences for a day of direct communication with scientists.

GMI SCIENTISTS INAUGURATE THE PLANT CELL'S MENDEL CELEBRATIONS

Did Mendel's discoveries withstand the test of time with regard to our modern-day knowledge of genetics? What could spur a modern Gregor Mendel's interest among the established and emerging fields of research? GMI Senior Group Leaders Ortrun Mittelsten Scheid and Frédéric Berger considered these questions in two perspective articles published in a series of reviews and articles to celebrate Mendel's 200th anniversary in *The Plant Cell*.

MENDEL'S LIFE & SCIENCE IN THE SPOTLIGHT

On its social media channels, GMI unveiled a film and exhibit about Mendel's life, education, and research. The film can be found on GMI's YouTube channel, while the exhibit is open for families and school classes visiting the Vienna Open Lab at the Vienna BioCenter. The exhibit links visitors to an in-depth exploration of Mendel's life and work on the "Mendel 200" jubilee website.



SIR PAUL NURSE AND THE MOST IMPORTANT QUESTION IN BIOLOGY

In a VIP event marked by the patronage of Dr. Alexander Van der Bellen, Federal President of Austria, the GMI celebrated the Gregor Mendel Bicentennial with a lecture by Nobel laureate Sir Paul Nurse. Nurse, who in 2020 wrote the book "What is Life?" presented five great ideas of biology.

THE FUTURE OF BIOLOGY AT THE LONG NIGHT OF RESEARCH

As the GMI stands in the tradition of Gregor Mendel, its researchers carry his legacy into the future. In May, visitors to the Long Night of Research joined GMI scientists for an evening of plant biology. Our team of researchers, including senior group leader Ortrun Mittelsten Scheid, gave guests a hands-on look at modern plant research, including the process of crossbreeding.

CORE SERVICES

The GMI is a member of the GMI/IMBA/IMP core services, providing researchers access to cutting-edge equipment and expert services. Core facilities are run by experts who assist researchers in experimental design, instrument usage, and data analysis. This high-level support allows researchers at the GMI to conduct internationally competitive research.



BIOOPTICS

Looking at the fine detail of cells and cellular structures can provide valuable insights into their functions and interactions. The BioOptics Facility supports research with specialized instruments for analysis and visualization of cells. Researchers have access to flow cytometry and cell sorting, more than twenty microscopy systems including CLSM, 2P, TIRF, SIM, and LSFM, as well as assistance in image processing and analysis.

MAX PERUTZ LIBRARY

In addition to providing a quiet and well-equipped study environment, the Max Perutz Library is a reference library. The Max Perutz Library maintains and develops literature collections and information services to support research and teaching needs.

MOLECULAR BIOLOGY SERVICE

The Molecular Biology Service offers a variety of services. The facility provides Sanger Sequencing,

preparation of competent *E. coli*, production of recombinant proteins and enzymes, monoclonal antibodies, a mycoplasma testing service for tissue culture cells, and 96-well format plasmid preparation. In addition, the Molecular Biology Service runs a full-service media kitchen and provides instrumentation and expertise for lab automation and high-throughput methods.

PROTEIN CHEMISTRY FACILITY

The Protein Chemistry Facility offers protein analyses. The facility runs mass spectrometers and chromatography systems to enable protein separation, identification, quantification, and post-translational modification characterization. The Protein Chemistry Facility offers peptide synthesis and affinity purification of antibodies, and also develops bioinformatics tools for data interpretation.

HIGH-PERFORMANCE COMPUTING

The Cloud Infrastructure Platform (CLIP) provides cutting-edge computing for the Life Sciences. CLIP offers an interdisciplinary, low entry barrier approach to High Performance Computing.

VBCF

Researchers at the GMI and other members of the Vienna BioCenter are supported by the Vienna BioCenter Core Facilities (VBCF), which offer state-of-the-art research infrastructure and scientific services. The VBCF encompasses nine core facilities, some of the most important facilities for researchers at the GMI are:

PLANT SCIENCES

The Plant Sciences Facility (PlantS) provides professional support to “green research” at the Vienna BioCenter. With 23 high-quality, highly specialized plant growth chambers, the Plant Sciences Facility can precisely control environmental conditions, reproducing abiotic plant stress conditions and simulating global environmental conditions.

The most recent addition to the plant phenotyping infrastructure is PHENOPlant – the only one of its kind in Austria. Here, thousands of plants grow in highly controlled environments under state-of-the-art LED illumination. The phenotyping process is fully automated, non-invasive, and high-throughput, allowing for highly controlled stress experiments. Thus, the Plant Sciences Facility can accurately simulate conditions predicted by climate models and analyze crop plants and model plants with state-of-the-art phenotyping technologies.



NEXT GENERATION SEQUENCING

Next Generation Sequencing (NGS) has become a key analysis method for biological research, enabling researchers to obtain a global view of biological processes. The Next Generation Sequencing unit accelerates research at the GMI with personalized guidance for sequencing projects offered by its team, which has 10 years of experience with sequencing systems, high-throughput data analysis, and the latest NGS technology and protocols, including STARR-seq, SARSeq, and SLAM-seq.

PROTEIN TECHNOLOGIES

The VBCF Protein Technology Facility (ProTech) offers services for the production, purification, and characterization of recombinant proteins. These include the design and cloning of expression constructs, the generation of constructs for multigene expression, and the production of recombinant targets in bacteria, insect cells, and mammalian cells.

ELECTRON MICROSCOPY

The VBCF Electron Microscopy Facility offers access to an extensive range of instruments, techniques, and expertise to visualize the ultrastructure of model systems. The unit analyzes diverse biological samples, from molecules, such as RNA, DNA, or protein, to organelles to entire prokaryotic or eukaryotic cells and tissues. The Facility also assists researchers with sample preparation techniques for on-site SEM, TEM, cryo-EM systems, and Correlative Light and Electron Microscopy (CLEM). The unit also provides access to the EM infrastructure for researchers interested in working independently.



ADMINISTRATION

Researchers at the GMI are supported by administrative staff, who ensure smooth day-to-day operations. To increase synergies, administrative staff is shared by GMI and IMBA, the two life science research institutes of the Austrian Academy of Sciences located at the Vienna BioCenter.

The Assistant to the Directors is responsible for organizing seminars, conferences, and the annual retreat and SAB meetings.

The Finance Department is responsible for accounting, financial controlling, and bookkeeping. The grant management team provides information on grant opportunities, assists in preparing proposals, and is responsible for all financial reporting and audits.

The Human Resources Officer supports staff in all matters relating to employment and living in Austria, including helping new employees organize visas or work permits.

The Lab Support team provides a range of services to support scientists in their experiments, ranging from offering a central supply of chemicals and consumables, to maintenance and repair of lab equipment, and plant pathogen control.

The Communications & Partnerships team makes GMI research and findings accessible for the wider public. The team organizes events, engages with the press, creates outreach opportunities, manages the website, and creates content for social media.

The Science Support team provides English editing services for grants and manuscripts, translation services, prepares official reporting, and serves as the tech transfer and public information office.

SCIENTIFIC ADVISORY BOARD

03 – SAB

Research at the GMI is evaluated annually by our Scientific Advisory Board (SAB). The SAB consists of independent international experts, whose primary role is to advise the institute's management and the Austrian Academy of Sciences on the quality of the science being undertaken at the GMI. The SAB meets over a two-day period when they conduct in-depth discussions with all research groups as well as Postdoc, PhD, and technical staff representatives.



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03 – ÖAW

THE AUSTRIAN ACADEMY OF SCIENCES

ÖAW

AUSTRIAN
ACADEMY OF
SCIENCES

The Gregor Mendel Institute is a basic research institute of the Austrian Academy of Sciences. The Austrian Academy of Sciences (ÖAW) is one of Austria's central institutions for science and research. Founded in 1847 as a learned society in Vienna, the Academy currently has over 760 members and 1,800 employees; it stands for innovative basic research, transdisciplinary

exchange of knowledge and dissemination of new insights – with the goal of contributing to progress in science and society.

The Academy's headquarters are located in Vienna's city center, in the former assembly hall of the University of Vienna. Today, the Academy fulfills two main functions. On the one hand, its 760 members form a scholarly society, advising decision-makers from politics, industry, and society and conveying scientific insights to the public. On the other, the Academy is Austria's major supporter of research outside the university system, funding 25 research institutions in both the natural sciences and humanities – including the Gregor Mendel Institute.

LOCATION

The Gregor Mendel Institute is located in the Vienna BioCenter, a world-leading international life science research center.



**GREGOR MENDEL INSTITUTE OF
MOLECULAR PLANT BIOLOGY**

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