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ANNUAL REPORT 2021

GMI

GREGOR MENDEL INSTITUTE OF MOLECULAR PLANT BIOLOGY

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Front page: Microscopy image of an Arabidopsis root tip. Legend: Green marker in the cytoplasm of specific root tip cells (quiescent center and columella), cell wall staining in magenta.
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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

2021 ANNUAL REPORT

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Dr. Magnus Nordborg
Scientific Director

Dr. Markus Kiess
Business Director

2021 DIRECTORS' STATEMENT

We are proud to be part of **one of very few research institutions worldwide devoted to basic plant biology.** The vision of the GMI is to contribute to our understanding of biology, in general, and plant biology, in particular, by carrying out excellent research, in particular the kind of fundamental research that is often poorly supported. Putting it another way, we want to understand how plants function, from basic cell biology 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 that humanity is currently partly reversing on a timescale of a few generations!

As directors, our main task is to create the kind of research environment that makes realizing this vision possible, through efficient administration, world-class services, and financial support for independent research groups. In addition to producing knowledge, we produce knowledgeable people, and are proud of their achievements, be they students, postdocs, or group leaders. Since last year's report, two junior group leaders moved on: Claude Becker is now professor at LMU Munich, and Michael Nodine is Assistant Professor at Wageningen University. We are delighted to welcome Silvia Ramundo as a new junior group leader.

It goes without saying that the last two years have been challenging, but we are happy to note that we have been able to stay open and productive — as we hope this report will convince you. As always, **we want to thank** the Austrian Academy of Sciences for its continued support of the GMI, and the Federal Ministry of Education, Science and Research as well as 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.

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INTRODUCING THE GMI

> *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)

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 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, genomics, 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, 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.

IMPORTANCE OF EXPERIMENTAL PLANT RESEARCH

Plants are the primary producers of the world's ecosystem and thus essential for all life on earth, a basic fact that is receiving new attention due to rising food prices, diminishing fossil fuel reserves, and a changing climate. Major innovations will be required to guarantee sustainable food and energy production in the 21st century, and some of them can only come from basic plant research like that carried out at the GMI.

Research on plants can also lead to fundamental scientific breakthroughs beyond plant biology, including many that can be applied to human medicine. Gregor Mendel's discovery of the basic principles of genetics, Barbara McClintock's discovery of transposons, and the recent work on epigenetics and RNA silencing are only a few of the dozens of examples. What critical discoveries will plant research bring in the future?

These are exciting times, for there is still much to learn, from the network interactions of receptor kinases, to 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 Program, 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 30 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 – which took place over Zoom this year wherever possible. 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.

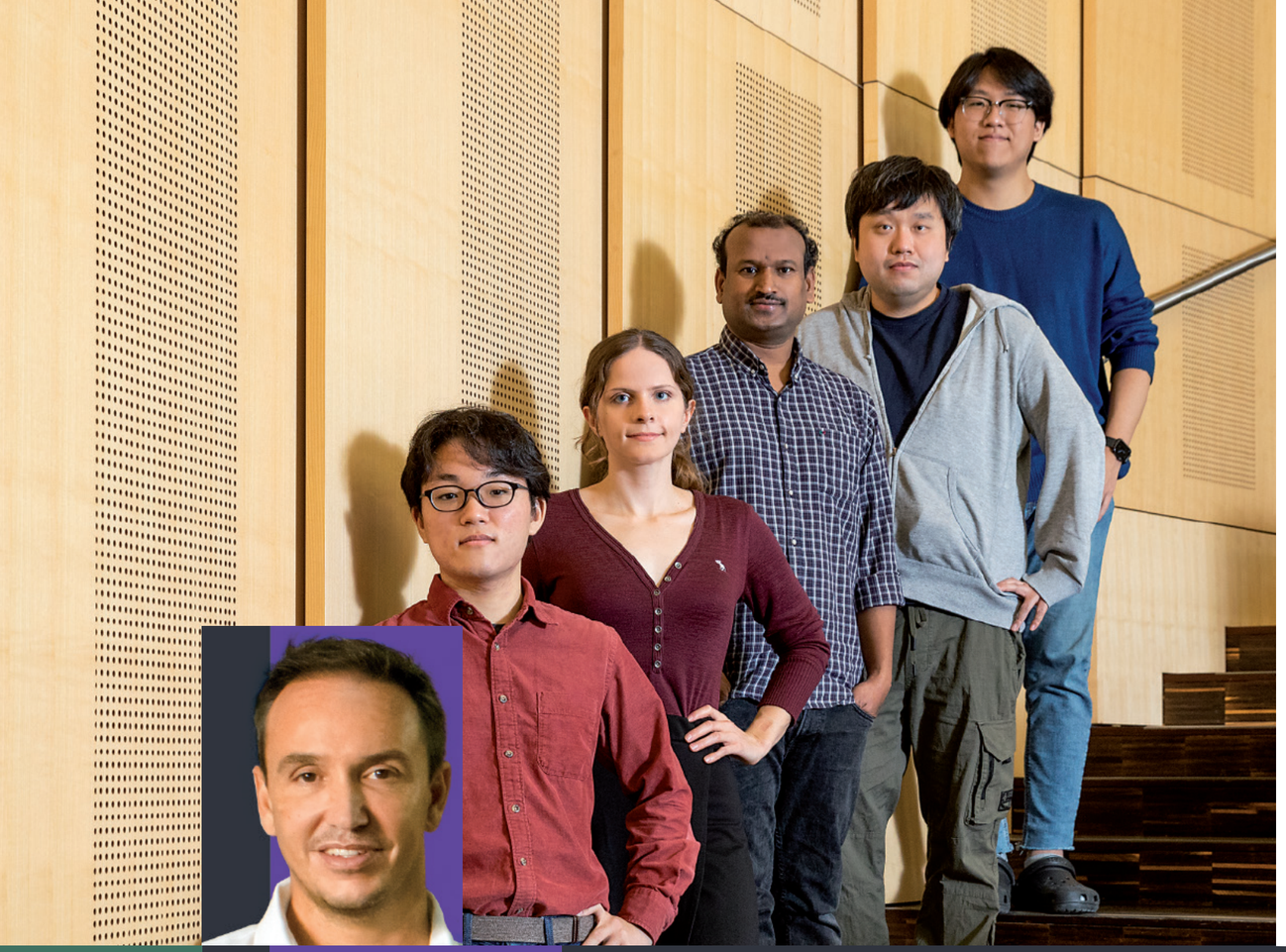
> *Plants are critical ecosystem components, provide humans with food, medicine, timber and generate the necessary oxygen to sustain most animal life on earth.*

(Kelly Swarts)

2021

GMI RESEARCH GROUPS

BELKHADIR GROUP
BERGER GROUP
DAGDAS GROUP
DOLAN GROUP
MARÍ-ORDÓÑEZ GROUP
MITTELSTEN SCHEID GROUP
NODINE GROUP
NORDBORG GROUP
RAMUNDO GROUP
SWARTS GROUP



YOUSSEF BELKHADIR

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Joined GMI in Jun 2014

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

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

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Duhwa Lee
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Julian Bünting*
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Jungmin Lee*
Julia Watzal*

(*left the lab in 2021)

DECISION MAKING THROUGH RECEPTOR KINASES

Youssef Belkhadir

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 (RKs). 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. The group is especially focused on understanding how plants choose to allocate resources between growth and pathogen defense. The knowledge they gain will help 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 2021

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 (CW) components. Microarrays displaying hundreds of different glycan structures are versatile tools for rapidly analyzing interactions between RKs and CW molecules. During 2021, we have continued to systematically test RK ECDs on these arrays and the results of these screening campaigns have revealed novel RK-glycan pairs that we are currently investigating in depth. The team has so far determined that one of these RK-glycan pairs act in plant immune responses to glycan ligands. In 2021, we have mainly focused on understanding the biological relevance of these receptor-ligand interaction when using specific types of microbes that are either detrimental or beneficial to plants.

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 plant immunity and bacterial motility. During 2021, the group decoded the immunogenic and motility profiles of the bacterial epitope and determined the spectrum of amino-acid mutations that drives antagonistic pleiotropy. In the process, the team 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, the group found that the output of these synthetic tracks occurs naturally in bacteria that co-exist with plants (→ Fig.). We have finalized the research and published the results of this work in two back-to-back publications in Cell Host & Microbe.

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. In 2019, 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, 14 of which are able to induce an immune response when exogenously applied to a plant. During 2021, the group has focused on understanding what the mode of action of these chemicals was by using mechanistic and biophysical approaches. We have also explored a chemical space of analogs that provides a better understanding of these sensory mechanism. In the process, we have devised an approach that could be used to activate plant immune responses with the rational design of analog molecules. We are currently investigating how we can hijack receptors with developmental functions by using chemicals.

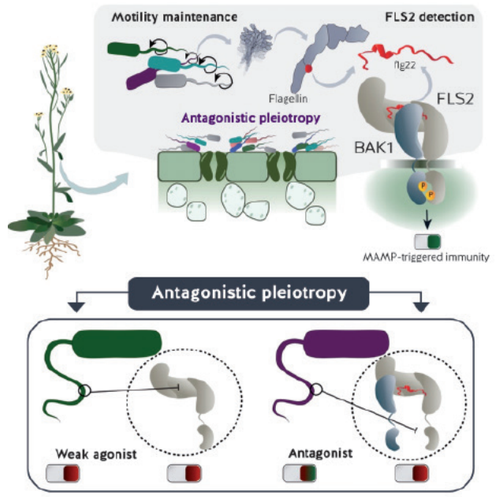

FIG.
Interrogation of a peptide array with the extracellular domain of FLS2 explains how some bacteria that associate with plants have been successful at doing so.

INSIGHTS

Natalie Edelbacher
Technician
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How did you come to the GMI?
During my research internship I gained my first experiences in plant immunity, which focused on investigating and deciphering molecular principles and mechanisms in plant-microbe interactions. I found studying and unraveling signaling pathways so intriguing, that right after I graduated, I decided to look for a place where I could continue this kind of research. I found the GMI, and it was an easy decision to make the jump.

What project are you working on?
When I first arrived, I was working with a PhD student, Kate, who was investigating the genetic trade-off between bacterial motility and host recognition. The project was based on the principle that the conserved microbial derived flagellin activates the host's antibacterial immune response and, thus, gets eliminated. Now, I support Duhwa on his ongoing project on discovering novel immunogenic molecules and their respective receptors. As a lab technician I also take care of tasks such as ordering supplies and introducing new students to protocols and equipment.

What do you especially like about working at the GMI?
I really enjoy working in an international institute and I have had many fascinating and inspiring conversations with my colleagues. The scientific facilities on site provide excellent support for our research and our technical and administrative staff make our life so much easier. Whenever I need scientific advice, a friend to lend an ear, or someone to do a spontaneous semi-professional photo shooting in a plant incubation chamber, I always have friends to count and rely on.

Where do you want to go next?
I am currently attending a graduate university course to learn more about how we can use biotechnological applications in plants to promote sustainable agriculture without damaging economic, social, and environmental integrity. In my future career step, I hope to help find solutions on current and emerging problems to control plant health and growth in a sustainable agriculture.

FRÉDÉRIC BERGER

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Joined GMI in Jan 2014

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

PREVIOUSLY

- Group Leader (2004-2014): Temasek Life Sciences Laboratory, SG
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(*left the lab in 2021)

Frédéric Berger

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 either modify the structural properties of the nucleosome or confer specific properties to chromatin. Some variants are found only in specific cells, some mark specific DNA sequences, while still others are involved in DNA repair and recombination. In addition to these variants, histone 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 investigating the evolution of histone variants and their roles in organizing the genetic information encoded by DNA into units that are readable by the machinery that translates the code into RNAs and proteins.

ADVANCES IN 2021

A new pathway that prevents activity from transposons in eukaryotes

Transposons are foreign elements that invade genomes of eukaryotes. These mobile elements are mutagenic and the activity of transposons' genes that enable their movement is suppressed. Non-coding RNAs and the associated DNA methylation suppress activity of a few transposons in plants. However how most transposons are suppressed remained unknown. This year the Berger lab elucidated this mechanism and published that the deposition of H2A.W by the chromatin remodeler DDM1 is sufficient to *de novo* silence most potentially mobile transposons in Arabidopsis. In plants, the chromatin of transposons is occupied by the H2A.W histone variants. We showed that these variants suppress chromatin accessibility and tend to prevent transcription. Chromatin remodelers are energy-dependent molecular machines that displace nucleosomes, and deposit or remove the histone variant H2A.Z. DDM1 had been identified 30 years prior in Arabidopsis but its mechanism of action remained enigmatic. We showed that heterodimers of H2A.W-H2B bind specifically to two binding sites close to the catalytic site of DDM1. In the absence of DDM1, H2A.W is lost from transposons. While this work identified the first pathway of deposition of H2A.W, the impact of our findings is more general. The deposition of H2A.W by DDM1 is responsible for silencing the activity of transposon genes and prevents the mobility of transposons. This mechanism is also valid in animals that evolved the variants macroH2A deposited over transposons. We showed that the H2A.W binding sites of DDM1 are conserved in the mammalian DDM1 orthologs LSH and HELLS. A parallel study by the Muegge lab showed that LSH acquired the capacity to deposit the variant macroH2A in a convergent manner. LSH-mediated deposition of macroH2A suppresses the activity of some transposons in mammals. The convergence between H2A.W deposition by DDM1 and macroH2A deposition by LSH highlights the broad importance of deposition of specialized H2A variants in silencing transposons. DDM1 stands for DECREASED DNA METHYLATION 1 because without DDM1, DNA methylation is lost throughout the genome. We are currently exploring how DDM1 controls DNA methylation, how it is recruited to heterochromatin and to which degree its action is independent of classical heterochromatin marks comprising DNA and H3K9 methylation. This research program changes our views on transcriptional suppression of transposons. Changes of chromatin properties by H2A variants now appear to play a central role in this process. This opens new possibilities in considering the interactions between transposons and hosts and its consequences on evolution of the genomes of eukaryotes.

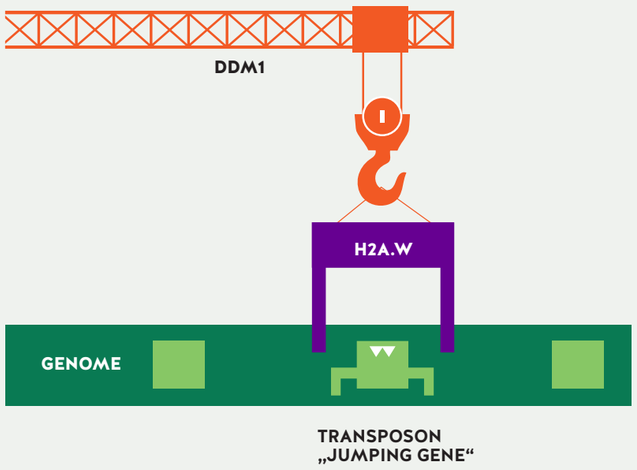
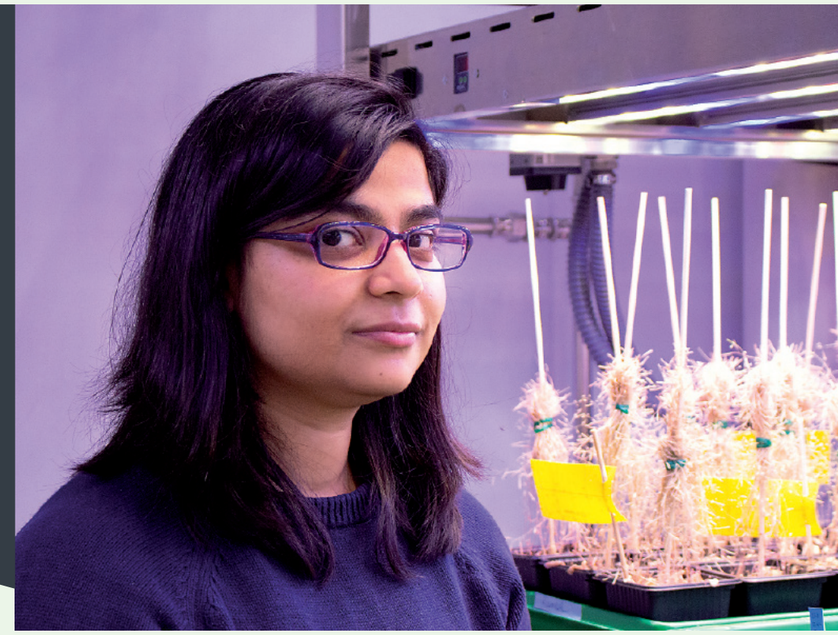


FIG.
Schematic representation of the chromatin remodeler DDM1 silencing a transposon by specifically depositing the histone variant H2A.W and "locking the transposon in". ©floorfour/GMI

INSIGHTS



Bhagyshree Babasaheb Jamge
PhD student
Kaudgaon, Maharashtra, India
MSc,
Institute of Bioinformatics and Applied Biotechnology (IBAB), Bangalore, India

How did you come to the GMI?

It all started with an email. I had just finished my Master's in Bioinformatics and Biotechnology at IBAB (Bangalore India). And I wanted to acquire some research experience before I committed to a PhD. So, I reached out to Ortrun for an internship, but she had no positions at that time. However, she suggested I apply to Fred's lab as our research interests aligned. After exchanging a couple of emails I interviewed with Fred on Skype and he gave me the opportunity to do an internship in his lab. And so began my research career. Eventually I also applied for the VBC PhD program and continued my research.

What project are you working on?

All information required for a cell to be "alive" is encoded in the DNA. But this information needs to be stored as well as be accessible for regulatory processes. Histone proteins play a crucial role in packaging this information. My research focuses on understanding how histone variants along with histone modifications contribute to organize the epigenetic landscape in Arabidopsis. My work also contributed to unravel a chromatin remodeler, DDM1, that deposits the histone variant H2A.W and maintains the transposon (jumping gene) in a silenced chromatin state.

What do you especially like about working at the GMI?

GMI is an excellent plant research institute. I really appreciate the international work environment here. Also, it gives you a lot of opportunity to interact with other researchers who are outside your field. People here are willing to give you feedback and are up for collaborations. And at last, we have the best research facilities at GMI and on campus (VBCF). As a researcher all you must do is come with an idea or an experiment to test your hypothesis. You will find someone who is willing to help you set up the experiment. It's a great place to start your research career as a PhD candidate!

Where do you want to go next?

I am now in my last year of PhD. Right now, I am focused on finishing my research projects and having successful publications and finally I will write my thesis. After my PhD, I am planning to work in the field of "international development" and am interested in working on agriculture and rural development policy. I am confident that I can use the skills that I have developed through my research career to make some meaningful impact on a policy level.

Yasin Dagdas

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 is studying 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 yield that are more tolerant to environmental stress and pathogens.

YASIN DAGDAS

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Joined GMI in Jan 2017

PhD: University of Exeter, UK

PREVIOUSLY
Postdoc (2013-2016): Sophien Kamoun Lab, The Sainsbury Laboratory, Norwich, UK

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Esther Kronthaler*
Marta Salas Gomez *
Adrijana Smoljan*

(*left the lab in 2021)

ADVANCES IN 2021

Our lab combines 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) crosstalk between selective autophagy and other quality control pathways (→ Fig.), 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 organelle recycling mechanisms in plants. Together with colleagues from all four Vienna BioCenter Institutes and other international collaborators, we discovered a novel cellular quality control pathway that mediates endoplasmic reticulum homeostasis. Through live cell imaging and biochemical experiments performed in *Arabidopsis thaliana, Marchantia polymorpha,* and human cell lines, we have shown that C53 forms a cross-kingdom conserved selective autophagy pathway that is involved in recycling polypeptide chains that are stalled in membrane bound ribosomes (→ Fig.). Furthermore, we have also shown that UFMylation, an enigmatic post-translational modification system, is involved in regulation of C53-mediated autophagy. Our findings established new connections between ribosome associated quality control pathways and autophagy and highlighted plants as exciting model systems to discover novel quality control mechanisms.

In parallel, together with our colleagues at the Chinese University of Hong-Kong, we have established a molecular framework to study mitophagy, mitochondria recycling via autophagy in plants. Furthermore, we have identified the first molecular player, named Friendly, which plays essential roles in mitophagy in plants. Finally, by showing the crucial role of Friendly-mediated mitophagy in de-etiolation, we have demonstrated a physiological response where mitochondrial recycling plays important roles. As de-etiolation is a major developmental transition that requires maturation of other organelles, our studies also highlight the role of autophagy in inter-organellar crosstalk.

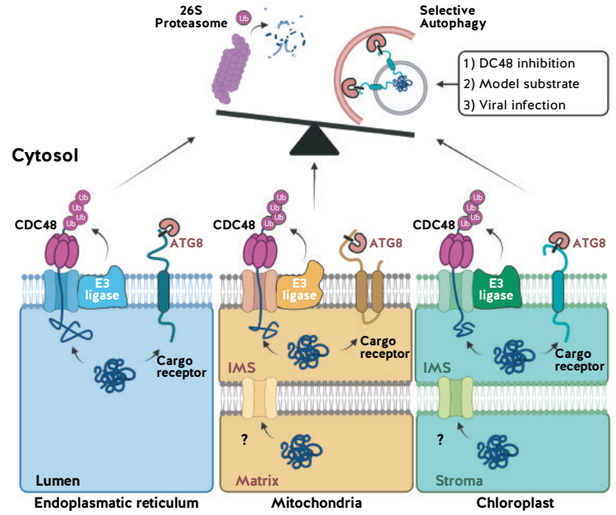
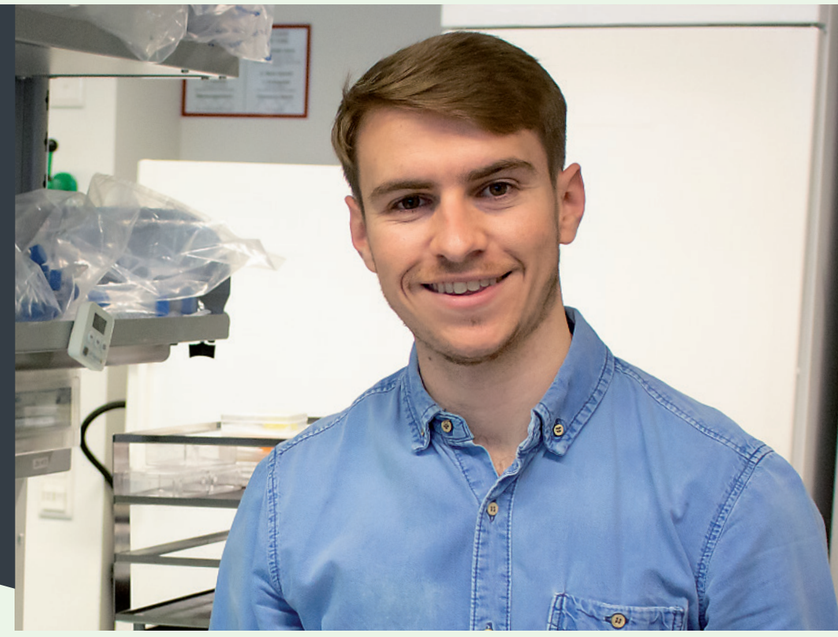


FIG. The balance between 26S proteasome and selective autophagy ensures organelle quality control.

Organelle associated degradation (OAD) is ensured by membranous ubiquitin E3 ligases present at the ER (blue), the mitochondria (yellow) and the chloroplast (green). Ubiquitinated misfolded organelle proteins are extracted by CDC48 and degraded by the 26S proteasome. Alternatively, damaged proteins in the organelles can be cleared by selective autophagy. Cargo receptor molecules anchored or recruited to the outer membrane recognize substrates in the organelle. Cargo receptors expose their ATG8 interacting motif (AIM) on the cytosolic side of the membrane, which recruits the autophagy machinery to initiate autophagosome biogenesis. Parts of the organelle that contain the damaged proteins or the whole organelle are degraded in the vacuole. The balance between 26S proteasome and selective autophagy can be shifted in favor of autophagy by several factors: **1)** *inhibition of CDC48, which leads to retention of ubiquitinated material at the organelle that can only be cleared by autophagy.* **2)** *Terminally aggregated substrates that require the autophagy pathway for complete clearance. This can be manipulated using model substrates.* **3)** *Viral replication complexes cause extensive damage to the organelle membrane and activate autophagy. IMS: inter membrane space.*

INSIGHTS



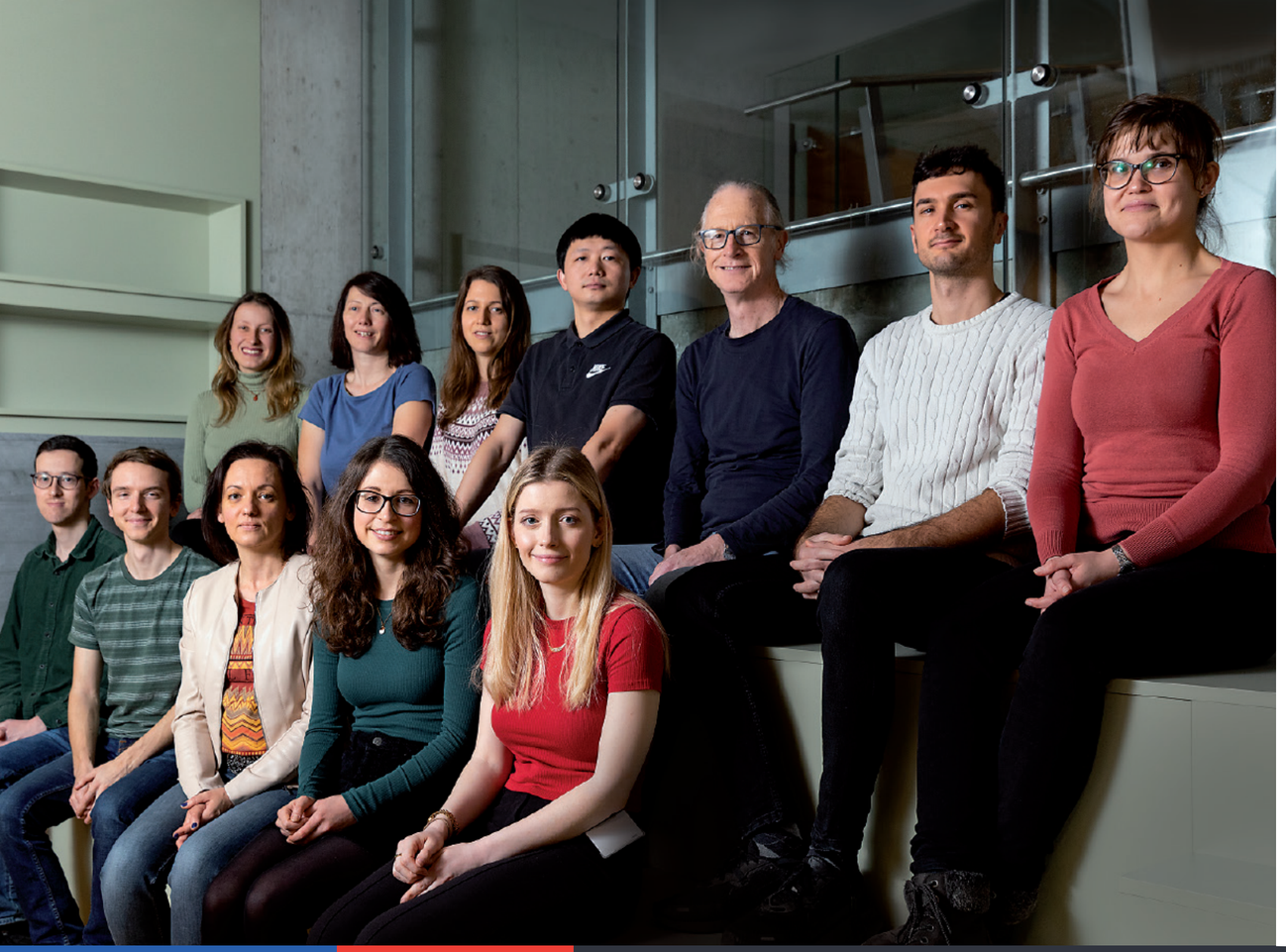
Víctor Sánchez de Medina Hernández
PhD student
Sevilla, Spain
MSc,
University of Sevilla, Spain

How did you come to the GMI?
My first adventure at GMI dates back to summer 2019, right after finishing my MSc Degree, when I did a 3-month internship in Yasin's group. After a short break, I re-joined the lab in January 2020 for a 6-month internship and applied for the VBC PhD Summer Selection 2020. I was honored to be accepted in the VBC PhD Program and started my PhD life in September 2020.

What project are you working on?
My PhD thesis focuses on understanding plant selective autophagy, using the emerging model plant system *Marchantia polymorpha.* Specialized proteins called selective autophagy receptors confer selectivity to autophagy processes. Therefore, they are the key to understanding how these processes work. In my PhD, I will combine biochemical, biophysical, and structural biology approaches as well as plant molecular biology to discover and characterize new selective autophagy receptors.

What do you especially like about working at the GMI?
I was amazed by the research community both at GMI and the VBC. Being part of a community with such diversity is truly inspiring for me as a student. Here, I could get to know people from different countries and research backgrounds who are always willing to help and assist and with whom I could have lively scientific discussions. I was also stunned by the world-class facilities, which make the researchers' life easier to fully focus on their research.

Where do you want to go next?
So far, I don't have any place in mind. Most probably I will apply for a Postdoc position and continue my research career in Academia, but it would be largely dependent on how my PhD experience is, as well as on how my research interests develop.



DEVELOPMENT AND EVOLUTION OF LAND PLANTS

The common ancestor of the land plants existed between 520 and 470 million years ago. The evolution of land plants dramatically changed the Earth System. The transition of life from water to land led to the evolution of many different developmental adaptations, including the formation of roots.

The Dolan group uses paleontology to classify the rooting structures of early land plants. By combining this with developmental genetics, the group seeks to understand the genetic mechanisms used to control development in extant plants and how these mechanisms have evolved throughout Earth history.

Liam Dolan

LIAM DOLAN

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Joined GMI in Sep 2020

PhD: University of Pennsylvania, Philadelphia, USA

PREVIOUSLY

- Head of Department (2012–2017): Dpt. of Plant Sciences, University of Oxford, UK
- Sherardian Professor of Botany (2009–2020): University of Oxford, UK
- Professorial Fellow (2009–2020): Magdalen College, Oxford, UK
- Project Leader (IMP 2/Band H) with tenure (1996–2009): John Innes Centre, UK
- Independent Research Fellow (1995–1996): John Innes Centre, UK
- Postdoctoral Researcher (1992–1995): John Innes Centre, UK
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ADVANCES IN 2021

Using fossils to reconstruct ancient roots

Interpreting the morphology of fossils poses a challenge. We adapted protocols for reconstructing the bodies of animals preserved in Devonian sediments to reconstruct the body of the 409-year-old *Asteroxylon mackiei* plant. This reconstruction demonstrated, for the first time, the relative positioning in space of the three different types of organs – shoot axes, root-bearing axes and rooting axes – that constitute the body of this plant. It demonstrated that each of these axes develops from the other by unequal branching – where the smaller axis adopts a new identity, and the larger axis maintains the identity of the parental axis. This process – anisotomous branching – occurs in extant lycopsids, the closest living relatives of *Asteroxylon mackiei*. However, roots of extant lycopsids do not originate by anisotomous branching. Taken together, these data indicate that the diversity of axes that formed the body plan of *Asteroxylon mackiei* arose through anisotomy. However, the developmental program by which roots originate through anisotomy has since disappeared. This suggests that mechanisms of root development that had evolved by the early Devonian period subsequently went extinct. It emphasizes that the morphological and developmental diversity of extant plants represents a subset of the diversity that has existed since land plants first evolved.

Using comparative developmental genetics to discover mechanisms that controlled the formation of the first rooting structures

Land plants comprise two monophyletic lineages: the bryophytes and the vascular plants. The comparative analysis of life cycle morphology suggests that the haploid body of these plants developed from spores – haploid cells produced by meiosis surrounded by a mechanically resistant wall, the sporoderm. We aim to reconstruct the genetic mechanism that controlled the development of the multicellular haploid phase of the life cycle of both the bryophytes' and vascular plants' common ancestor. Achieving this aim requires the identification of mechanisms that operated in the developing spores of each lineage. As a first step in investigating how the haploid phase of the land plant life cycle developed in these extinct ancestors, we are using the spore of the bryophyte *Marchantia polymorpha* as a model. There, we seek to define the molecular mechanisms regulating the early stages of development of the multicellular haploid plant.

We have shown that the spore polarizes to form an apical regenerative cell that forms the plant body, and a basal rhizoid cell, a rooting structure that anchors the sporeling in place. In addition, we identified environmental factors that orient the polarity of the germinating spore and set up the apical-basal body axis. Furthermore, we demonstrated that the apical and basal cell regulate each other's development and cellular identity through lateral inhibition. Together, these are some of the molecular mechanisms that regulate the formation of the early body plan of the haploid plant as it develops from a spore. Future comparative analysis will test if these mechanisms likely acted in the common ancestor of the bryophytes and vascular plants between the late Cambrian and middle Ordovician periods when land plants are thought to have evolved from aquatic, algal ancestors.

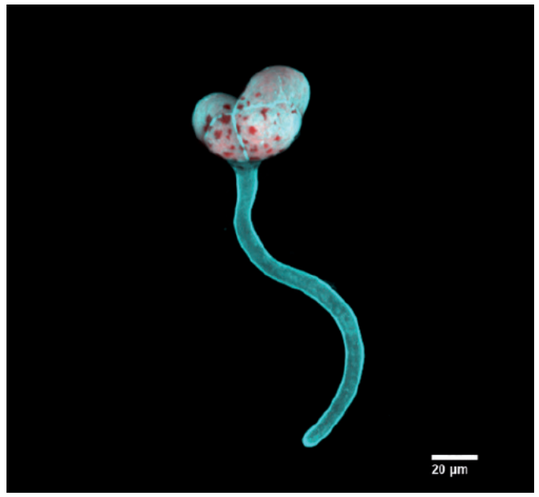
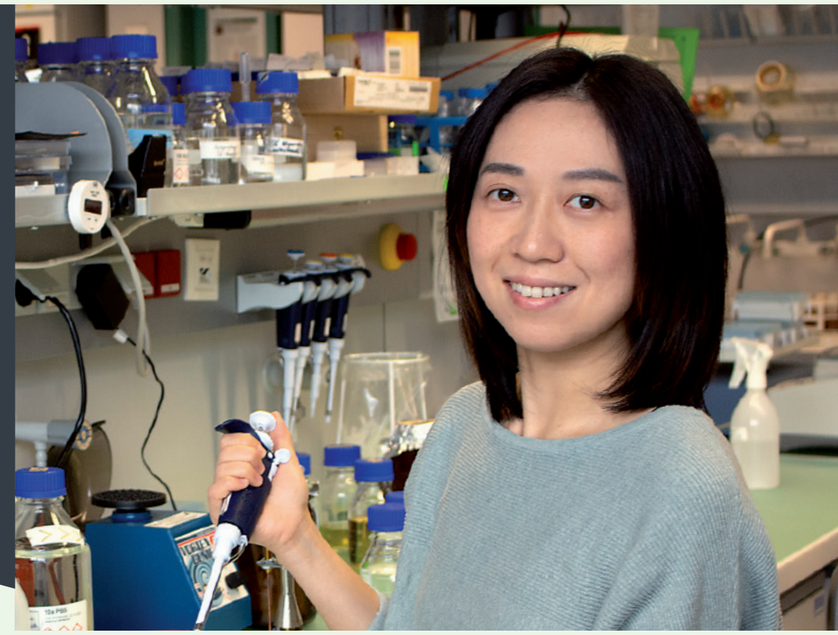


FIG.
A Marchantia polymorpha *haploid plant that developed from a spore. The first division was asymmetric and formed an apical cell that further divided to form the four round cells visible at the top of the plant. The asymmetric cell division also formed a basal cell that did not divide further, but instead elongated by tip growth to form the tubular rhizoid at the base of the plant.*

INSIGHTS



Pin Guo
Postdoc
Wuhan, China
PhD,
Wuhan University

How did you come to the GMI?

I met Liam in a conference when I was in Japan as a postdoc, and we had a chat following his presentation. In 2020, I was in Wuhan for 10 months due to an unexpected lockdown. During the pandemic, I got Liam's email telling me that he was planning to move from Oxford to GMI and might have the possibility to offer me a postdoc position. As a result, I applied to the VIP2 program, and finally managed to come to GMI as a VIP2 fellow!

What project are you working on?

I am working on cell fate determination and patterning focusing on rhizoid cells in the model liverwort, *Marchantia polymorpha*. Marchantia generates unicellular transparent rhizoids which provide nutrition and anchorage in the haploid gametophyte of the life cycle. Rhizoids develop from single epidermal cells that grow out of the plane of epidermis and arrange in a chain-shape pattern on disc-like shape gemmae. One of my projects is to know the mechanism of how rhizoid cells pattern on the gemmae. My second project focuses on single-cell spore development. After the first cell division, a regenerative stem cell and a basal differentiated rhizoid cell are generated. I am working on the mechanism of how these two different cell fates are established.

What do you especially like about working at the GMI?

I enjoy working at GMI. The research atmosphere is quite open-minded. The facilities offer a wonderful assistance in technical training. I am also grateful for the media kitchen and Sterile Processing Department. They take lots of weight off my shoulders and allow me to focus better on my research.
Meanwhile, I benefit a lot from the research networks in GMI. I learnt what other colleagues are studying through Wednesday seminars. People here are open with regards to their research projects and we frequently have discussions on projects among different labs.

Where do you want to go next?

I am thinking about staying in academia, either to have my own lab or work as a research assistant. But I am also open to other career opportunities, such as industry or technique counselor.

ARTURO MARÍ-ORDÓÑEZ
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Joined GMI in Jan 2019

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Arturo Marí-Ordóñez

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. This knowledge will help the research group understand how these selfish genetic elements affect genomes. As part of this goal, the Marí-Ordóñez lab is investigating a group of plants that have not been traditionally used in science, called duckweeds. Duckweeds are rapdily 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.

ADVANCES IN 2021

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. Although the mechanisms that maintain TEs in a silenced state are well described in Arabidopsis, the question of how transcriptional gene silencing (TGS) is initiated before its faithful propagation through generations remains elusive as such pathways act on already silenced TEs. We have recently observed that defects during translation of TE transcripts might represent the first step in the recognition of actively invading transposons. This results in the initiation of small RNA-based antiviral defense mechanisms targeted against the invasive genomic elements.

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. Duckweeds are aquatic plants that mostly reproduce asexually through clonal propagation. Although genomic resources are still scarce, a closer look at the *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. As part of our efforts to understand silencing mechanisms in duckweeds, we have re-sequenced the genomes of two species (*Spirodela polyrrhiza* and *Lemna minor*) and have initiated the genome sequencing of *Wolffia brasiliensis*. Our analysis of small RNA and DNA methylation patterns of both Spirodela and Lemna have confirmed the absence of TE-derived small RNAs and associated DNA methylation patterns. Interestingly, while Spirodela has little DNA methylation only present on a subset of TEs, the majority of transposons remain silenced albeit largely free of DNA methylation. On the other hand, Lemna displays extremely high levels of DNA methylation over TEs. How DNA methylation is deposited over TEs in the absence of small RNAs and how transcriptional silencing can be achieved in Spirodela in the absence of DNA methylation are fascinating questions we are actively investigating.

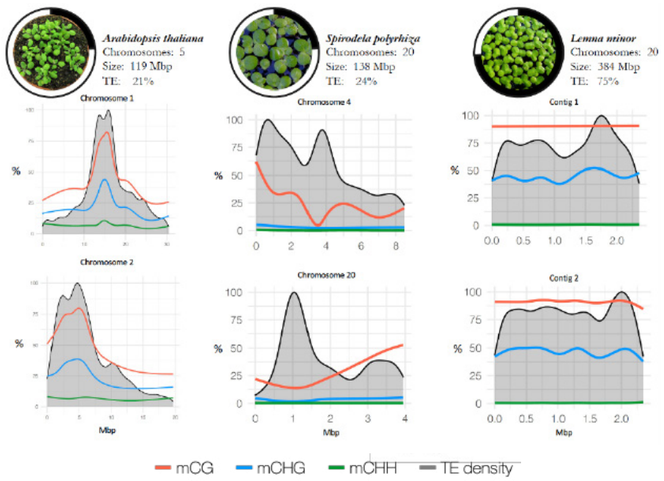
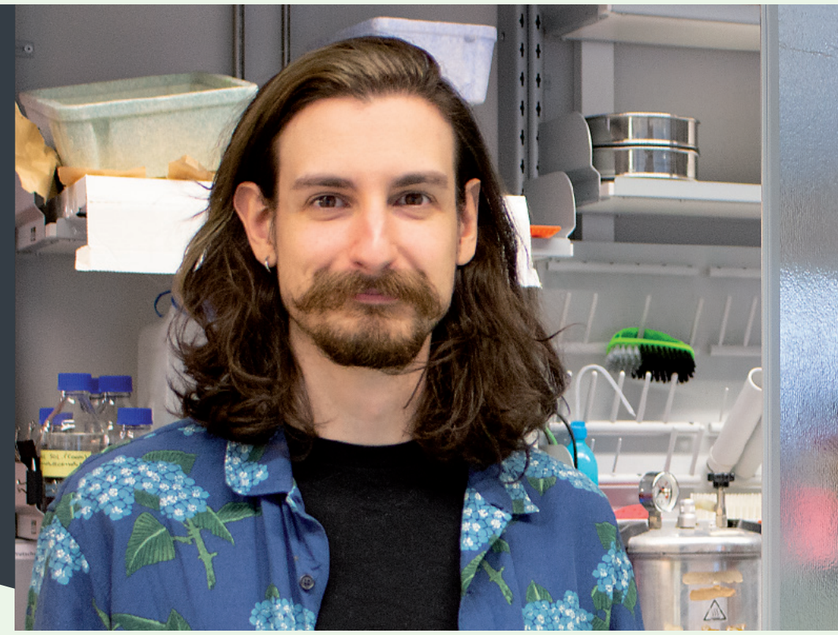


FIG.
Density and distribution of TEs and DNA methylation in Arabidopsis, Spirodela and Lemna.
Density of TE's (Grey) and DNA methylation in the CG (Red), CHG (blue) or CHH (green) context, along two chromosomes (or contigs/scaffolds) for each species.

INSIGHTS



Rodolphe Dombey
PhD student
Lyon, France
MSc,
Montpellier University, France

How did you come to the GMI?
I first joined the GMI as a master student in the Berger lab in 2019. During one of the social hours, I met Arturo, who introduced me to his idea to investigate a new plant family to understand transposon (TE) regulation. The project instantly appealed to me. Therefore, I decided to apply to the PhD program.

What project are you working on?
Until recently, plant research has been seen through the prism of *Arabidopsis thaliana*, however this angle has some serious limits. Hence, in the lab we are working on new model plants, called duckweeds. The latter have lost a major pathway (RdDM) involved in TE silencing. My project is to understand how these plants manage to restrain transposon activity in this context, using genomics approaches.

What do you especially like about working at the GMI?
I really appreciate the working atmosphere at the GMI, you can feel the willingness to help other people to improve your research. Moreover, as a part of the Vienna BioCenter, the GMI offers some core cutting-edge scientific facilities, multidisciplinary seminars by world-class researchers, and excellent training programs to help develop as a scientist.

Where do you want to go next?
My long-term goal is to understand what the rules and the exceptions in transposon silencing are. My thesis project already shows that our current paradigm remains incomplete. I believe that studying different species on an evolutionary scale will greatly contribute to shedding light on TE regulation. I would therefore like to pursue this path with a post-doc, working with more ancestral organisms (e.g., *Chlamydomonas reinhardtii*).

ORTRUN MITTELSTEN SCHEID

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(*left the lab in 2021)

EPIGENETICS

Ortrun Mittelsten Scheid

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 at the DNA (without changing the sequence), variants and modifications 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. The research group studies how epigenetic information is inherited between generations, how it changes during stress or virus infection, how it keeps a memory of light exposure, and how it is involved in DNA repair.

ADVANCES IN 2021

While the genetic inheritance via DNA sequences in nuclear and organellar genomes is well documented, it is still unclear whether and which epigenetic information is transmitted between generations and whether external factors can influence it. Paramutation, a process in which the expression state of one gene copy is permanently changed following an encounter with another copy that has a different expression state, is one of the best examples for heritable epigenetic states. We found that different types of small RNA, the structure and number of the gene copies, as well as the temperature during plant growth determine the degree and timing of paramutation (Bente et al., 2021).

A bottleneck for genetic and epigenetic inheritance in sexually reproducing plants is the shoot apical meristem (SAM), as aerial organs including flowers and seeds originate from the few stem cells in the SAM. The heritable information in these cells determines the performance of the progeny, but its integrity is challenged by transposon activity and other mutations. Suppression of deleterious transposition and mechanisms for DNA repair, though also active in somatic cells, are therefore even more important in cells that contribute to the germline. Further, the exclusion of pathogens from the meristem is important to avoid transmission through seeds.

We found that several novel, long non-protein-coding RNAs that are induced and connected with DNA damage signaling have a role in the capacity for DNA repair, adding to the multiple components that secure genome stability. For a chromatin remodeling complex, we identified phosphorylation sites that are necessary for its function in DNA repair. Based on the analysis of gene expression and DNA methylation in nuclei of SAM stem cells, we identified two proteins from the AGO family that are specifically expressed throughout the plant life cycle in cells potentially contributing to the germline. We extended the analysis to single nuclei, analyzed the small RNA cargo of the AGO proteins, and connected it to transposon suppression and DNA methylation patterns. We followed the dynamic localization of the AGO proteins with different methods, including live imaging. The latter technique was also applied to visualize virus infection in wild type and mutants affected in epigenetic or defense pathways. This is expected to provide insight on how virus entry into the meristem and vertical transmission of virus infections are avoided (Bradamante et al., 2021).

The projects described above are based on experiments with the model plant *Arabidopsis thaliana.* In addition, we contributed to growing genome and gene expression data for the related species *Aethionema arabicum* (Fernandez-Pozo et al., 2021) and followed an interesting aspect of its seed biology. Seeds of some accessions do not germinate if they are exposed to light, and a longer period in the light can install a lasting inhibition of germination, likely adapting this important developmental step to the optimal season. Mutagenesis with high energy radiation and screening for plants that either lost the light inhibition or the memory effect of the light resulted in several candidates. For some of these plant candidates, we were able to identify the affected genes and connected the phenotype to light reception and signaling.

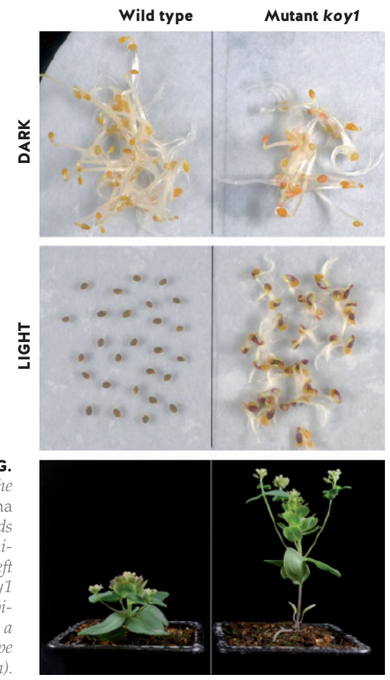

FIG. *One candidate from the mutant screen in* Aethionema arabicum. *Normally, seeds of this plant cannot germinate in the light (middle left panel), but the mutant koy1 (right) has lost this inhibition. Mutant plants show a "shade avoidance" phenotype (bottom).*

INSIGHTS

Nathalie Durut
Postdoc
Neuilly-sur-Marne, France
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How did you come to the GMI?
After finishing my PhD, I had the great opportunity to work as a Junior Lecturer at the University of Perpignan in France. It became quickly evident to me that I wanted to continue in both teaching and research. Thus, I decided to look for a post-doctoral position to gain more experience and to be able to apply for a professorship in the future. I contacted Ortrun Mittelsten Scheid as I was 1) impressed by her research quality and 2) interested in both epigenetics and DNA repair, topics addressed in her team. After a successful interview, she encouraged me to develop my own research project, which was then granted by the Lise Meitner Fellowship from the Austrian Science Fund (FWF).

What project are you working on?
When DNA is damaged, efficient repair must be carried out to ensure faithful transmission of genetic information. My research project consists of exploring the role of an emerging class of molecules: the long non-coding RNAs (lncRNAs) in DNA repair. Using transcriptomic, genetic and molecular approaches, we identified several promising candidates showing a clear connection with DNA damage. Our next steps focus on understanding what the role of these molecules in DNA repair is and how they participate in the maintenance of plant genome stability.

What do you especially like about working at the GMI?
The GMI is an internationally recognized center for basic plant research that provides state-of-the-art technology for molecular biology as well as excellent plant growth facilities. It offers several services with experienced people helping us in our research. It is a great place to work in, with a friendly and interdisciplinary environment. A special thanks to the VBC for providing us a safe workplace especially during the Covid pandemic.

Where do you want to go next?
In my next career step, I would like to teach at the University and continue doing research. I am also open to join the private sector if opportunities arise.

Michael Nodine

RNA BIOLOGY OF PLANT EMBRYOS

Soon after fertilization of the egg and sperm, genes in the zygote are turned on and initiate a precisely coordinated developmental program. Already during very early stages of development, the basic blueprint of the plant body plan and (epigenetic) modifications are re-established. Specialized cell types within these organs are also established at this time, and each of these cell types must turn on specific sets of genes. Although decades of research in animals have found how many of these processes are regulated in animals, relatively little is known in plants because developing plant embryos are deeply embedded in maternal tissues, which makes them difficult to study.

The Nodine Group is interested in learning more about how these very early stages of development are regulated. They developed an array of genomic, microscopy and bioinformatic tools to study RNA biological processes from limited amounts of material including early plant embryos. They are especially interested in how small RNAs that do not encode proteins regulate developmental and epigenetic processes during the initial steps of plant embryogenesis.

MICHAEL NODINE*

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Joined GMI in Jul 2012

PhD: University of Arizona, Tucson AZ, US

PREVIOUSLY

Postdoc (2007-2012): David Bartel Lab, Whitehead Institute for Biomedical Research, Cambridge MA, US

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TECHNICIAN
Magdalena Mosiołek*

(*Left the lab in 2021 – Michael Nodine moved to Wageningen University, Netherlands)

ADVANCES IN 2021

We continue to develop molecular biology, microscopy, and bioinformatic approaches to characterize the establishment of the nascent epigenome and the most fundamental plant cell types at the beginning of life using Arabidopsis as a model system. Below are highlights of three projects that we published in 2021.

Generating a gene expression atlas across embryonic cell types has been a major goal for plant embryologists at least since the original root cell atlases were published 18 years ago (Birnbaum et al., 2003). However, previous efforts to profile embryonic transcriptomes have been hampered by the notorious difficulty in isolating early embryos deeply embedded in maternal seed tissues. Previous attempts have employed methods such as cell sorting, laser capture microdissection and INTACT-based methods, but all resulting datasets have suffered from either a lack of cell-type resolution or contaminating RNAs from surrounding seed tissues. We developed a method that enables the generation of high-quality transcriptomes from single nuclei of early *Arabidopsis thaliana* embryos (Kao et al., 2021). In addition to providing the community with an early embryonic gene expression atlas at single-nucleus resolution, we also highlighted gene expression variations across cell types associated with differential evolutionary trajectories, epigenetic mechanisms, and transcriptional programming.

Developmental phase transitions are often controlled by quantitative regulation of gene expression by multiple factors at precise developmental time points. Decades of research have revealed how multiple pathways converge to establish the expression of FLC at levels that prevent flowering until favorable environmental conditions. However, it remains poorly understood how and when during development such factors interact to quantitatively regulate FLC expression. Together with our collaborators from the UK, we demonstrated that FLC activators and repressors antagonize each other in a specific stage of early Arabidopsis embryos to modulate polyadenylation site usage of FLC transcripts (Schon et al., 2021). Excitingly, this antagonism quantitatively regulates flowering time much later in life and provides a conceptual advance in understanding quantitative regulation of gene expression in a developmental context.

Understanding how DNA methyltransferases are regulated to balance the sensitivity needed to silence mutagenic transposable elements (TEs) while limiting ectopic methylation of genes is a key research goal in the field of epigenetics. Fine-tuning of DNA methyltransferase activities is particularly demanding during plant embryogenesis when dynamic cell cycle activities generate the precursors of all future cell types including the gametes. We demonstrated that a single microRNA, as well as chromatin features, helps prevent CHROMOMETHYLASE 3 (CMT3) from ectopically methylating thousands of endogenous genes (Papareddy et al., 2021). Such epigenetic off-targeting can reduce transcript levels from genes that switch from transcriptionally inert to active states. We further showed that the repression of CMT3 in embryos helps prevent the mitotic propagation of hypermethylated cytosines in the CHG context throughout most of Arabidopsis development. Interestingly, CMT3-induced CHG hypermethylation occurs on genes in an identical pattern as observed for CG gene-body methylation. Ectopic CMT3 can occasionally induce CG methylation (Wendte et al., 2019). Based on our results, we propose a model that may help resolve the ongoing debate regarding the functionality, or lack thereof, of gene-body methylation in plants. We suggest alternative explanations for the main features associated with gene-body methylation.

In addition, we propose that these may be related to functional consequences of transient CHG methylation that occurred in the past and were fixed as gene-body methylation on evolutionary time scales in nearly all flowering plants.

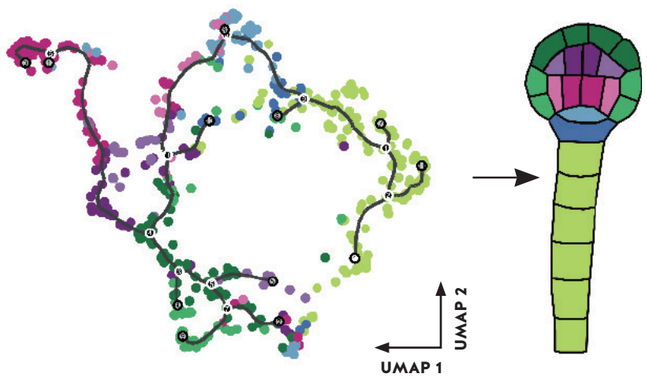

FIG.
The supervised clustering approach used by Kao et al. resolves nine different cell types in the plant embryo. This hypergeometric test calculates scores for cell types based on marker genes. Each dot represents a nucleus and is assigned to the cell type with the highest calculated score. UMAP: Uniform Manifold Approximation and Projection for Dimension Reduction. ©Kao/Nodine/Development/GMI

INSIGHTS

Michael Schon
PhD student
Cedar Rapids, Iowa, USA
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How did you come to the GMI?
As an undergrad in Iowa I worked in a fly neural development lab, but growing up in the "heartland" gave me an enduring interest in agriculture and plant biotechnology. I decided to pursue a PhD in plant development, so I applied for the VBC PhD program and fell in love with the campus. The GMI offers world-class plant research uniquely situated in a vibrant center for molecular biology.

What project are you working on?
For my PhD I focused on tackling the challenges that come from working with very small samples of RNA. The Nodine lab uses Arabidopsis embryogenesis as a model for understanding plant development, but early embryos are tiny and surrounded by maternal tissue. I developed a collection of RNA sequencing and data analysis techniques that enabled us to get a comprehensive and precise picture of the embryonic transcriptome. We now have a spatiotemporal atlas of transcript dynamics during embryogenesis, including sites of transcription initiation, termination, and site-specific cleavage by microRNAs.

What do you especially like about working at the GMI?
The GMI fosters a great collaborative and social atmosphere. It's been wonderful to freely share ideas, materials, and strategies for ongoing projects with colleagues at the GMI and across campus. Open science is science at its best.

Where do you want to go next?
I am joining Michael Nodine as a postdoc in his new lab at Wageningen University & Research in the Netherlands. With its strong focus on plant research for agriculture and the environment, WUR sits on the interface between basic and applied science. I'm excited to bring the tools and expertise I've built at the GMI to a new environment!

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Zahra Panahy*

(*left the lab in 2021)

EXPLORING GENOMIC VARIATION

Magnus Nordborg

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 seeks 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 2021

What is genetic variation?
The first human genome, published in 2003, cost an estimated 1 billion dollars. By 2014, the cost of additional human genomes had dropped to $1000, and the goal now is to reach $100 per genome. Or so it is said: these latter numbers represent a truth with modification, because these genomes are produced by sequencing millions of short DNA fragments that can be compared to the 2003 reference genome in order to find differences –in particular Single Nucleotide Polymorphisms (SNPs) that can then be used to search for genetic variants that may be associated with various diseases, and so on. But 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. Thanks to advances in long-read sequencing technologies, this is now becoming possible. A major effort of the group is to complement the previous "1001 Arabidopsis Genomes Project" with many independently assembled genomes. By the end of 2021, we had generated more than a hundred such genomes.

No more artifacts!
An obvious use for such data is to assess how much we have been missing by aligning short sequencing reads to a single reference genome. For example, over 40% of all SNPs called this way in the 1001 Genomes data using standard methods are ostensibly heterozygous. Because Arabidopsis lines are inbred, this is impossible, and it seemed likely that they were pseudo-SNPs resulting from cryptic duplication. This means that if the genome of the target individual contains multiple copies of a sequence that only occurs once in the reference genome, bioinformatics methods will align all sequencing reads to this one location. This approach would identify any difference between loci in the sequenced individual as heterozygous polymorphisms. In this line, we found that 10% of all annotated genes in the Arabidopsis reference genome are duplicated, wholly or partly.

The problem is not limited to variant detection. Many standard approaches in genomes are based on aligning short sequencing reads to a reference genome. For example, genome-wide transcription measurements are done using so-called RNA-seq, where mRNA fragments are converted to DNA fragments and aligned to their putative source to quantify expression levels. However, expression levels can also differ because of copy number variation in the underlying loci, and this will generally be missed. We are systematically evaluating the seriousness of this and related problems.

How do genomes evolve?
The most important use for our new genomes, however, is to understand how genomes evolve. While the mutational processes causing SNPs are reasonably well understood, the same is not true for structural variants. We have developed methods for comparing whole genomes and identifying all structural variants. Armed with these data, we can then ask how they arose. We are particularly interested in mobile DNA that has been inserted from somewhere else and has a high and variable copy number, because these sequences are effectively transposable elements – here identified because they do, in fact, transpose. Typically, transposons are identified using bioinformatic algorithms that try to recognize known transposons, a biased approach, because you can only find what you are looking for. By looking for things that have actually moved, we find new things. For example, we identified a new transposon that consists of a tandem arrangement of an annotated transposon and an annotated gene. Both annotations are wrong, and the true transposon is larger.

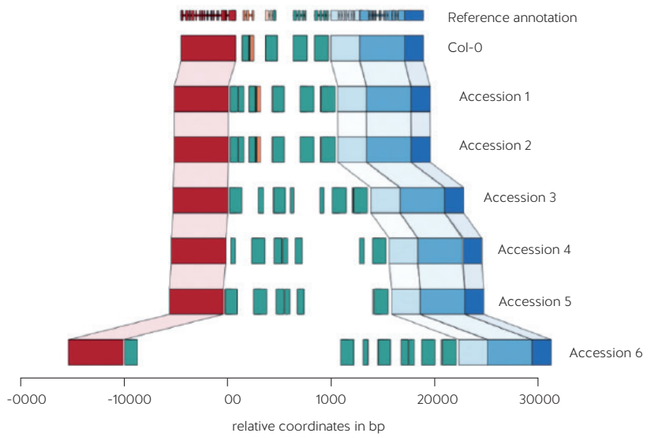
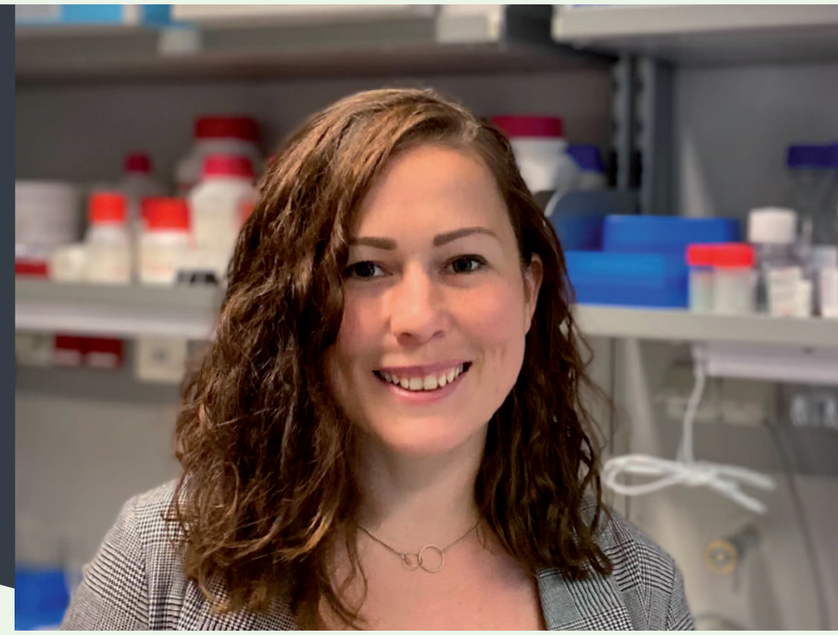


FIG.
Example of gene duplication across 6 Arabidopsis accessions: The different colors represent the genes in the region. When the reference and Col-0 have 4 copies of the same gene (green), all other accessions included here contain 5 or 6 copies as well as other unknown fragments. The flanking regions, red and blue here are fully conserved.

INSIGHTS



Aleksandra Kornienko
Postdoc
Smolensk, Russia
PhD,
CeMM + Medical University of Vienna, Austria

How did you come to the GMI?
After finishing my Ph.D., I was very torn about where to go next, but then finally decided to join the Nordborg lab at the GMI because here I had complete freedom to develop and work on my own project. I also received an FWF Hertha Firnberg Fellowship which was another great support in my research and independence.

What project are you working on?
I am trying to understand how a special kind of genes - long non-coding RNAs – differ between individuals of the same species (in this particular case – our model organism – a little weed plant *Arabidopsis thaliana*). Long non-coding RNAs are often called "the dark matter" of the genome because there are so many of them and because they have been overlooked for decades. I am trying to learn as much as possible about their evolutionary origin, diversity in the population, genome biology. I hope to find (among thousands) some interesting lncRNAs that can be studied for specific functions in plants.

What do you especially like about working at the GMI?
I like that people in the GMI are really chilled and open and that we, as scientists, don't need to worry about anything but science because of all the administrative and technical support. I also really like the equality and respect here and that you never feel in any way intimidated or looked down upon by the PIs and the directors, who are way more advanced in their careers than you are. GMI is like a second big home, with lots of plants and people who really love plants and want to know everything about them.

Where do you want to go next?
I am still undecided but I am leaning towards moving to the intersection of science and public policy hoping to increase the interaction and understanding between science and society.

SILVIA RAMUNDO

silvia.ramundo@gmi.oeaw.ac.at

Joined GMI in Oct 2021

PhD: University of Geneva, Switzerland

PREVIOUSLY

Post Doc, Peter Walter Lab, University of California, San Francisco, USA (2013-2021)

GROUP MEMBERS

TECHNICIAN
Nicole Lettner

Silvia Ramundo

CHLOROPLAST BIOGENESIS AND PROTEIN QUALITY CONTROL

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 a process commonly known as photosynthesis. Chloroplasts have a fascinating evolutionary history and are a marvellous example of the relationship between structure and function. They contain a highly organized system of membranes where chemical reactions take place with remarkable precision. These reactions are orchestrated by multiprotein complexes whose subunits are often encoded by the physically separated chloroplast and nuclear genomes.

The Ramundo lab aims to investigate poorly understood aspects of chloroplast biogenesis and protein quality control. With their work, the research group envisions to answer fundamental questions in biology while developing or applying innovative research tools.

MEET SILVIA RAMUNDO, NEW GMI GROUP LEADER!

The cornerstone of the Ramundo lab at GMI was set in October 2021. Silvia Ramundo came to us following a postdoctoral position at the University of California, San Francisco, USA. At GMI, the Ramundo lab will investigate chloroplast biogenesis and protein quality control using the model organism Chlamydomonas. In this short interview, Silvia Ramundo talks about her research interests and plans, and why she chose GMI. In addition, she provides insight on the challenges of young parents in science and talks about her hobbies. Dive with us into the mind of a successful young scientist who champions #WorkLifeBalance!

Silvia Ramundo was interviewed by Daniel F. Azar from the GMI-IMBA Communications & Partnerships.

Dear Silvia, welcome to the Gregor Mendel Institute, it is great to have you on board! Please tell me, how do you summarize your research interests and plans for your lab at GMI?

SR: Thank you Daniel, it is a pleasure to be here! On my research interests and plans: I am a "chloroplast aficionado" and use the green alga *Chlamydomonas reinhardtii* as a model system. Chlamydomonas is one of the few organisms whose chloroplast genome can be easily engineered via gene targeting. In addition, Chlamydomonas is unicellular, has a haploid nucleus and a single chloroplast, thus it enables one to combine genetic, cellular, and biochemical studies.

At the GMI, I want to advance our understanding of the molecular mechanisms involved in chloroplast biogenesis, signaling and protein quality control. Here I bring in Chlamydomonas as a new model organism to the Institute. In exchange, I am excited at the prospect of collaborating with groups that use other model organisms, such as *Arabidopsis thaliana* or *Marchantia polymorpha*, or have complementary research expertise to mine.

What made you choose GMI? What is the added value with regards to other institutions where you applied for group leader positions?

SR: The Vienna BioCenter offers a very stimulating research environment with a wide range of research topics, and the GMI core funding is incredibly generous. The lack of teaching obligation is attractive, too. It is not that I do not like teaching (quite the opposite), but not having this obligation is helpful at this stage of my life, as I am establishing a lab in a new country while I also have a family with two very young children. I am also happy with my colleagues here! In fact, let me tell you more. I got infected with Covid-19 around the time when my interview with GMI was scheduled. I requested to postpone this interview for two weeks to allow myself some time to recover. Two weeks later, when I showed up to my rescheduled online interview, my future colleagues noticed that I was still suffering and asked me if I was sure about doing the interview in such a state. I had not fully recovered yet but would have never thought of postponing the interview further. However, my colleagues insisted on the importance of being "at my top" for this crucial career step. This was another important sign that the GMI would be the right place for me!

How is the move going? Do you feel supported by GMI in establishing your research group?

SR: Moving overseas in the middle of the pandemic has been quite a challenge, I will not hide it. However, people at the GMI have been incredibly helpful at all levels. This goes from helping me with the official requirements for moving biological material and equipment to Austria, to more personal matters like arranging childcare for my children.

What are your thoughts on women/mothers in academic research? How do you feel about joining GMI as a female group leader/a mother?

SR: You know, it's great that you ask. Rather than looking at this question from the perspective of a specific gender, I would approach it from the perspective of a parent. I am well aware of VBC institutes' efforts to promote hiring female group leaders, but this alone is insufficient. The women who are more likely to be recruited still tend to be women without children and family commitments. In my opinion, the key for making science and academia more embracing for women is to make it more embracing for working parents in general. In addition, we should find an effective way to factor-in the challenges of those scientists whose partner is also a full-time working parent when measuring their overall success during hiring and/or promotion decisions.

What hobby/activity/interest helps you clear your mind from work? Would Vienna be a suitable location for your "extracurricular interests"?

SR: One of my hobbies is traveling and exploring other cultures! That's probably why I chose this job, and I moved a lot during my professional career. I'm from Nardó, a town near Lecce, in Southern Italy, but I studied Pharmaceutical Biotechnology in Bologna, which is in Northern Italy. From there I moved first to Barcelona, at the CRG for my master thesis, then to San Diego for a summer internship at the Salk Institute, then to the University of Geneva for my PhD, then to the University of California in San Francisco for my postdoctoral studies and now to Vienna, at the GMI! Being in Vienna is great for traveling as the city has very good connections within Europe and the world. Another passion is cooking. I'm a total foodie and am lucky to be married to an excellent cook – and yes, he is Italian, too (laughs). What people might find a bit unusual for a scientist is that I love fashion design, too, especially Chanel's and Missoni's personal accessories. I also appreciate art and music in general – so I very much look forward to enjoying the great cultural and artistic offer in Vienna once this pandemic will be over!

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
Vasilina Akulova

POSTDOC
Miguel Vallebueno

TECHNICIANS
Alex Arizpe
Julia Riefler
Lucyna Slusarz

STUDENTS AND INTERNS
Sana Naderi*
Krisztian Nemeth
Anni Nurmisto
Sonja Steindl*
Lisa Weidlich
Nora Wittmann
Chieh Yen Chun

(*left the lab in 2021)

TREE RING GENOMICS

Kelly Swarts

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 2021

As of this summer, we have sampled 3,748 genotypes from 52 plots across 12 locations in the Alps, Bohemian, and Carpathian regions (→ Fig.) 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. Over the past year, we have also intensively sampled the spruce bark beetle *(Ips typographus)*, a biotic environment. Up to 79 trees are sampled for DNA and two increment cores, and tree metrics (height, diameter) recorded.

A 20Gbp genome makes whole-genome sequencing cost prohibitive. However, Miguel Vallebueno developed a reduced representation, massively multiplexable Genotyping-by-Sequencing (GBS) restriction digest library protocol. In a small population, we discovered over 1.5 million variants and directly covered more than 56% of coding regions. These results are comparable to the current standard but with 30 times more unbiased markers for less than one Euro per sample, and the manuscript is currently in preparation. Because this approach is sampling a small fraction of the total genomic space, we sampled haploid megagametophytes from managed and unmanaged plots across Europe that we can use to estimate the power this variant set provides for climate associations. Early reduced-representation genotyping data from three populations across Europe implies that populations are more structured in coding regions than genome-wide, suggesting selection (→ Fig.). Additionally, we recently sampled outgroups to help untangle the mode of action.

Hand measurement of annual growth is not only unfeasible but would be error prone since many individuals would be required to participate. With Core Services, we have successfully developed an automated phenotyping platform that relies on high-quality images generated from a Zeiss broad-spectrum light microscope. In addition, this automated phenotyping platform requires 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). 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 0.95 and a recall (the proportion of true rings that are called) of 0.99. A paper focused on the CNN is currently in preparation. Furthermore, we are developing a Shiny app in R that allows for human correction of the CNN and subsequently generates ring-width measurements and provides tools for predicting the tree center (pith) and ensuring that rings are correctly dated. This pipeline allows for the fast and accurate generation of millions of ring-width measurements.

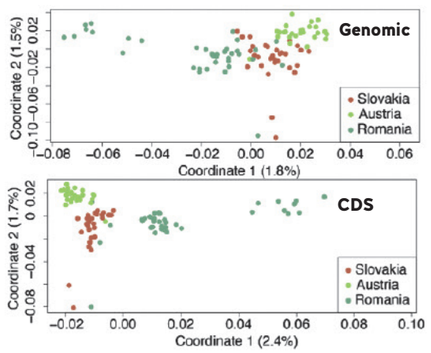


FIG.1
Multidimensional scaling based on variants across the genome versus only in the coding regions.

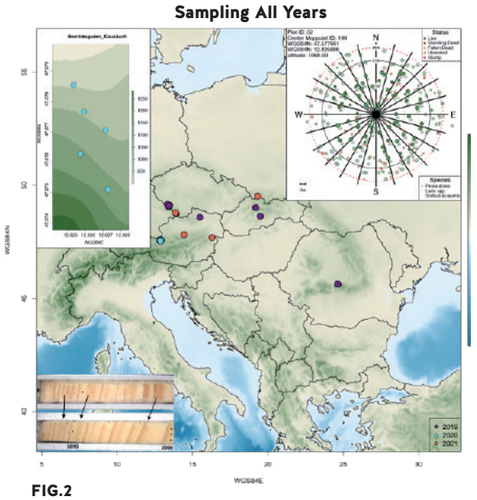


FIG.2
Multiscalar sampling design.

INSIGHTS

Alexis Arizpe
Technician
Tucson, Arizona, USA
MSc,
University of Arizona, USA

How did you come to the GMI?
I met Kelly in summer 2018. At that time, I had a position as a lab and field instructor in an intensive tree ring course offered by the University of Arizona. Kelly was a student in this course. One evening she said she'd recently been offered a job at the GMI. I told her to let me know if she needed a technician and by the following January I was in Vienna.

What project are you working on?
Our group is interested in the role of genetics and the environment in influencing tree growth. To do this, we are collecting samples from trees from across Europe. We need to know the calendar year that each ring of the tree was formed so that we can compare it to that year's climate and understand how it grew relative to its neighbors. I focus mainly on collecting the tree-ring samples in the forest, then preparing and dating them back at the lab.

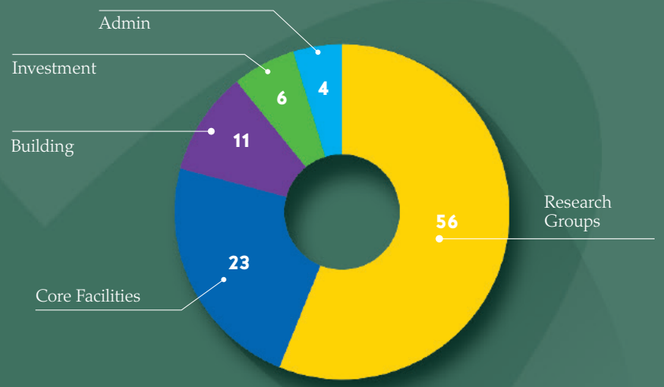
What do you especially like about working at the GMI?
The workshop is the most impressive workshop I've ever seen. They can really make anything happen! In addition, all the support at GMI is really impressive. Lab support, bio-optics and the workshop all make it so easy to focus on your research. I've never worked at a place that has so much support for such a wide variety of projects. It is amazing to come up with an idea, wonder if it's possible and then see that it is with the assistance of all these groups.

Where do you want to go next?
As someone that spends so much of their time looking at the past through tree rings, I have a harder time looking forward. I like both the GMI and Vienna so hope to stay for a while longer.

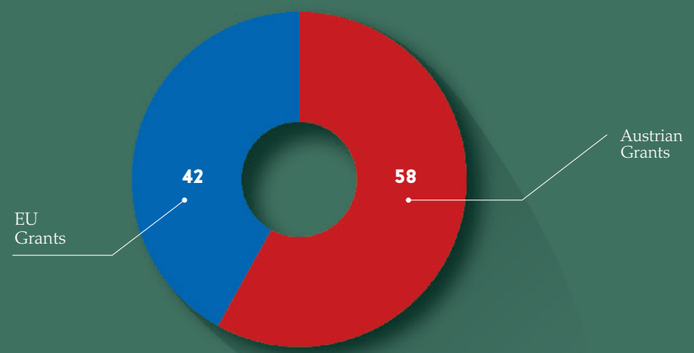
2021

KEY FACTS *(as of Dec 31, 2021)*

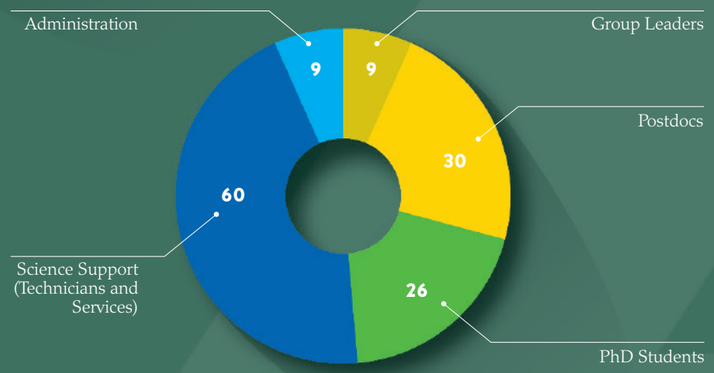
EXPENDITURES (%)



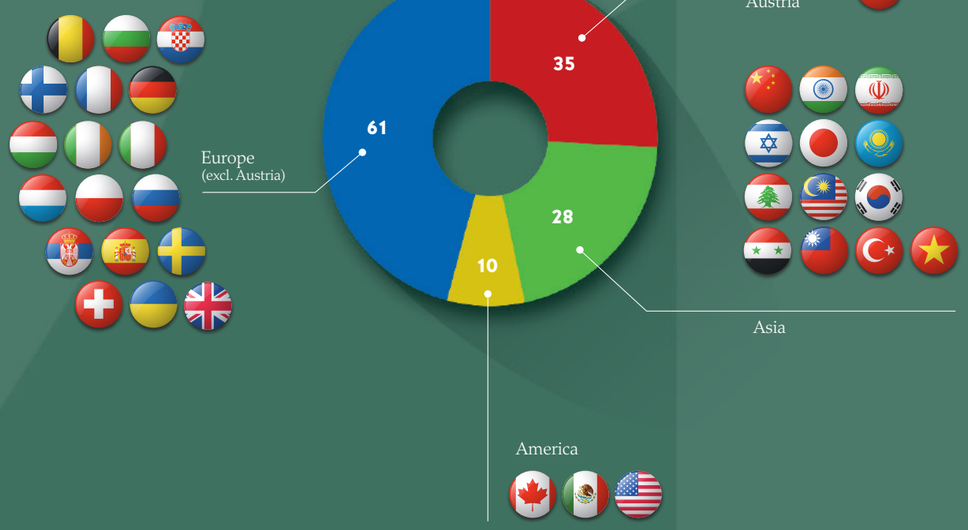
RESEARCH GRANTS (%)



STAFF BY FUNCTION (Head Count)



STAFF - NATIONALITIES (Head Count)



2021 PUBLICATIONS

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Colaianni NR, Parys K, Lee HS, et al. (2021) **A complex immune response to flagellin epitope variation in commensal communities.** *Cell Host Microbe 29(4):635-49.*

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Lee DH, Lee HS, Belkhadir Y (2021) **Coding of plant immune signals by surface receptors.** *Curr Opin Plant Biol 62:102044.*

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BERGER GROUP

Borg M, Jiang D, Berger F (2021) **Histone variants take center stage in shaping the epigenome.** *Curr Opin Plant Biol 61:101991.*

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Déléris A, Berger F, Duharcourt S (2021) **Role of Polycomb in the control of transposable elements.** *Trends Genet [epub].*

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DAGDAS GROUP

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Klionsky DJ, Abdel-Aziz AK, Abdelfatah S, et al. (2021) **Guidelines for the use and interpretation of assays for monitoring autophagy (4th edition).** *Autophagy [epub].*

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DOLAN GROUP

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MITTELSTEN SCHEID GROUP

Bente H, Foerster AM, Lettner N, et al. (2020) **Polyploidy-associated paramutation in Arabidopsis is determined by small RNAs, temperature, and allele structure.** *PLoS Genet 17(3):e1009444 preprint bioRxiv:2020.10.21.348839.*

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NODINE GROUP

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PUBLICATIONS

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Schon M, Baxter C, Xu C, et al. (2021) **Antagonistic activities of cotranscriptional regulators within an early developmental window set FLC expression level.** *PNAS 118 (17) e2102753118.*

NORDBORG GROUP

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RAMUNDO GROUP

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SWARTS GROUP

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FORMER GROUPS & SERVICES

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2021 GRANTS

BECKER GROUP

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

Bacterial activation and degradation of allelochemicals
(Lise Meitner fellowship Knoch)
Austrian Science Fund: M 2482-B21
€ 169,260
November 2018 – January 2021

BELKHADIR GROUP

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 - January 2022

BERGER GROUP

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
May 2019 – April 2022

Chromatin dynamics at fertilization in early land plants (Tetsua Hisanaga)
H2020-MSCA-COFUND-2018:
GA: 847548 VIP² (GEUP0018BER)
€ 98,640
January 2020 - December 2022

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

The histone variant H2A.W promotes heterochromatin accessibility for efficient DNA methylation in Arabidopsis (Pierre Bourguet)
H2020-MSCA-COFUND-2018:
GA: 847548 VIP² (GEUP0018BER)
€ 98,640
January 2021 - December 2023

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

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

Viruses as probes to dissect selective organelle recycling (Marion Clavel)
H2020-MSCA-COFUND-2018:
GA: 847548 VIP² (GEUP0018DAG)
€ 98,640
January 2020 – December 2022

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

Protein engineering expands the effector recognition profile of a rice NLR immune receptor (Juan Carlos de la Concepción)
H2020-MSCA-COFUND-2018:
GA: 847548 VIP² (GEUP0018DAG)
€ 98,640
March 2021 – February 2024

EMBO Long-Term Fellowship (Marta García León)
European Molecular Biology Organization: ALTF1107-2020
€ 53,811
January 2021 – October 2021

CURIE - C53 and Ufmylation Regulation In Endoplasmic Reticulum-Autophagy
(ER-phagy) (Ni Zhan) H2020-MSCA-IF-2020:
GA: 101028611
€ 186,167
May 2021 - April 2023

Functional evolutionary analysis of a novel autophagy adaptor in plants (Jierui Zhao)
ÖAW Doc Fellowship: 25966
€ 38,000
August 2021 - July 2022

MENTOR - Molecular Mechanisms to Improve Plant Resilience
Austrian Science Fund: 111-B
€ 201,029
October 2021 – September 2025

DOLAN GROUP

DENOVO-P De novo Development of Polarity in Plant Cells
H2020-ERC: GA: 787613 Denovo
€ 1,965,757
(October 2018 – Sept 2020 UOXF, € 533 466,60)
GMI: October 2020 – September 2023

Study on Spatial Patterning of Rhizoid Cells Regulated by Lateral Inhibition in Marchantia polymorpha (Pin Guo)
H2020-MSCA-COFUND-2018:
GA: 847548 VIP² (GEUP0018DAG)
€ 98,640
May 2021 – April 2024

Untersuchung von Mechanismen der Zellpolarität in Bezug auf Zellschicksal und Musterbildung während der Entwicklung von Vaskulatur und Spaltöffnungen in Arabidopsis (Sophie Wallner)
DFG WA4709/1-1
€ 33,504
April 2021 – March 2022

MITTELSTEN SCHEID GROUP

Graduate program "Chromosome Dynamics"
Austrian Science Fund: W1238
€ 182,800 + € 142,020 (prolongation)
March 2012 – August 2021

AUgmented REsilience After Transmission of Epimutations (Ruben Gutzat)
Austrian Science Fund: I 3687-B25
€ 302,719
January 2018 – June 2021

A novel model to study light-regulated seed germination (Zsuzsanna Merai)
Austrian Science Fund: I 3979-825
€ 382,032
February 2019 – February 2023

Transgenerational antiviral barrier in plants
(Lise Meitner fellowship Marco Incarbone)
Austrian Science Fund: M – 2921
€ 169,260
July 2020 – June 2022

NODINE GROUP

Graduate program "RNA Biology"
Austrian Science Fund: DK W1207-B09
€ 286,680
January 2014 – November 2021

NORDBORG GROUP

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

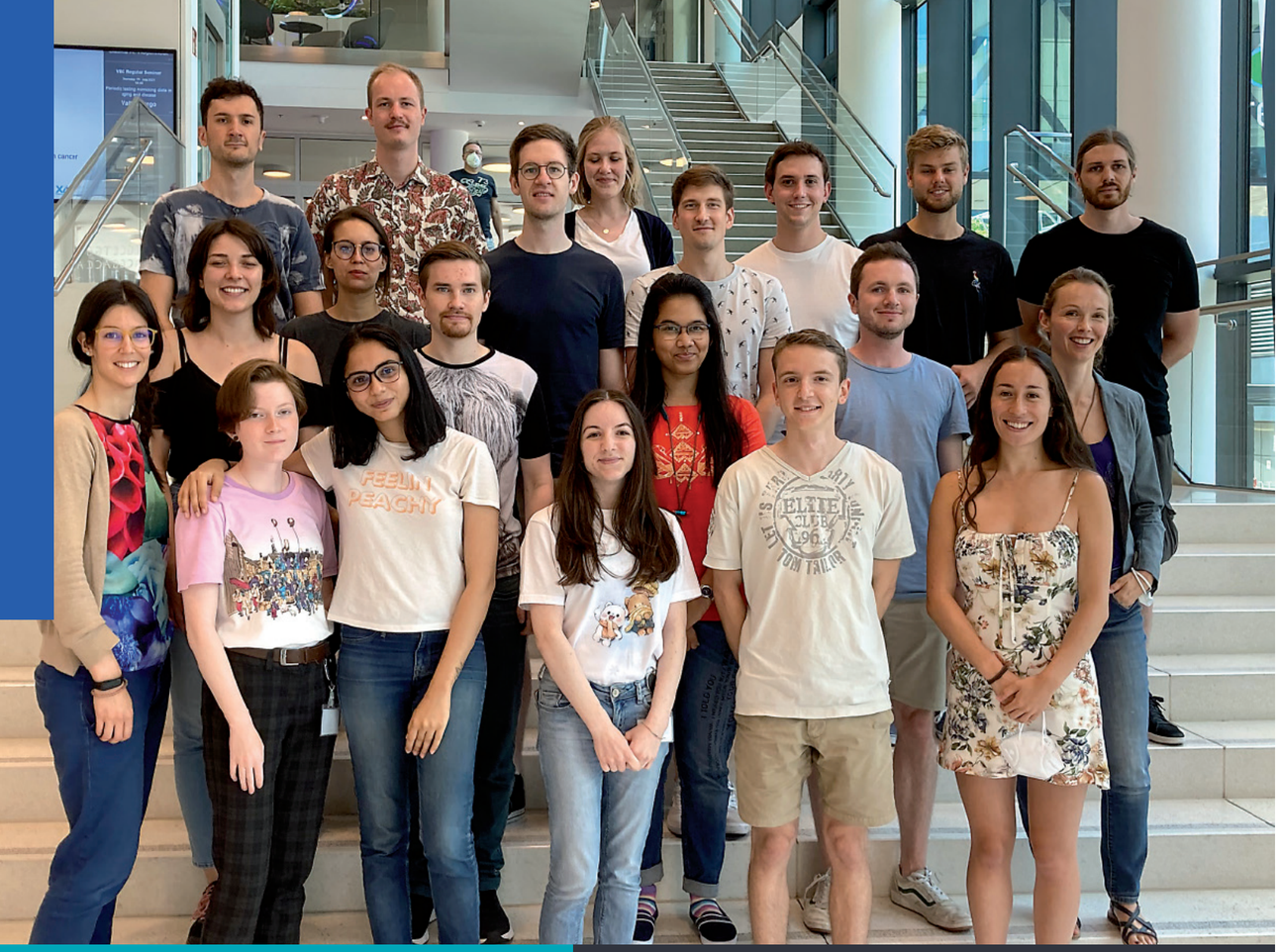
1001 Genomes Plus
Austrian Science Fund: I 3684-B25
€ 355,541
January 2018 – June 2021

CUBIC: An Atlas of Genetic Architecture Promises Directed Maize Improvement
(Haijun Liu)
H2020-MSCA-COFUND-2018:
GA: 847548 VIP² (GEUP0018NOR)
€ 98,640
January 2021 - December 2023

Climate adaptation in A rabidopsis thaliana through evolution of transcription regulation
(Yoav Voichek)
H2020-MSCA-COFUND-2018:
GA: 847548 VIP² (GEUP0018NOR)
€ 98,640
January 2021 - February 2022

SWARTS GROUP

Plant adaptation to rapidly changing environments (Miguel Vallebueno)
European Commission (Horizon 2020):
GA: 847548 VIP² (GEUP0018SWA)
€ 98,640
January 2020 – December 2022



The new students that started their PhD at the Vienna BioCenter in 2021, as well as Eva Schmid, Head of the Scientific Training Unit and Chiara Ceriotti, Training Coordinator.

GMI PHD STUDENTS

Marintia Mayola Alibek Abdrakhmanov
Gabriele Bradamante
Daniel Buendia
Sebastian Deiber
Rodolphe Dombey
Vu Hoang Nguyen
Patrick Hüther
Bhagyshree Jamge
Jianyi Kok
Marintia Mayola Nava García
Lorenzo Picchianti
Daniela Ramos Cruz
Johannes Rötzer
Victor Sánchez de Medina Hernández
Anna Schmücker
Marieke Trasser
Jierui Zhao

2021 VIENNA BIOCENTER INTERNATIONAL PHD PROGRAM IN LIFE SCIENCES

EMPOWERING CURIOUS RESEARCHERS

The mission of the Vienna BioCenter PhD Program is to promote interdisciplinary research in the Life Sciences at the highest level, and to help excellent PhD students develop into tomorrow's leading scientists through a comprehensive training program.
By promoting the exchange of ideas, by bringing together different and often complementary disciplines, and by supporting the development and adoption of novel cutting-edge technologies, we provide outstanding opportunities for ambitious and motivated students. Enrolled students are expected to contribute to the advancement of science by making important scientific discoveries and by publishing these in international, peer-reviewed journals.

Our training program educates students in all areas relevant for a career in science and provides additional opportunities to acquire skills relevant for other career paths.

For detailed information and application procedures, please consult the Program's website **www.training.vbc.ac.at/phd-program.**

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 and competitive .DOC Fellowships from the Austrian Academy of Sciences.

Vienna BioCenter PhD PROGRAMME

2021 PROFESSIONAL TRAINING & PERSONAL DEVELOPMENT

As part of the responsibility of a leading international research institute, the Gregor Mendel Institute fosters the development of our scientists' research skills and careers by providing a range of training and development opportunities specifically tailored for PhD students, postdoctoral fellows, and group leaders. Through external partners and on-campus specialist services, we aim to develop our employees' research performance, future employability, professionalism, and social engagement.

GENERAL TRAINING

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

TRAINING FOR PHD STUDENTS AND POSTDOCTORAL FELLOWS

- Career development workshop
- Career 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 POSTDOCTORAL FELLOWS

- 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

2021 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. 2021 saw the departure of several PhD students and postdocs moving to various academic and industry positions. We said „Auf Wiedersehen und viel Glück" in 2021 to:

CLAUDE BECKER
Group Leader, LMU Munich, Germany

MICHAEL BORG
Group Leader, MPI for Developmental Biology, Tübingen, Germany

ROBIN BURNS
Postdoc, University of Cambridge, UK

DEJAN DUKIC
Machine Learning Engineer, Smiles Projektentwicklungs GmbH, Vienna, Austria

MARTA GARCIA LEON
Owns and runs two restaurants in Spain

PING KAO
Assistant Professor, Tohoku University, Sendai, Japan

LEE HO-SEOK
Research professor, Yonsei University, Seoul, Korea

LEI BINGKUN
Associate PI, Fudan University, Shanghai, China

MICHAEL NODINE
Group Leader, University of Wageningen, The Netherlands

KATALIN PALDI
Postdoc, University of Florida, Gainesville, USA

RANJITH PAPAREDDY
Postdoc, University of California, Los Angeles, USA

SUBRAMANIAN PAULRAJ
Postdoc, University of Wageningen, The Netherlands

DANIELA RAMOS CRUZ
PhD, LMU München

MICHAEL SCHON
Postdoc, University of Wageningen, The Netherlands

MADLEN STEPHANI

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:

ALMOST 1,900 SCIENTISTS
(including 359 PhD students)

141 RESEARCH GROUPS

38 BIOTECH COMPANIES

SCIENTISTS FROM 79 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 of Molecular Plant Biology (GMI)** have rapidly developed into two of the most renowned Austrian research institutes in their respective fields.

A growing number of **biotech-companies** and space for **start-up labs** 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 more than 45,000 visitors with an interactive glimpse into the Life Sciences.

Achievement, recognition, and support for research is reflected by **numerous grants and awards:** 75 ERC research grants, 29 EMBO Members, 13 Wittgenstein Awards (the most highly endowed science award in Austria) and 2 Breakthrough Prizes (the most highly endowed scienctific award in the world). 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.

2021 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.

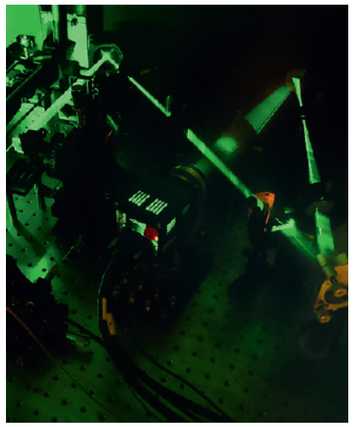
PROTEIN CHEMISTRY FACILITY

The Protein Chemistry Facility offers protein analyses. Their services include protein identification, characterization of posttranslational modifications, protein quantitation 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, on 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.

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



Vienna BioCenter CORE FACILITIES

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

NEXT GENERATION SEQUENCING

Advice and guidance of sequencing projects are offered by their team that relies on more than 10 years of experience with sequencing systems, high-throughput data analysis, and cutting-edge NGS technology. All common sequencing applications are supported, and the development of novel methods and protocols is encouraged.

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.
For the objective, reproducible and high-throughput assessment of plant phenotypic traits they operate numerous phenotyping devices for Arabidopsis and crop plants; shoot and root systems. For the subsequent image analysis, they use classical image analysis approaches but also state-of-the-art deep learning pipelines. Data analysis, statistics and data visualization, up to publication-ready figures, complement the phenotyping service.

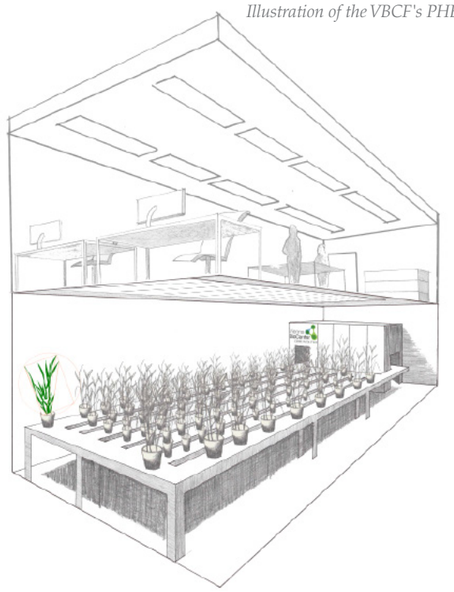
The mission of the Protein Technologies Facility (ProTech) is to further research in molecular and cell biology, protein biochemistry, and structural biology by overcoming major bottlenecks in these fields. Their core services include molecular cloning, protein production and purification, and biophysical characterization of proteins. Since 2014, they also offer services surrounding CRISPR/Cas9 genome engineering technology.

CHILD CARE CENTER

The VBC Child Care Center promotes the compatibility of career and family at the Vienna BioCenter. They are proud to offer professional, reliable, and flexible child care for all Vienna BioCenter employees. Their team of qualified pedagogues works every day to create a loving and caring atmosphere for children from 3 months to 6 years of age. The daycare is a positive and stimulating environment that provides everything a child's heart desires.

The Child Care Center is a creative place for children where they undertake excursions into the countryside, visit kids theatre, grow vegetables, go ice skating, and do everything else a children's heart desires.

Illustration of the VBCF's PHENOPlant.



The Child Care Center at the Vienna BioCenter.

2021

FINANCE & ADMINISTRATION

BUSINESS DIRECTOR'S OFFICE

MARKUS KIESS
Business Director

MARTINA GSUR
Assistant to the Directors

FINANCE

MIREIA VERDAGUER
Head of Finance

BIANCA JELL
Accountant

SIMONA WOJCIK
Bookkeeper

NORMA SCHÖNHERR
Grant Manager

HUMAN RESOURCES

MARIOLA GLAWISCHNIG
Human Resources Officer

LAB SUPPORT

BORRIES LUBERACKI
Head of Lab Support

JENS SCHIACH
Lab Support Specialist

HANSJÖRG STAMPFL
Lab Support Specialist

ANNELIESE AUER
Senior Plant Facility Technician

COMMUNICATIONS & PARTNERSHIPS

PETRA NIECKCHEN
Head of Communications & Partnerships

DANIEL F. AZAR
Communications Officer

ALEXANDER BODMANN
Communications Officer

SYLVIA WEINZETTL
Senior Relationships Manager

SCIENCE SUPPORT

J. MATTHEW WATSON
Head of Science Support and Tech Transfer

BARBARA WEIGEL
Assistant to Science Support

2021

VBC CAFETERIA

MONIKA LECHNER

Cheffe pâtissière at the cafeteria

joined GMI and the VBC cafeteria in October 2021

INSIGHTS

Monika Lechner
Cheffe pâtissière
(right)

Ingrid Vermeulen
Assistant to the VBC cafeteria
(left)

The new pastry chef Monika Lechner enchants the campus with a wide variety of cake and sweet recipes! Her creations can be found every day both at the cafeteria for lunchtime, as well as at the Bridge, where Monika's colleague Ingrid Vermeulen caters for the afternoon cravings of the whole campus. Working from the cafeteria and only rarely appearing at Ingrid's side at the Bridge, Monika's face remained a mystery for far too long. Get to know the face and mind behind the fabulous new pastries in this exclusive interview!

Dear Monika, welcome to GMI and the VBC! How did you become a Cheffe pâtissière?

ML: *As a young child I already loved sweets and said, once I grow up, I want to become a pastry chef! I had a three-year training program in confectionery after which I performed seasonal work for three years. The seasonal jobs took me to Carinthia (southern Austria), Italy and Mexico. Following these travels, I passed the Master examination and started working as a "Cheffe pâtissière".*

Where did you work before? Did you bring secret recipes with you?

ML: *In Vienna, I led the bakery of "Café Glorietteʺ in Schönbrunn for 17 years. Ix surely brought with me knowledge and expertise from my previous workplaces. "Secret recipes" definitely come along, but if I tell everyone about them, they will no longer be secret! (laughs).*

Do you like to explore and improvise new recipes just to try something new?

ML: *Of course! Inspiration often strikes when I see or read a recipe, and I feel compelled to try it out and give it my personal twist!*

What is your favorite pastry or recipe?

ML: *That would be Cremeschnitte (puff pastry cream slice) or chocolate mousse. I have a general preference for cream cakes, cream gateaux, and Viennese cake slices.*

What do you enjoy about your new workspace and team here on campus?

ML: *My colleagues are all very kind and instantly embraced me within their team! I particularly enjoy having absolute freedom to try all the recipes that inspire me. Trust me when I say that it is so much fun! In addition, every now and then I get to hear positive feedback and encouragement on my cakes and recipes, which makes me feel grateful!*

What do you enjoy doing in your free time?

ML: *I greatly enjoy outdoor activities. Hiking, jogging, cycling… Everything that involves nature and fresh air!*

2021 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.

LEIF ANDERSSON
Uppsala University, Uppsala, SE

HARMIT MALIK
Division of Basic Sciences, Fred Hutchinson Cancer Research Center, US

NIKO GELDNER
Dept. of Molecular Biology, University of Lausanne, CH

> *The GMI continues to hold its position as a premier plant science institute. The SAB enjoyed hearing reports of the excellent scientific progress towards understanding fundamental processes of gene regulation, evolution and ecological and environmental responses. The GMI continues to attract exceptionally high caliber group leaders, postdocs and students.*

CATHIE MARTIN
John Innes Centre, Norwich, UK

KEIKO SUGIMOTO
RIKEN Center for Sustainable Resource Science, Tokyo, JP

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

SUSAN WESSLER
Dept. of Botany and Plant Sciences, University of California Riverside, US

THE AUSTRIAN ACADEMY OF SCIENCES

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

The Austrian Academy of Sciences (ÖAW) is Austria's central institution for science and research. Founded in 1847 as a learned society in Vienna, the Academy currently has about 1,800 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 760 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 26 research institutions in both the natural sciences and humanities. The Academy also organizes events and lecture series, and supports talented young and established scientists alike through its awards and scholarships programs.

ÖAW AUSTRIAN ACADEMY OF SCIENCES

2021 VIENNA COVID-19 DETECTION INITIATIVE (VCDI) 2020-2021

The Vienna Covid-19 Detection Initiative (VCDI) was established in 2020 as a collaborative, inter-institutional effort to combat the SARS-CoV-2 coronavirus. The initiative of research institutes at the Vienna BioCenter and the University of Vienna has repurposed existing resources and expertise and invested in new infrastructure to develop capacities for detecting SARS-CoV-2.

The VCDI operated smoothly until the end of 2021. This ensured the successful transfer of the technology and testing capacities to the City of Vienna, thus making PCR testing accessible to all Viennese residents.

The VCDI and its stakeholders promoted a strategy for frequent, large-scale population screening to avoid further lockdowns and damage caused by uncontrolled spreading of the virus through asymptomatic individuals. To this end, VCDI scientists committed themselves to developing novel, faster and cheaper approaches to detect SARS-CoV-2.

Between April 2020 and December 2021, a PCR testing pipeline operated and was consolidated and expanded within the Vienna BioCenter Core Facilities to allow for a capacity of about 6000 tests per day. Testing capacity was provided for humanitarian initiatives of broader public interest.

The initiative freely disseminated its know-how, operating procedures, and latest developments. The VCDI was supported by the University of Vienna (Max Perutz Laboratories, Centre for Microbiology and Environmental Systems Science, Division of Microbial Ecology DOME), the Research Institute of Molecular Pathology IMP (Boehringer Ingelheim), Institute of Molecular Biotechnology IMBA and Gregor Mendel Institute of Molecular Plant Biology GMI (both Austrian Academy of Sciences); and funded by the Federal Ministry of Education, Science and Research and a grant from the COVID-19 Rapid Response Call of the Vienna Science and Technology Fund (WWTF).

2021 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.

ND-QUEST

ND-quest is an expansion of Botanic Quest to natural monuments of which there are several thousands throughout the city. It was developed as a cooperation of the Gregor Mendel Institute and the Environmental Protection Department of the City of Vienna (MA22). In a first step, 17 natural monuments in different districts were chosen to be represented, with plans to expand to more areas of the city. The quiz started in spring 2020 and proved to be an ideal activity for people of all ages during the pandemic.

www.ndque.st

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

Michael Ludwig, the major of Vienna presents the App "Naturdenkmäler Quest" (ND-quest) in the Rathauspark.

2021 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, or better yet cycle!, 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, Organization for Security and Cooperation in Europe, International Centre for Migration Policy Development, European Fundamental Rights Agency, and a number of other international corporations and organizations, Vienna is a dynamic, multicultural, and cosmopolitan city.

2021 LOCATION AND TRAVEL DIRECTIONS

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

Vienna BioCenter

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).

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)

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