



## ANNUAL REPORT



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

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# GMI ANNUAL REPORT 2020

# DIRECTORS' STATEMENT



Dr. Magnus Nordborg

Scientific Director



Dr. Markus Kiess
Business Director

We are proud to be one of very few research institutions worldwide devoted to basic plant biology. The decision by the Austrian Academy of Sciences to establish the GMI is looking increasingly visionary given that human activities, in particular fossil-fuel usage, are rapidly changing the global climate. The importance of understanding the biology of the world's primary producers is difficult to overstate in this context. As plant biology is important to everyone, we hope this annual report makes our research more accessible to a broad audience. We've also chosen to highlight some of the many people carrying out this important research.

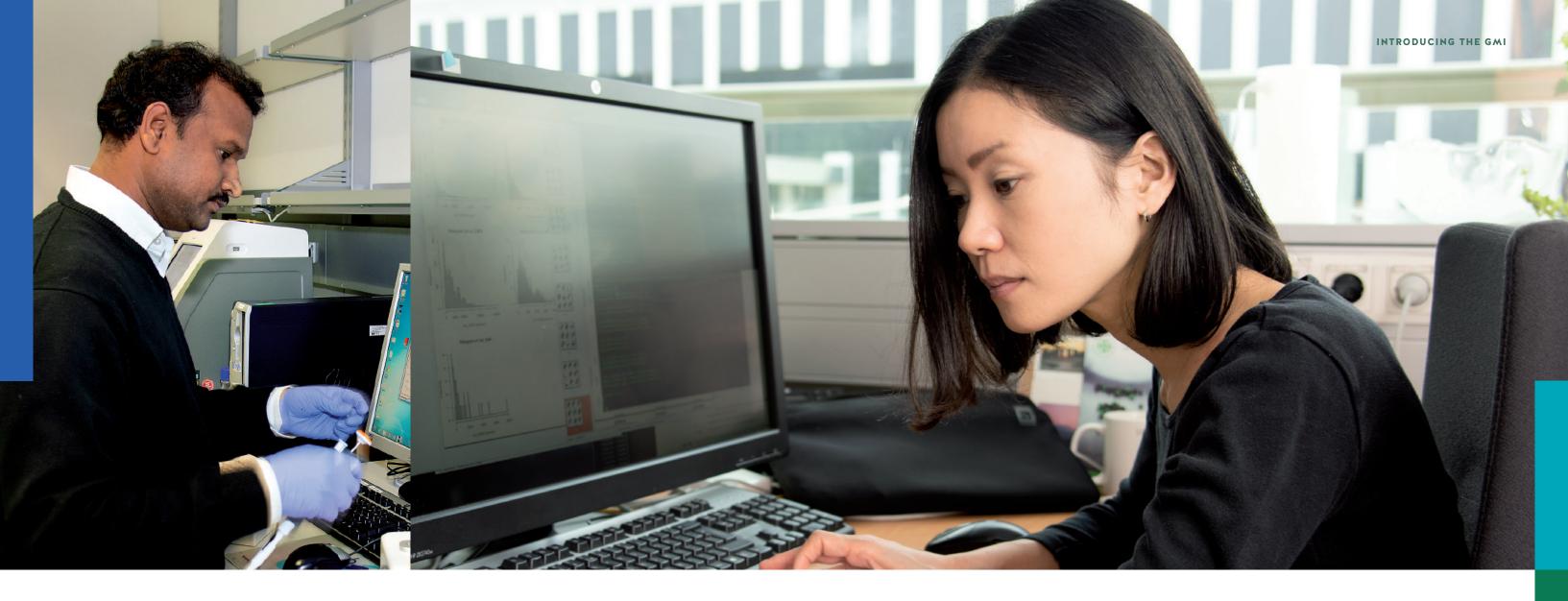
The goal of the GMI is to contribute to our understanding of plants (and biology in general) by carrying out world-class research, in particular the kind of fundamental research that is poorly supported elsewhere. Like the other institutes that are part of the Vienna Bio-Center, we strive for excellence and emphasize creativity and independent thinking at every level. We are supported by an efficient administration and world-class services. As directors, our most important task is to create a fantastic

research environment and to recruit and promote young scientists, allowing them to develop into researchers capable of securing scientific positions worldwide. In this regard, we are happy to announce that Michael Nodine has accepted a position as an Assistant Professor at the Plant Developmental Biology Group in Plant Sciences Division at Wageningen University & Research.

It goes without saying that this year has been extraordinarily challenging, but thanks to our outstanding facilities developing SARS-CoV-2 testing pipelines as a demonstration of how the epidemic might be combated, we have been able to continue working without too much interruption — as evidenced by this report.

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





INTRODUCING THE GMI

#### **PROFILE**

The Gregor Mendel Institute of Molecular Plant Biology (GMI) was founded by the Austrian Academy of Sciences (ÖAW) in 2000 to promote research excellence in molecular plant biology. It is one of the few institutes throughout the world that focuses on basic plant biology. The GMI is located in the purpose-built ÖAW Life Sciences Center 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**

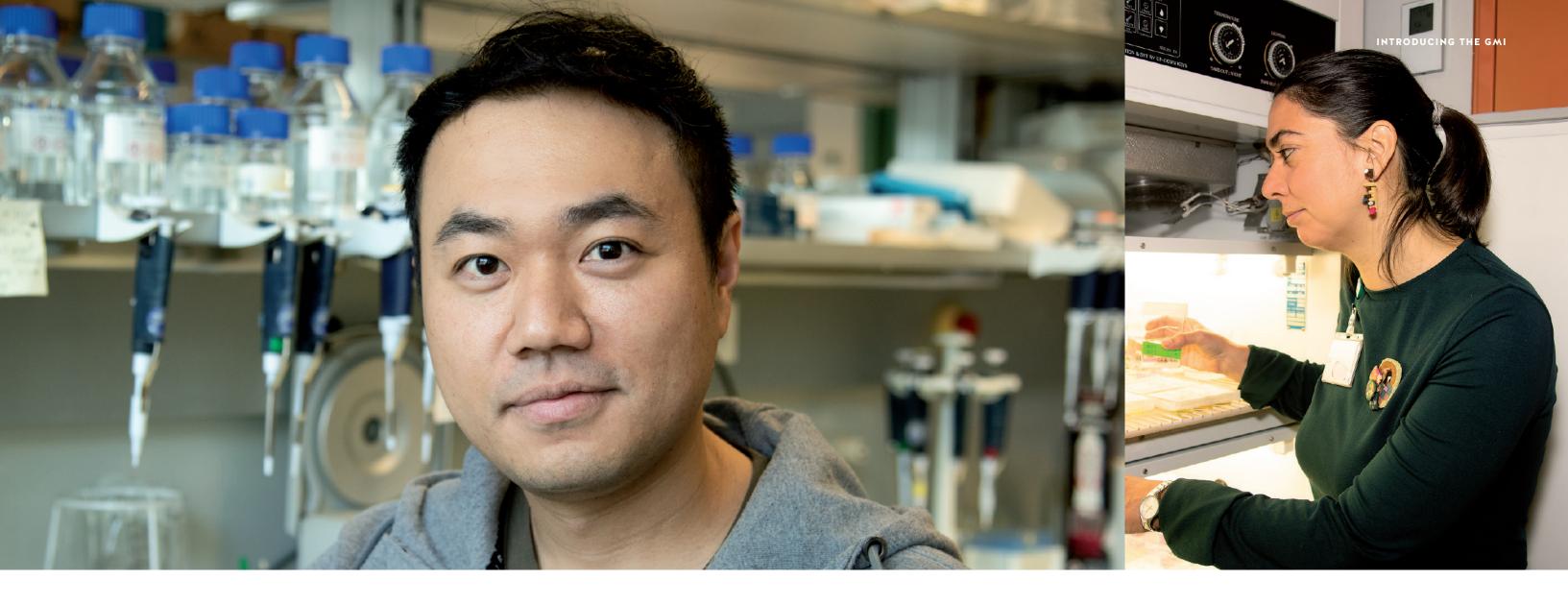
Research at the GMI covers many aspects of molecular plant genetics, including epigenetics, transposon biology, population genetics, genomics, chromosome biology, developmental biology, stress signal transduction, autophagy, and defense. During the last 20 years, the model plant *Arabidopsis thaliana* 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 sen-

ior 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.

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. **QQ**(Claude Becker)



#### IMPORTANCE OF EXPERIMENTAL PLANT RESEARCH

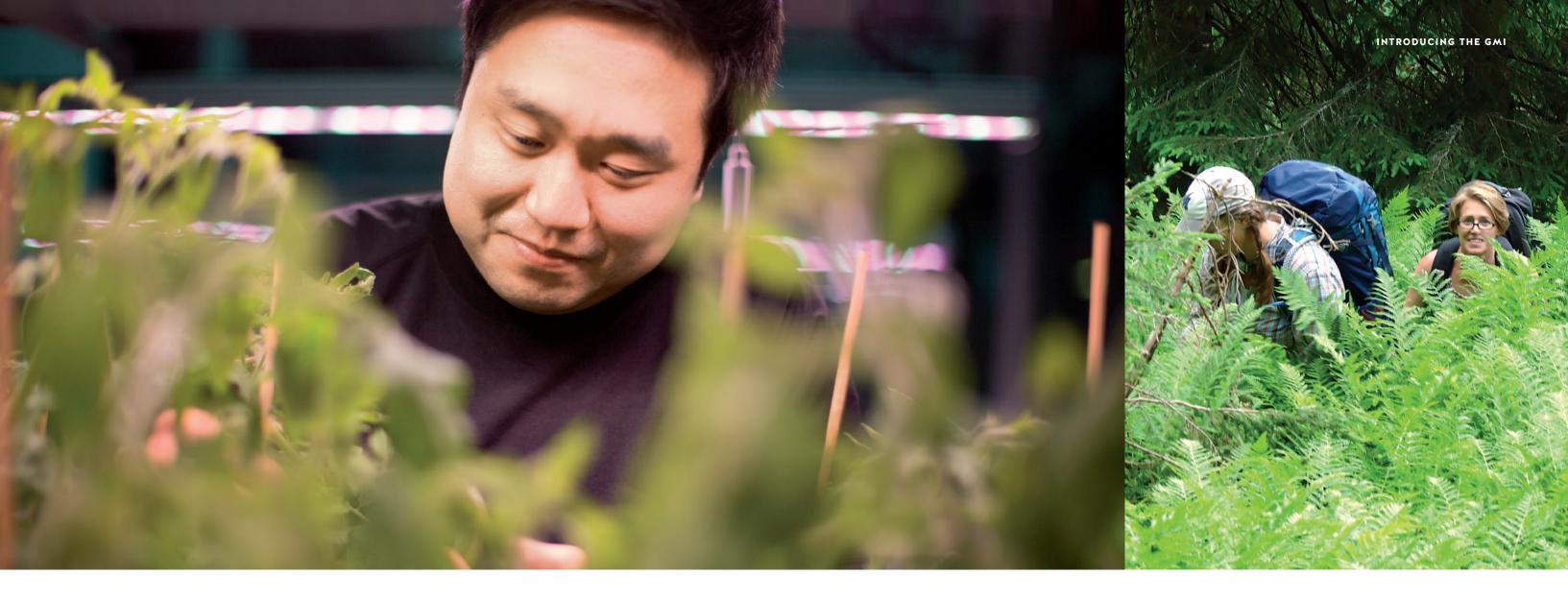
Plants are the primary producers of the world's ecosystem and thus essential for all life on earth, a basic fact that is receiving new attention due to rising food prices, diminishing fossil fuel reserves, and a changing climate. Major innovations will be required to guarantee sustainable food and energy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

Research on plants can also lead to fundamental scientific breakthroughs beyond plant biology, including many that can be applied to human medicine. Gregor Mendel's discovery

of the basic principles of genetics, Barbara Mc-Clintock'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**

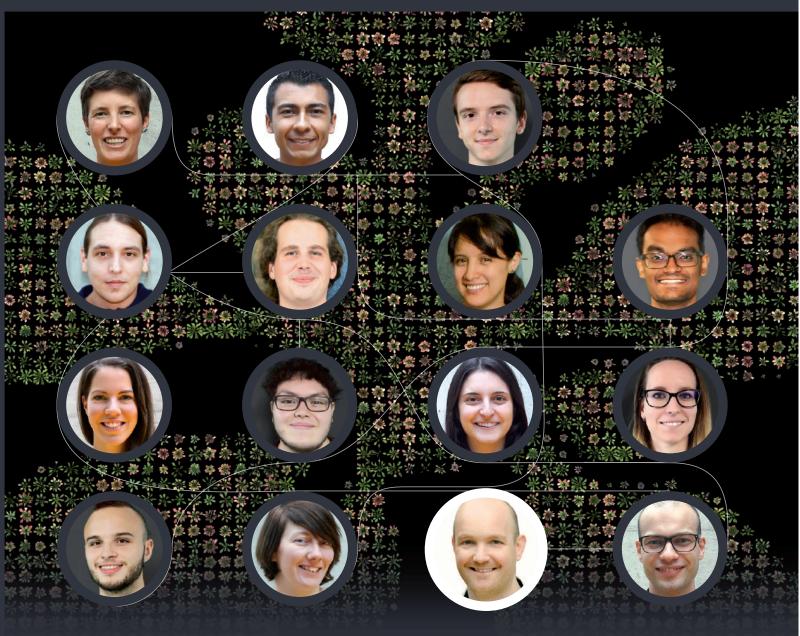
The GMI focuses on providing a perfect environment for cutting-edge science as well as education, which makes it an excellent place to develop a scientific career. We offer an exciting setting for undergraduates, PhD students, postdocs, and principal investigators alike. All researchers have access to 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.

**99** 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)





#### **CLAUDE BECKER**

claude.becker@gmi.oeaw.ac.at



Joined GMI in Dec 2016

PhD: Albert-Ludwigs-University, Freiburg, DE

#### **PREVIOUSLY**

- Research Associate (2011-2016): Detlef Weigel Lab, Max Planck Institute for Developmental Biology, Tübingen,
- Postdoc (2010-2011): Detlef Weigel Lab, Max Planck Institute for Developmental Biology, Tübingen, DE
- Postdoc (2010): Klaus Palme Lab, Albert-Ludwigs-University, Freiburg,

#### **GROUP MEMBERS**

#### PHD STUDENTS

Patrick Hüther Daniela Ramos Jorge Isaac Rodríguez Arévalo Núria Serra Serra\* Reshi Shanmuganathan

#### **POSTDOCS**

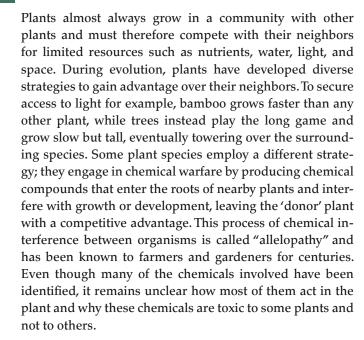
Zane Duxbury\* Eva Knoch Judit Kovacs Niklas Schandry

#### TECHNICIAN Katharina Jandrasits

STUDENTS AND INTERNS Sebastian Deiber Zuszsanna Günther Jakob Reimann\* Mateo Vasconez

(\*left the lab in 2020)

#### **CHEMICAL WARFARE BETWEEN PLANTS**



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





One major theme of the lab is the allelopathic potential of benzoxazinoids, compounds that are produced in many grass species, including major crops such as maize, rye, and wheat. While the actual substances that are produced in these plants are only mildly toxic to other plants, they are rapidly converted in soil to more potent derivatives. The soil microbiome, i.e. the community of microorganisms living on and around the plant roots as well as freely in soil, plays a double role in this process: on the one hand, some of these microorganisms are essential for these conversions to take place; on the other hand, these compounds can affect the well-being of these microorganisms and the configuration of the microbial community as a whole. We observed substantial variability in the sensitivity of different root-associated bacterial strains, even among genetically

closely related ones. Using machine learning approaches, we identified bacterial genes associated with the level of tolerance towards plant-derived metabolites and currently investigate the function of these genes to determine whether the corresponding gene products might be targets of these compounds or, alternatively, whether they might be enzymes metabolizing the plant-derived substances. To test whether these compounds can disrupt microbial communities, we designed synthetic bacterial communities to study the effect of benzoxazinoids and their derivatives on community establishment and development over time. In a next step, we are going to assess how such chemically conditioned communities in return affect plant growth.

Another crop with significant allelopathic potential is rice (*Oryza sativa*). Rice is not only

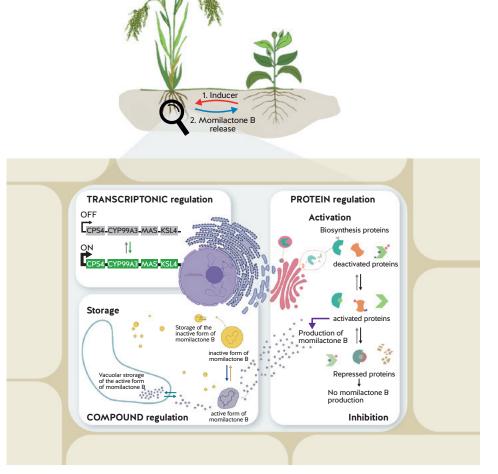
able to produce compounds that inhibit the growth of weeds frequently infesting agricultural areas, it also does so on cue: the biosynthesis and the release of these compounds only take place when the rice plant perceives a neighbouring plant that is of another species (Figure). We are investigating the nature of the signal that informs the rice plant about the presence and the identity of the neighbouring plant using metabolomic approaches. In collaboration with partners at Tokyo University, we explore the genetic diversity of rice cultivars to better understand the regulation of the biosynthesis. Moreover, we want to understand how momilactones, the compounds produced and released in response to those neighbours, act in the plant cell to inhibit growth.

FIG. Momilactone B content and exudation increase in presence of (some) non-kin neighbours. A yet unknown signal from the neighbouring plant is recognised by the rice plant. Upon perception, different processes can result in higher momilactone B content, all of which currently remain hypothetical. Downstream signalling could lead to transcriptional activation of the biosynthetic cluster, ultimately resulting in higher production rate. Alternatively, biosynthetic enzymes might already be present in the non-induced state but exist in an inactive form. Upon induction, they could be modified or released from a putative repressor, and the synthesis rate could be increased. Finally, momilactone B itself could be regulated in two ways:

momilactone B could exist in an inactive or conjugated form and become activated upon induction; alternatively, momilac-

tone B might be compartmentalised in

the cell.





#### **INSIGHTS**

**Eva Knoch,** Postdoc Flensburg, Germany PhD, University of Copenhagen

#### How did you come to the GMI?

I was doing a postdoc in Japan working with plant specialized metabolites and was looking for opportunities back in Europe. I was curious to learn more about the interaction between plants and microorganisms, and Claude Becker's group had started research into the role of plant compounds in this interaction. So, I applied for and received a Lise Meitner Fellowship from the Austrian Science Fund (FWF) to come here.

#### What project are you working on?

My research project is focused on the interaction between plants and soil bacteria, and the role that plant specialized metabolites play in this interaction. I am curious how these metabolites, which are secreted by the plants,

affect the microbial community, and how the microbes might use the metabolites. To investigate this, we are using both bacterial transcriptomics and genomics, and also a tracer-based metabolomics approach, in collaboration with the Analytical Chemistry Group at the BOKU in Tulln

As a side project, in my spare time, I started a YouTube channel about plant science this year. An outreach activity planned for this summer (KinderUni) was converted to online videos because of Covid-19, and I enjoyed participating. Because of the Covid-19 measures, where many things were closed, I also spent much more time at home than normal, so I started my channel "Der molekulare Garten" to explain some of the molecular mechanisms of plant life that non-plant scientists might enjoy.

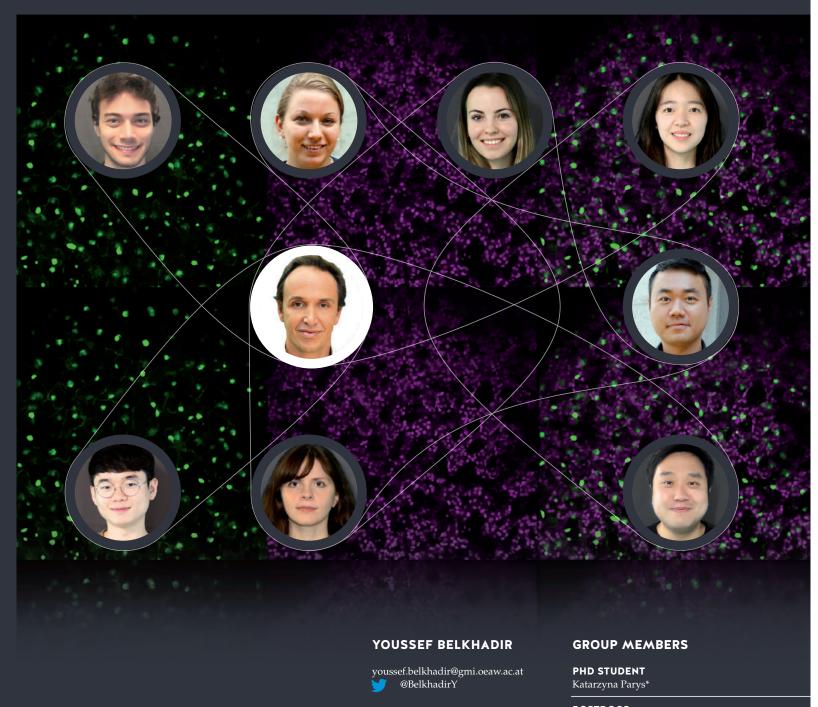
#### What do you especially like about working at the GMI?

Thanks to my fellowship and my group leader, I have a lot of freedom in my research, and can follow my curiosity. And then there is the location in the beautiful city of Vienna which is also close to the mountains, both of which I really enjoy.

#### Where do you want to go next?

I have a few years of postdoc experience now where I have explored different aspects of plant metabolomics and formed my own research agenda. I am hoping to soon start my own research group, so I'm looking for opportunities and applying for funding.







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

#### **POSTDOCS** Ho-Seok Lee Duhwa Lee

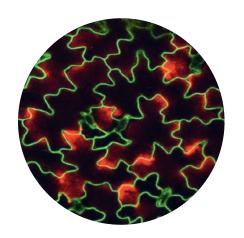
TECHNICIAN Natalie Edelbacher

#### STUDENTS AND INTERNS:

Kerstin Dürr Tobias Hrovat Jungmin Lee Sunghee Lee\*

(\*left the lab in 2020)

#### **DECISION MAKING** THROUGH RECEPTOR **KINASES**



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

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



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 2020, we have systematically tested 450 RK ECDs on these arrays and the final 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.

## FIG. Interrogation of a glycan array with the extracellular domain of a CERK1 as a proof-of-concept. The

three red dots represent a positive interaction between the receptor kinase and glycans.

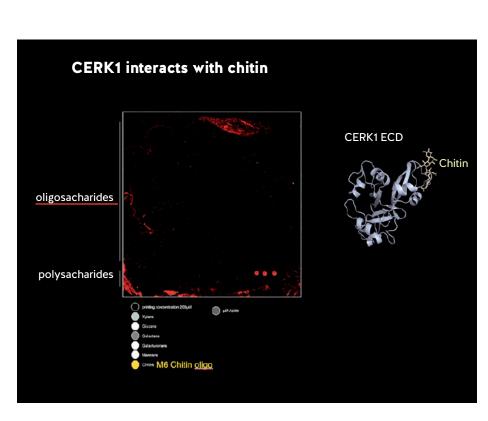
#### Pairing receptors with ligands by high density peptide arrays.

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 2020, 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.

## Engineering ligands to rationally control RK-signaling and modulate plant cell behaviors.

In conventional chemical genetic screens, small chemicals are used to perturb a biolog-

ical system to then explore the molecular outcome. Here the laboratory is proceeding in the opposite direction by interrogating molecular interactions of all of 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 2020, the group has also performed other screens with these chemicals and established that these compounds can also activate marker gene expression in the roots and shoots of Arabidopsis. Thus, we obtained information that could be used to activate the immune receptor with the rational design of cheap analog molecules that could be chemically synthesized for direct use on crops. The systematic understanding of receptor interactions with non-natural ligands has important implications for engineering disease resistance in crops.





#### **INSIGHTS**

**Duhwa Lee**, Postdoc Seoul, South Korea PhD, Yonsei University

#### How did you come to the GMI?

After I finished my PhD, I was anxious to broaden my horizons with an overseas postdoc. At the same time, one of my best friends, Ho-Seok, visited Korea to marry his wife. He strongly recommended that I apply to the lab he works at with Youssef Belkhadir. Just in time, Youssef also visited Korea for an international conference, thus I had the good fortune to have an interview with him in person. After meeting him, I was fascinated by his biological approach and unique view of science. Fortunately, he gave me a chance to join his lab. Additionally, 10 years ago as I was travelling across Europe, Austria was the country that impressed me the most. This is another big reason I was happy to start at the GMI.

#### What project are you working on?

I am working on developing a small chemical engineering pipeline to manipulate plant receptor kinase (RK) signaling. RKs are ideal targets for "druggability" to identify both com-

petitive and non-competitive small-molecule probes for pathway-specific signaling modulation. With our high-throughput, large-scale screening method to examine molecular interactions between RKs and a comprehensive chemical array with >24,000 chemicals, 84 small molecules were identified to interact with our target RK. To further characterize these small molecules, we developed a complex strategy using an *in silico* computational approach, *in vitro* biochemical analysis, and *in vivo* studies for phenotypic output. In addition, cost-effective, engineered novel RK ligands could lead to their utilization as chemical tools in crops such as Tomato.

#### What do you especially like about working at the GMI?

The GMI provides access to a diverse set of core cutting-edge scientific facilities and services that will help accelerate my research. Together with other institutes at the Vienna BioCenter, the GMI hosts various professional

training programs and encourages active interdisciplinary collaborations between groups. Besides these core services, I was very happy to be at the VBC during the pandemic with our great in-house testing. The fantastic working conditions even during this year are the result of many efforts of GMI/VBCF staff, and I really appreciate their support. Without their effort, I could not have done anything during my first

#### Where do you want to go next?

During my post-doc period, I would like to explore a brand-new field of biology. In order to answer new questions in plant science, I will try to develop my own toolbox at the GMI. I hope to establish a more general high-throughput pipeline that comprises identification, validation, and application using these tools. This pipeline and the scientific network I build will be especially important for my future position.







Joined GMI in Jan 2014

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

#### PREVIOUSLY

**¬** Group Leader (2004-2014): Temasek Life Sciences Laboratory, SG

■ Research assistant professor (1997–2004): Institut National de la Recherche Agronomique (INRA)

Bhagyshree Jamge Jian Yi Kok Sean Montgomery Anna Schmücker

#### POSTDOCS

Michael Borg Pierre Bourguet Tetsuya Hisanaga Bingkun Lei Akihisa Osakabe

#### STAFF SCIENTIST

Zdravko Lorković

#### TECHNICIAN

Svetlana Akimcheva

#### STUDENTS AND INTERNS:

Philipp Karall Michael Klingenbrunner Nicolas Nemeth Isabelle Skrzypek Christian Waltl

#### **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.



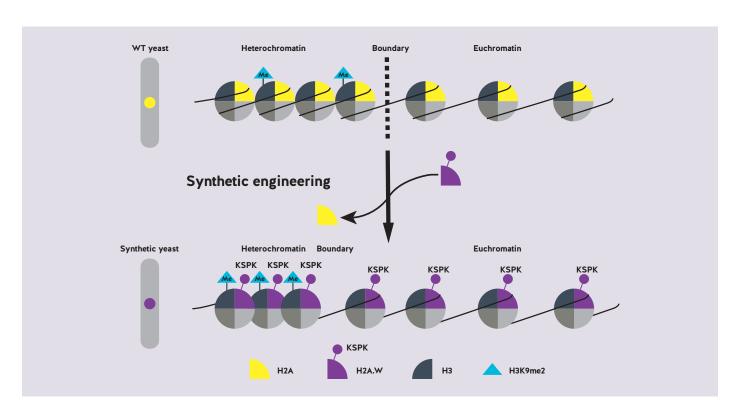
The Berger lab used a new strategy to interrogate the properties and evolution of variants in the histone H2A family, the most diversified class of histone variants that are characterized by distinct C-terminal tail motifs, and occupancy of specific chromatin states. In addition to H2A.Z, H2A.X and replicative H2A present in most multicellular eukaryotes, the plant-specific H2A.W variant exclusively occupies the silent heterochromatic regions of the genome and possesses a long C-terminal tail with a KSPK motif. We asked whether this motif could confer specific silencing properties. To do this, we used a synthetic approach in fission yeast, which possesses only H2A and H2A.Z. Expression of chimeric H2A variants with a long C-terminal tail and KSPK motif in yeast showed an impact comparable to the silencing role ascribed to H2A.W in Arabidopsis. Remarkably, in yeast the KSPK motif did not constrain the location of the variant spH2A.W

to silent heterochromatic regions and yet primarily affected only heterochromatin properties. In conclusion, synthetic reconstruction of H2A.W variant evolution in yeast supported the potential for emergence of the motif KSPK prior to mechanisms responsible for segregation of H2A.W to heterochromatin (Figure). Based on these findings we will initiate a new series of experiments to understand how more complex organization of chromatin arose during evolution of eukaryotes.

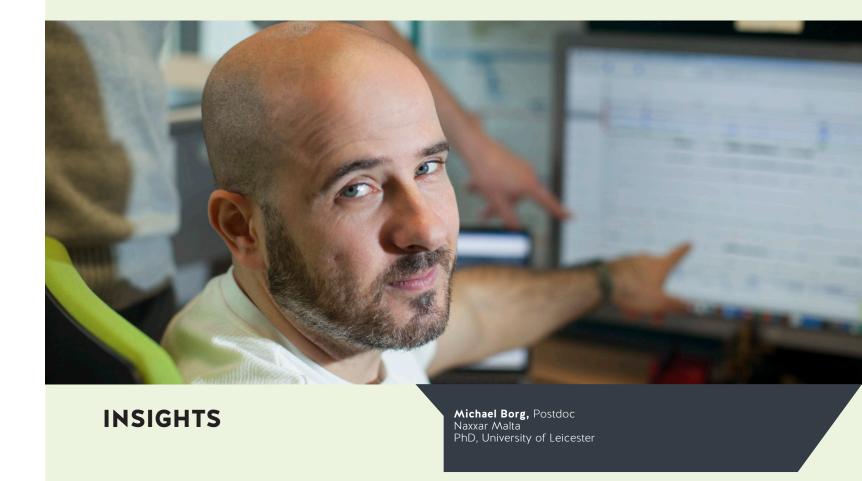
## Synthetic organization of silent chromatin in fission yeast by the plant histone variant H2A.W.

Fission yeast was engineered to replace the endogenous H2A with a mimic of plant H2A.W. H2A.W enhanced silencing by heterochromatin that is marked by H3K9 methylation (H3K9me2) but did not affect euchromatin. While most histone variants have been uncov-

ered and studied amongst members of the H3 and H2A families, we have identified an unsuspected diversity of histone variant in the H2B family. This family has expanded dramatically in plants and mammals. We showed how Arabidopsis H2B expression varies across development and identified a new class of highly divergent H2B variants, H2B.S, that specifically accumulate during chromatin compaction of dry seeds in multiple species of flowering plants. We identified two groups of H2Bs expressed in Arabidopsis somatic tissues with preferential deposition in silenced and expressed regions of the genome. This work thus expands our knowledge of the evolutionary history and distinct properties of plant histone H2Bs, paving the way for mechanistic studies into their impact on chromatin dynamics and development.



**FIG.** Adapted from Lei et al. (2020) A Synthetic Approach to Reconstruct the Evolutionary and Functional Innovations of the Plant Histone Variant H2A.W. Current Biology.



#### How did you come to the GMI?

I met Fred Berger at a conference and heard he was moving to the GMI in Vienna. We got chatting and he encouraged me to apply for an FWF Lise Meitner fellowship. This was successful and I moved from the University of Leicester in the UK to the GMI in January 2015.

#### What project are you working on?

In my research career thus far, I have strongly focused on male germline biology and at the GMI my expertise expanded to chromatin biology and epigenomics both at the bench and *in silico*. During my time at the GMI, I developed a body of work addressing the epigenetic and transcriptional transitions occurring during early cellular development in Arabidopsis using pollen as a developmental system. My main work has addressed how the paternal epigenome is reprogrammed in Arabidopsis, where we uncovered a novel mechanism whereby H3K27me3 is globally and specifically

erased from sperm chromatin. I have also addressed how transcription is rewired during the alternation of generations in Arabidopsis, which is a fundamental developmental process observed during the life cycle of all plants and algae. By profiling chromatin accessibility in pollen, we revealed how cis-regulatory element activity is extensively rewired during pollen development and have shown how this is tightly linked with the differential reprogramming of epigenetic marks to drive the alternation of generations.

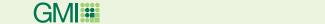
#### What do you especially like about working at the GMI?

The GMI is a special plant biology institute for many reasons. It's placed very centrally in the cool metropolitan city of Vienna and is one of the few places in the world to do basic fundamental plant science that is well-supported both financially but also scientifically, given that the GMI is embedded within the Vienna

BioCenter. This means access to world-class facilities that are run by dedicated scientists well-versed in their field of expertise that provide excellent guidance, be this in microscopy, next-generation sequencing, or plant growth and phenotyping. Being part of the VBC also means access to great talks by world class scientists both within and outside of the VBC, which provides a stimulating environment for new scientific ideas and fields and different ways of thinking. And if that isn't enough, there are the fantastic social events that are topped by the now famous GMI summer party!

#### Where do you want to go next?

After six successful years at the GMI, I am happy to have secured a new group leader position at the Max Planck Institute for Developmental Biology in Tuebingen, Germany. It is sad to leave the GMI, but I am also thrilled that it provided me with a solid platform to further my scientific career.





@PlantoPhagy



Joined GMI in Jan 2017

PhD: University of Exeter, UK

#### PREVIOUSLY

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

Alibek Abdrakhmanov Lorenzo Picchianti Victor Sánchez de Medina Madlen Stephani Jierui Zhao

#### POSTDOCS

Marion Clavel Marta García Leon

#### TECHNICIANS

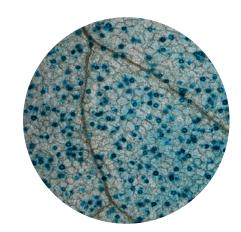
Nenad Grujic

#### STUDENTS AND INTERNS

Jeppe Ansbol\* Luca Argiro\* Mai Thu Bui Alexander Gajic\* Esther Kronthaler Azadeh Mohseni Emilio Skarwan\*

(\* left the lab in 2020)

#### **ADAPTATION THROUGH AUTOPHAGY**



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

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

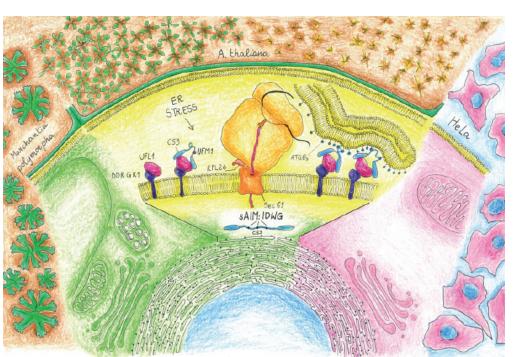


Our lab combines a variety of mechanistic tools to understand how plants employ selective autophagy to maintain cellular homeostasis. Using Marchantia and Arabidopsis as comparative model systems, we are using a three-layered approach to explore (i) organelle recycling mechanisms (ii) cross-talk between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

Over the last year, we have made significant progress on the 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 biochemistry 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 (Figure). Furthermore, we have also shown that Ufmylation, an enigmatic posttranslational 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 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. C53 is a cross-kingdom conserved autophagy receptor that is crucial for endoplasmic reticulum homeostasis during stress.

C53 is highly conserved throughout eukaryotes. It interacts with ATG8 via a novel binding motif that we named the shuffled ATG8 interacting motif (sAIM). When ribosomes start colliding at the endoplasmic reticulum, the C53 receptor complex formed by C53, UFL1, and DDRGK1 proteins is activated by the transfer of UFM1 to the stalled ribosomes. This allows the cell to recycle the toxic stalled nascent chains. Image credit: Dorotea Fracchiolla, Art&Science (https://my-art-science.com)



#### **INSIGHTS**

**Jierui "Jerry" Zhao,** PhD Student Jinan China MSc Leiden University

#### How did you come to the GMI?

I applied to the 2019 VBC PhD winter selection online (just one day before the deadline) and was accepted for the interview. I came to Vienna for the interview from the Netherlands and was honored to be admitted as a PhD in Yasin's group. I finally started my PhD life in GMI in April 2019.

#### What project are you working on?

My PhD thesis focuses on selective autophagy in Arabidopsis. I am studying how autophagosomes are transported to the vacuole in Arabidopsis. It is mainly plant molecular and cell biology.

#### What do you especially like about working at the GMI?

I especially like the working atmosphere here. People are really nice and willing to help you. In addition, the facilities at the GMI are world-class and the technicians are always available to help

#### Where do you want to go next?

I will probably continue a post-doc position in Vienna, it would be great if I can continue somehow at the GMI.

GMI**:** 



#### LIAM DOLAN

liam.dolan@gmi.oeaw.ac.at



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,
- Independent Research Fellow (1995–1996): John Innes Centre, UK
- Postdoctoral Researcher (1992-1995): John Innes Centre, UK
- Postdoctoral Researcher (1991–1992): University of Pennsylvania, USA

#### **GROUP MEMBERS**

#### PHD STUDENTS

Sarah Attrill Sam Caygill Alexandra Casey Chloe Casey Hugh Mulvey

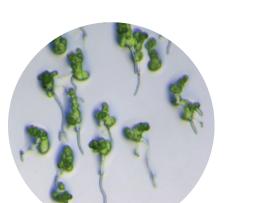
#### POSTDOC

Susanna Streubel

#### TECHNICIANS

Katharina Jandrasits Magdalena Mosiolek

#### **DEVELOPMENT** AND EVOLUTION OF **LAND PLANTS**



Plants moved out of the water to colonize the land roughly 450 million years ago, dramatically changing the Earth System. The transition from a liquid to solid environment 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 and combines this with developmental genetics to understand the genetic mechanisms used to control development in modern plants and how these mechanisms have evolved throughout Earth's history.



In 2020 we reported two important findings. The first was the discovery that dichotomously branching roots evolved many times in the early evolution of vascular plants with true leaves (euphyllophytes). The second was the discovery of a novel mechanism of cell patterning through a miRNA.

There are two forms of root proliferation in extant vascular plants; lateral branching where new root meristems develop from internal root tissues, and dichotomous branching where an existing root meristem splits in two. Lateral branching is found in extant euphyllophytes which include the seed plants and monilophytes (ferns and horsetails). Dichotomous branching is only found among extant Lycophytes. To determine if euphyllophytes always developed lateral roots, we investigated root development in euphyllophyte fossils from 420 to 350 million years ago. Surprisingly, we discovered that many extinct euphyllophytes formed new roots through dichotomy. Our analysis suggests that root proliferation by dichotomy evolved many times independently in early-diverging groups of euphyllophytes and disappeared when these plants went extinct. Our discovery highlights the importance of including fossils in our analysis when determining how and when plant organs evolved.

Lateral inhibition is a mechanism that patterns different cell types in sheets of cells during development. The conserved Notch-Delta receptor-ligand signaling system mediates lateral inhibition among all metazoans but is not conserved among land plants where different mechanisms evolved in different lineages.

Combining genetics and theoretical modelling we demonstrated that the MpFRH1 miRNA is a repressor that acts in lateral inhibition during the patterning of rhizoid cells in the Marchantia epidermis. Our data is consistent with the hypothesis that the MpFRH1 miRNA is produced by developing rhizoid cells and moves to adjacent cells where it represses rhizoid cell differentiation by destroying the MpRSL1 mRNA. If correct, this would be the first example of a miRNA acting as a repressor during lateral inhibition in any organism.

Comparative developmental genetics has shown that RSL genes control the formation of

tip-growing cells with rooting functions (rhizoids and root hairs) in all groups of land plants. The conserved function in the development of these cell types allows us to conclude that RSL genes acted in the common ancestor of all groups of extant land plants which lived some time before 450 million years ago. MpFRH1 miRNA, on the other hand, is found only in the liverwort lineage and probably evolved around 380 million years ago. This suggests that while the mechanism specifying the identity of tip-growing cells with a rooting function was inherited from the earliest land plants, different mechanisms that pattern these cells evolved later in different plant lineages.

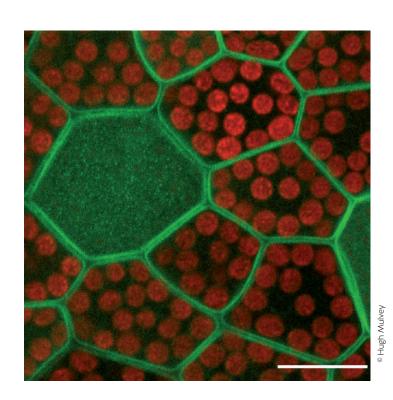


FIG. The patterning of rhizoid cells (pale green) and flat epidermal cells (red fluorescence) in the epidermis of the Marchantia polymorpha gemma

This plant expresses a fusion protein which labels the surface of every cell in the epidermis green. The rhizoid cell has expanded out of the plane of the image and leaves a dark void (faint green color) while the chloroplasts near the upper surface of the flat epidermal cells are visible as red fluorescence. Scale bar = 20 µm.



#### **INSIGHTS**

**Sarah Attrill,** PhD Student Southampton, England BA, University of Oxford

#### How did you come to the GMI?

I started my PhD in Liam Dolan's group at the University of Oxford last year. This year the lab moved from Oxford to the GMI, attracted by the great facilities and the opportunity to be near other *Marchantia* research groups. For my PhD project, I am particularly excited about utilizing the microscopy expertise and plant growth facilities available here. Also in being part of the VBC's diverse research community.

#### What project are you working on?

My project looks into the mechanisms driving cell polarization and asymmetric division

during early plant development. To do this, I am using the spores of *Marchantia polymorpha*. These single cells polarize and divide to form a small rhizoid cell and a larger apical cell. My work investigates how the cytoskeleton is organized during these critical events to define the first apical-basal axis in *M. polymorpha*.

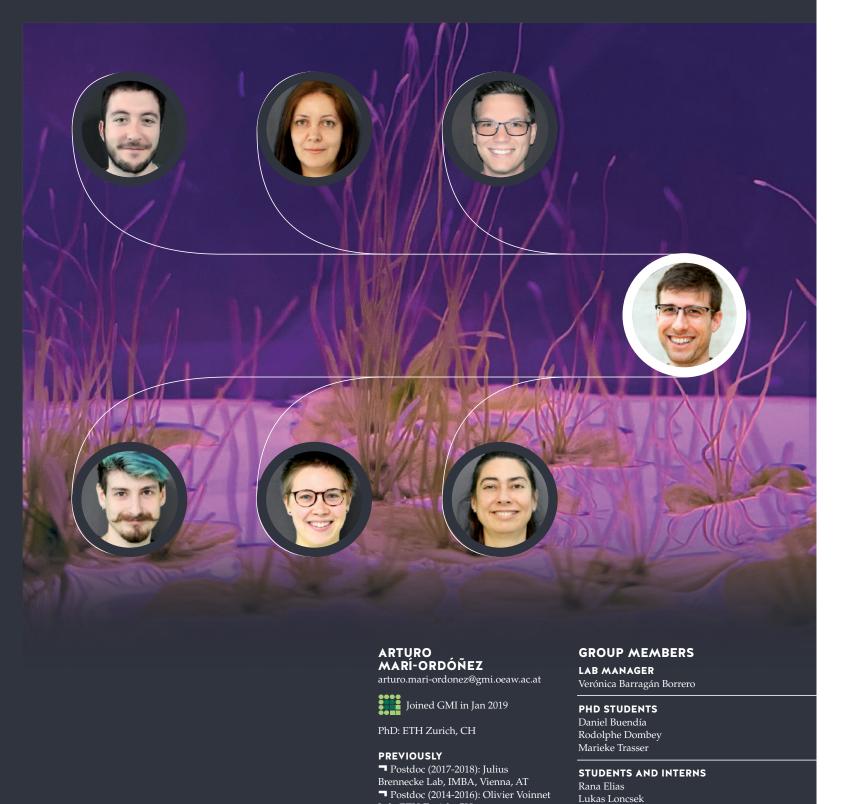
#### What do you especially like about working at the GMI?

Everyone has been very welcoming and helped our lab to quickly settle in. The atmosphere here is friendly and the high number of technical and administrative staff provide great support to each researcher. With this support, I am positive my research will progress further much faster.

#### Where do you want to go next?

I have only just completed the first year of my PhD, so I will be at the GMI for the next 3 years. After my PhD, I am interested in working in industry to develop new plant technologies and help achieve food security.

GMI**:** 



Lab, ETH Zurich, CH

## HOW TO RECOGNIZE A TRANSPOSON



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

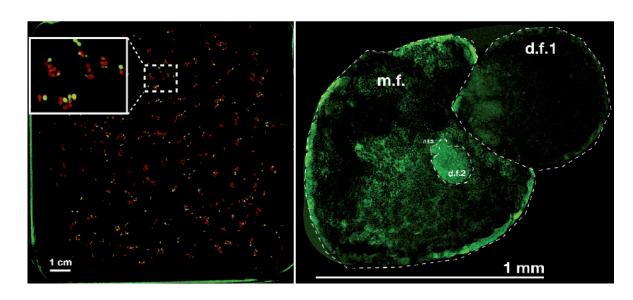
The Marí-Ordóñez lab is investigating this first step, how cells recognize new transposons, which will help us understand how they affect genomes. As part of this goal, they are developing a new group of plants that have not traditionally been used in science, called Duckweeds. Duckweeds are rapdily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

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, how transcriptional gene silencing (TGS) is initiated before its faithful propagation through generations re-

mains elusive as such pathways act on already silenced TEs. We have recently observed that some TE transcripts remain attached to chromatin and can potentially serve as scaffolds to recruit the silencing machinery to deposit the initial wave of chromatin modifications. Although still in progress, this finding indicates that initiation of epigenetic silencing of TEs is closely linked to TE biology as chromatin-bound transcripts are required for the TE to fulfill its life cycle within the plant.

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 ancestral *Spirodela polyrrhiza* genome has

revealed that many of the factors involved in TE silencing are absent. Hence, duckweeds represent a unique opportunity to investigate non-canonical silencing pathways to elucidate the basis of silencing in plants as well as the complex evolutionary interplay between TEs and their hosts. As part of our efforts to understand silencing mechanisms in duckweeds, we have resequenced the genomes of two species (Spirodela polyrrhiza and Lemna minor). Annotation of their genomes based on RNA-seq and epigenomes is ongoing. We are also expanding our analysis to other duckweeds species from the Wolffia genus, from which a survey to identify diploid strains to use as model for our studies is nearly completed. Moreover, we have succeeded in our efforts to transiently express transgenes in duckweeds (Figure) as a means to genetically modify duckweeds for functional studies.



#### FIG. Transient expression of GFP in Wolffia arrhiza.

**Left** Fluorescent scanning of transiently transformed Wolffia fronds. RED: chlorophyll autofluorescence (not transformed). GREEN: GFP positive Wolffia plants. **Right** Confocal microscopy image of a GFP positive Wolffia arrhiza frond (m.f.: mother frond, d.f.: daughter fronds numbered from older to younger).



#### **INSIGHTS**

Marieke Trasser, PhD Student Chambéry, France MSc University of Montpellier

#### How did you come to the GMI?

I got to know about the GMI during my master's degree through one of my professors, who also drew my attention to the VBC PhD program. I was considering continuing my studies after obtaining my master's degree. I was looking for a PhD position in plant biology, and more specifically in epigenetics, a new and exciting field to me. I applied to the VBC PhD program and met Arturo during the recruitment process. He was about to start his own lab at that time and had a project on transposon silencing in Arabidopsis that piqued my interest.

#### What project are you working on?

Transposons are mobile elements and are generally maintained silenced throughout the genome. Using the features of a specific transposon found in *Arabidopsis thaliana*, *ÉVADÉ*, I aim to understand how transposons are initially recognized and the mechanisms involved in the process of *de novo* silencing.

#### What do you especially like about working at the GMI?

I really appreciate the working climate at the institute. Here, I can knock on all doors and engage with everyone to get input on results, have a discussion about new papers, or just chit-chat over a coffee. This is making my time at the GMI very rich scientifically, but also on a human level.

Additionally, the state-of-the-art facilities and the many research fields represented on campus provides a very stimulating and interesting environment.

#### Where do you want to go next?

I have not thought about what is going to happen after my PhD, for the moment I am focusing on my project. I can imagine however looking for a post-doc position, but I would not exclude the possibility of going into the private sector if the opportunity presents.





for Cell Biology, Ladenburg, DE

Katarina Lalatovic\* Johannes Rötzer Marlene Wedler\* Fei Xu

(\*left the lab in 2020)

#### **EPIGENETICS**



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

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



Inheritance refers to passing information to progeny, in the case of higher plants through the formation of flowers and seeds. Like all aerial parts, these originate from a few stem cells in the shoot apical meristem (SAM). Therefore, genetic and epigenetic information in these cells is expected to be safeguarded against unwanted perturbations by external factors.

In the case of genetic information, plants have multiple pathways to repair DNA damage. These involve diverse proteins as well as RNA molecules. While some of the core protein complexes are well known, we have identified novel interacting subunits, and we found previously unknown long non-protein-coding RNAs associated with DNA damage. Defects in the corresponding genes render the plants sensitive to DNA damage, supporting the relevance of their gene products for the DNA repair capacity. The necessary mutants are mostly generated by the CRISPR/Cas technology, which has been adapted to support easy and cost-efficient genotyping of the mutations (Bente et al. 2020).

Many abiotic and biotic factors can also modify epigenetic parameters. How epigenetic information is maintained, reset during development, or restored after perturbations, is less clear than for the DNA sequence conservation, but of high importance in the stem cells. Based on fluorescence-activated nuclear sorting (FANS) (Gutzat and Mittelsten Scheid 2020), the Mittelsten Scheid lab investigated gene expression and DNA methylation in pure fractions of SAM stem cell nuclei during the development of Arabidopsis. This revealed a core set of genes differentially expressed in stem cells, among them some components associated with RNA-directed DNA methylation (RdDM), an epigenetic control mechanism mainly of transposons. A transient activation of some transposable elements in the stem cells and characteristic changes in DNA methylation suggests a programmed (epi-)genome protection prior to flowering and seed set (Gutzat et al. 2020). In addition to transposons, viruses are a threat for genome integrity and interfere with RdDM but are rarely able to enter seeds. Applying fluorescence microscopy in living wildtype and mutant plants infected with tagged virus derivatives allows us to investigate the degree and kinetics of virus spreading in the meristem (Figure).

While research with model plants like Arabidopsis provided invaluable, generally valid knowledge, studying other plants can reveal alternative principles. This is the case for the regulation of seed germination: Arabidopsis seeds require light exposure, while seeds of different accessions of its close relative Aethionema arabicum have light-inhibited germination, likely an adaptation ensuring that this process occurs only when short day conditions indicate the optimal season. The seeds seem to have a "memory" for light exposure, which has stimulated the development of epigenetic tools in this species (Kreutz et al. 2020). Screening a newly generated mutant collection identified several candidate plants with seeds that could germinate also in light, and some responsible genes were already identified. Their corresponding gene products will allow us to study the hormonal and signalling pathways that regulate the alternative germination process.

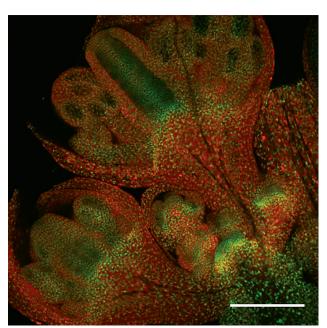
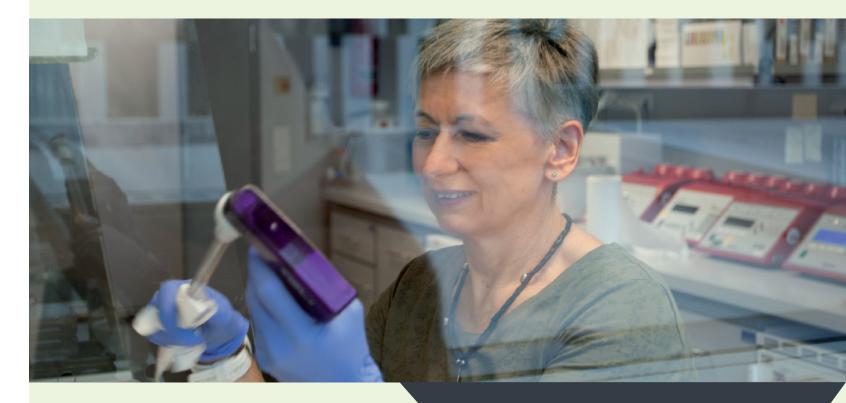


FIG.
Fluorescence microscopy allows
to investigate how far and how fast
a virus can spread within living
plants. The image shows a section
through flower buds of Arabidopsis
thaliana in which the nuclei are labelled
in green. The plant was infected with a
virus that contains a protein labelled in
red. Size bar = 200 µm.



#### **INSIGHTS**

**Nicole Lettner,** Technician Wiener Neustadt, Austria Kolleg für Technische Chemie, Rosensteingasse Vienna

#### How did you come to the GMI?

Luck? Chance? I have worked in different labs, dealing with inorganic chemistry and trace analyses to pharmaceutical research. When my previous workplace closed down, I came across an announcement for a technician job at the GMI and got very excited. Working with plants was new for me, but otherwise I had experience with all the techniques that were required, so I applied, and this was it. The decision was made within a week and since I am still here more than a decade later, I would say it worked out very well.

I always liked to learn something new, wanted some challenge, and plants were new to me. Also, epigenetics was a field I had not explored so far or, to be honest, was not much aware of. Getting this chance was and is great.

#### What project are you working on?

As a technician, I ensure the lab runs smoothly on an everyday basis. I make sure things function, materials are available, knowledge is maintained, and I try to be the helping hand in all projects where this is needed. I also keep an eye on the budget, communicate with the lab support team, and I train new lab members how to use equipment and protocols.

#### What do you especially like about working at the GMI?

I enjoy the international atmosphere. I get to interact and work with people from a lot of different cultures and backgrounds. That is very interesting and exciting.

I see a lot of goodwill, of acceptance, of trying to achieve something together, which makes me feel that there is a chance for a more peaceful world.

And on a smaller scale, I like the freedom I have in my everyday work. I am relatively free to structure my day and nobody will interfere. The jobs need to get done, but that is my responsibility. The people in my group are a great lot. We work well together and I get support when needed.

Also, as this is science, the tasks are varied and keep changing and I am still learning new things. For myself I just cannot imagine doing a total routine job day in day out.

#### Where do you want to go next?

Hopefully, when my current group closes down in 2022, to another group at the GMI. I would like to stay on for the coming years and starting a new lab from scratch would be a great new challenge.

And then eventually I will retire. Sort of.

GMI**#** 



PhD: University of Arizona, Tucson

#### **PREVIOUSLY**

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

Michael Schon

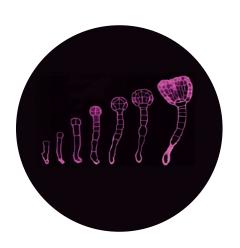
#### **POSTDOCS**

Balaji Enugutti Subramanian Paulraj

#### **TECHNICIAN**

Magdalena Mosiołek

#### **RNA BIOLOGY OF PLANT EMBRYOS**



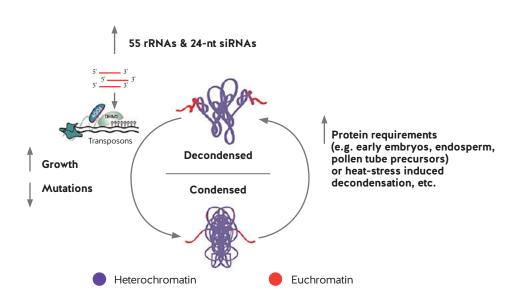
Soon after fertilization of the egg and sperm, genes in the zygote are turned on, beginning a precisely coordinated developmental program. Already during very early stages of development, this program has established the basic blueprint of the plant body, including the root, shoot, and first leaves. Specialized cell types within these organs are also established at this time, and each of these cell types has to turn on 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 the developing 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 are developing new tools to help study early plant embryos and are especially interested in how small RNAs that do not encode proteins regulate these processes.



We continue to develop molecular biology, microscopy, and bioinformatic approaches to characterize zygotic genome activation, establishment of the nascent epigenome, and body plan formation at the beginning of plant life using Arabidopsis as a model system. Below, I have highlighted a project that we published in 2020, and which revealed how small RNAs establish epigenetic modifications on DNA during early plant life.

Eukaryotic genomes are partitioned into euchromatic and heterochromatic domains to regulate gene expression, cell division, and other fundamental cellular processes. However, chromatin is dynamic during growth and development, and must be properly re-established after its decondensation. Small interfering RNAs (siRNAs) are a class of small RNAs that promote heterochromatin formation, but little is known about how chromatin regulates siRNA expression. We demonstrated that thousands of transposable elements (TEs) produce exceptionally high levels of siRNAs in Arabidopsis thaliana embryos (Papareddy et al., 2020). TEs generate siRNAs throughout embryogenesis according to two distinct patterns depending on whether they are located in euchromatic or heterochromatic regions of the genome. siRNA precursors are transcribed in embryos and siRNAs are required to direct the re-establishment of DNA methylation on TEs from which they are derived in the new generation. Decondensed chromatin also permits the production of 24-nt siRNAs from heterochromatic TEs during post-embryogenesis, and siRNA production from bipartiteclassified TEs is controlled by their chromatin states. Therefore, decondensation of heterochromatin in response to developmental, and perhaps environmental, cues promotes the transcription and function of siRNAs in plants. In contrast to models proposing that TEs are silenced in gametes and embryos by mobile siRNAs produced from surrounding "companion" cells, our results indicate that chromatin-mediated siRNA transcription provides a cell-autonomous homeostatic control mechanism to help reconstitute pre-existing chromatin states during growth and development including those that ensure silencing of TEs in the future germ line (Figure).



#### FIG. Model of how interplay between chromatin states and siRNAs provides epigenome homeostasis.

Hundreds of rRNAs are colocalized with thousands of TEs in pericentromeric regions. Reduced heterochromatin upon karyogamy, cell division or heat-stress allows sharp increases in transcription of both rRNAs and precursors of siRNAs derived from TEs. While rRNAs fuel cell growth, siRNAs direct re-methylation of TEs to help silence them and prevent their mutagenic activities. This may be a general mechanism for cells to simultaneously achieve maximal growth while maintaining genome stability.



#### **INSIGHTS**

#### How did you come to the GMI? What project are you working on?

I had my first taste of plant epigenetic inheritance during my masters at the University of Glasgow. I thought I wasn't ready for a PhD and therefore worked as a research technician with Prof. Jose Gutierrez-Marcos. Because I relish studying how epigenetics marks behave after fertilization in embryos, Jose introduced me to the research happening at the GMI. I was pretty impressed by the research in both epigenetics (Fred Berger and Ortrun Mittelsten Scheid Labs for example) and embryogenesis (Nodine lab). I was confident that having an opportunity to pursue my PhD in the Nodine lab, surrounded by experts in epigenetic, would nourish me into a better researcher in this subject.

My PhD research focuses primarily on understanding how small RNAs and DNA methylation help each other in establishing the nascent epigenome soon after fertilization in Arabidopsis embryos. Recently, we published a paper trying to explain how chromatin states promote transcription of non-coding small RNAs and establishment of DNA methylation during seed development. I am currently wrapping up a project where we are studying the regulation of methyltransferases during seed development.

Mallam, Nellore, India MSc University of Glasgow

#### What do you especially like about working at the GMI?

Working at the GMI is definitely a unique opportunity. I could go on and on listing rea-

sons why GMI is an outstanding place to do plant research. To mention just a handful: apart from the vibrant scientific community at the Vienna BioCenter, it would not be an understatement to say that the GMI is one of the very few institutes that offers outstanding core facilities and support, multidisciplinary seminars by world-class researchers, and excellent training programs to help develop as a

#### Where do you want to go next?

I would love to be a group leader, and will continue to work towards this goal. My current plan is to graduate by April 2021, after which I will move to the University of California, Los Angeles to do my post-doctoral training in Prof. Steve Jacobsen's lab.

GMI #







Joined GMI in Feb 2009

PhD: Stanford University, US

#### PREVIOUSLY

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

#### PHD STUDENTS

Gökce Aköz\* Robin Burns Dejan Đukić Rahul Pisupati Luz Mayela Soto Jiménez

#### POSTDOCS

Pieter Clauw Thomas Ellis Danièle Filiault Benjamin Jaegle Aleksandra Kornienko Haijun Liu Eriko Sasaki\* Yoav Voichek

#### TECHNICIANS

Joanna Gunis Viktoria Nizhynska

#### STUDENTS AND INTERNS Mirjam Bissmeier\*

Sonia Celestini\* Tarik Cerimagic\* Tal Dahan\* Yalcin Ege Okyar\*

(\*left the lab in 2020)

#### **EXPLORING GENOMIC VARIATION**



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

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



#### Polyploidy and whole-genome duplication

The genomes of most higher organisms show traces of ancient whole-genome duplications, or polyploidy, in the form of chromosomal segments that are obviously copies of each other, and that still harbor the same genes, albeit diverged. It is generally believed that the process of whole-genome duplication followed by gene loss and divergence of retained copies has played a major role in evolution — essentially by providing new material for natural selection to work on.

Whole-genome duplication have been particularly common in plants, for reasons that are not understood, although hermaphroditism likely plays a role because it allows individuals with unusual chromosome numbers to reproduce by mating with themselves. Sex between individuals with different ploidy levels usually result in sterile offspring. Therefore, in species with separate sexes, an individual with an unusual chromosome number may have a hard time finding a partner with which it could produce fertile offspring.

Most flowering plants (the core eudicots) stem from a hexaploid ancestor, i.e., a species carrying three copies of the diploid genome. Our work on the columbine (*Aquilegia sp.*) genome provided insight into how this happened. By analyzing the pattern of segment-sharing, we were able to show that the columbine genome is tetraploid, and that the whole-genome duplication that led to tetraploidy was the same as the one that led to tetraploidy in the core eudicots. The third diploid genome must have been added later, which means that the core eudicots were probably the product of ancient hybridization between a tetraploid and a diploid ancestral species.

#### The evolution of polyploidy

The fact that polyploidization is frequent in plants mean that we are able to see the process "in action". In addition to studying the traces of ancient processes, we can look at recently established polyploid species. We have looked at one such example, Arabidopsis suecica, a tetraploid species known to be the product of mating between the main model plant, A. thaliana and a different species in the same genus, A. arenosa. The two parent species are separated by at least six million years of evolution, and differ in genome size, chromosome number, and ecology (A. thaliana is a tiny, self-fertilizing weed, whereas A. arenosa is a much larger outcrossing species). Mating works only because of polyploidy: presumably an unreduced, diploid

egg from *A. thaliana* was fertilized by a diploid pollen from the already tetraploid *A. arenosa*. Our estimates suggest that the new hybrid species was formed multiple times about 16 thousand years ago, at the end of the last glacial maximum.

The existence of a recent polyploid hybrid allowed us to investigate the process of polyploidization. In particular, how is it possible for two very different genomes to co-exist and create plants that are not only fully functioning, but evolutionarily successful (although restricted to boreal forest areas of Fennoscandia and parts of Russia) It has been suggested that polyploidy and hybridization would lead to a so-called "genome shock", characterized by massive genome rearrangements, rapid silencing of one (sub-)genome or the other, and a dramatic increase in the activity of transposable elements.

Our study found no evidence for any of this. On the contrary, there appeared to have been slow-but-steady adaptation towards being polyploid. Darwin famously argued that evolution was gradual — "nature doesn't make leaps" — and our results suggests that polyploidy may not be an exception.

# ~6-8 mya ~16 kya A. thaliana A. suecica A. aren

2n = 4x = 26

Selfing

Multiple origins

2n = 10

Selfing

#### The origins of Arabidopsis suecica.

A. suecica is a allotetrapolyploid, i.e., it contains two diploid genomes from two different species — 2 set of 5 chromosomes from A. thaliana, and two sets of 8 chromosomes from A. arenosa for a two sets of 5+8=13 chromosomes. This occurred via regular crosses, but with diploid instead of haploid gametes.

**A. arenosa**2n = 2x(4x) = 16(32)
Outcrossing



#### **INSIGHTS**

**Almudena Mollá Morales,** Lab Manager Elche, Spain PhD Miguel Hernández University

#### How did you come to the GMI?

Before joining the GMI I was doing my second postdoc at the CNB-CSIC in Madrid. The project was coming to an end and I needed to think what my next step would be. I wanted to stay in research, but I knew I didn't want to be a PI, so I started looking for jobs. One of my friends saw the advertisement for the position of lab manager in Magnus Nordborg's lab and sent it to me with a note saying that it sounded like a good fit. He was right: I applied and, not too much later, I moved to Vienna.

#### What project are you working on?

As a lab manager, I have to be on top of everything happening in the lab. People come

to me for help, advice in experimental design, and discussions. I am also in charge of purchasing and organizational matters and I also still do some benchwork. It may seem that I need to be a superhuman to manage it all, but I get a lot of help from my coworkers, which makes my day to day work easier to handle, and I am really grateful for that.

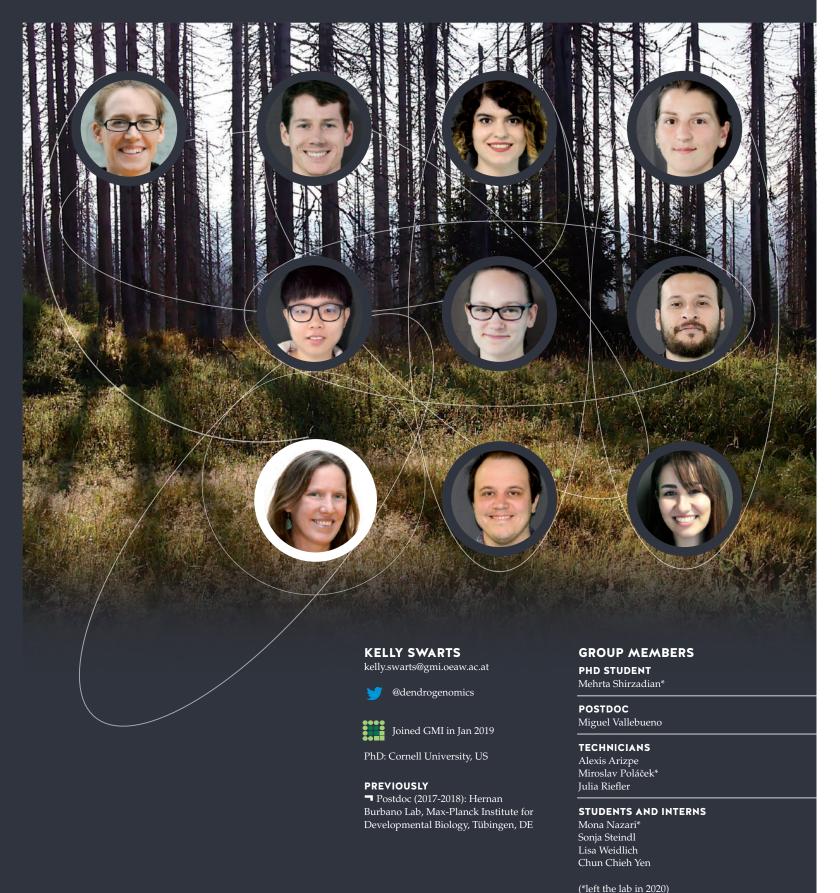
#### What do you especially like about working at the GMI?

It cannot be denied that the GMI is a privileged institute. Its facilities and resources allow science to proceed without the hurdles other places have, plus it is located in one of the most livable cities in the world! But what I really like about working at the GMI is its international and diverse community, which allows open and interesting conversations about many different topics (not just about science!).

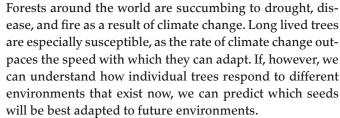
#### Where do you want to go next?

After a PhD and two postdocs (and even a semester as a high school teacher!), I have finally found a stable position in science as a lab manager, a job that I enjoy. I haven't ruled out doing something different in the future (who knows?), but, for now, I see myself staying here for a while.

GMI**:** 



### RING **GENOMICS**



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.





ease, 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



We focus on the economically and ecologically important conifer Norway spruce (*Picea abies*) to

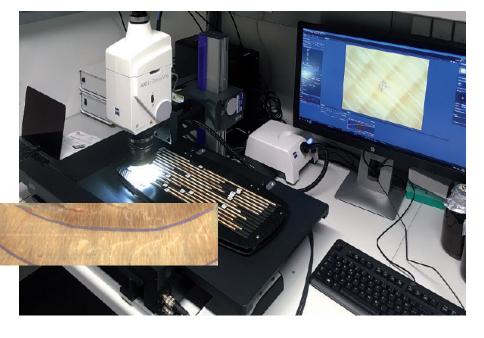
- 1) develop models and infrastructure to understand the fraction of annual growth that can be attributed to genotype, environment, and genotype-by-environment interactions (GxE),
- **2)** map the genetic basis of adaptive response using estimates for GxE as a response in genome-wide association studies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

Over the past year, extensive fieldwork was limited due to COVID restrictions but we still collected data from 15 plots in Berchtesgaden

National Park in Germany, adding over 1,000 new tree samples. Over the past two years we have collected from nearly 3,000 trees and each of these has two core samples typically capturing more than 100 years of growth. Hand measurement of annual growth is not only unfeasible but would be error prone since many individuals would be required to participate. We've successfully developed an automated phenotyping platform that relies on high-quality images generated from a Zeiss broad-spectrum light microscope and a custom robotic stage that allows us to digitize microtome-prepared increment cores in reusable aluminum core mounts in a single run (up to 650 cm of cores/run) that was developed in collaboration with the core service departments. Accurate measurement relies on correctly identifying annual rings and Miroslav Polacek has led the development and testing of a Convolutional Neural Net (CNN) deep learning approach to identify annual ring boundaries, cracks and other wood anatomical traits such as resin

canals and pith. Training of the CNN is overseen by Alexis Arizpe, our dendroecologist (→ Fig. 1). The previous best model has a precision of .99 and recall of 0.82 on the validation set and is still being iteratively improved by adding failed detections back into the training. (On real data, the recall is 0.98).

Efficiently genotyping large numbers of trees is critical to the project. Due to the large genome size of spruce (20 Gbp), Miguel Vallebueno developed a cheap (<one euro/sample) Genotyping-by-Sequencing (GBS) restriction digest library protocol that is very highly multiplexable to take advantage of Illumina NovaSeq technologies. GBS reduces the sampled genome from 20 Gbp to less than 0.5 Gbp but targets functional genomic regions due to the methyl-sensitive ApeKI restriction enzyme. Sonja Steindl led testing in spruce and, by replacing error-prone Taq polymerase with a high fidelity Phusion and decreasing the cycle number, has developed a protocol that is highly replicable ( $\rightarrow$  Fig. 2).



Automated microscopy system for digitizing tree rings.

FIG. 1

FIG. 2

MaskR-CNN predictions for a representative spruce sample where purple indicates high confidence prediction after post-processing. The center of the tree is especially challenging because of the curves in the rings



**INSIGHTS** 

**Miguel Vallebueno,** Postdoc Durango, Mexico PhD National Laboratory of Genomics for Biodiversity

#### How did you come to the GMI?

I met Kelly Swarts during an Internship at the Max Plank Institute, where we collaborated on a project to explore ancient maize diversity and adaptation. Since we share interests on the use of time as a proxy to undercover adaptation processes, I was excited to join her lab in 2019. In her lab I found a team of diverse specialists, that together bring a revolutionary perspective to the study of forest adaptation through hundreds of years of history stored in the tree rings.

#### What project are you working on?

The project I have been developing the last two years is understanding adaptation of maize to novel environments. My work focuses on the use of paleogenomics to study maize population dynamics across time in the American continent. I am particularly interested in understanding the process of local adaptation of maize populations.

#### What do you especially like about working at the GMI?

I fully enjoy the diverse and friendly environment, the colleagues in the institute are not only open to discuss challenging scientific ideas but also to warm you with their friendship. Also, the facility members are always happy to guide across the multiple platforms that the VBC provides.

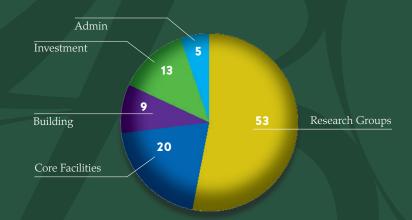
#### Where do you want to go next?

The next step in my scientific career would be applying for a Junior group leader position. The biggest treasure of Mexico is its diversity. Therefore, I will apply there for positions that allow me to continue exploring the Mexican ancient maize diversity.

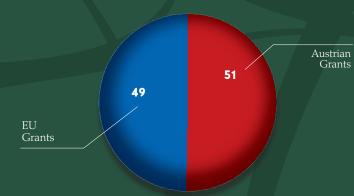
GMI**:** 

# KEY FACTS (as of Dec 31, 2020)

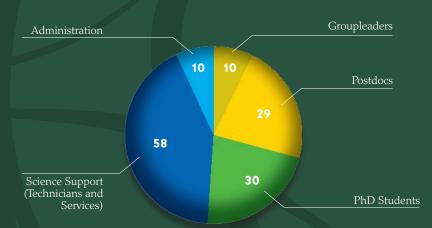
#### **EXPENDITURES** (%)



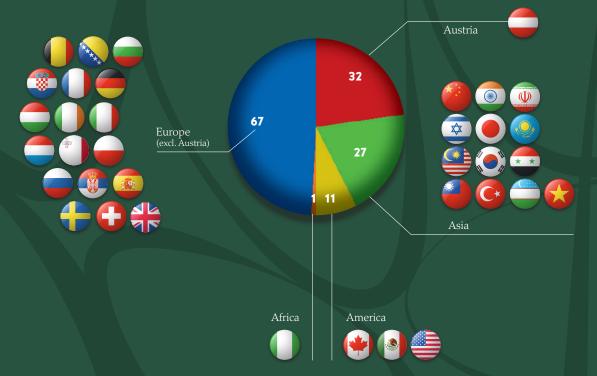
#### RESEARCH GRANTS (%)



#### STAFF BY FUNCTION (Head Count)



#### STAFF - NATIONALITIES (Head Count)



# PUBLICATIONS

#### **BERGER GROUP**

Borg M, Jacob Y, Susaki D, et al. (2020) Targeted reprogramming of H3K27me3 resets epigenetic memory in plant paternal chromatin. Nature Cell Biology 22(6):621-9.

Bourguet P, Picard CL, Yelagandula R, et al. (2020) The histone variant H2A.W promotes heterochromatin accessibility for efficient DNA methylation in Arabidopsis. bioRxiv:19.998609.

Jiang D, Borg M, Lorković ZJ, et al. (2020) The evolution and functional divergence of the histone H2B family in plants. PLoS Genet 16(7):e1008964.

Julca I, Flores M, Proost S, et al. (2020) Comparative transcriptomic analysis reveals conserved transcriptional programs underpinning organogenesis and reproduction in land plants. bioRxiv:2020.10.29.361501.

Karaaslan ES, Wang N, Faiß N, et al. (2020) Marchantia TCP transcription factor activity correlates with three-dimensional chromatin structure. Nat Plants [epub].

**BECKER GROUP** 

Hüther P, Schandry N, ... Becker C (2020)

Aradeepopsis, an Automated Workflow for

**Top-View Plant Phenomics using Semantic** 

preprint bioRxiv:2020.04.01.018192v1.

**Segmentation of Leaf States**. *Plant Cell [epub]* 

Ramos-Cruz D and Becker C (2020) A Critical

**Guide for Studies on Epigenetic Inheritance** 

Hajný J, Prát T, Rydza N, et al. (2020) Recep-

tor kinase module targets PIN-dependent

auxin transport during canalization. Science

Control: Cellular Logic in the Root Immune

**Response.** *Cell Host Microbe* 27(3):308-10.

Lee HS and BelkhadirY (2020) Damage

in Plants. Methods Mol Biol 2093:261-70.

**BELKHADIR GROUP** 

370(6516):550-7.

Lei B, Capella M, Montgomery SA, et al. (2020) A Synthetic Approach to Reconstruct the Evolutionary and Functional Innovations of the Plant Histone Variant H2A.W. Curr Biol

Loppin B and Berger F (2020) Histone Variants: The Nexus of Developmental Decisions and Epigenetic Memory. Annu Rev Genet [epub].

Montgomery SA, Tanizawa Y, Galik B, et al. (2020) Chromatin organization in early land plants reveals an ancestral association between H3K27me3, transposons, and constitutive heterochromatin. Curr Biol [epub].

Yan A, Borg B, Berger F, et al. (2020) The **Atypical Histone Variant H3.15 Promotes** Callus Formation in Arabidopsis thaliana. Development [epub].

#### **DAGDAS GROUP**

Acheampong AK, Shanks C, Chang CY, et al. (2020) EXO70D isoforms mediate selective autophagic degradation of Type-A ARR proteins to regulate cytokinin sensitivity. bioRxiv:938712.

Acheampong AK, Shanks C, Cheng CY, et al. (2020) EXO70D isoforms mediate selective autophagic degradation of type-A ARR proteins to regulate cytokinin sensitivity. PNAS

Ma J, Liang Z, Zhao J, et al. (2020) Friendly regulates membrane depolarization induced mitophagy in Arabidopsis. bioRxiv:2020.07.12.198424.

Pandey P, Leary AY, Tümtas Y, et al. (2020) The Irish potato famine pathogen subverts host vesicle trafficking to channel starvation-induced autophagy to the pathogen interface. bioRxiv:2020.03.20.000117.

Petre B, Contreras MP, Bozkurt TO, et al. (2020) Host-interactor screens of Phytophthora infestans RXLR proteins reveal vesicle trafficking as a major effector-targeted process. bioRxiv:2020.09.24.308585.

Rodriguez E, Chevalier J, Olsen J, et al. (2020) Autophagy mediates temporary reprogramming and dedifferentiation in plant somatic cells. EMBO J 39(4):e103315.

Stephani M, Picchianti L, ..., Dagdas Y (2020) A cross-kingdom conserved ER-phagy receptor maintains endoplasmic reticulum homeostasis during stress. *eLife:58396 preprint* bioRxiv:995316.

Stephani M, Picchianti L, Dagdas Y (2020) C53 is a cross-kingdom conserved reticulophagy receptor that bridges the gap betweenselective autophagy and ribosome stalling at the endoplasmic reticulum. Autophagy [epub].

#### **DOLAN GROUP**

Cannell N, Hetherington AJ, Emms D, et al. (2020) Multiple metabolic innovations and losses are associated with major transitions in land plant evolution. Curr Biol 30(10):1783-800.

Dolan L (2020) Plant Evolution: An ancient mechanism protects plants and algae from heat stress. Curr Biol 30(6):R277-8.

Hetherington AJ, Berry CM, Dolan L (2020) Multiple origins of dichotomous and lateral branching during root evolution. Nat Plants 6(5):454-9.

Thamm A, Saunders TE, Dolan L (2020) Independent evolution of lateral inhibition mechanisms in different lineages of land plants: MpFEW RHIOZIDS1 miRNA-mediated lateral inhibition controls rhizoid cell patterning in Marchantia polymorpha. Curr Biol 30(10):1905-15.

#### MITTELSTEN SCHEID GROUP

Bente H, Foerster AM, Sarazin A, et al. (2020) Polyploidy-associated paramutation in Arabidopsis is determined by small RNAs, temperature, and structure. bioRxiv:2020.10.21.348839.

Bente H, Mittelsten Scheid O, Donà M (2020) Versatile in vitro assay to recognize Cas9-induced mutations. Plant Direct 4(9):e00269.

Gutzat R and Mittelsten Scheid O (2020) Preparing Chromatin and RNA from Rare Cell Types with Fluorescence-Activated Nuclear Sorting (FANS). Methods Mol Biol 2093:95-105.

Gutzat R, Rembart K, Nussbaumer T, et al. (2020) Arabidopsis shoot stem cells display dynamic transcription and DNA methylation patterns. EMBO J [epub] preprint bioRxiv:430447.

#### **NODINE GROUP**

Gutierrez-Marcos J, Lee YS, Maple R, et al. (2020) A transposon surveillance mechanism that safeguards plant male fertility during stress. bioRxiv:2020.10.03.324764.

Gutzat R, Rembart K, Nussbaumer T, et al. (2020) Arabidopsis shoot stem cells display dynamic transcription and DNA methylation patterns. EMBO J [epub] preprint bioRxiv:430447.

Kao P and Nodine MD (2020) Profiling Transcriptomes of Manually Dissected Arabidopsis Embryos. Methods Mol Biol 2122:113-26.

Kao P and Nodine M (2020) Application of expansion microscopy on developing Arabidopsis seeds. Methods Cell Biol [epub].

Nodine MD (2020) Parental contributions to early embryos. Nat Plants [epub].

Páldi K, Mosiolek M, Nodine MD (2020) Small RNA In Situ Hybridizations on Sections of Arabidopsis Embryos. Methods Mol Biol 2122:87-99.

Papareddy R, Páldi K, ... Nodine MD (2020) **Chromatin Regulates Bipartite-Classified** Small RNA Expression to Maintain Epigenome Homeostasis in Arabidopsis. bioRx-

Papareddy RK, Páldi K, ..., Nodine MD (2020) Chromatin regulates expression of small RNAs to help maintain transposon methylome homeostasis in Arabidopsis. Genome Biol 21(1):251.

#### **NORDBORG GROUP**

Burns R, Mandakova T, Jagoda J, et al. (2020) Gradual evolution of allopolyploidy in Arabidopsis suecica. bioRxiv:264432.

Gutzat R, Rembart K, Nussbaumer T, et al. (2020) Arabidopsis shoot stem cells display dynamic transcription and DNA methylation patterns. EMBO J [epub] preprint bioRxiv:430447.

Tsuchimatsu T, Kakui H, Yamazaki M, et al. (2020) Adaptive Reduction of Male Gamete Number in the Selfing Plant Arabidopsis Thaliana. Nat Commun 11(1):2885.

Weiszmann J, Clauw P, Jagoda J, et al. (2020) Plasticity of the primary metabolome in 241 cold grown Arabidopsis thaliana accessions and its relation to natural habitat temperature. bioRxiv:2020.09.24.311092.

#### **SWARTS GROUP**

Morales L, Repka AC, Swarts KL, et al. (2020) Genotypic and phenotypic characterization of a large, diverse population of maize near-isogenic lines. Plant J 103(3):1246-55.

#### **FORMER GROUPS & SERVICES**

Alcântara A, Seitner D, Navarrete F, Djamei A (Epub: 2020) A high-throughput screening method to identify proteins involved in unfolded protein response of the endoplasmic reticulum in plants. Plant Methods, Bd. 16, S. 4.

Gordon S, Contreras-Moreira B, Levy J, et al. (Epub: 2020) Gradual polyploid genome evolution revealed by pan-genomic analysis of Brachypodium hybridum and its diploid **progenitors.** *Nat Commun, Bd. 11 (1), S. 3670.* 

Raxwal V, Simpson C, Gloggnitzer J, Entinze J, Guo, W, Zhang R, Brown J, Riha K (2020) Nonsense-Mediated RNA Decay Factor UPF1 Is Critical for Posttranscriptional and Translational Gene Regulation in Arabidopsis. Plant Cell, Bd. 32 (9), S. 2725-2741.



# **GRANTS**

#### BECKER GROUP

**Epidiverse - Epigenetic Diversity in Ecology** European Research Council (ERC), Life Sciences:

H2020-MSCA-ITN-2017

#### € 255,374

September 2017 – August 2021

Function and evolution of attack and response strategies during allelopathy in plants
European Research Council (ERC), Life

ERC Starting Grant: FEAR-SAP

#### € 1,500,000

January 2018 – December 2022

EPPN Transnational Access proposal (ID 180): in-kind contribution (service and instrument time @ IPK Gatersleben); starting 1st Q 2018

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

November 2018 – November 2020

#### EMBO Long-Term Fellowship Duxbury

European Molecular Biology Organization: ALTF 875-2017

#### € 93,667

April 2018 – April 2020

#### FWF – JSPS: Genetic variation in rice momilactone biosynthesis

Austrian Science Fund: I 4808-B

#### € 362,370

June 2020 – May 2024

## Unravelling the molecular and genetic mechanisms of the innate weed suppression capacity of rice

ÖAW Doc Fellowship, Núria Serra Serra

#### € 76,000

July 2020-June 2022

#### BELKHADIR GROUP

An extracellular interactome map of plant receptor kinases (Hertha Firnberg fellowship Elwira Smakowska)

Austrian Science Fund: T947-B29

#### € 230,010

August 2017 – July 2020

#### Manipulation of plant innate immune responses by small molecules probes

Vienna Science and Technology Fund:

#### € 324,800

January 2018 – December 2021

#### Regulation of growth defense tradeoffs by temperature

Austrian Science Fund: I 3654-B29

#### € 299.533

January 2018 - December 2020

#### BERGER GROUP

**Graduate program "Chromosome Dynamics"** Austrian Science Fund: DK W1238-B20

#### € 142,020

April 2016 – February 2020

#### A mechanism of histone exchange involved in heterochromatin (Lise Meitner fellowship Akihisa Osakabe)

Austrian Science Fund: M 2539-B21

#### € 169,260

August 2018 – July 2020

#### The role of histone variants in chromatin organization

Austrian Science Fund: P32054-B21

#### € 397,745

May 2019 – April 2023

#### Tracing the origins of male germline specification in plants

Austrian Science Fund: I 4258-B21

#### € 306.589

May 2019 – April 2022

## Chromatin dynamics at fertilization in early land plants (Tetsua Hisanaga)

H2020-MSCA-COFUND-2018): GA: 847548 VIP<sup>2</sup> (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

#### 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)

European Commission (Horizon 2020): GA: 847548 VIP<sup>2</sup> (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

#### **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, EUR 533 466,60)

GMI: October 2020 – September 2023

#### MITTELSTEN SCHEID GROUP

#### Graduate program "Chromosome Dynamics" Austrian Science Fund: W1238

€ 182,800 + € 142,020 (prolongation)

March 2012 – February 2020

#### AUgmented REsilience After Transmission

of Epimutations (Ruben Gutzat)

#### € 302,719

January 2018 – December 2020

#### The role of long ncRNAs during DNA repair in Arabidopsis (Lise Meitner fellowship

Austrian Science Fund: M 2410-B21

#### € 156,140

May 2018 – April 2020

#### A novel model to study light-regulated seed

**germination** (Zsuzsanna Merai) Austrian Science Fund: I 3979-825

#### € 382,032

February 2019 – January 2021

#### **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 – June 202

#### Small RNA regulation of the body plan and epigenome in Arabidopsis embryos

European Research Council: Starting Grant No. 637888

#### € 1,499,989

July 2015 – June 2020

#### NORDBORG GROUP

1001 Genomes Plus

Austrian Science Fund: I 3684-B25

#### € 355,541

January 2018 – December 2020

## ERC Advanced Grant: Elucidating the causes and consequences of the global pattern of epigenetic variation in Arabidopsis thaliana European Research Council: Advanced Grant

#### No. 789037 **€ 2,498,468**

June 2018 – May 2023

#### Role of long non-coding RNA variation in

A. thaliana (Hertha Firnberg Aleksandra

#### Austrian Science Fund: T 1018-B29

#### € 234,210

September 2018 – August 2021

#### **SWARTS GROUP**

## Plant adaptation to rapidly changing environments (Miguel Vallebueno) European Commission (Horizon 2020): GA:

#### € 98.640

January 2020 – December 2022

847548 VIP<sup>2</sup> (GEUP0018SWA)









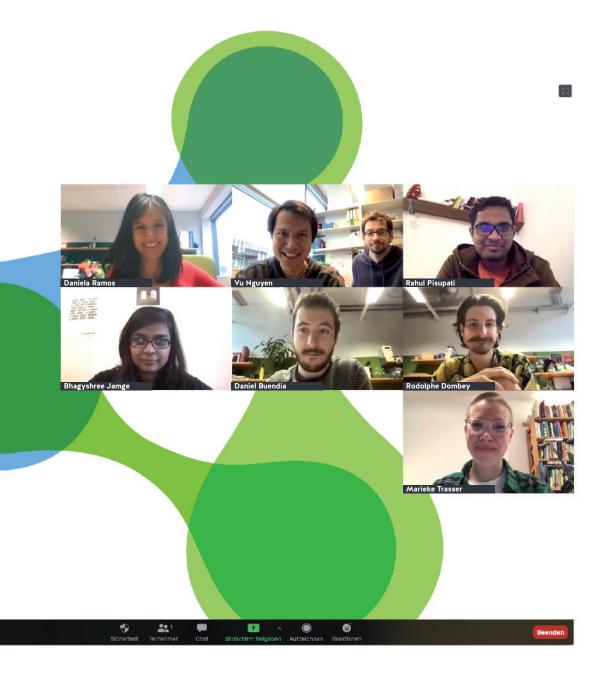








# VIENNA BIOCENTER INTERNATIONAL PHD PROGRAM IN LIFE SCIENCES



#### **EMPOWERING CURIOUS RESEARCHERS**

A major milestone was reached this year - the research institutes at the Vienna BioCenter campus GMI, IMBA, IMP, and the Max Perutz Labs signed a collaboration agreement with the University of Vienna and the Medical University of Vienna to form a unique doctoral school with joint degrees from both universities. The aim of the new school is to promote interdisciplinary research in the Life Sciences at the highest level, recruit the best talent to the VBC campus, and to provide a comprehensive training program to motivated PhD students. This program is supported by a comprehensive infrastructure to support all fac-

ulty members and students, and to meet the ever-changing training needs of the scientific research endeavor.

Students are selected twice-yearly with an emphasis on academic and technical excellence. The official language of the program is English, and students are enrolled through the University of Vienna. PhD salaries are offered at an internationally competitive level for up to 4 years. Many GMI faculty are involved in giving lectures, seminars, and practical courses in Molecular Plant Biology in the context of this program.

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.



## 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

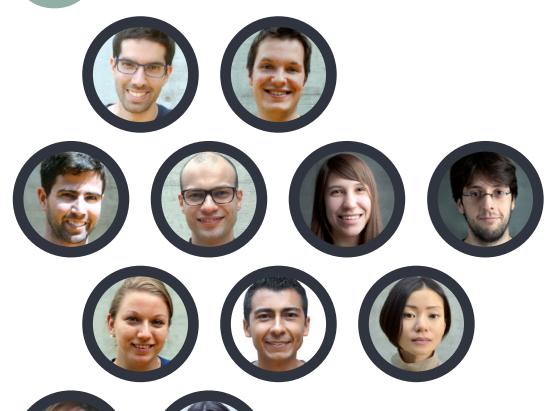
- Facing the challenge of effective writing
- Professional development course for young scientists (aka Lab management course)
- Entrepreneurship

#### 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

# 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. 2020 saw the departure of several PhD students and postdocs moving to various academic and industry positions. We said "Auf Wiedersehen und viel Glück" in 2020 to:

#### ANDRE ALCANTARA

Molecular Biologist, Neoplants, Paris France

#### HEINRICH BENTE

Postdoc, Swedish University of Agricultural Sciences, Uppsala Sweden

#### MARTIN DARINHO

#### ZANE DUXBURY

Scientist, Syngenta, UK

#### GÖKCE AKÖZ

FERNANDO NAVARRETE

#### KATARZYNA PARYS

Postdoc, LMU Munich, Germany

#### JORGE ISAAC RODRÍGUEZ

PhD, LMU Munich, Germany (Becker Group)

#### **ERIKO SASAKI**

Associate Professor, Kyushu University, Japan

#### DENISE SEITNER

Information Designer, Austrian Agency for Health and Food Safety, Vienna Austria

#### NURIA SERRA

European Association of Nuclear Medicine, Vienna Austria







Vienna BioCenter is a leading life sciences location in Europe, offering a unique combination of research, education and companies on a single campus:

> ALMOST 1,500 SCIENTISTS (including 260 PhD students)

> > 91 RESEARCH GROUPS

33 BIOTECH COMPANIES

**SCIENTISTS FROM 81 COUNTRIES** create a highly dynamic environment of international standards.

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

A growing number of biotech-companies 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

Achievement, recognition, and support for research is reflected by numerous grants and awards: 54 ERC research grants, 24 EMBO Members, 11 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 infra**structure** offer unique working conditions that enable scientists here to operate at the forefront of Life Science research.



# 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 produc-

tion 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.



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 pro-

viding 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 highthroughput 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.

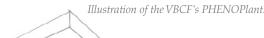
The mission of the Protein Technologies Facility (ProTech) is to further research in molecular and cell biology, protein biochemistry, and structural biology by overcoming major bottlenecks in these fields. Their core services include

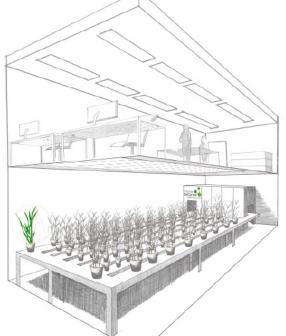
molecular cloning, protein production and purification, and biophysical characterization of proteins. Since 2014, they also offer services surrounding CRISPR/Cas9 genome engineering technology.

#### 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.











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BioOptics.

# FINANCE & ADMINISTRATION



**MARKUS KIESS**Business Director

BORRIES LUBERACKI Head of Lab Support

MARIOLA GLAWISCHNIG Human Resources Officer

J. MATTHEW WATSON
Head of Science Support

MIREIA VERDAGUER Head of Finance

MARTINA GSUR Assistant to the Directors ANNELIESE AUER Senior Plant Facility Technician

BARBARA WEIGEL Assistant to Science Support

BIANCA JELL Accountant

HANSJÖRG STAMPFL Lab Support Specialist

SIMONA WOJCIK Bookkeeper

NORMA SCHÖNHERR Grant Manager

JOHANNA OSTAH\* Grant Manager

**EVA SCHMID** Head of Scientific Training (VBC)

DANIELA MACHEEV Trainee

JENS SCHAICH Lab Support Specialist

<sup>\* (</sup>left the GMI in 2020)

## **GMI SCIENTIFIC ADVISORY BOARD**

Research at the GMI is annually evaluated by experts whose primary role is to provide the Academy of Sciences, with feedback on the staff representatives.

quality of the science being undertaken. The the GMI Scientific Advisory Board (SAB). The SAB meet over a two-day period (typically SAB comprises independent international each November) during which time they conduct in-depth discussions with all Research Institute's management, and the Austrian Groups as well as Postdoc, PhD, and technical

The GMI continues exceptionally high caliber group

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LEIF ANDERSSON Uppsala University, Uppsala, SE



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



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



STEVEN HENIKOFF Fred Hutchinson Cancer Research Center, Seattle



CATHIE MARTIN John Innes Centre. Norwich, UK



SCHUMACHER Cell Biology, Centre for Organismal Studies Heidelberg, DE



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



#### THE AUSTRIAN **ACADEMY OF SCIENCES**

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

The Austrian Academy of Sciences (ÖAW) is Austria's central institution for science and research. Founded in 1847 as a learned society in Vienna, the Academy currently has over 770 members and 1,600 employees; it stands for the transdisciplinary exchange of knowledge, innovative basic research, and progress for society. Its headquarters are in Vienna's city center in the former assembly hall of the University of Vienna, built between 1753 and 1755 by the French architect Jean Nicolas Jadot.

The Austrian Academy of Sciences has two sections, the Section for Mathematics and Natural Sciences, and the Section for the Humanities and Social Sciences. Today, the Academy fulfills two main functions. On the one hand, its 770 members form a scholarly society, advising decision-makers from politics, industry, and society and conveying scientific insights to the public. On the other, it is Austria's major supporter of research outside the university system, funding 27 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.





# VIENNA COVID-19 DETECTION INITIATIVE (VCDI)

The Vienna Covid-19 Detection Initiative (VCDI) is 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 and its stakeholders promote 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 are committed to developing novel, faster and cheaper approaches to detect SARS-CoV-2.

Since April, a PCR testing pipeline is in operation that is currently consolidated and expanded within the Vienna BioCenter Core Facilities

to allow for a capacity of about 6000 tests per day. Testing capacity is provided for humanitarian initiatives of broader public interest.

The initiative freely disseminates its know-how, operating procedures and latest developments. The VCDI is 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).

# 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



GMI■

The VCDI activities are overseen by a su-

BioCenter Core Facilities.

pervisory board and operated by the Vienna

# THE CITY OF VIENNA

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? around the world and they might give these reasons: of any European city.

Vienna is a fantastic city to ITS LOCATION - in the heart of Europe, And public transport, housing, schooling, live in – and that's not just our with easy connections in all directions, whether to go home or on a weekend excursion to another European capital.

elegant splendor of the former Austro-Hungarian capital with a modern infrastructure, Ask GMI employees from lots of nearby countryside for outdoor excursions, and one of the richest cultural offerings other international corporations and organiza-

#### IT'S SAFE, CLEAN, AND PRACTICAL

where in Vienna, even at night, and you feel safe. The air, the streets, everything is clean.

health care and all the other everyday needs work well and are affordable.

**COSMOPOLITAN** - with the United THE LIFESTYLE - Vienna combines the Nations, Organization for Security and Cooperation in Europe, International Centre for Migration Policy Development, European Fundamental Rights Agency, and a number of



