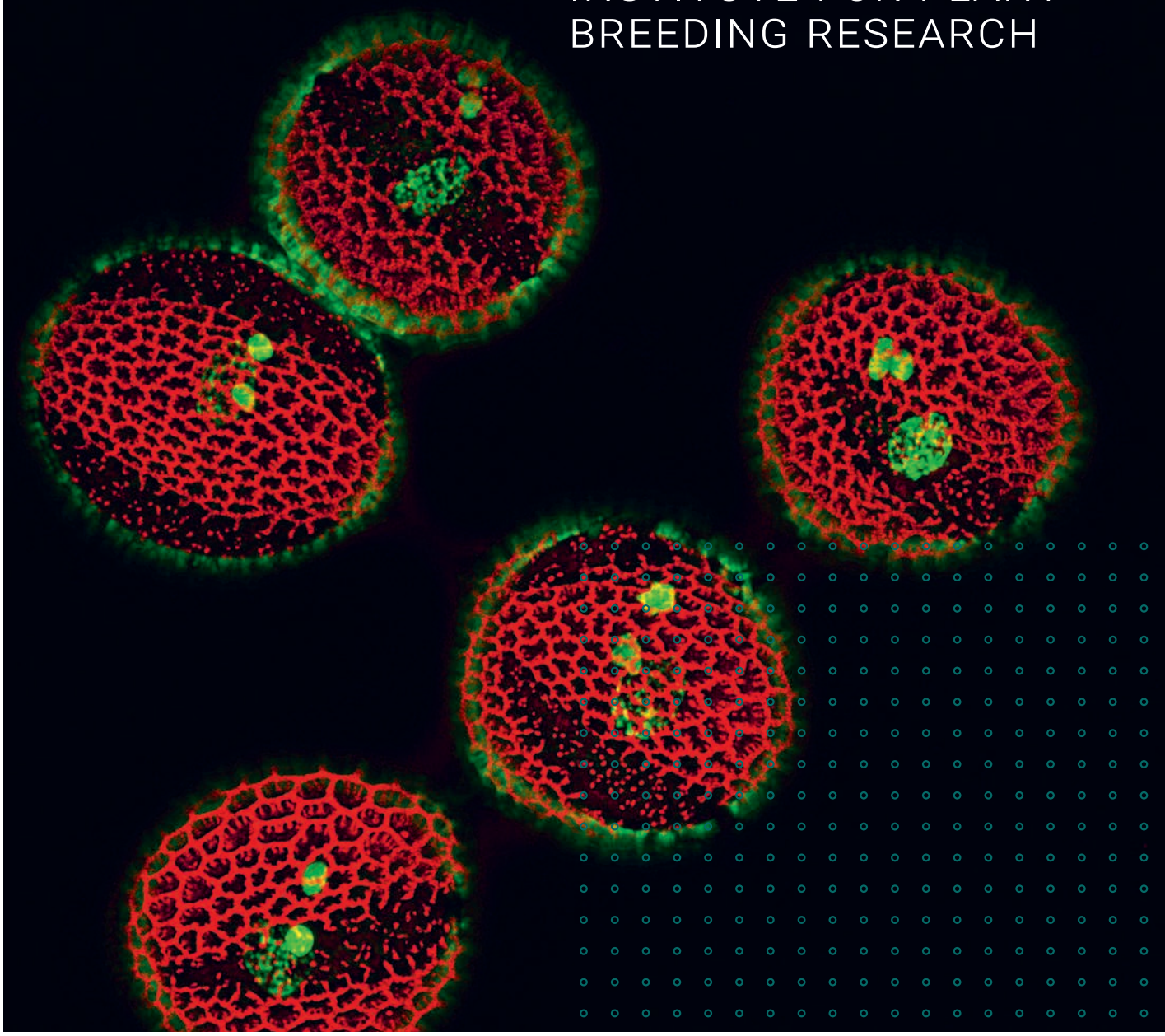
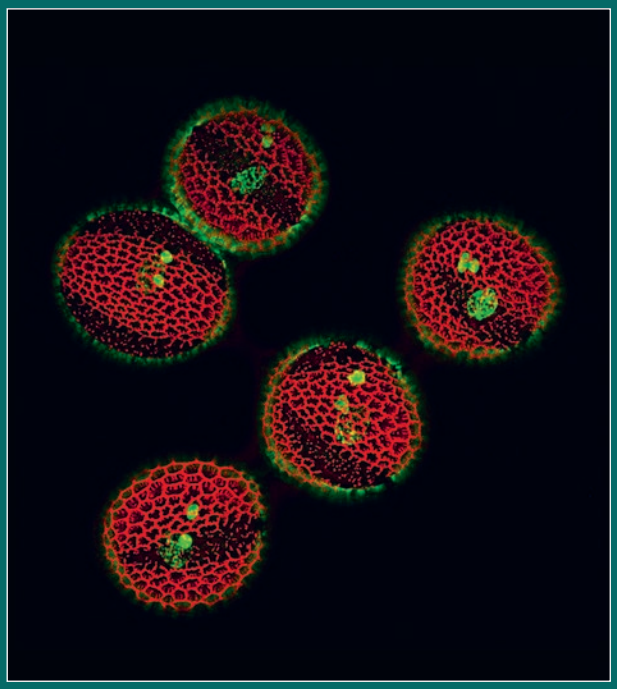
24

SCIENTIFIC OVERVIEW

MAX PLANCK INSTITUTE FOR PLANT BREEDING RESEARCH





Confocal Image of *Brassica nigra* pollen grains

This high-resolution confocal image illustrates the structural components of *B. nigra* pollen, showing five mature grains (~30 µm in diameter). It is taken within the project exploring interspecific diversity in recombination frequency using single-nuclei sequencing of gametes within the Brassicaceae family.

The green fluorescence highlights three nuclei within each pollen grain:

- Two small, condensed and round sperm cells (~2.5 *µ*m each) are responsible for double fertilisation; one fertilises the egg cell to form the diploid zygote (2n), while the other fertilises two polar nuclei to produce the triploid endosperm (3n).
- A larger, irregularly shaped vegetative nucleus (~6 *µ*m), which migrates into the pollen tube to direct its growth.

The red fluorescence marks the exine, the patterned outer layer of the pollen grain, with visible apertures through which the pollen tube germinates.

The pollen grains were stained overnight with Aberrior LIVE 560, a DNA-specific fluorescent dye and imaged using a Leica STELLARIS Confocal Microscope by Samija Amar (Schneeberger Lab, Department of Chromosome Biology) in collaboration with Ton Timmers (Central Microscopy).

SCIENTIFIC OVERVIEW 2024

MAX PLANCK INSTITUTE FOR PLANT BREEDING RESEARCH

MAX PLANCK INSTITUTE
FOR PLANT BREEDING RESEARCH

Welcome to our Institute

We have compiled this overview to provide you with an introduction to the research carried out at the Max Planck Institute for Plant Breeding Research. We summarise the scientific goals and organisation of the institute and outline the projects of the individual research groups. We have tried to present our work in a style that will appeal to a general audience as well as to scientists, and we hope you will find the text both engaging and informative. We encourage a curiosity-driven approach to plant science that stimulates collaboration and yet provides the freedom to shape individual careers.

The report describes the work of 22 research groups. A vast majority of the directors, group leaders, postdoctoral fellows and PhD students, come from abroad, underlining the international character of the Institute. In addition to the departmental groups, the Institute houses independent research groups and service groups that focus on topics not covered by any of the four departments. We attach great importance to the training and supervision of doctoral students. With over 75 members, this group represents a significant proportion of the 400 staff on campus. Many participate in structured programmes such as the International Max Planck Research School (IMPRS), the MPIPZ Graduate School or the Centre of Excellence on Plant Sciences (CEPLAS), a regional research and training initiative run jointly with the Universities of Düsseldorf and Cologne. Our PhD coordinator closely monitors the progress of all students, offers additional courses and advice, and organises retreats and annual student meetings. In addition, more than 50 post-doctoral fellows have found the Institute's state-of-the-art infrastructure and intellectual environment to be a training ground and stepping stone to a research career in academia or the plant science industry.

Members of our Institute play a major role in plant science nationally and internationally, making our campus a premier site for basic plant research in Europe. We have particularly close links with the regional universities of Cologne and Düsseldorf, which participate in our IMPRS and provide the academic framework for our PhD students. We also collaborate with them in four Collaborative Research Centres funded by the German Research Foundation (DFG) and CEPLAS. We are particularly grateful to the Max Planck Society for providing an annual core grant which enables us to carry out many of our scientific activities.

Whatever your background, we hope you will enjoy reading about our science in the following pages.

RAPHAËL MERCIER
Managing Director

Directors at the Institute in Cologne (since 1955)

1936 – 1961	Wilhelm Rudorf
1961 – 1979	Josef Straub
1967 – 1978	Wilhelm Menke
1978 – 2000	Jeff Schell
1980 – 2009	Heinz Saedler
1983 – 2002	Klaus Hahlbrock
1985 – 2004	Francesco Salamini
2000 – present	Paul Schulze-Lefert
2001 – present	George Coupland
2004 – 2016	Maarten Koornneef
2012 – present	Miltos Tsiantis
2018 – present	Raphaël Mercier

Historical Background of the Institute

The Institute was originally founded in 1928 as part of the Kaiser-Willhelm-Gesellschaft, and at that time was located in Müncheberg (Brandenburg). The founding Director, Erwin Baur, initiated breeding programmes with fruits and berries, as well as basic research on Antirrhinum majus and the domestication of lupins. After the Second World War, the Institute moved west to Voldagsen (Niedersachsen), and was relocated to new buildings on the present site in Cologne in 1955. The modern era of the Institute began in 1978 with the appointment of Jeff Schell and the development of plant transformation technologies and plant molecular genetics. The focus on molecular genetics was extended in 1980 with the appointment of Heinz Saedler. The appointment in 1983 of Klaus Hahlbrock broadened the expertise of the Institute in the area of plant biochemistry, and the arrival of Francesco Salamini in 1985 added a focus on crop genetics. From 1978-1990, the Institute was greatly expanded, and new buildings were constructed for the departments led by Schell, Hahlbrock and Salamini, in addition to a new lecture hall and the Max Delbrück Laboratory building that housed independent research groups over a period of 10 years.

After 2000, a new generation of Directors was appointed in view of the approaching retirements of Klaus Hahlbrock and Jeff Schell. Paul Schulze-Lefert and George Coupland were appointed in 2000 and 2001 respectively, and Maarten Koornneef arrived three years later upon the retirement of Francesco Salamini. Miltos Tsiantis began work on establishing a Department of comparative development and genetics in 2013 after the retirement of Heinz Saedler. Raphaël Mercier, the latest arrival, established the Department of Chromosome Biology in 2019 following Maarten Koornneef's retirement. The new scientific departments brought a strong focus on utilising model species in order to understand the regulatory principles and molecular mechanisms underlying plant biology.

The arrival of a new generation of Directors also required modernisation of the infrastructure. So far, this has involved the complete refurbishment of the building that houses the Plant Developmental Biology laboratory (2004), construction of a new guesthouse and library (2005), as well as new buildings for Stores, the Outreach Department and Workshops along with a new entrance gate (completed in spring 2009). The new laboratory building for the Koornneef Department (now the Department of Chromosome Biology) was completed in 2012, as was the communal building that links all four science departments, and which houses meeting rooms, offices and the bioinformatics groups. An extensive new space to accommodate the Genome centre's servers was opened in the spring of 2012, while a partial overhaul of the Department of Comparative Development and Genetics was begun in mid-2013. Modernisation of a glasshouse complex was completed at the end of 2015 and will be extended in the near future. Finally, a new hall hosting growth chambers and phenotyping facilities was open in 2024.

Organisation and Governance of the Institute

The Institute comprises four scientific departments, five independent research groups, three scientific service groups, the greenhouse service group, an outreach department that presents plant science to the public and press, and the administrative department, which includes the technical workshops and library.

The **Board of Directors** is responsible for the management of the Institute. The Board is made up of the Directors of the four scientific departments and the Head of Administration. It meets once a month under the chairmanship of the Managing Director. The Board of Directors takes decisions on matters such as how the budget of the Institute should be allocated, recruitments, promotions and the purchase of major equipment. The Board frequently invites senior scientists and/or service managers to these meetings for consultation on these issues and to provide a broader basis for decision making.

BOARD OF TRUSTEES

INSTITUTE SCIENTIFIC COORDINATOR
Francesca Stomeo

BOARD OF DIRECTORS
Managing Director: Raphaël Mercier

SCIENTIFIC ADVISORY BOARD

HEAD OF ADMINISTRATION
Karsten Schürmann

DEPARTMENT OF PLANT DEVELOPMENTAL BIOLOGY
Director: George Coupland

- **Reproductive Development and the Evolution of Perennial Life History**
  George Coupland
- **Plant Population Genetics and Adaptation Genomics**
  Andrea Fulgione
- **Quantitative Approaches to Multicellular Dynamics in Plant Development**
  Pau Formosa-Jordan
- **Epigenetic Regulation of Plant Development**
  Franziska Turck

DEPARTMENT OF PLANT-MICROBE INTERACTIONS
Director: Paul Schulze-Lefert

- **Integrative Bioinformatics**
  Ruben Garrido-Oter
- **Multitrophic Plant-Microbe Interactions**
  Stéphane Hacquard
- **Resistance Pathway Dynamics in Plant Immunity**
  Jane Parker
- **Innate Immunity and the Plant Microbiota**
  Paul Schulze-Lefert

DEPARTMENT OF CHROMOSOME BIOLOGY
Director: Raphaël Mercier

- **Evolution of Meiosis**
  André Marques
- **Molecular Mechanisms of Meiosis**
  Raphaël Mercier
- **Genomics of Extreme Adaptation in Polyploids**
  Polina Novikova
- **Genome Plasticity and Computational Genetics**
  Korbinian Schneeberger
- **Meiosis in Crops**
  Charles Underwood

DEPARTMENT OF COMPARATIVE DEVELOPMENT AND GENETICS
Director: Miltos Tsiantis

- **Plant Development and Genetics**
  Miltos Tsiantis
- **Mathematics and Mechanics of Plant Morphogenesis**
  Hadrien Oliveri
- **MPG Partner Group**
  Adam Runions, University of Calgary

INDEPENDENT RESEARCH GROUPS

- **Root Communication with the Environment**
  Tonni Grube Andersen
- **Molecular Basis of Adaptive Evolution**
  Angela Hancock
- **Genetic Basis for Phenotypic Evolution**
  Angela Hay
  (affiliated with the Department of Comparative Development and Genetics)
- **Basic Immune System of Plants**
  Hirofumi Nakagami
- **FIND-CIS Group MPIPZ**
  Thomas Hartwig

SCIENTIFIC SERVICE GROUPS

- **Max Planck-Genome-Centre Cologne**
  Bruno Hüttel
- **Central Microscopy (CeMic)**
  Ton Timmers
- **Protein Mass Spectrometry Service**
  Hirofumi Nakagami

TRAINING

- **PhD Office**
  International Max Planck Research School (IMPRS)
  MPIPZ Graduate School
  Monika Schlosser
- **Postdoc Office**
  Postdoc Program
  Francesca Stomeo

ADMINISTRATION

- **Head of Administration**
  Karsten Schürmann
- **Human Resources**
  Stefan Schüller
- **Purchase Department**
  Mike Quadbeck
- **Accounting Department**
  Lars Kruener
- **International Office**
  Melanie Doerk
- **Third Party Office**
  Heike Meier-Nieragden
- **Travel Reimboursement & Seminars**
  Olaf Schüller

GENERAL SERVICES

- **Public Relations & Outreach**
  Mia von Scheven
- **Library / Web Content Management**
  Britta Hoffmann
- **Laboratory and Occupational Health Management**
  Diana Hofmann

TECHNICAL SERVICES

- **IT Services**
  Marc Thoben
- **Greenhouses Management**
  Aristeidis Stamatakis
- **Technical Services & Workshops**
  José Costa Blanco
- **Building Coordinator**
  Dominik Oesterreich

G PLANT DEVELOPMENTAL BIOLOGY
George Coupland

E CHROMOSOME BIOLOGY
Raphaël Mercier

H PLANT-MICROBE INTERACTIONS
Paul Schulze-Lefert

J COMPARATIVE DEVELOPMENT AND GENETICS
Miltos Tsiantis

C PROTEIN MASS SPECTROMETRY SERVICE
Hirofumi Nakagami

B MAX PLANCK-GENOME-CENTRE COLOGNE
Bruno Hüttel

S CEMIC: CENTRAL MICROSCOPY
Ulla Neumann / Ton Timmers

C ADMINISTRATION
PR AND OUTREACH
PHD OFFICE

A MIXED SCIENTIFIC USE

F BUILDING WITH OFFICES

K PURCHASING, MAIL, OFFICE SUPPLIES
TECHNICAL SERVICES

O WORKSHOPS

L ENTRANCE / GATE

N LIBRARY
GUEST ROOMS 1ST FLOOR
IT SERVICES

Each **Director** is also head of a scientific department and is responsible for the scientific programme, budget and personnel of that department. Each department comprises several research groups that are led by research scientists, who in turn are responsible for the scientific programme, personnel and budget of their research groups.

The **service groups** provide support in technical areas that underpin the work of the scientific departments. Each service group is managed by a service facility leader, who is responsible for the services provided and the management of staff within the group. Each service group consults with a Users' Committee comprising a scientist from each scientific department and the head of the service group. Each of these groups is chaired by a Director.

The **Head of Administration** is responsible for managing the administration department, workshops, library and security. The administration department manages issues such as appointment contracts, the budget of the Institute, the building programme, the Institute canteen, Institute housing and maintenance of the Institute grounds.

The Institute **Scientific Coordinator** assists primarily the Managing Director but also all other Directors in directing ongoing scientific matters of the Institute relating to their respective area of responsibility.

The **PhD Coordinator** manages the International Max Planck Research School (IMPRS) and is responsible for the welfare of the students and provides them with advice and support.

The **Postdoc Coordinator** supports MPIPZ postdocs in their professional training and development and provides guidance and resources on all postdoc matters.

The **Faculty of the Institute** comprises the Directors of the Institute, all group leaders from each department, heads of service groups and independent research group leaders. This committee meets monthly to discuss issues raised by its members. Major issues are discussed concerning scientific strategy, purchase of large pieces of equipment, and new recruitments. This committee has proven to be an important conduit for channelling the views of research scientists to the Board of Directors and has helped create a more horizontal management structure within the Institute. The faculty meeting is precedent by a Research meeting to which all scientists are invited.

The **scientific programme** of the Institute is assessed every three years by the Scientific Advisory Board, which reports to the President of the Max Planck Society.

The **Board of Trustees** meets annually and oversees the management of the Institute. The Board also provides important links with local and national organisations within the sphere of activity of the Institute.

Research Objectives and Major Emphases

BACKGROUND AND PRESENT STATUS

A deep understanding of plant biology can be a boost for plant breeding. This conviction, in line with the Max Planck Society's motto "Insight must precede application", is the motivation behind all the Institute's research programs. We carry out basic molecular biology and genetics research on plants with the ultimate aim of developing more efficient breeding techniques and environmentally sound crop management.

The last two decades have tremendously increased our knowledge of the molecular mechanisms underlying plant biology. This progress is largely based on studies on model species, principally *Arabidopsis thaliana*. The work of the Institute aims to test whether a deeper understanding of regulatory mechanisms obtained in model species will allow rational approaches to making desirable changes in selected traits in crop plants. This also requires the study of biological processes in a diversity of plant species, with particular emphasis on understanding the underlying natural variation. Genetic variation is the raw material with which plant breeders work. Greater knowledge of the processes and genes that control trait variation will allow much more efficient breeding, using either marker-assisted selection or the edition of genes in crop plants.

Even in *Arabidopsis,* our understanding of the regulatory mechanisms that control plant traits is limited, and the connections between the proteins they encode are often poorly understood. Therefore, focused programs have been established within the Institute to elucidate the molecular mechanisms controlling traits of agronomic importance. These programs investigate plant-pathogen interactions and the plant microbiota (Schulze-Lefert), flowering time control (Coupland), how biological forms develop and diversify (Tsiantis) and how genetic information is transmitted and modified through generations (Mercier). All of these traits are studied within a genetic framework. In addition to intensive studies based on induced mutations and reverse genetics, natural genetic variation is exploited to provide an understanding of the natural plasticity of complex traits under the influence of quantitative genetic variation. Comparative studies of the function of similar genes in different species and computational modeling help us to understand how genetic variation between species can alter conserved regulatory networks to create new structures or responses to the environment. Model plants are carefully chosen to provide meaningful comparisons with *Arabidopsis,* based on their relatedness (*Arabis alpina* and *Cardamine hirsuta*) or because they display specific genetic complexities or properties (barley, tomato). Furthermore, we have increasingly complemented our genetic approaches with biochemistry and cell biology. These methods both identify proteins that are refractory to genetic approaches and reveal further layers of regulation beyond transcriptional control. We believe that integrated approaches that bridge the boundaries between traditional research disciplines such as genetics, molecular biology, biochemistry, cell biology and computational biology are crucial for developing a multi-scale understanding of selected plant traits.

The Institute has developed an extensive technological infrastructure to help answer such questions. Since 2010, an integrated 'Max Planck Genome Centre' (MP-GC) has been located on our campus which provides state-of-the-art next-generation DNA- and RNA-sequencing services. The MP-GC provides next-generation sequencing services to three core Max Planck Institutes located in Cologne, Bremen and Plön. The MP-GC continuously develops new protocols and integrates the most recent developments in genome/bioinformatics technologies. In addition, the Institute has significantly enhanced its resources in the area of bioinformatics and modeling, by integrating expertise in computational biology and regulatory networks.

Our technology platform in protein mass spectrometry has been greatly improved over the past few years, and in 2016 we appointed Hirofumi Nakagami as the head of research and service group, whose research combines advanced proteomics technologies and evolutionary biology. In recent years, we have significantly invested in confocal, light super-resolution, and electron microscopy to visualize dynamic processes at subcellular resolution and/or in live tissues. These infrastructures are heavily utilised by all four departments and provides attractive training opportunities for students.

FUTURE ORIENTATION

The Institute's mission requires coordinated efforts to balance research in model systems and crop plants. The long-term goal of our research is to transfer the gained knowledge to breeding programs and new methods in plant breeding. We have begun to extend our research activities to a diversity of plants, including *Cardamine hirsute, Arabis alpina, Rhynchospora pubera* as a representative of a species with holocentric chromosomes and the liverwort *Marchantia polymorpha* representing one of the early divergent land-plant lineages. This enables comparative approaches that are driven by evolutionary trait analysis in a phylogenetic framework to reveal mechanisms underlying inter-species trait variation and the origin of evolutionary novelties. Across departments, the Institute focuses its crop-related research on barley and tomato, by exploring how knowledge gained on fundamental traits and trait variation in model plants can be transferred to a crop context. We believe that future trait modeling, based on quantitative interactions of its genetic components, will empower rational, predictive plant breeding. Widening our research to evolutionary trait analysis with phylogenetically related reference plants also opens up opportunities to understand the molecular basis of their ecological adaptations to different natural environments.

Co-operation and Communication within the Institute and with local Universities

INTERACTIONS WITHIN THE INSTITUTE

Numerous collaborative research projects are ongoing, between individual research groups both within and between departments. These research collaborations are vital in order to test new ideas at the interface between seemingly distinct plant processes or to enable the dissection of complex traits using different methods. Both the International Max Planck Research School (IMPRS) and the Cluster of Excellence on Plant Sciences (CEPLAS), a joint regional research and training activity together with the Universities of Düsseldorf and Cologne, provide incentives for joint PhD research projects between research groups that have complementary skills and expertise. The mission of CEPLAS is to contribute new paradigms in order to solve urgent problems in plant performance and production through exploitation of natural variation and biodiversity. A combination of evolutionary analysis and synthetic biology is applied for interdisciplinary research on four major themes: plant performance, by mapping the interface between development and metabolism, plant microbiota metabolic networks and edaphic adaptation, synthetic and reconstruction biology, and data science and data management.

CO-OPERATION WITH DÜSSELDORF AND COLOGNE UNIVERSITIES

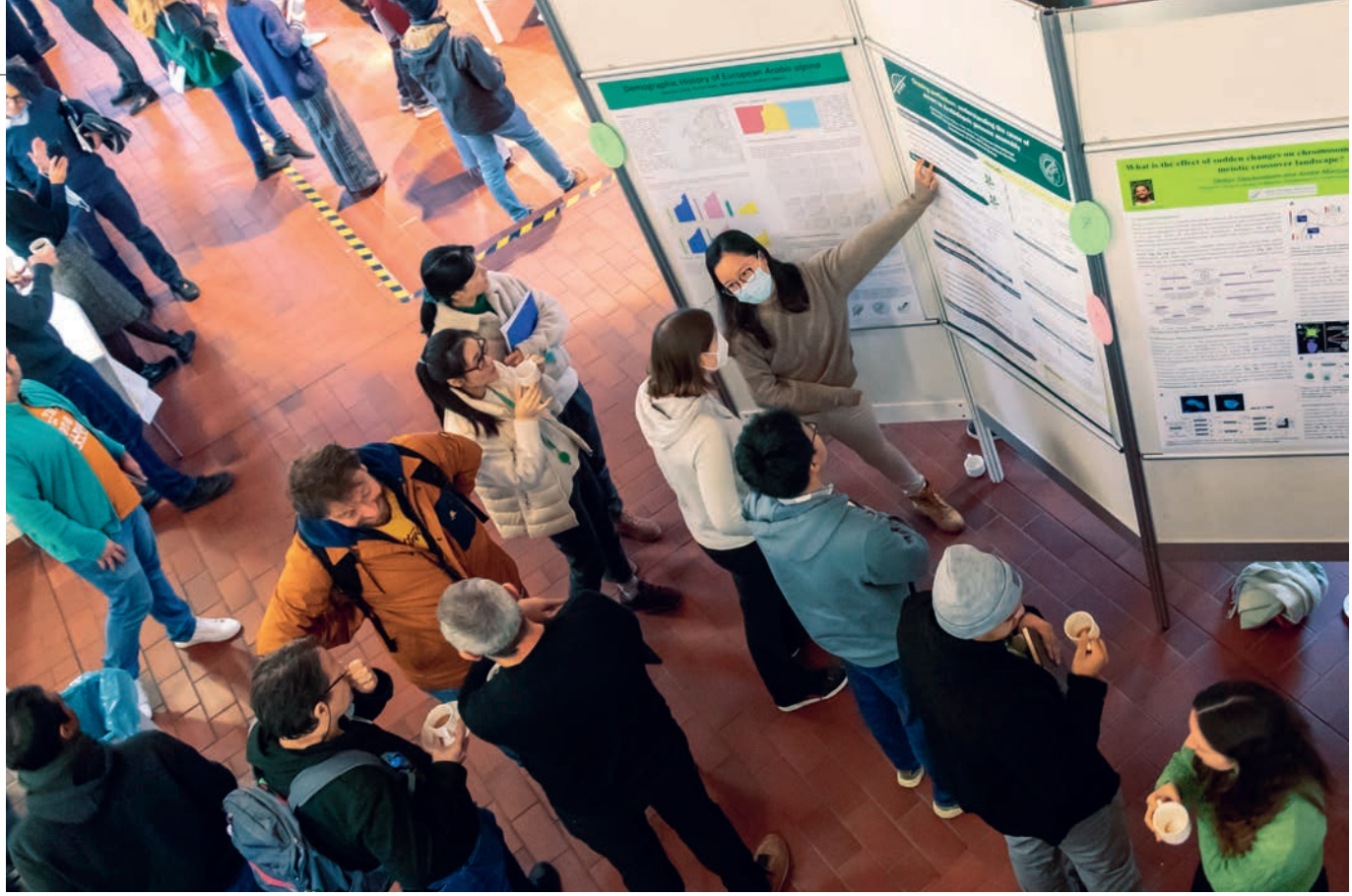
A large proportion of the groups in the Institute participate in collaborative projects funded by the Deutsche Forschungsgemeinschaft (DFG), together with the Universities of Cologne and Düsseldorf: The SFB 1403 on Cell Death in Immunity, Inflammation and Disease in plants and animals began in 2020, SFB1535 Microbial networks - from organelles to cross-kingdom communities, Priority programs DECRyPT (Deconstruction and Reconstruction of the Plant Microbiota) and MAdLand (Molecular Adaptation to Land) and the TRR341, Ecological Genetics of Plants.

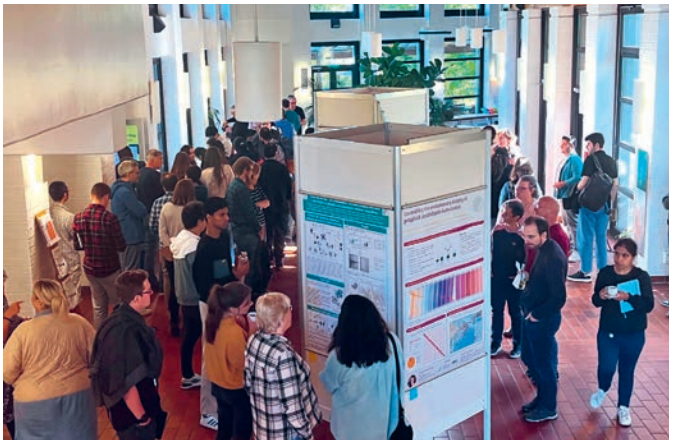
The Cluster of Excellence in Plant Science (CEPLAS) is a major focus of collaboration with the Universities of Cologne and Düsseldorf. It incorporates retreats and monthly science meetings as well as funding professors, post-docs, students and technical assistants at MPIPZ.

The Institute's International Max Planck Research School (IMPRS), a coordinated graduate programme, is run in close collaboration with the regional Universities of Cologne and Düsseldorf. The International Max Planck Research School (IMPRS) includes faculties from both the Institute and the University. It provides a forum for scientific communication and improves contacts and collaborations between plant science groups in both organisations on a daily basis, giving a thorough overview of all plant research activities at the annual IMPRS retreats involving both faculties and students.

PhD PROGRAMME AND EDUCATION

Providing high-quality education for young researchers is of particular concern to the MPIPZ. We support the future of plant science by creating an environment that provides a solid base for best possible education outcomes of young scientists. This includes the opportunity to test new ideas, novel concepts and unconventional approaches, as





well as fostering creativity and scientific curiosity. We promote multilateral collaboration in an increasingly complex scientific network. Here, young scientists from all over the world with diverse scientific backgrounds find a research environment that supports their development as researchers. The Institute's research would be unthinkable without the contribution of our students. Moreover, the international character of the Institute offers valuable insights into intercultural differences that allow the students to reconsider their position in a globalised world and to prepare for the international challenges to come.

The doctoral programmes, especially the IMPRS graduate programme, also promote scientific collaboration among European institutions. Training in modern plant sciences thus contributes to the future of the whole continent.

Our IMPRS helps to curb the loss of scientific talent and counteract the diminishing interest in plant science as a career path. This interdisciplinary approach ensures that the students not only obtain a Ph.D. degree, but also have the opportunity to learn complementary skills that will be recognised as a valuable career qualification. Within the IMPRS, each student receives scientific support from a Ph.D. Thesis Advisory Committee (TAC), as well as general support from fellow students and scientists from neighbouring disciplines. The demands of the modern scientific community are met through complementary training, including training in the communication of science and preparation for an increasingly dynamic and flexible global job market.

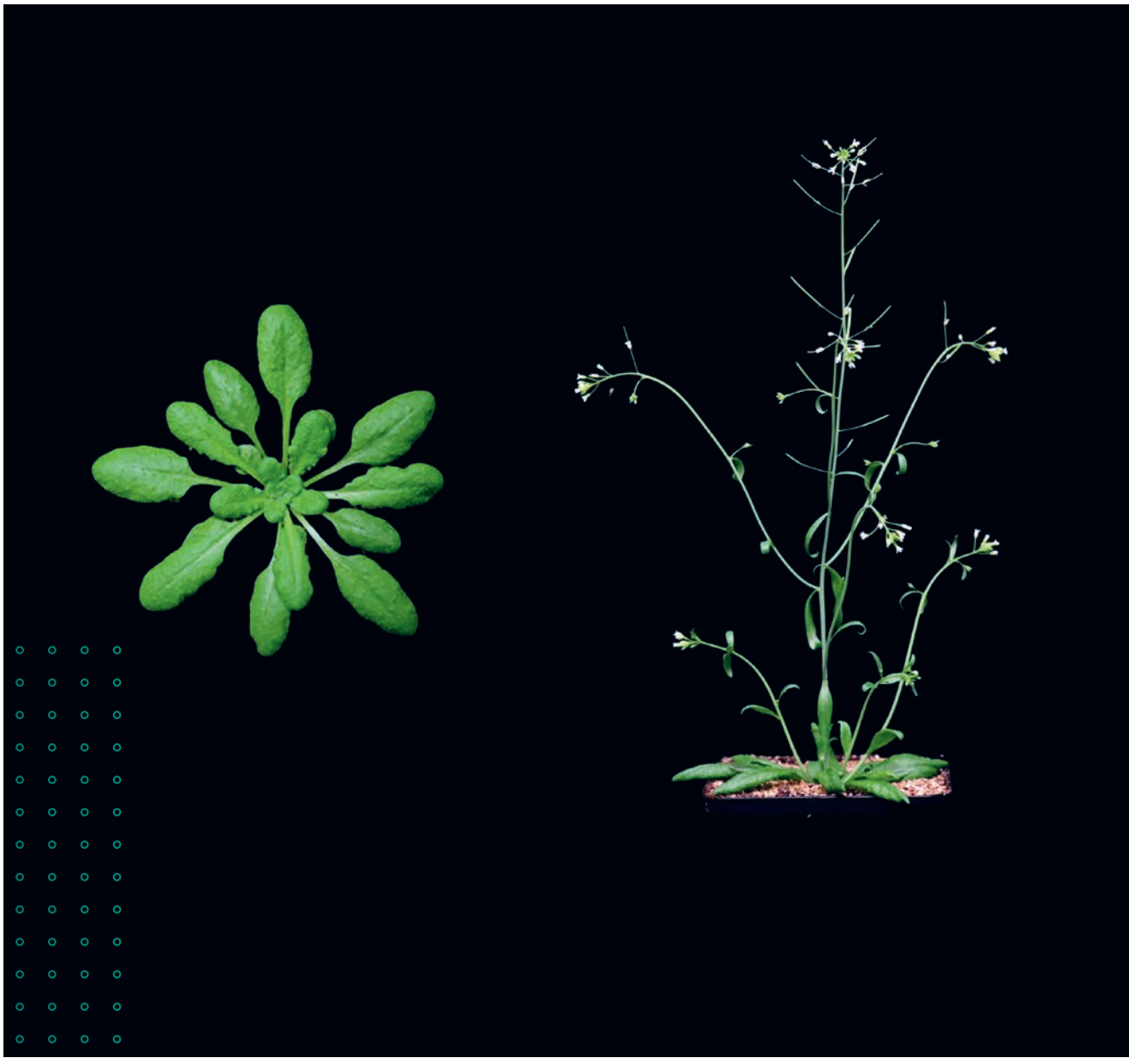
The statistical data for the past several years reveal a continuously high level of interest in joining our research programmes among applicants from all parts of the world. This clearly demonstrates that the Ph.D. education provided at the Max Planck Institute for Plant Breeding Research is internationally recognised and underlines the reputation of the MPIPZ as an attractive institution for a qualified PhD education.

Plant growth and development are highly responsive to environmental cues. This versatility enables plants to succeed in diverse environments. We investigate the genetic, molecular and cellular mechanisms that control the decision to initiate reproductive development and form flowers in response to environmental signals. We also examine how genetic variation alters these processes during evolution to adapt plants to different environments. This genetic variation was important during crop domestication and is exploited by plant breeders to maximize the yield of crops in different environments.

We employ computational, molecular-genetic, biochemical and cell biology-based methods in the crucifer family to study the environmentally controlled switch from vegetative development to flowering. We use computational approaches to study the regulation of this developmental transition, and to apply population genetics methods to study adaptation and evolution of plants across their wide geographical ranges. Our biological interests include the molecular mechanisms by which the growth and identity of meristems change in response to environment during floral transition, comparative analysis of annual and perennial flowering patterns, the assembly and specificity of transcriptional complexes that regulate gene expression in response to environmental signals, and the importance of chromatin structure in controlling epigenetic regulation of flowering-time genes. Our activities generate a collaborative, multi-disciplinary environment in which to study plant reproductive development.

DEPARTMENT OF
PLANT DEVELOPMENTAL BIOLOGY

Director: George Coupland



GEORGE COUPLAND

Two phases of FT transcription separately control the time of flowering and development of floral organs.

Reproductive Development and the Evolution of Perennial Life History

Reproduction is strictly controlled in all organisms. In higher plants, reproduction starts with the decision to form flowers. This transition from vegetative growth to flowering is controlled by environmental cues such as seasonal changes in day length or temperature. The interaction between environment and the floral development programme ensures that plants flower at the appropriate age, on specific branches and at the optimal time of year. These responses optimize fitness in nature and are exploited in agriculture to ensure maximal yield. We study the mechanisms controlling flowering of annual and perennial species. Annual plants live for less than one year, flower profusely and die after flowering. In contrast, perennials live for many years, and flower several times during their lives. We use a combination of genetics, molecular biology, biochemistry and imaging to understand how floral transition is controlled and varies during evolution.

FLORAL TRANSITION IN THE MODEL ANNUAL SPECIES *ARABIDOPSIS THALIANA*

Arabidopsis thaliana is used as a model annual plant to study mechanisms controlling floral transition. It flowers a few days after germination under long summer days, but if exposed to short winter days takes around 6 weeks to flower. We have defined a regulatory pathway that triggers rapid flowering under long days, and a second default pathway responsible for flowering under short days. Differences in day length are perceived in the leaves, whereas floral development occurs at the shoot apical meristem, the growing tip of the plant. On exposure to long days, the *FT* gene is activated in the leaf vasculature and movement of FT protein to the shoot apex first induces increases in size and height of the shoot apical meristem. This morphological change is accompanied by a switch in developmental identity leading to the production

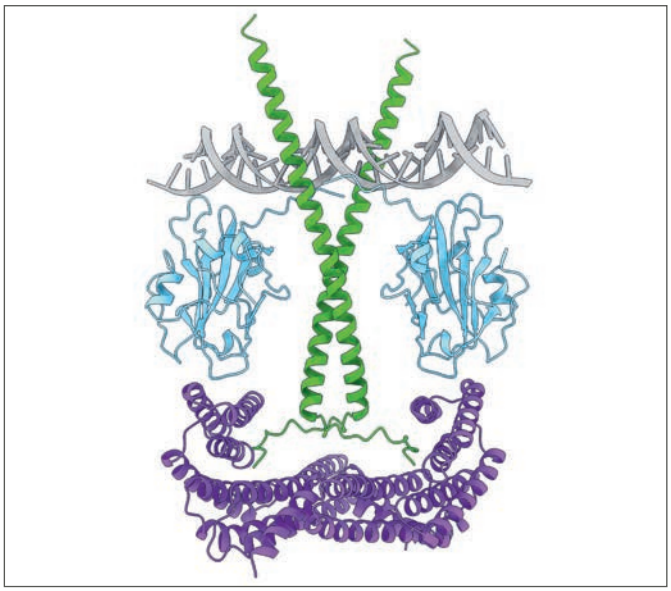


Figure 1: *Model of a transcriptional complex containing the FT protein and a bZIP transcription factor bound to DNA. Blue: FT protein. Green: bZIP transcription factor. Purple: 14-3-3 protein. Grey: DNA.*
Image credit: He Gao

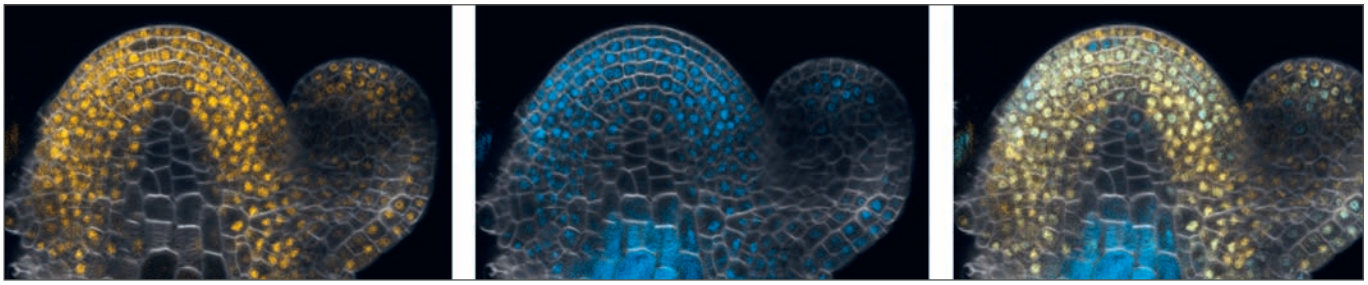


Figure 2: *Two bZIP transcription factors that interact with FT coexpressed in the shoot apical meristem and developing flower. Left: bZIP factor 1 fused to VENUS fluorescent protein. Middle: bZIP factor 2 fused to mCHERRY fluorescent protein. Right: co-detection of both VENUS and mCHERRY. Image provided by Vítor Falavigna. More details in Martignago, Falavigna et al (2023) PloS Genetics 19, e1010766.*

of flowers rather than leaves. Recently, we have studied how the FT protein causes changes in meristem shape and identity. We showed that increases in meristem size and height require the APETALA2 transcription factor that is expressed in the meristem as it increases in size during floral transition. APETALA2 is then repressed through the action of *FT* to prevent excessive growth of the meristem and to allow floral development. Unexpectedly, we found that a second wave of *FT* transcription then occurs in the developing floral primordium, and that this is required for development of the appropriate number of floral organs and properly timed induction of carpel development. Currently, we are studying the biochemical action of FT protein, and how it facilitates assembly of transcriptional complexes on the promoters of flowering genes. These complexes include different members of the bZIP family of transcription factors that are expressed in spatially distinct domains of the shoot meristem and floral primordium. Several of these factors affect shoot meristem size and identity, as shown for FT, but also influence stem growth. Under short days, *FT* is not expressed in leaves, but is still activated in floral primordia, and we are exploring the connections between the default flowering pathway that triggers floral transition under short days and the role of *FT* in floral development.

COMPARATIVE ANALYSIS OF PERENNIAL *ARABIS ALPINA*

We developed *A. alpina,* a close relative of *A. thaliana,* as a model system to study perennialism. *A. alpina* shows classical features of perennials. For example, in contrast to annuals, it restricts the duration and extent of flowering allowing it to survive and flower over several years. We are using CRISPR-Cas9 based reverse genetics and genetic variation among accessions of *A. alpina* collected in different environments to explore the mechanisms underlying perennial flowering behaviour. Inactivation of the *FT* genes of this species abolishes floral development, indicating that *FT* has a more critical role in inflorescence development of *A. alpina* after floral transition than is evident in *A. thaliana.* Moreover, in many accessions of *A. alpina* the switch to flowering is controlled by whether floral buds mature and form floral organs, not whether floral buds are formed by the shoot apical meristem, as described for *A. thaliana.* We are studying the mechanisms by which winter cold triggers development of *A. alpina* floral buds, and its significance for adaptation of perennials to extreme environments.

SELECTED PUBLICATIONS

Bertran Garcia de Olalla E., Cerise M., Rodríguez-Maroto G., Casanova-Ferrer P., Vayssières A., Severing E., López Sampere Y., Wang K., Schäfer S., Formosa-Jordan P., and Coupland G. ***Coordination of shoot apical meristem shape and identity by APETALA2 during floral transition in Arabidopsis.*** *Nature Communications 10.1038/s41467-024-51341-6. (2024)*

Gao H., Song W., Severing E., Vayssières A., Huettel B., Franzen R., Richter R., Chai J. and Coupland G. ***PIF4 enhances DNA binding by CDF2 to co-regulate target gene expression and promote Arabidopsis hypocotyl cell elongation.*** *Nature Plants 8, 1082-1093. (2022)*

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PAU FORMOSA-JORDAN

We combine quantitative imaging and modelling to understand how plant tissues and organs develop.

Quantitative Approaches to Multicellular Dynamics in Plant Development

Throughout plant development, cells grow, divide, and differentiate to form tissues and organs that perform specific functions. This process results from the interplay of cell signalling (mediated by gene regulatory networks and hormone transport) and mechanical cues, in response to the integration of environmental signals (e.g., temperature and light). However, we still have a limited quantitative understanding of the complex multicellular dynamics that occur in developing plant tissues, as well as how these dynamics lead to reproducible developmental outcomes.

In our group at the MPIPZ, we study the multicellular dynamics of plant developmental processes by combining confocal microscopy imaging of developing plant tissues, quantitative image analysis, and mathematical modelling.

DYNAMICS OF CELLULAR PATTERNING

In developing tissues, cells that are initially indistinguishable from one another differentiate and form tissues containing different cell types. The arrangement of these different cell types is referred to as a cellular pattern. We study how complex cellular patterns are formed in different plant tissues as a result of the interplay between cell signalling, cell growth, and cell division, with a particular focus on the sepal and leaf epidermis of the plant *Arabidopsis thaliana*. The leaf and sepal epidermises contain cellular patterns of different cell types (Figure 1): stomatal guard cells (for gas exchange) and giant cells (large cells that have been related to organ curvature control and plant immunity) are scattered throughout the epidermis and are interspersed among undulated pavement cells. Using a combination of experimentation, quantitative image analysis, and computational and mathematical modelling, in collaboration with the Roeder lab (Cornell University), we have quantitatively studied the spatial pattern of giant cells in sepals and leaves. We showed that in both organs, giant cells are more clustered than expected by chance. Moreover, our analyses suggest that giant cell specification occurs randomly throughout the epidermis and that cell divisions lead to giant cell clustering.

In the longer term, we want to understand how different cellular patterns that include giant cells, guard cells, and pavement cells arise and are maintained in plant tissues.

MULTICELLULAR DYNAMICS OF THE FLORAL TRANSITION

Plants undergo fundamental developmental transitions such as seed germination or the initiation of flowering, known as the floral transition. These processes can be understood as multicellular dynamical systems that undergo important dynamic changes due to their exposure to environmental cues. However, little is known about the dynamics of the key regulators of these complex developmental processes at the single-cell and multicellular levels.

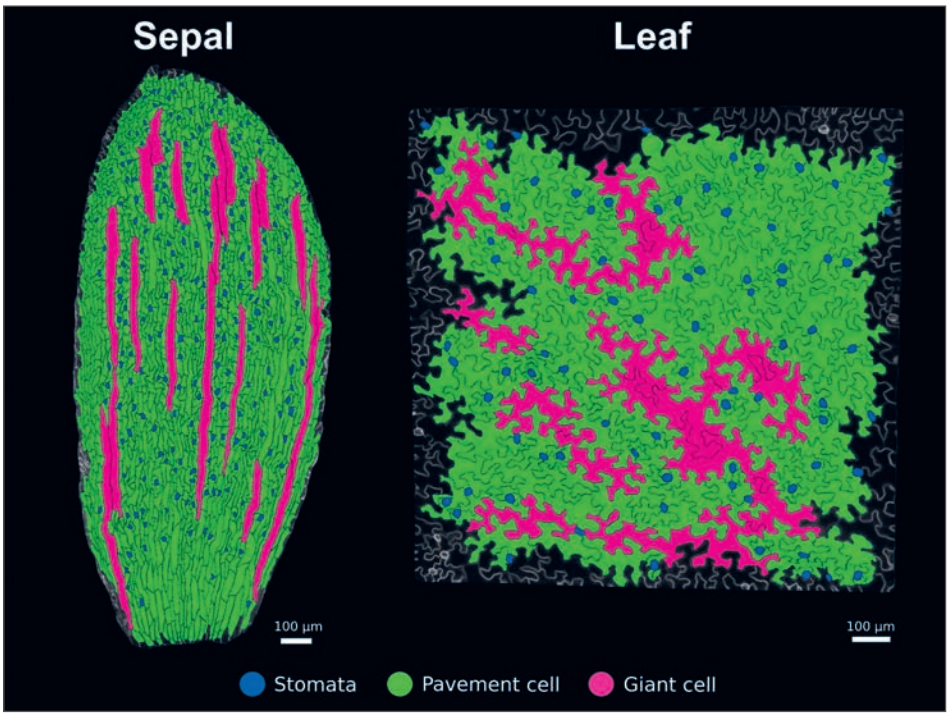

Figure 1: *Epidermal patterning of different cell types shown by microscopy images of the abaxial side of a mature leaf and sepal of Arabidopsis thaliana. Cells are coloured according to an automatic computational classification analysis pipeline on the basis of cellular morphological features.*
Image credit: F. Clark and G. Weissbart.

During the floral transition in *A. thaliana,* the shoot apical meristem (SAM), which is the tissue that produces the plant aerial organs, undergoes a dramatic morphological change from a flat to a domed structure (Figure 2). In collaboration with the Coupland group at the MPIPZ, we are investigating how the SAM undergoes this morphological change and how this morphological change is influenced by spatio-temporal patterns of gene expression within the SAM. Our studies combine quantitative information at the single-cell level with morphological measures of the SAM. Furthermore, using our microscopy data, we are developing the theoretical basis to understand the dynamics of the gene regulatory network underlying the floral transition.

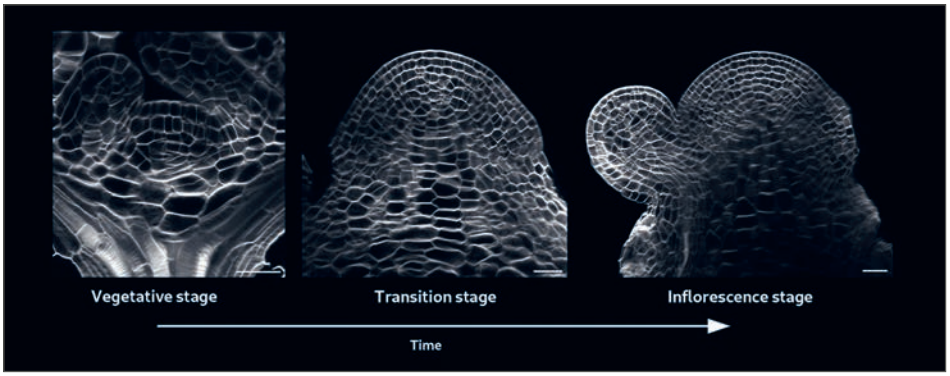

Figure 2: *Confocal microscopy images of the shoot apical meristem from Arabidopsis thaliana before, during, and after floral transition.*
Image credit: G. Rodríguez-Maroto and K. Wang

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** equal contributors*
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ANDREA FULGIONE

We aim to unravel the complex feedback between developmental, ecological, and evolutionary processes in shaping genomic variation in natural plant populations

Plant Population Genetics and Adaptation Genomics

In natural plant populations, plants often differ in their genomic DNA sequence. Some of these differences are neutral, that is, do not have an effect on plant performance in the natural environment (fitness). Other variants influence phenotypic traits, and can have a negative or a positive effect on survival or fecundity, and therefore evolve under the effect of natural selection. In the group, we study how genomic variation in plants originates and evolves through time and space, as a result of mutation, recombination, genetic drift, migration and selection. In turn, the configuration of variants across the genome retains information on the past history of populations and species. This information ranges from the place of origin of a species, the degree and timing of isolation across populations, population size expansions and contractions, admixture, and adaptation to ecological and environmental conditions. We analyze large-scale genomic data to retrieve this information and reconstruct past events in the biogeographic and evolutionary history of plants (see for example, Durvasula et al. 2017, Fulgione et al. 2018, Fulgione et al. 2022). Understanding the history of past adaptation in plants can help us build a framework to predict future responses to climate change, and to understand the stability of natural and agro-ecosystems.

RESEARCH AIMS

Research in the group focuses on population genetics, genomics and evolutionary biology of plants, with the main aim of understanding adaptation to the biotic and abiotic environment. We use methods in computational biology, bioinformatics and modeling applied to large-scale genomics data, in combination with the study of molecular function, plant phenotype and fitness in controlled experiments and in natural conditions.

Research in the group currently focuses on the perennial, Arctic-alpine species *Arabis alpina* (Figure 1), which has several advantages complementary to *Arabidopsis thaliana* and other model plants and crops (Wötzel et al. 2021). First, the perennial life-history and its developmental and evolutionary consequences have not been studied as systematically as in annuals. In the group we are exploring the consequences of life-history strategies on the evolution of plant genomes. Further, *A. alpina* is found in Arctic-alpine environments across a wide geographic range, which represents a deep history of colonisations across the continents, and provides the potential for local adaptation. The Arctic-alpine environment is extremely harsh, with prolonged frost, drought, high UV irradiation and a short growing season, likely resulting in strong

Figure 1: *Our model species for adaptation genomics, the perennial, Arctic-alpine plant Arabis alpina, growing in its natural environment. The top left and right panels show plants from outcrossing populations in the Apennine Mountains, Central Italy, the bottom left panel shows plants from self-compatible populations in the Kjølen Mountains, Central Norway.*
Image credit: Andrea Fulgione

selective pressures. *A. alpina* is therefore a powerful model to study biogeographic dynamics and genomics of adaptation to natural, harsh environments. *A. alpina* also shows unusual variation in mating system, with outcrossing, mixed mating, and selfing populations across the range. These populations also vary in selfing syndrome traits, a set of reproductive traits associated with mating system variation in plants (e.g. flower size, pollen count, and floral scent). In the group we use population genomics to study the evolution of variable mating systems, of mixed mating strategies, and of selfing-syndrome traits. Finally, *A. alpina* accessions show phenotypic variation at ecologically relevant traits related, for instance, to the perennial life-history, to the variation in mating system, and to adaptation to the harsh Arctic-alpine environment.

We are building a large panel of natural genomic and phenotypic variation in *A. alpina,* which will support projects focused on local evolutionary scenarios, on populations with potentially adaptive phenotypic peculiarities, as well as projects with a species-wide focus. Currently ongoing projects are: 1) Reconstructing the demographic and biogeographic histories of *A. alpina,* 2) Ecological adaptation of flowering phenology in perennial plants, 3) Population genomics of variable and mixed mating system, and 4) Adaptation of perennial *A. alpina* along a latitudinal gradient in Scandinavia.

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FRANZISKA TURCK

Telomere Repeat Binding Factors promote the vegetative growth phase in plants, but how, why and when have they have integrated into two regulatory complexes with opposing functions to do their job?

Epigenetic Regulation of Plant Development

Gene repression by Polycomb group (PcG) proteins is achieved by local packaging of nuclear DNA into an inaccessible chromatin structure. PcG-mediated repression can epigenetically switch target genes between expressed and non-expressed states that are maintained across cell divisions, independently of environmental or developmental signals. Examples of epigenetically controlled genes in plants are the flowering repressor *FLOWERING LOCUS C,* which is permanently silenced in winter, and a group of seed maturation genes that are silenced during seedling establishment. By contrast, genes that promote floral organ identity are epigenetically repressed until the shoot apical meristem enters the reproductive state.

In plants, PcG components locate their target genes through interactions with sequence-specific DNA-binding proteins. Our group focuses on a family of DNA-binding proteins called TELOMERE REPEAT BINDING FACTORS (TRBs), which are responsible for maintaining PcG-mediated repression of floral organ identity genes during vegetative growth. The DNA motifs bound by TRBs are similar or identical to those found in several thousand copies at telomeres, and TRBs contribute to telomere maintenance. Moreover, TRBs are also part of plant-specific PEAT complexes, which are primarily involved in gene activation. PEAT complexes recruit histone acetyl transferases, which create a less condensed chromatin structure that favours transcription.

TRB-MEDIATED EPIGENETIC GENE REPRESSION IS IMPORTANT DURING VEGETATIVE GROWTH

As part of the PEAT complex, TRBs are involved in the activation of genes that promote vegetative growth, including genes that encode ribosomes, while suppressing the formation of reproductive organs by inhibiting floral organ identity genes together with PcG components. Plants lacking functional *TRB* genes show a so-called embryonic flowering phenotype and bypass normal vegetative development (Figure 1). A similar phenotype is observed in mutants that exhibit severe

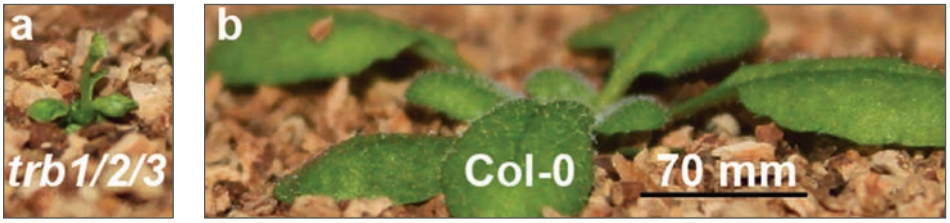

Figure 1: *Comparison of triple TRB mutant plants and wild-type control plants grown side-by-side in culture conditions that delay flowering (cold ambient temperature, short light period during the day). The triple trb mutant (a) already forms a terminal flower while the wild-type control (b) will form around 40 additional vegetative leaves before the first flower emerges.*
Image credit: Franziska Turck

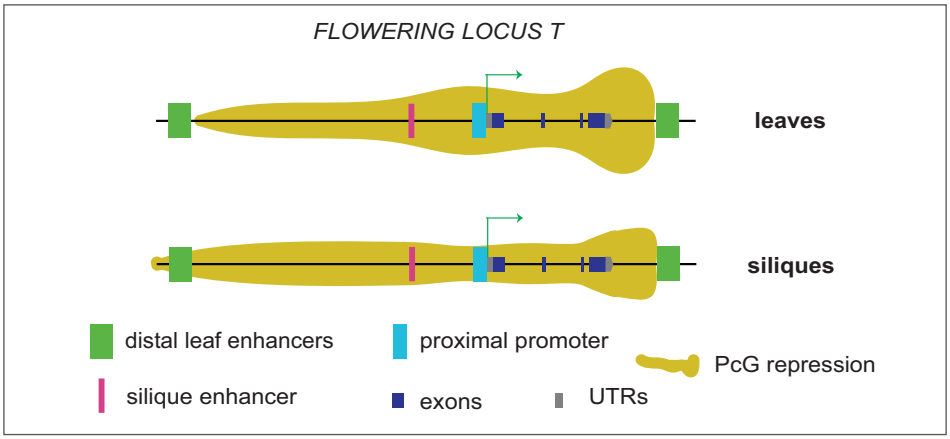

Figure 2: *Depiction of the FLOWERING LOCUS T locus in Arabidopsis thaliana. Expression of FLOWERING LOCUS T in leaves requires the presence of two distal enhancers that are outside of the region targeted by PcG-mediated repression. In siliques, expression uses a different gene regulatory network that acts through a silique-specific enhancer. The PcG-mediated repression is less prominent at FT and the promoter in a more accessible state. Image credit: Franziska Turck*

defects in the PcG signaling pathway, suggesting that the embryonic flowering phenotype is caused by the lack of epigenetic gene repression. By contrast, mutants affected in only two out of three *TRB* genes show only very subtle phenotypic changes. These mutants are only early flowering under certain environmental conditions, and it is not yet clear whether defective epigenetic repression or PEAT function causes the phenotype. To answer this question, we are currently aiming to identify TRB target genes whose deregulation is mainly responsible for the early flowering of plants with different mutant combinations and under different growth conditions.

THE NEXT CHALLENGE: UNDERSTANDING MULTIFUNCTIONALITY

The biological function of TRBs is to promote vegetative growth, but their molecular function is undefined because they participate in protein complexes with opposing functions. The TRB-mediated coordination of chromatin complexes with opposing functions might serve to maintain target genes in an intermediate state, thereby allowing regulatory responses to external cues. We are interested to learn how and when during plant evolution TRBs acquired their roles in different protein complexes. These PEAT- and PcG-complexes might affect many common target genes or specialized subsets. The TRB dosage might be one factor in the regulation, with lower and higher TRB levels promoting and inhibiting floral development, respectively. In such a scenario, telomeres might act as a buffer by binding a large proportion of the cellular pool of TRBs.

EPIGENETIC SWITCH OF THE REGULATORY NETWORK OF THE FLOWERING LOCUS T GENE

FLOWERING LOCUS T (FT) encodes florigen, a mobile signal (or hormone) that is expressed in the leaves when plants are exposed to long days. *FT* moves as protein to the shoot apical meristem to induce flowering. *FT* expression is regulated by the PcG pathway; however, the gene can be switched on and off in immediate response to the photoperiod signal. In the past, we have identified two distal enhancer regions that are necessary to induce *FT* in response to long days. These regions also require a proximal promoter with binding sites for the CONSTANS activator complex, which is only stable when leaves are exposed to long days. After flowering, *FT* has a second function in developing fruits, where strong, photoperiod-independent expression provides developmental feedback to stabilize flower production. A different gene regulatory network that does not require distal enhancers or the CONSTANS activator complex controls *FT* expression in developing fruits. We have mapped the *FT* enhancer regions that are required in developing fruits and have indications that the enhancer switch is associated with differences in the chromatin structure at the *FT* promoter.

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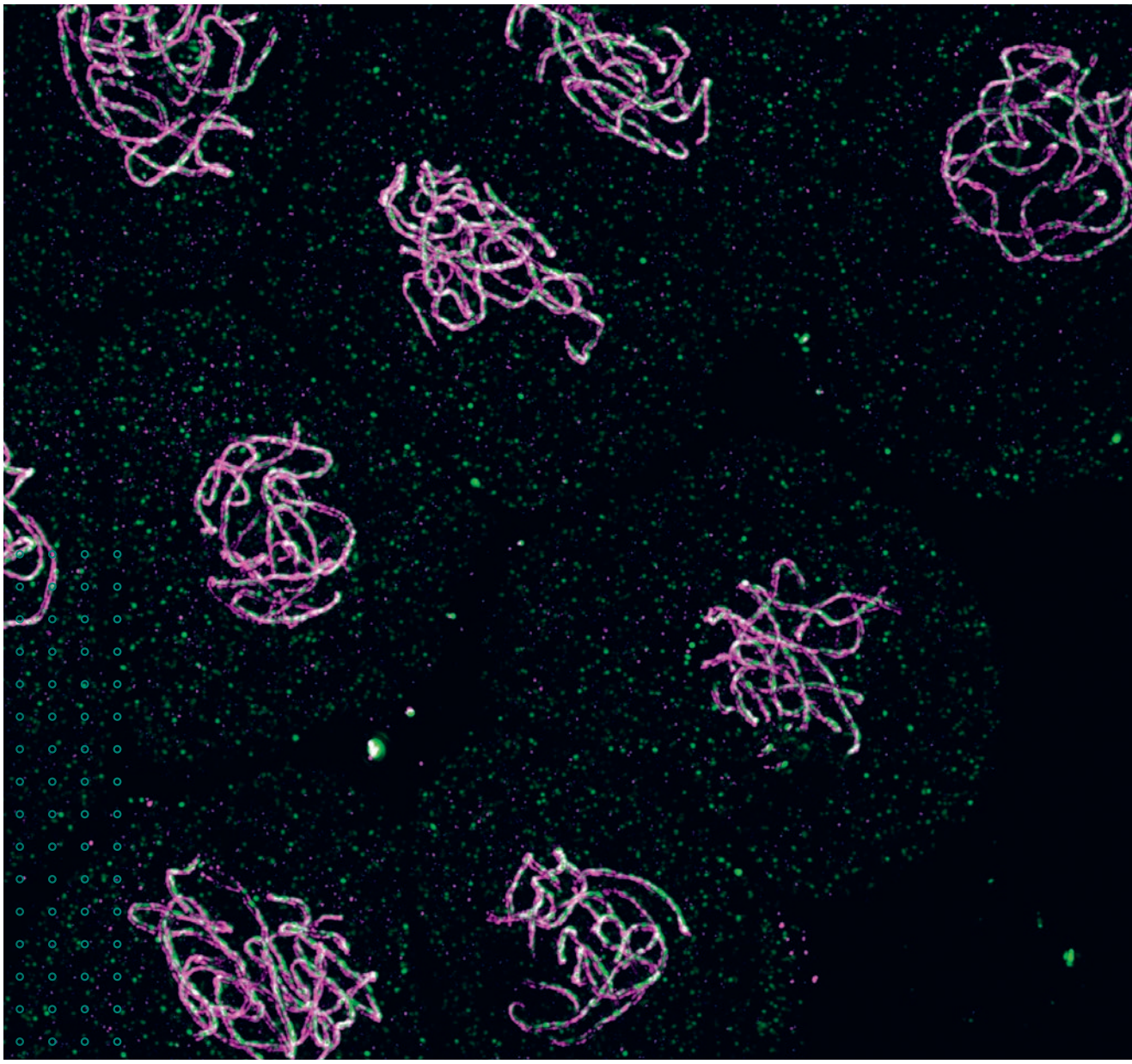
The ability to reproduce and transmit genetic information is one of the few key characteristics that define life. Both natural selection and breeding can optimize the gene pool to adapt to the environment or to confer useful traits for agriculture. The Department of Chromosome Biology at the MPIPZ aims to understand how genetic information is transmitted and modified over generations.

The engine of heredity is meiosis, a special form of cell division that produces sexual cells during which genetic information is recombined, creating genetic diversity in the progeny. A major focus of the Department of Chromosome Biology is meiosis and meiotic recombination. However, we also explore other key sources of genomic variation such as mutations, genome rearrangements, and polyploidisation. We develop multiple-scale approaches – from molecules and cells to populations – and use cutting-edge technologies in microscopy, cell biology, genetics, and genomics to address questions such as: How is meiotic recombination regulated regarding the number and localization of genetic exchanges along chromosomes? How are chromosomes faithfully transmitted to gametes? How does meiosis evolve in response to changes in chromosome structure or whole genome duplication? Conversely, how do meiosis and genome reorganization shape adaptation? Finally, we explore the possibility opened by a better understanding of meiosis and heredity to develop transformative innovations for plant breeding.

DEPARTMENT OF CHROMOSOME BIOLOGY

Director: Raphaël Mercier



ANDRÉ MARQUES

Life's diversity extends beyond species and phenotypes, appearing at every level of biological organisation.
It's fascinating to explore the many ways life manifests.

Evolution of Meiosis

Based on centromere organisation, chromosomes are essentially classified into two main types, **monocentric chromosomes** – one centromere domain per chromosome – and **holocentric chromosomes** – multiple centromere domains distributed genome-wide (Figure 1). This kind of chromosomal organisation evolved several times independently in animals and plants, with specific adaptations along with it. Most of what we know about adaptations to deal with holocentric chromosomes is derived from the animal model *Caenorhabditis elegans*. A holocentric plant model is, thus, necessary because, as this kind of chromosomal organisation evolved independently in different lineages, all the adaptations do deal with it are also expected to be different. In my team, we aim to understand the impact of this unique chromosome structure on the genome evolution and meiotic adaptations of holocentric plants from the genus **Rhynchospora** (beaksedges) (Figure 2).

GENOME ORGANISATION AND EVOLUTION OF HOLOCENTRIC PLANTS

With the recent advances in long-read sequencing technologies, high-quality genome assemblies of non-model species have become feasible. We have sequenced the genomes of the breaksedge *Rhynchospora pubera* (2n = 10) and related *Rhynchospora* species to establish holocentric plant models with diverse genome features (Hofstatter et al. 2022). Analysis of genomes from additional holocentric plants allows us to further understand how holocentricity evolved in land plants and influences genome architecture and karyotype evolution (Hofstatter et al. 2022; Mata-Sucre et al. 2024). Some of the specific questions we are interested in are, how does chromosome structure influence genome evolution in this highly diverse group? Does meiotic recombination occur in or around centromeric regions?

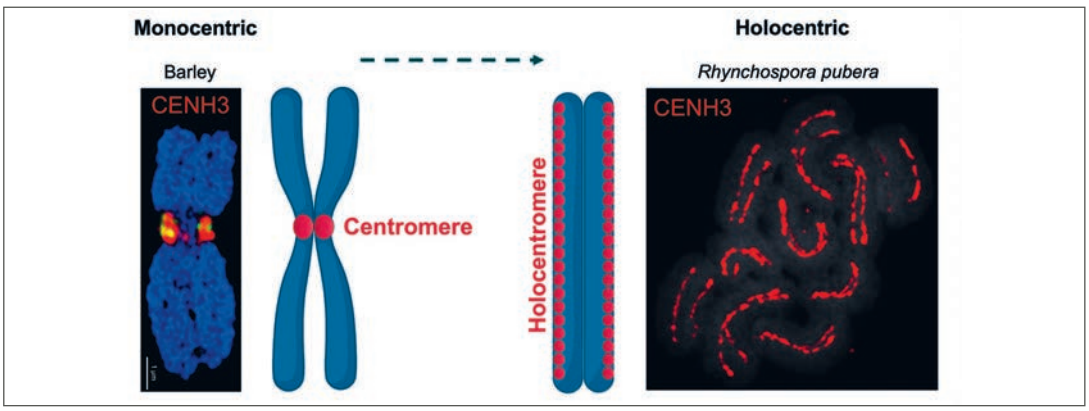


Figure 1: *Centromere organisation differences between monocentric and holocentric chromosomes. Monocentric chromosome CENH3 staining modified from Schubert et al. 2020.*

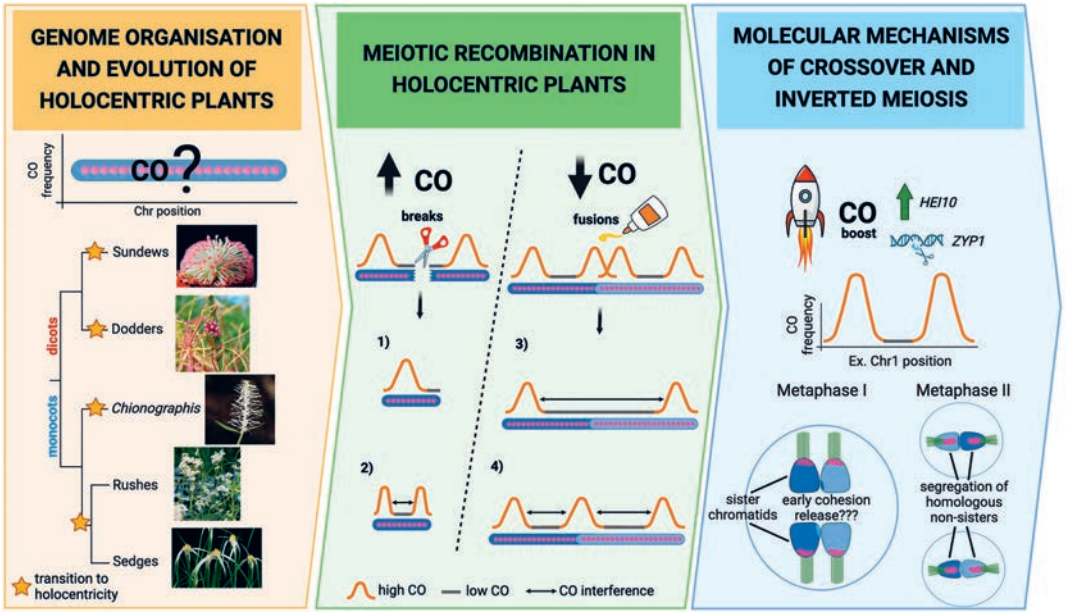


Figure 2: *Overview of the main research activities in the Evolution of Meiosis group. Image created with Biorender.*

MEIOTIC RECOMBINATION IN HOLOCENTRIC PLANTS

Monocentric organisms show restricted meiotic or even non-meiotic recombination at and near centromeres (cold regions), but the reasons for this remain unclear. We therefore aim to better understand how meiotic recombination is regulated in plants with holocentric chromosomes. Using cutting-edge technologies, we are performing analyses to characterise meiotic recombination rates and identify the meiotic proteins involved in the evolution of meiotic adaptations in these organisms (Castellani et al. 2024). Using holocentric plants as a model to understand how meiotic recombination is regulated at centromeric regions should unveil new strategies to interfere with recombination in monocentric organisms. Furthermore, we want to address how the rapid karyotype evolution within holocentric plants influences crossover patterning and frequency.

MOLECULAR ADAPTATIONS OF INVERTED MEIOSIS

Holocentric plants engage in an unusual mode of meiotic division called inverted meiosis, characterised by the early segregation of sister chromatids at the end of the first meiotic division. In the genus Rhynchospora, both chiasmatic *(Rhynchospora pubera)* and achiasmatic *(Rhynchospora tenuis)* inverted meiosis are observed (Hofstatter et al. 2021). Genes related to cohesion, condensation, and chiasmata may play important roles in the structural changes associated with inverted meiosis, and special focus will be placed on studying the role of these genes. Therefore, we are establishing functional studies in Rhynchospora, using different species as models for plant transformation. The first CRISPR/Cas9 knockout experiments targeting meiotic recombination- and cohesion-related genes are currently ongoing.

FUTURE PERSPECTIVES

I am deeply interested in the structure and function of plant chromosomes. My research focuses on exploring chromosomal organisation and centromere architecture, and their impact on plant development and evolution. Using advanced molecular biology and genomics techniques, I aim to uncover fundamental aspects of plant biology, with potential applications in biotechnology. My work includes studying centromeres, chromatin, and epigenetic modifications, as well as applying CRISPR/Cas9 for chromosome engineering.

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Hofstatter P. G., Thangavel, G., Lux, T., et al. ***Repeat-based holocentromeres influence genome architecture and karyotype evolution.*** *Cell 185: 3153–3168 (2022)*

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RAPHAËL MERCIER

Meiosis makes each eukaryote – including you and the plants you eat – genetically unique.

Molecular Mechanisms of Meiosis

Meiosis has two key functions in the life cycle of eukaryotes:

- it halves the number of chromosomes in the gametes
- it creates new combinations of alleles on which natural or artificial selection can act

Increasing our knowledge on meiosis has important implications in medicine. This is because meiotic errors are astonishingly frequent in humans, being the major cause of trisomy and pregnancy loss. Deciphering the how and why of meiotic recombination is also crucial in understanding eukaryotes' evolution. Finally, gaining control over the process of meiosis and recombination is important for plant breeders.

Four unique features define meiosis:

- chromosome pairing
- crossovers that generate genetic exchanges
- modified kinetochore orientation to segregate homologous chromosomes
- altered cell cycle machinery allowing two successive divisions

Our group aims to elucidate the mechanisms of meiosis using *Arabidopsis* as the main model system and combining the power of genetic screening, molecular genetics, genomics, and advanced microscopy.

MECHANISMS AND REGULATION OF MEIOTIC RECOMBINATION

Crossovers enhance genetic diversity and are essential for proper chromosome distribution in most eukaryotes. The number and distribution of crossovers along the chromosomes are tightly regulated. There is at least one crossover per chromosome, rarely more than three, some very hot genome spots, and other regions (e.g. peri-centromeric regions) completely lacking crossovers. Furthermore, crossovers tend to away from each other along chromosomes, a phenomenon described and named "interference" more than a century ago and whose mechanism is elusive.

We use diverse genetic screens to identify the factors involved in crossover formation and decipher their function with a combination of advanced microscopy, genomics, genetics, and structural analysis. We have identified and characterized both pro- and anti-crossover factors and aim to get a global understanding of the multiple levels of regulation that determine the frequency and distribution of crossovers along chromosomes, including the mysterious interference.

DIVERSITY OF MEIOTIC RECOMBINATION

Beyond the analysis of recombination mechanisms in a few laboratory strains, we aim to explore the extent of the diversity of crossover frequencies in

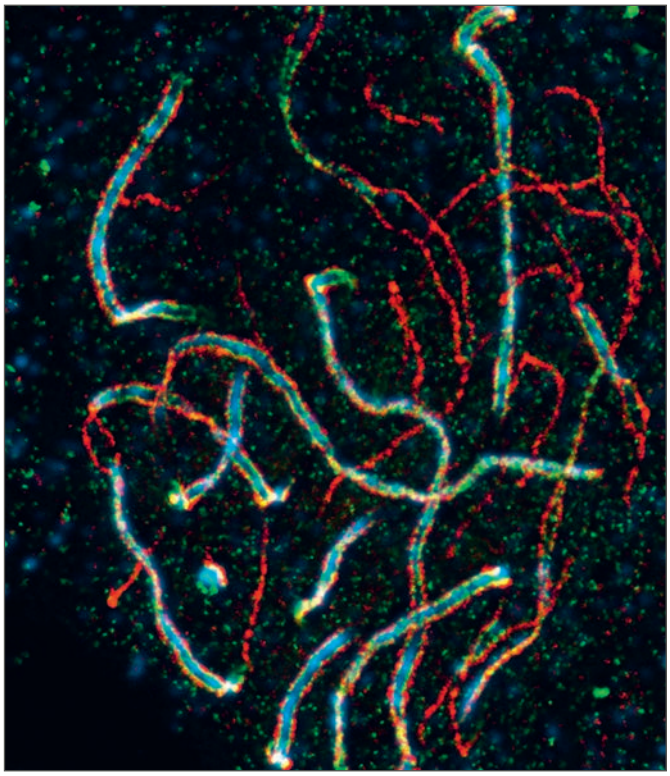

Figure 1: *Arabidopsis chromosomes in meiotic prophase. Each chromosome is arranged along an axis (Red, REC8). Pairs of homologous chromosomes are progressively tightly associated along their length and connected by the transverse element ZYP1, the C-terminal end (Green) of which is associated with the axial element. Meiotic recombination occurs in this structure and is promoted by the HEI10 protein (Blue). STED microscopy.*
Image credit: Stéphanie Durand

the wild as well as the underlying genetic determinants. Recent advances in DNA sequencing now make it possible to analyse recombination in multiple individuals. Because of its large geographic distribution, Arabidopsis is a highly suitable model for exploring the question of recombination diversity and its potential adaptive value.

MODIFICATION OF CELL CYCLE AND CHROMOSOME DISTRIBUTION DURING MEIOSIS

In this project, we analyse two key features that allow ploidy reduction at meiosis:

- the control of the number of cell divisions, which must be exactly two
- the control of chromosome distribution, which separates homologues at the first division and sisters at the second division

Dedicated genetic screens and downstream functional analyses allow us to decipher mechanisms that prevent meiocytes from exiting meiosis after a single division or prevent entry into a third division. We are also exploring what regulates kinetochore orientation and sister chromatid cohesion during meiosis I and II.

EXPANDING THE TOOLBOX FOR PLANT BREEDING

A better understanding of meiosis allows us to propose disruptive innovations for plant breeding. Through international collaborations, we have shown that crossovers can be massively increased in various crops. We also took advantage of accumulated knowledge on meiosis to engineer clonal reproduction through seeds and aim to improve this revolutionary technology and apply it to diverse crops.

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POLINA YU. NOVIKOVA

Exploring natural variation in the context of broad geography and evolutionary history allows us to describe environmental and genetic interactions that affect polyploids' origin, establishment, and evolution.

Genomics of Extreme Adaptation in Polyploids

Polyploid organisms have more than two sets of chromosomes due to whole-genome duplication or hybridization. Polyploidy is abundant and non-random throughout space, time, and the Tree of Life. It is often associated with extreme environments, where whole-genome duplications can be triggered by external stress or established more easily due to the lack of competition. Polyploidy is more common in plants than animals, but not without exceptions. What explains the abundance of polyploids in some cases and the complete lack thereof in others? Environmental factors and genetic predisposition could increase the initial formation of polyploids, affect their establishment success, and determine the pace of gradual loss of redundancy and return to a diploid state. We work on different models addressing each phase of the described polyploid evolutionary cycle.

Our genomics studies aimed to cover large geographical territories with different environments, for which we developed methods for accessing the full genetics of existing collections, such as herbaria and museums, for a wholesome description of natural variation (Figure 1).

ORIGIN AND ESTABLISHMENT OF POLYPLOIDS

Arabidopsis lyrata, with its vast geographical distribution across the Northern Hemisphere, covering territories of mild and extreme environments, is one of our models for studying the birth and death rates of whole-genome duplications. Analyzing full genomes of over 400 samples from herbarium and live collection, we found over 30 autotetraploid

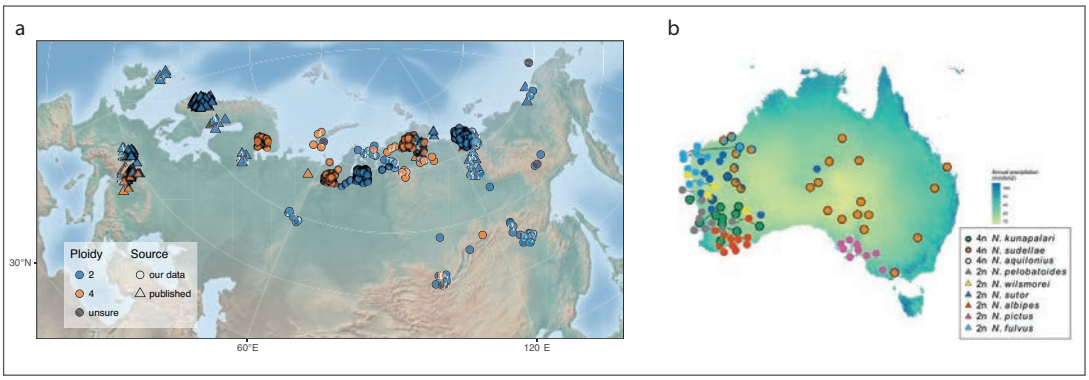

Figure 1:
(a) Distribution of sequenced diploid and tetraploid A. lyrata across Eurasia; herbarium and seed collection.
(b) Distribution of sequenced diploid and tetraploid Australian frogs Neobatrachus species, museum collection.

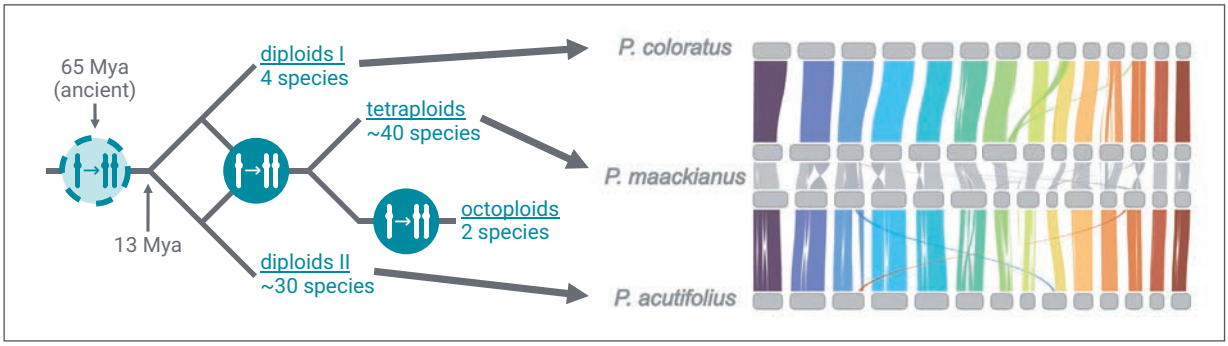

Figure 2: *Evolution of polyploidy in Potamogeton. Genome collinearity analysis of diploid and tetraploid Potamogeton species indicates conserved structure evolution of tetraploids' subgenomes.*

populations split into two distinct lineages, originating soon after the Last Glacial Maximum. We explore if the persistence of autotetraploids in *A. lyrata* is determined by harsh environment or genetic predisposition. *A. lyrata* is also one of the progenitors of allotetraploid *Arabidopsis kamchatica,* whose establishment was facilitated by the immediate transition to self-compatibility determined by standing genetic variation in the mating system of *A. lyrata* species-complex. The origin, on the other hand, coincides with environmental upheavals. To understand if the birth rate of polyploids in *A. lyrata* is also affected by genetics or if environmental triggers are sufficient, we experiment with different accessions, measuring the production of 2n gametes under different conditions.

To understand what explains polyploidy prevalence on a larger evolutionary scale, we include animal systems, such as *Neobatrachus* diploid-tetraploid species complex of Australian burrowing frogs, in our studies. Comparing tetraploid-specific selection signatures, we aim to see if there are any similarities in mechanisms of adaptations, such as changes in the synaptonemal complex to reduce crossover numbers between plants and animals. We also investigate what animal-specific challenges can explain their lower tolerance to whole-genome duplications, including the effect of sex chromosomes on polyploid formation and evolution.

GAIN, MAINTENANCE, AND LOSS OF GENETIC REDUNDANCY

Ultimately, all surviving polyploids return to a diploid state, leaving only small (non-random) traces of past duplication events. To understand how the ecology of a species shapes its rediploidization patterns, we study *Potamogeton* – a genus of widespread aquatic flowering plants (>90 species). We reconstructed the evolutionary history of the genus and dated two duplication events, 65 Mya and 12 Mya, that are shared by all (the former) and half (the latter) of present-day *Potamogeton* species (Figure 2). Now, we aim to describe lineage-specific changes after whole-genome duplications at different time scales in the context of environmental niches.

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**equally contribution*
§ corresponding author

KORBINIAN SCHNEEBERGER

Understanding the complex differences between genomes will help create sustainable crops of the future.

Genome Plasticity and Computational Genetics

Genomes are the product of millions of years of evolution. We live in times when we are gaining deep insights into the precise sequence of this exciting molecule for the first time. Knowledge of the genome sequence allows us to understand, manipulate and improve organisms.

Despite drastic technological improvements, efficient reconstruction and comparison of genomic sequences aren't solved problems yet. Our group is focussed on advancing genomic technologies and on translating methods and resources to plant breeding.

HAPLOTYPE-RESOLVED PAN-GENOMES

We have developed methods to reconstruct the complex sequences of crop genomes based single-cell genome sequencing of individual pollen grains (Figure 1). We use these methods to generate the first phased pan-genome of potato, which has the highest sequence diversity in a domesticated species described to date. In contrast, haplotype diversity of potato in Europe is very low due to multiple bottlenecks during domestication and transition to Europe some hundred years ago offering the unique possibility to create the first near-to-complete, phased pan-genome of a domesticated species. Such an unprecedented resource will allow us to create a genome-graph to generate phased, pseudo-genome assemblies of any modern potato cultivars using efficient short-read sequencing only.

MEIOTIC RECOMBINATION

Besides mutations, the key ingredient for the diversification of genomes is meiotic recombination. To understand the exact make-up of meiotic recombination, we develop single-cell sequencing methods to analyse recombinant genomes and apply these methods to understand the natural variation of meiotic chromosome arm exchanges across populations and species. But crossing-overs are not the only type of meiotic recombination that exists. Alternatively, short stretches of a chromosome can be replaced by the haplotype of the homologous chromosomes. If the haplotypes of the two chromosomes differ, such 'non-crossover' recombination events cause a change in the DNA sequence in one of the chromosomes, which are known as gene conversions. Even though such changes are orders of magnitudes more frequent than point mutations, little is known about their occurrence across populations or non-model plants. We use high precision, single-cell genomic technologies to study the impact of gene conversion in different environments, populations and species.

Genetic variation can cause differences in gene expression, which in turn is the basis for phenotypic change. Expression quantitative trait locus (eQTL) mapping is a method by which we can identify variants that cause the change of gene expression. Using single-cell RNA sequencing of individual pollen cells we have developed a method for rapid eQTL

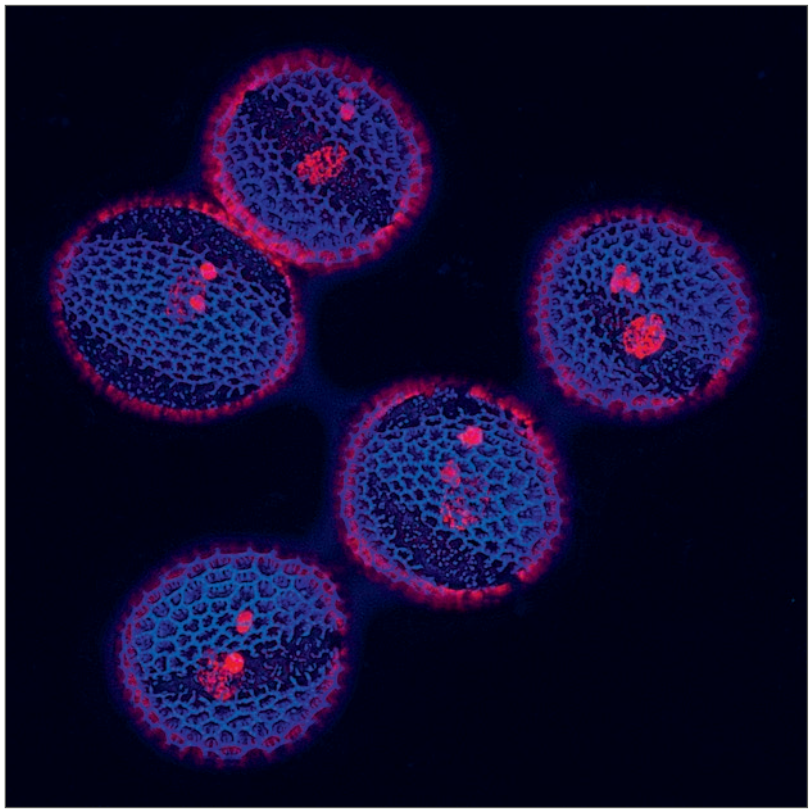

Figure 1:
Microscopic image of five pollen grains. Each of them includes three different nuclei.
Image credit: Samija Amar

mapping which already works with a small number of heterozygous individuals. This allows us to identify the variation in the master gene expression regulators that determine developmental difference.

SOMATIC MUTATIONS IN FRUIT TREES

Each eukaryote with more than one cell carries more than one genome. In fact, most eukaryotic individual consists of billions of cells and thus carry billions of genomes, which not all are identical. During development, the genomes of some cells can undergo mutations. We use single-cell genome reconstruction to understand the somatic differences in the genomes of individual organisms, using fruit trees as model. Fruit tree breeding is often based on spontaneous mutations that introduce agronomically beneficial traits specific to some parts of tree. Insights into the somatic mutations underlying such changes can help understand the genetic basis of agronomic traits and can guide future breeding efforts.

THE PROTEIN POTATO

Aardaker *(Lathyrus tuberosus)* is a forgotten crop in Europe that has recently come back to greater attention. Aardaker is an attractive, low-input alternative crop that can fix its own nitrogen and provides consumers with a high-protein alternative to potatoes. We are developing the first genomic resources including a reference sequence and global diversity information that will form the basis for genomics-assisted breeding.

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CHARLIE UNDERWOOD

Exploring meiosis and plant reproduction in a wider number of species – including the cultivated tomato and wild relatives – allows us to better understand how these processes have been shaped by evolution.

Meiosis in Crops

During the meiotic cell division, the combination of the random segregation of homologous chromosomes and meiotic recombination generate genetic diversity in gametes and offspring. The study of meiosis in diverse model systems, is allowing us to understand how meiosis has been shaped and modified over evolutionary time. Plant meiosis research is largely focused on *Arabidopsis thaliana* yet the cultivated tomato *(Solanum lycopersicum)* has been long proven to be a powerful system for meiotic cytology. We have applied molecular genetics approaches to establish tomato and wild relatives as an additional dicotyledonous plant model species for studying meiosis. An offshoot of this research is the development of novel approaches that can expedite plant breeding.

HARNESSING CLONAL GAMETES IN HYBRID CROPS TO ENGINEER POLYPLOID GENOMES

Heterosis (hybrid vigor) contributes to the high performance of modern crops; however due to the segregation of genetic information in meiosis the offspring of hybrid plants have different phenotypes. In this project that was published in *Nature Genetics* in 2024, we bioengineered a *'mitosis instead of meiosis' (MiMe)* system in tomato via ablation of three meiotic factors. The mutation of *SlSPO11-1* abolishes meiotic recombination, loss of *SlREC8* removes sister chromatid cohesion and removal of *SlTAM* leads to skipping of the second meiotic division. Through this *MiMe* system we could generate unreduced, clonal gametes in three hybrid tomato genotypes and used it to establish a new breeding system that we called "polyploid genome

Figure 1: *A "4-haplotype" plant produced by the fusion of clonal gametes.* Image credit: Yazhong Wang

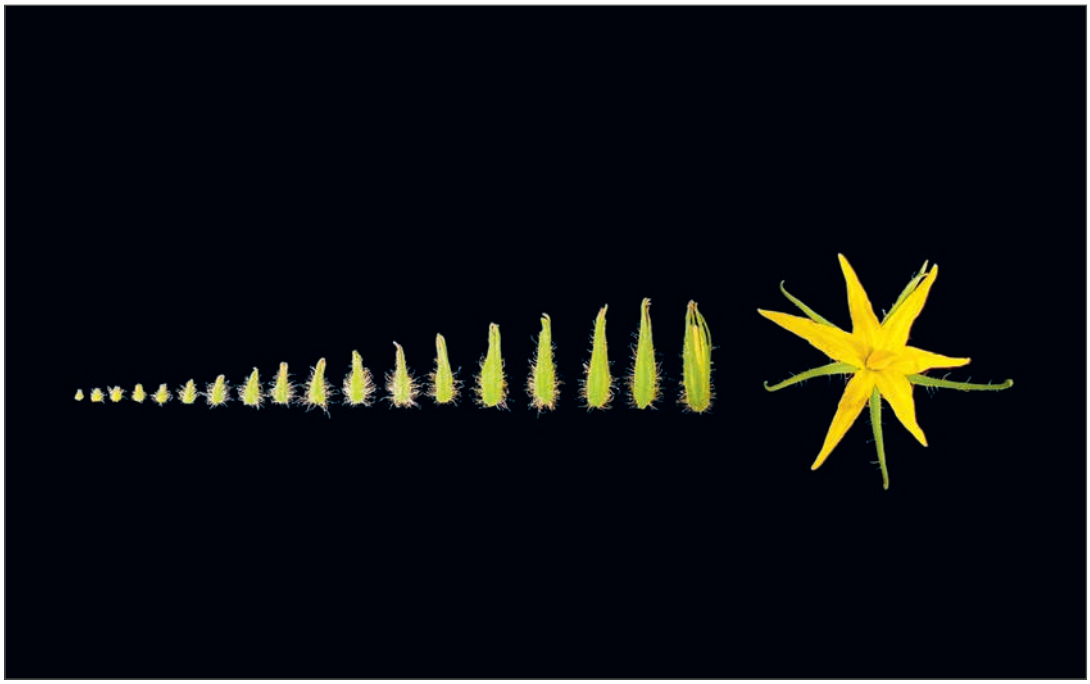

Figure 2: *Different stages of floral bud development in tomato variety Moneyberg-TMV. The smaller buds contain meiotic cells. Image credit: Yazhong Wang*

design". Through the hybridization of two distinct MiMe hybrids, we generated '4-haplotype' plants that encompassed the complete genetics of their four inbred grandparents. Essentially the fertilization of a clonal egg from one parent by a clonal sperm from another parent led to plants containing the complete genetic information of both parents. This project providing a blueprint for establishing de novo polyploidy in crops through genome engineering approaches.

A CHROMOSOME SCALE TOMATO GENOME REVEALED EXTENSIVE LINKAGE DRAG DURING BREEDING

The assembly of a genome sequence represents the characterization of the complete genetic code of a given plant. The cultivated tomato *(Solanum lycopersicum)* has been improved through the introgression of genetic material from related wild species, including resistance to pandemic strains of tobacco mosaic virus (TMV) from *Solanum peruvianum*. In this project that was published in *The Plant Journal* in 2022, we applied PacBio HiFi and ONT Nanopore sequencing to develop independent, highly complete assemblies of an inbred TMV-resistant tomato variety. We merged the independent genome assemblies to generate an assembly where all 12 chromosomes were represented as 12 near-complete sequences. The genome assembly revealed that a complex series of structural variants in chromosome 9 (where the TMV resistance gene is located) likely contributed to linkage drag of a 64.1-Mbp region of the *S. peruvianum* genome during tomato breeding. Through genetic marker studies we found that this introgression region is present in six cultivated tomato hybrid varieties developed in three commercial breeding programs. Our results show that complementary long read technologies can facilitate the rapid generation of near-complete genome sequences.

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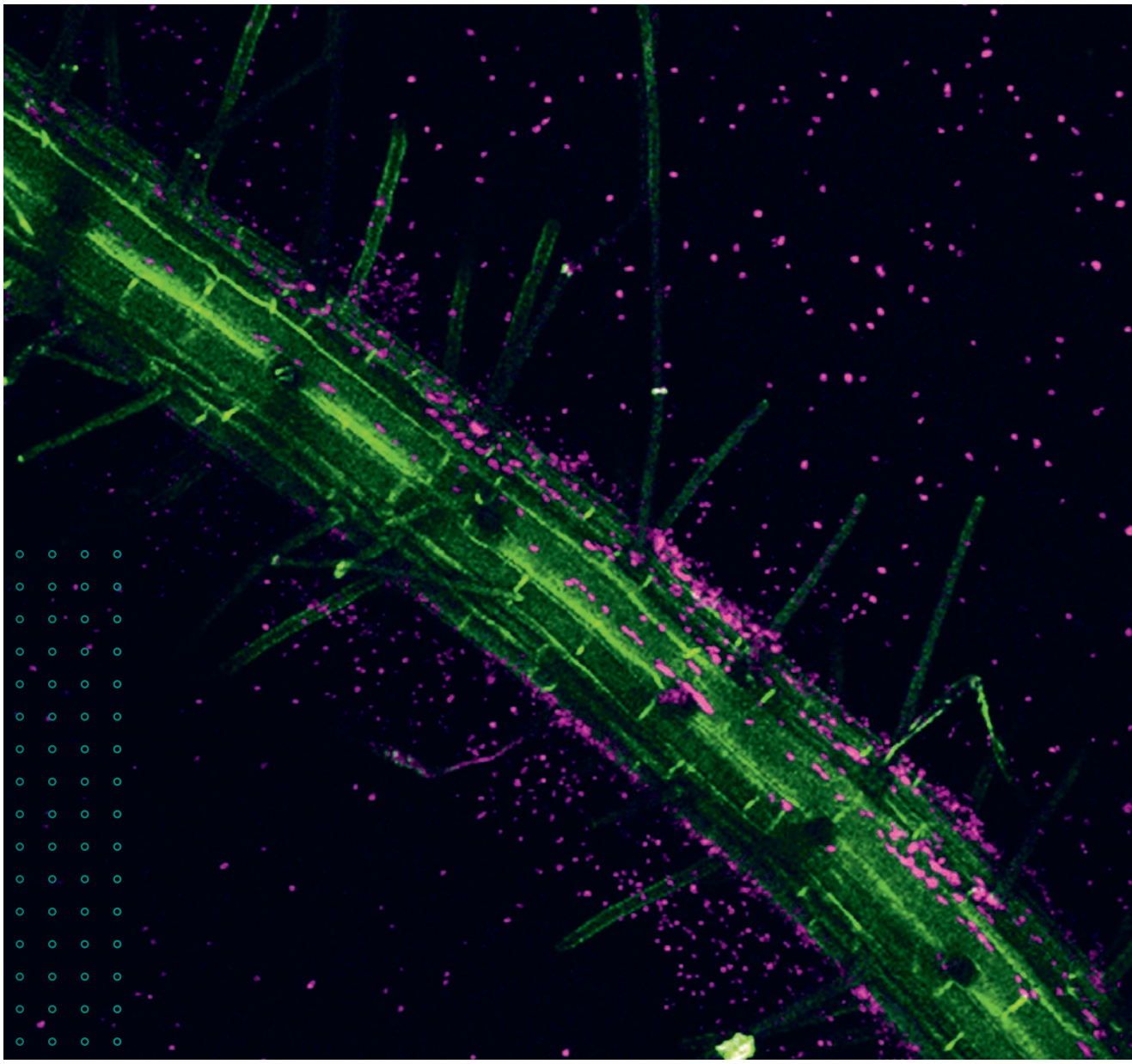
Research in the Department is aimed at understanding how plants interact with microorganisms and specifically how they protect themselves from pathogenic microbes while harnessing the useful properties of beneficial microorganisms. One major research theme focuses on the interplay between the plant innate immune system and harmful microbial invaders. By studying instances in which immunity fails and infection ensues, we aim to identify key regulatory steps in plant immunity that can be manipulated to boost plant growth and health. Understanding the establishment and functions of microbial communities associated with healthy plants, called the plant microbiota, defines a second major research theme. We seek to understand the plant and microbial factors governing microbiota establishment as well as how plants take advantage of the microbiota to adapt to nutrient-poor environments and to protect themselves from microbial pathogens. These insights are a pre-requisite for the rational development of probiotics to improve plant performance. As well as genetics, molecular biology and biochemistry, we take full advantage of the power of bioinformatics to study the structures and functions of plant-associated bacterial communities.

DEPARTMENT OF
PLANT-MICROBE INTERACTIONS

Director: Paul Schulze-Lefert



RUBEN GARRIDO-OTER

We study the ecological and molecular principles that govern plant- and algae-microbiota interactions, exploring how hosts and environmental conditions shape microbial communities and their evolution.

Integrative Bioinformatics

HARNESSING THE POWER OF SYNTHETIC ECOSYSTEMS

Microorganisms form complex communities that interact with photosynthetic eukaryotic hosts, such as plants and algae, in intricate ecological networks. My group's research aims to uncover the ecological and molecular principles governing these interactions, with a particular focus on understanding and engineering plant-microbiota systems (Fig. 1). By developing reductionist experimental frameworks and computational approaches, we aim to move beyond descriptive studies to reveal causal relationships within these dynamic communities. Our work builds on synthetic ecosystems, enabling controlled perturbations and reproducibility, and bridging experimental and computational approaches to explore microbial diversity, community stability, and evolution.

To enable this research, we have developed advanced gnotobiotic systems called EcoChambers, which allow precise control of environmental parameters, including CO_2 concentration, temperature, humidity, and light intensity. Using these systems, we observed that elevated CO_2 levels enhance plant growth in the presence of nutrient-mobilizing microbes, providing valuable insights into how plant-microbiota interactions respond to anthropogenic environmental changes. Such findings inform predictive models of ecosystem responses to climate change and support the development of microbial interventions to improve plant resilience and soil health under future environmental conditions.

STRUCTURE AND FUNCTIONS OF TERRESTRIAL PHYCOSPHERES

Building on the discovery of conserved principles linking microbiota establishment in land plants and unicellular algae, we are leveraging the model chlorophyte alga *Chlamydomonas reinhardtii* to study the structure and functions of terrestrial phycospheres. This ERC-funded project aims to address fundamental questions in microbial ecology and plant biology by integrating experimental, computational, and evolutionary approaches. Our research involves characterizing microbial communities associated with diverse chlorophyte and streptophyte algae, revealing shared core taxa and distinct communities influenced by host-specific factors.

Comparative experiments with synthetic microbial communities (SynComs) derived from *C. reinhardtii* and *Arabidopsis thaliana* allow us to explore the ecological principles of microbiota assembly. These experimental approach allow us to asses host support for cross-kingdom microbiota and uncover conserved mechanisms and host-specific factors through phenotypic and transcriptomic analyses. To investigate molecular and genetic drivers of host-microbiota interactions, we are profiling the exometabolome and transcriptome of *C. reinhardtii,* identifying algal exudates that recruit and shape microbial communities as metabolic currencies or signalling molecules.

Our aim is to deepen our understanding into the origins and conservation of these interactions by comparing genetic mechanisms in *C. reinhardtii* and land plants, providing insights into their development

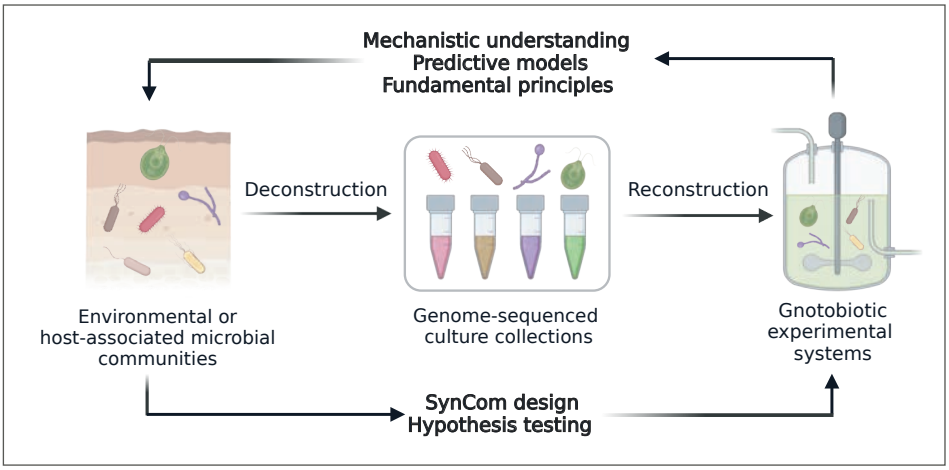


Figure 1: *Workflow illustrating the integrative approach to studying microbial communities, from genome-sequenced culture collections to gnotobiotic experimental systems. This pipeline enables the deconstruction and reconstruction of microbial communities, facilitating SynCom design, hypothesis testing, and the development of predictive models to uncover fundamental ecological principles.*

over hundreds of millions of years. Additionally, we are constructing synthetic phototrophic microcosms using bioreactors to study microbiome dynamics and evolution under controlled environmental conditions. This project has the potential to reveal universal principles governing host-microbiota interactions, enhancing our understanding of ecosystem functions and informing strategies for microbiome engineering.

ENGINEERING AND DIRECTED EVOLUTION OF PLANT-ASSOCIATED SYNTHETIC MICROBIOMES

We are employing directed evolution and microbial community engineering to investigate the molecular and genetic mechanisms driving host preference in plant-associated microbiomes. By conducting long-term artificial evolution experiments with synthetic microbial communities (SynComs) across multiple plant generations, we aim to uncover how microbial populations adapt to their host environment.
We build on our previous findings (Wippel *et al.*, 2021), which demonstrated that bacterial communities isolated from *Arabidopsis thaliana* and *Lotus japonicus* exhibit host preference, with increased colonization and persistence in their native hosts. Using a novel experimental approach to successfully propagate microbial communities and populations across multiple plant generations, we have shown that the plant host exerts a strong evolutionary pressure, driving reproducible genomic adaptations in associated microbes. These adaptations reveal how host species influence microbiome evolution, offering key insights into the mechanisms underpinning host-microbe interactions and their potential applications in microbiome engineering.

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STÉPHANE HACQUARD

Mechanistic understanding of microbe-induced plant phenotypes will drive agricultural innovations.

Multitrophic Plant-Microbe Interactions

Over the last five years, the plant microbiota research field has rapidly moved from efforts aimed at gaining a descriptive understanding of microbiota composition to a focus on acquiring mechanistic insights into microbiota functions. Reconstitution experiments with synthetic microbial communities representative of naturally-occurring microbiomes have been critical for unravelling host-microbe and microbe-microbe interactions that drive community establishment and plant health. In my research group, we aim at understanding these fundamental mechanisms using *Arabidopsis* as a model system (Figure 1).

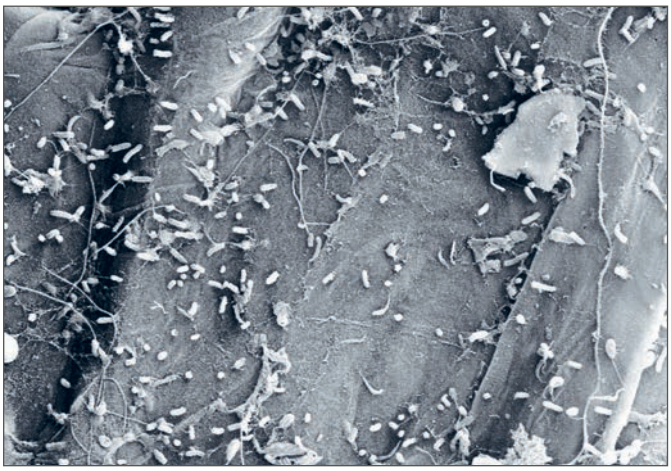

Figure 1: *Scanning electron microscopy picture of A. thaliana root surface colonized by a large diversity of different microbes.*
Image credit: Stéphane Hacquard

ROOT IMMUNITY AND BACTERIA JOINTLY PREVENT FUNGAL DYSBIOSIS

Root-colonizing fungi reproducibly detected in natural *Arabidopsis* population are often detrimental when mono-inoculated on germ-free *Arabidopsis* under laboratory conditions. We discovered that these fungi are very efficient at colonizing roots and causing disease due to their ability to aggressively degrade plant cell wall constituents such as pectin, one of the most abundant carbohydrate of the primary cell wall of *Arabidopsis*. However, the detrimental activity of these fungi is often kept in check in natural populations, illustrating the existence of mechanisms that prevent fungal dysbiosis in nature. We reported that both host- and bacterium-encoded functions act in concert to maintain fungi in check in *Arabidopsis* roots, thereby promoting plant health. The observation that the protective activity of the bacterial community is as important as the host innate immune branch involving tryptophan-derived specialized metabolites for controlling fungi is remarkable. It indicates that the plant immune system is insufficient to fully protect plants from fungal burden, and that bacterial partners residing in roots provide an additional layer of protection, which is needed for plant survival in nature. We are now aiming to identify the bacterial genes that modulate fungal growth in plant roots via direct competition or indirectly through modulation of the host immune system.

COCKTAIL OF BACTERIAL EXOMETABOLITES DRIVES ROOT INFECTION

Unlike fungi, most root-colonizing bacteria remain harmless for plants, except for very few exceptions (< 5%). We identified such a strain within the bacterial root microbiota called *Pseudomonas brassicacearum* R401 and showed that production of molecules in the environment (called exometabolites) is needed to drive R401 dominance in

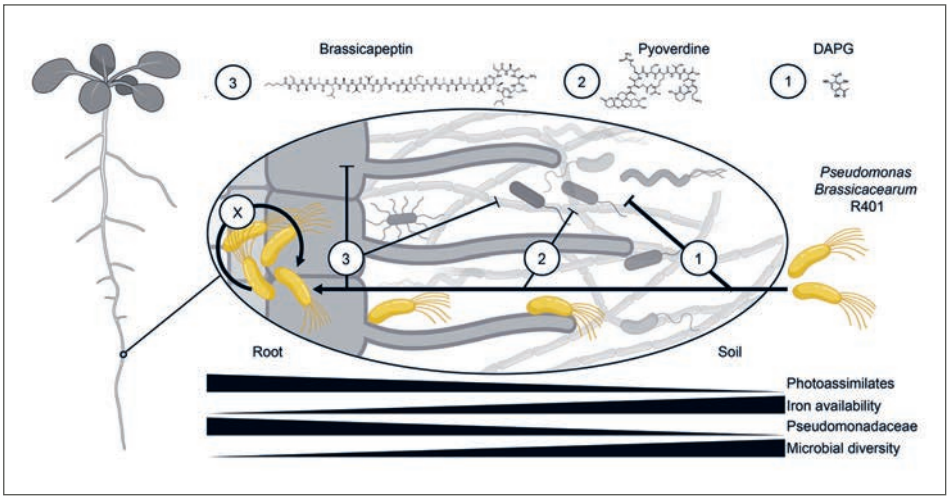

Figure 2: *Pseudomonas brassicacearum R401 deploys three unrelated exometabolites during host colonization that drive microbiota assembly, promote colonization success and modulate plant health.*
1: Diacetylphloroglucinol (DAPG) antimicrobial; 2: Iron-chelating pyoverdine; 3: Pore-forming cyclic lipopeptide Brassicapeptin; x: multiplication of the strain.

roots (Figure 2). Those include an antimicrobial (diacetylphloroglucinol) and an iron-chelating molecule (pyoverdine) that co-function via chemical and nutrient blocking, respectively, to inhibit a broad range of microbial competitors and to modulate root microbiota assembly (Figure 2). We therefore uncovered that keeping competitors away drives colonization success of this strain. We recently identified a third exometabolite produced by R401 that also promotes infection. The molecule is a newly discovered cyclic lipopeptide called Brassicapeptin that forms pores in host plasma membranes and disturb ion homeostasis. Consequently, the molecule is phytotoxic for *Arabidopsis*, especially under osmotic stress, but also has moderate antimicrobial activity against specific microbiota members (Figure 2). Therefore, we start to appreciate the remarkable diversity of small bioactive molecules produced by bacteria during host colonization and the extent to which these molecules contribute to microbial assembly, strain competitiveness, disease emergence, as well as microbiota-induced plant phenotypes. We are now interested at better understanding the chemical language driving host-microbe-microbe associations and particularly how it shapes high-level biological organisation.

MICROBIOTA-ROOT-SHOOT CIRCUITS PROMOTE PLANT HEALTH

Recent evidence suggests that bidirectional signalling between below-ground microbial commensals and distant aboveground host organs is critical for maintaining host-microbe homeostasis and plant health. Reminiscent of the critical role of the microbiota-gut-brain axis for modulating brain functions in animals, we recently obtained evidence supporting the role of the microbiota-root-shoot axis for integrating response to microbes belowground and response to light aboveground. We uncovered that plant growth and defence responses are engaged in different feedback loops with the root microbiota depending on aboveground light conditions. Light-induced change in root exudation profiles is likely an important mechanism that stimulates the growth of particular beneficial root commensals that boost plant growth under low light. The results suggest that bacterial root and gut commensals have important functions in modulating stress responses not only locally, but also in distant host organs. We are currently investigating these fascinating circuits and envision to utilize belowground microbes to promote aboveground stress responses in plants.

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**Joint first authors; #joint corresponding authors.*

JANE E. PARKER

Determining plant defence metabolite modes of action creates new possibilities for disease resistance in crops

Resistance Pathway Dynamics in Plant Immunity

Plants use receptors at the cell surface and inside cells to detect pathogens, while also supporting beneficial microbes in the environment. We study how plants regulate their immune responses, both at the level of preventing disease and accommodating useful microbes. One goal is to elucidate dynamic processes by which immune receptor recognition of specific pathogens is transmitted to conserved defence execution machineries in cells and tissues. Another goal is to understand how particular plant metabolites and nutrients influence microbial colonization and disease. We continue to use *Arabidopsis thaliana (Arabidopsis)* extensively as a model dicot host-microbe system but have extended the scope and tools to other dicot (*Nicotiana* and tomato) and monocot (barley and rice) species to characterize conserved vs. clade-specific mechanisms in plant disease resistance.

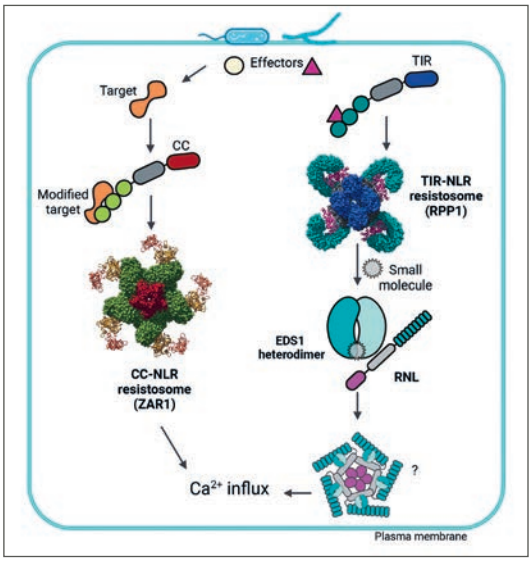

Figure 1: *Pathogen-activated CC-NLR and TIR-NLR resistosome oligomers converge on Ca^{2+} influx for immunity. Left: the pathogen effector-induced CC-NLR pentamer (ZAR1) forms a CC-domain Ca^{2+}-permeable ion channel at the plasma membrane. Right: pathogen effector-induced TIR-NLR (RPP1) forms a TIR-domain NADase enzyme generating ribosylated nucleotide SMs. Via its binding to an EDS1 dimer receptor, the SM activates an RNL, probably to form a ZAR1-like ion channel and thus also promote Ca^{2+} influx.*
Image credit: Federica Locci

CENTRALITY OF TIR-DOMAIN NADase ENZYMES IN PLANT IMMUNITY

Our long-standing research interest has been on the workings of intracellular 'NLR' immune receptors with Toll-Interleukin-1 Receptor (TIR) signalling domains whose members (called TIR-NLRs) detect diverse pathogens in dicot plants. While TIR-NLRs were lost from monocot lineages, a group of smaller but highly immune-responsive TIR-only proteins contributes to disease resistance in dicot and monocot species. Both TIR-NLR and TIR-only protein generated signals converge on a conserved family of lipase-like proteins - EDS1, SAG101 and PAD4 which promote resistance by activating particular coiled-coil (CC)-domain NLRs (called RNLs). The activated RNLs form oligomers with calcium permeable ion channel activity that promotes rapid cellular reprogramming. In collaboration with Prof. Jijie Chai at MPIPZ we established that pathogen-activated TIR-NLR and TIR-only proteins are NAD+ hydrolysing enzymes. Through TIR-encoded NADase and ADP-ribosylation activities, the TIR enzymes generate a set

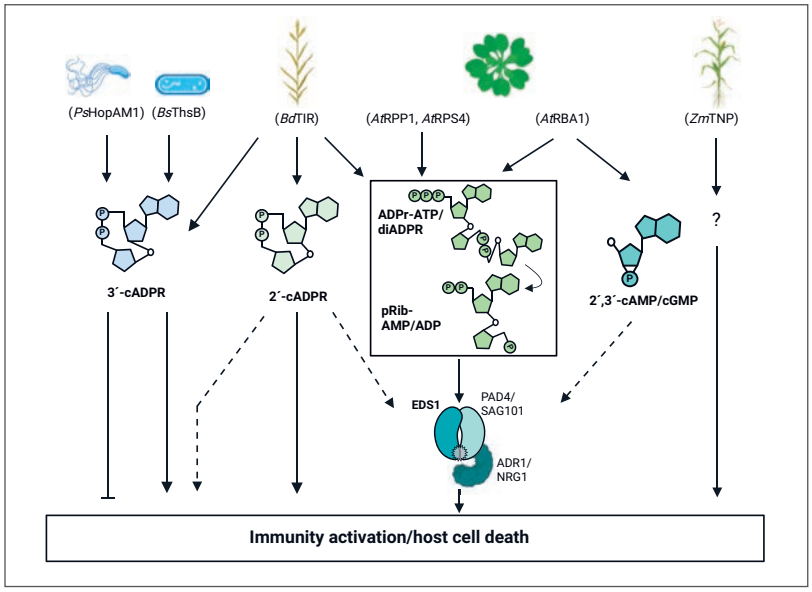

Figure 2: *A range of cyclic and non-cyclic nucleotide small molecules have emerged as important signalling intermediates in plants, bacteria and mammals. For details see Locci et al. Current Opinion in Plant Biology, https://doi.org/10.1016/j.pbi.2023.102373 (2023).*

of non-cyclic ribosylated nucleotide small molecules (SMs). Particular TIR-catalysed SM types bind to and activate distinctive EDS1-family/RNL branches to confer immunity (Figure 1).

TRACKING A NEW CLASS OF NUCLEOTIDE-BASED IMMUNE 2ND MESSENGER

Our current protein structural, biochemical and genetic data suggest that TIR-NLR- and TIR-only produced nucleotide signals and their downstream EDS1-RNL machineries constitute a control hub for resistance to diverse pathogens. Notably, the SM-binding pockets of *Arabidopsis* EDS1-family dimer complexes are conserved across a wide range of seed plant species. Hence, SMs represent a new type of plant immune-stimulating 2nd messenger with the potential for protecting crops from disease. Together with the team of Prof. Stephanie Kath-Schorr at the University of Cologne, we are designing various engineered SM compounds and response assays to track SM bioactivities inside plant cells and tissues. The TIR-generated SMs described here are among a growing number of nucleotide-based signals with immune-activating or suppressing activities in plants, bacteria and mammals. This offers exciting prospects for immune-metabolism research across kingdoms (Figure 2).

IMPACT OF COUMARINS ON PLANT INTERACTIONS WITH FUNGI

As part of our research into plant immunity mechanisms we are exploring the actions of induced defence metabolites in discriminating between beneficial, neutral and harmful (pathogenic) fungi that associate with roots or leaves. We focus on a family of secondary metabolites – the coumarins which are derived from phenylpropanoid precursors, are produced in a broad range of seed plant species and have known roles in shaping root-bacteria associations. Certain coumarin derivatives act as iron chelators which, in cooperation with root-associated bacterial strains, promote microbial colonization and plant resilience to low iron availability. By dissecting the role of particular coumarin molecules in an interaction between *Arabidopsis* and a natural root-colonizing fungal endophyte we have uncovered a metabolic collaboration between the fungus and its host in which the fungus steers coumarin-based iron provision for mutual benefit. This represents a positive outcome for the plant and a potentially important niche for the fungus, limiting competition at the root. In a related project we are examining the metabolic interplay between leaves of tobacco with an aggressive and agronomically costly necrotrophic pathogen, *Botrytis cinerea*. In this interaction, plant-generated coumarins are re-purposed by the fungus to aid its colonization. These two studies begin to reveal how plant-fungal cross-talk at the level of coumarin usage and metabolism can shape plant – microbe interactions.

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PAUL SCHULZE-LEFERT

Understanding how plants interact with both harmful and beneficial microorganisms will facilitate the development of sustainable strategies to improve plant health and growth.

Innate Immunity and the Plant Microbiota

Healthy plants in nature host a huge diversity of commensal microorganisms, called the plant microbiota. In the past several years, we have contributed to establishing plant microbiota science as a novel research field. Building on foundational work describing the composition of plant-associated microbial communities, we are now starting to learn about the principles underlying microbiota establishment and maintenance as well as the functions of these microbial assemblages. Plants have evolved elaborate immune systems that recognize the presence of potential pathogens and mount powerful immune responses that stave off infection by microbial intruders. We aim to elucidate the molecular mechanisms of plant immunity against pathogenic microbes.

ASSEMBLY AND FUNCTIONS OF THE ROOT MICROBIOTA

We have shown that soil type is a major driver of the composition of root-inhabiting bacterial communities and that membership of the root microbiota is limited to only a fraction of the large diversity of microbes found in soil. We have also succeeded in isolating and culturing microorganisms from the majority of bacterial and fungal groups of the leaf and root microbiota, which has allowed us to reconstitute synthetic microbial communities that are representative of the diversity found in nature. Introduction of these synthetic communities to germ-free plants then allows us to disentangle the impact of different microbes on plant physiology. One breakthrough has been our discovery that the bacterial root microbiota is essential for plant survival in soil and protects plants against root-associated fungi and oomycetes.

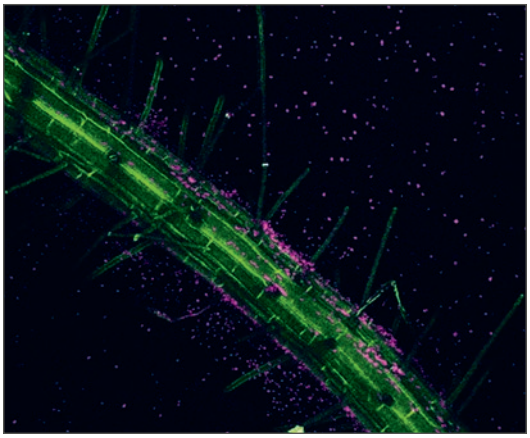

Figure 1:
Live microscopy image
Colonization of the Arabidopsis thaliana root surface by commensal soil-derived rhizobacteria. Arabidopsis thaliana plants expressing the fluorescent YFP protein localized at the plasma membrane (green-colored) were inoculated with a commensal rhizobacterium constitutively expressing the fluorescent RFP protein (magenta-colored). Bacterial colonization of the primary root and root hair surfaces was visualised by confocal laser scanning microscopy and is shown as a 3D projection. Image credit: Thomas Nakano

We hypothesize that the plant immune system plays an important role in microbiota establishment, and we aim to identify the underlying molecules and pathways. To understand the inner working of the microbial assemblages, we explore metabolic diversity and metabolic interdependencies among commensal members and with the plant host as potential determinants of community stability and

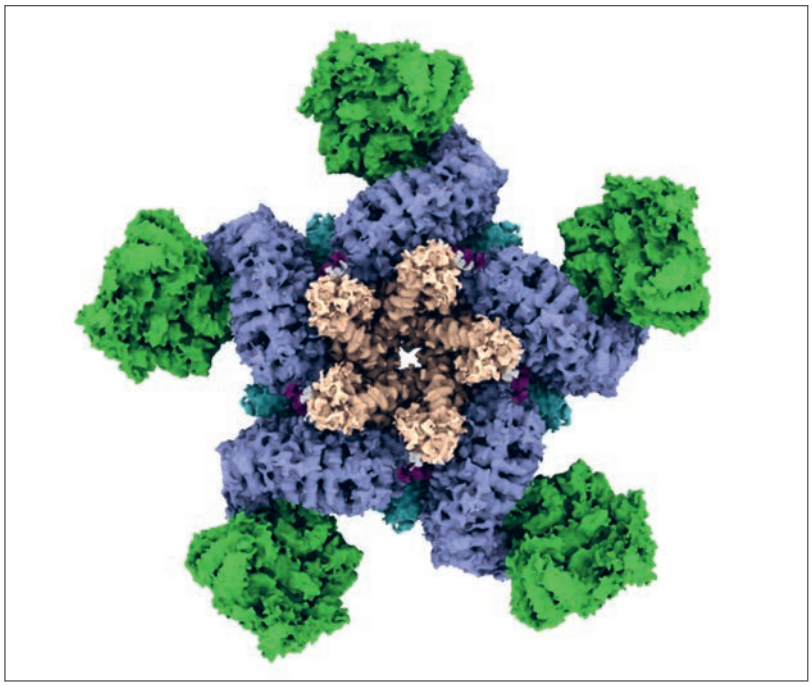

Figure 2: *The wheat Sr35 resistosome. Cryo-EM based structure model of the pentameric Sr35 resistosome with 3 Å resolution (top view). The AvrSr35 pathogen effector is coloured green and Sr35 domains are shown in magenta and light ochre. Note the central pore, which is critical for non-selective cation channel activity of the plant membrane-inserted heterocomplex.*
Image credit: Alexander Förderer

microbial services. These community services (traits) include indirect pathogen protection, mineral nutrient mobilization from soil, and abiotic stress tolerance. The insights that we gain may enable the development of rational probiotics for low-input agricultural ecosystems with reduced utilization of fertilizers and pesticides.

RECOGNITION OF PATHOGENIC MICROBES BY INTRACELLULAR IMMUNORECEPTORS

We investigate how immunoreceptors that reside inside plant cells detect the presence of pathogen-delivered molecules, so-called effectors, and activate powerful immune responses that terminate pathogen growth. The immune receptors are encoded by plant disease resistance (R) genes that are often used by plant breeders to select resistant crop varieties. Immunity mediated by these receptors is typically associated with host cell death at sites of attempted pathogen invasion. The diversified receptors in plants comprise a protein family, designated Nucleotide-Binding Domain and Leucine-Rich Repeat containing proteins (NLRs). Intriguingly, plant NLRs are structurally related to intracellular receptors of the innate immune system in animals and humans.

We primarily use the crops barley and wheat and the model plant *Arabidopsis thaliana* to address the co-evolutionary dynamics between host and pathogen at the level of populations and conservation of receptor function across different plant lineages. In collaboration with the structural biology group of Jijie Chai, we have made step-change advances in understanding how NLRs are activated and initiate immune signalling and immunity-associated cell death. Our discoveries have laid the foundation for the rational development of synthetic NLR receptors with novel pathogen effector recognition capabilities.

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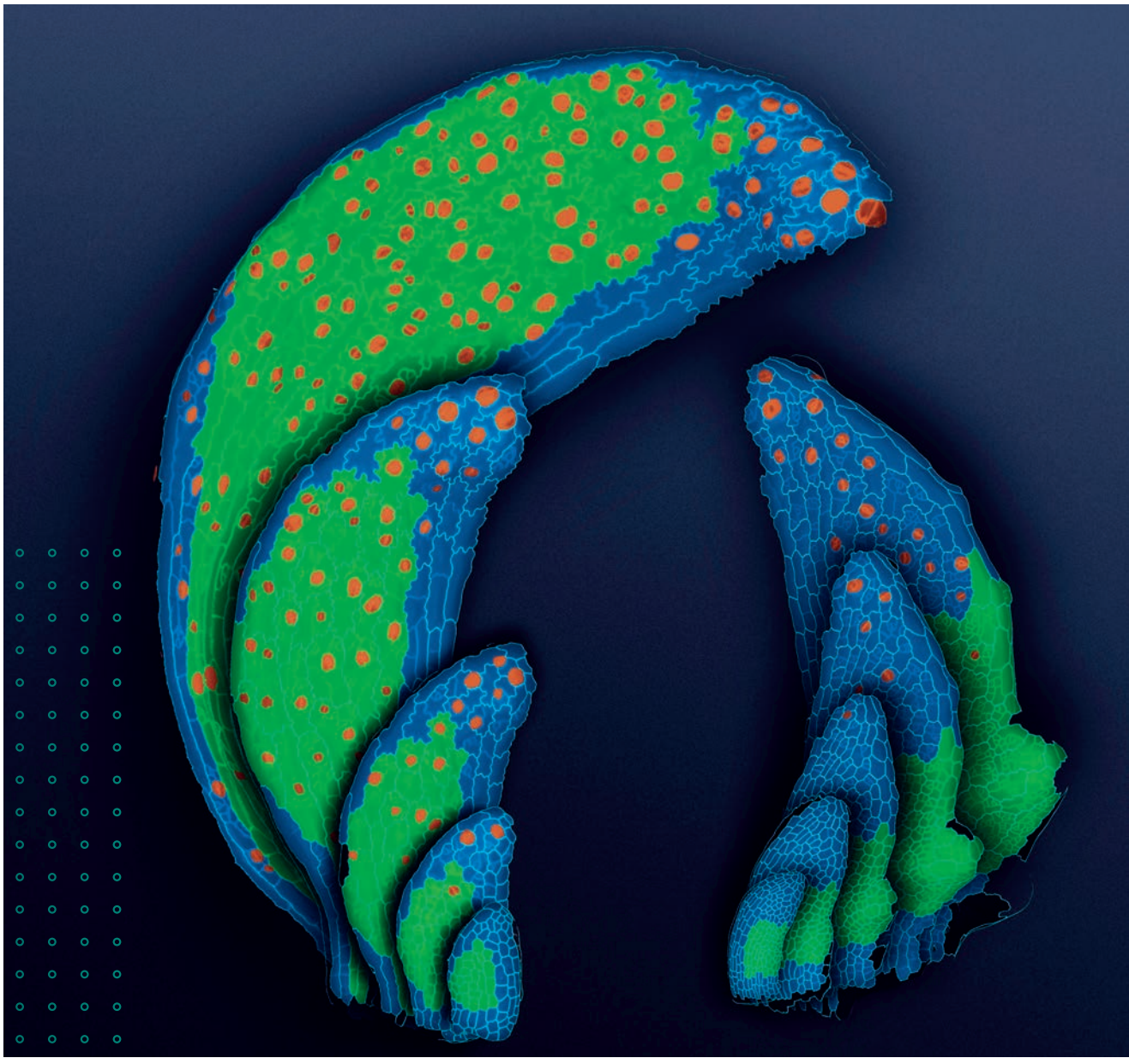
** corresponding author*

Plants show considerable morphological variation in organ shape, size and number. Work in our department seeks to elucidate the basis for such variation. We address two fundamental questions: first, how do plants develop and grow into complex organisms starting from a fertilized egg and, second, how did plant form diversify through evolution? To answer these questions, we work at the interface of developmental genetics, comparative development and biomechanics. This combination of approaches helps us to identify genetic networks that underpin the generation of different aspects of morphology and understand how the balance between conservation and divergence of these networks generates diversity during evolution. One key challenge arises from the fact that an organism's form is determined by a cascade of processes that take place at different levels of organisation, and yield the final form through complex feedback loops of genetic regulation, signalling, cell proliferation patterns, and tissue growth. Thus, it becomes increasingly difficult to conceptualize how the processes that influence growth and patterning are combined and integrated to produce organismal form. To resolve these issues and synthesize our biological findings, we use computational approaches to help reveal fundamental principles that govern the development and diversity of plant form. Our work is important for two reasons: by building a predictive framework that conceptualizes how biological forms develop and diversify, we attain a clearer understanding of the natural world and improve the knowledge base that underpins plant breeding.

DEPARTMENT OF COMPARATIVE DEVELOPMENT AND GENETICS

Director: Miltos Tsiantis



HADRIEN OLIVERI

Exploring mechanistic, mechanical, and mathematical models of plant growth to uncover the principles guiding the development of plant living matter.

Mathematics and Mechanics of Plant Morphogenesis

Morphogenesis is the process by which biological organisms establish their form. This phenomenon relies upon multiple genetic, chemical, mechanical, and physical regulations, which are typically multi-scale and coupled, forming what is called a complex system. Characterising the behaviour of this system is one of the most fundamental problems in biology. To achieve a rational understanding of morphogenesis, dedicated mathematical modelling is indispensable. Mathematics offers a set of tools, a framework for thinking, and a language that enables systematic predictions, the rationalisation and integration of biophysical phenomena, the characterisation of quantitative and qualitative relationships within the system, and a symbolic understanding of these phenomena.

Our goal is to design and explore physically-based mathematical models of plant growth, development and behaviour. These models are grounded in fundamental physical principles and integrate various regulatory mechanisms across different scales. Our approach lies on simple mathematical models that can be analysed analytically, asymptotically, or numerically to uncover fundamental guiding principles at play in plants.

TOWARDS A FIELD THEORY OF PLANT MORPHOGENESIS

A grand challenge in mathematical biology is to build field theories that describe the physical behaviour of living matter at the tissue level. Indeed, physical field theories such as continuum mechanics and reaction-diffusion systems based on partial differential equations are built on solid mathematical grounds and benefit from exact, asymptotic and numerical techniques dedicated to their analysis. The construction of such theory for plants is an open challenge.

The aim is still to develop a theory of plant morphogenesis – a comprehensive mathematical framework where growth phenomena arise from the interaction of multiple coupled physical, chemical, and mechanical fields, described from first principles. Here we combine the theories of reaction-diffusion equations (which describes the reaction and diffusion of chemical species), poroelasticity (the mechanics of fluid-saturated solids), and morphoelasticity (a modern mechanical theory of growth), to capture chemical, elastic, anelastic, and hydromechanical effects in plant growth.

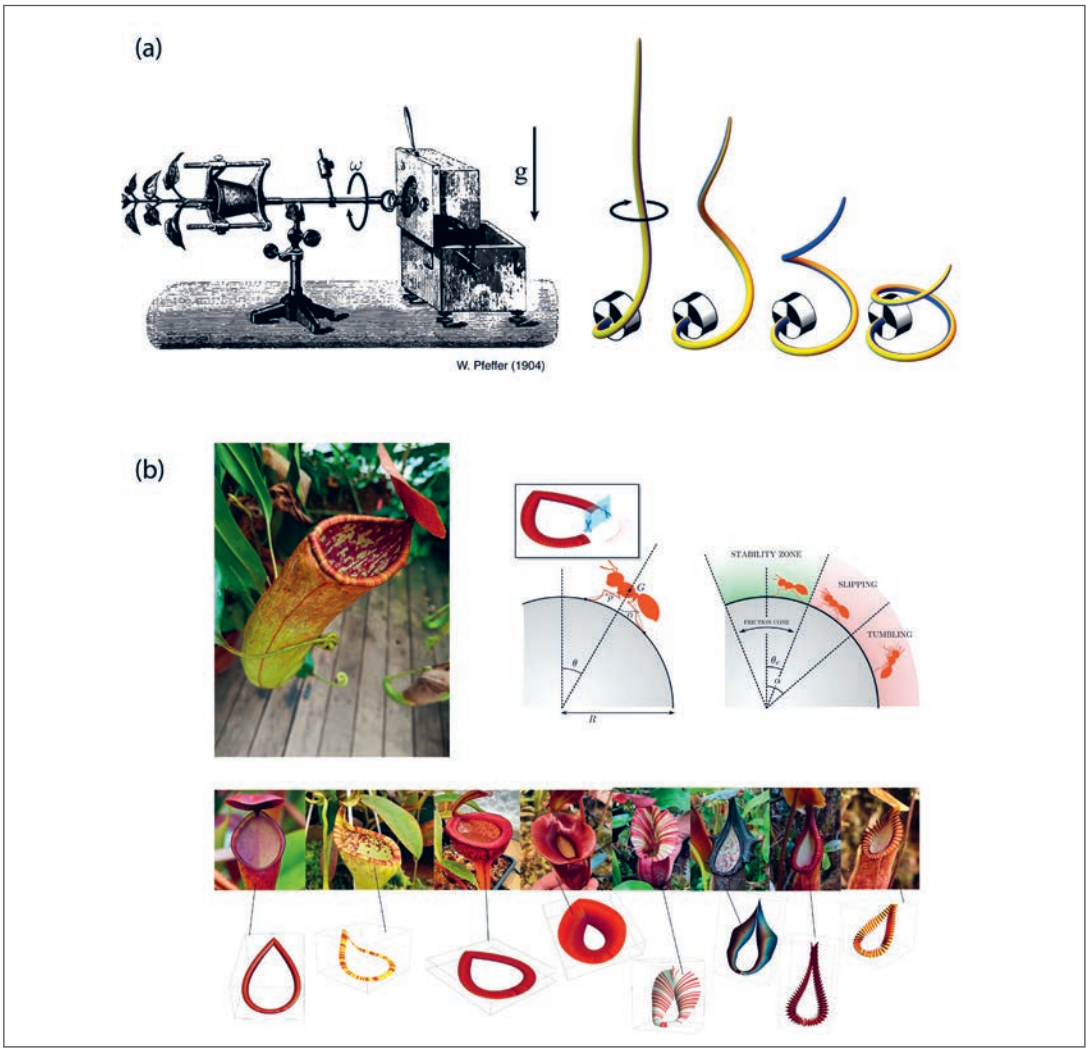


Figure 1: *(a) Plant gravitropism: The shape of a plant rotating in a clinostat under gravitropic influence (see Oliveri et al., Physical Review E, 2024). (b) Mechanical selection of carnivorous pitcher plants Nepenthes: assessing the role of shape and size in the mechanics of prey capture using mathematical modelling (see Moulton et al., PNAS, 2023).*

PLANT TROPISMS

To survive and thrive, plants rely on their ability to sense various environmental signals, such as gravity and light, and respond by growing and changing their shape. This response is known as tropism, the directed movement of a plant in response to a stimulus. Tropism is a multiscale process involving sensing, hormonal transport, and growth. Typically, a tropic signal is sensed by the cells, which respond by redistributing growth hormones within the organ (e.g. shoot or root). These hormones then regulate growth, leading to a global change in shape. Viewing the plant as an active filament, we explore mechanistic, multiscale models to study the dynamics of plant organs in the presence of multiple changing stimuli.

FUN

Plants provide a fantastic playground for scientists fascinated by solid mechanics, geometry and dynamics. As applied mathematicians, we have a broad curiosity about a diversity of problems, including fundamental problems in mechanics, and applied problems in all sorts of plants, whether pretty, ugly, or bizarre, that hunt, eat, pop, dance, twine, twist, and bend.

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MILTOS TSIANTIS

We seek to address two fundamental questions in biology: How do biological forms develop and what is the basis for their diversity?

Plant Development and Diversity

To address these questions, we first aim to elucidate how genotypes are translated into organismal forms through the process of morphogenesis. Secondly, we seek to conceptualize how the balance between conservation and divergence in morphogenetic regulatory networks yield different organismal forms during evolution. We approach these problems using genetics based on both induced and natural variation, while also employing biological imaging, genomics and computational modelling. We believe that working at the interface of these areas will allow us to attain a predictive understanding of how biological forms develop and diversify.

Our research programme is empowered by the use of *Cardamine hirsuta* (hairy bittercress), a common weed we developed as a model system for studies in the evolution of development. *C. hirsuta* is related to the reference plant *Arabidopsis thaliana* (thale cress) and is also amenable to both forward and reverse genetics approaches, including efficient transgenesis. However, *C. hirsuta* and *A. thaliana* differ in key morphological traits, including leaf shape, shoot branching, floral structure and fruit development, so comparative studies between the two species can greatly enrich our knowledge of the molecular mechanisms that drive the evolution of form. The analysis of both induced and natural variation within this comparative framework, coupled with broader, phylogenetically informed studies will help us understand the genetic basis for evolutionary change.

MORPHOGENESIS AND THE CONTROL OF FORM

Can we conceptualize morphogenesis in a predictive fashion? The form of an organism is determined by a cascade of developmental processes that take place at different levels of organisation and yield the final form through complex feedback loops of genetic regulation, signalling and tissue growth. We aim to delineate such interactions and develop predictive models that conceptualize the process of development. Examples we study are leaf morphogenesis and patterning, and cell fate delimitation during embryo, shoot and root development (Figure 1).

THE MECHANISTIC BASIS FOR MORPHOLOGICAL DIVERSITY

Is morphological diversity between species generated by a large number of small-effect genetic differences, or by a few large-effect genetic changes? Are a handful of key genes responsible for the evolution of multiple morphological traits? How are genes

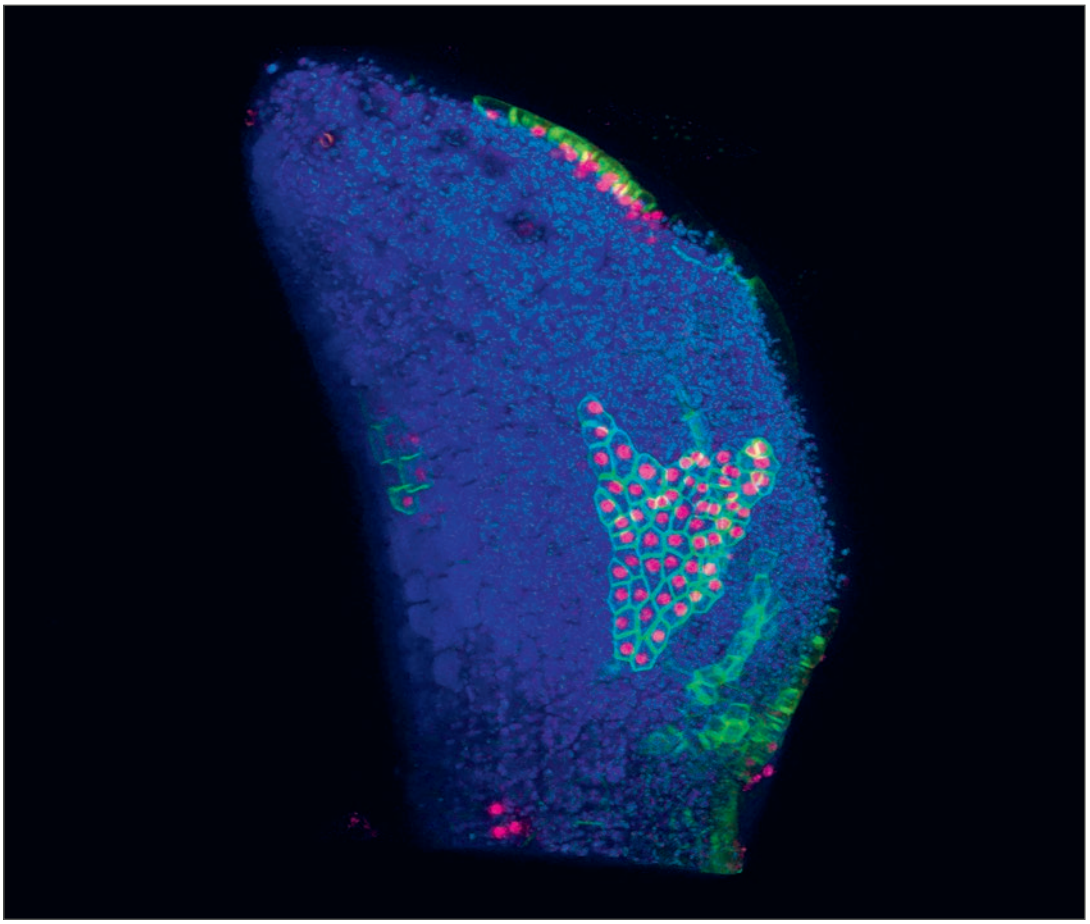

Figure 1: *An Arabidopsis leaf with a "heart-shaped" clone of the transcription factor CUP-SHAPED COTYLEDON1 (CUC1; magenta) from its close relative Cardamine hirsuta and auxin transport protein PIN-FORMED 1 (PIN1; green). We found that species-specific expression of CUC1 is a key determinant of leaf-shape differences between the two related plant species. CUC1 acts as a polarity switch through transcriptional activation of kinases that influence the polarity of PIN1. This mechanism provides instructive input into PIN1-auxin-based leaf marginal patterning that regulates leaf shape.* *Image credit: Neha Bhatia.*

that drive diversification positioned within genetic regulatory networks that influence form? Which specific genes have changed to produce the vast degree of morphological diversity seen in nature? And how do these genes change e.g. are mutations that result in stable morphological change more likely to lie in coding or regulatory segments of genes, do they behave in a dominant or recessive fashion, are they already present in populations or does their sudden appearance generate diversity?

PATHS OF EVOLUTIONARY CHANGE

How repeatable is evolution? Does diversity in the same types of genes or pathways underlie variation in the same trait in different instances? Does inter- and intra-specific variation in morphology of the same traits arise via equivalent morphogenetic avenues? How prevalent is the role of positive selection in sculpting diverse plant forms and can the agents of selection be identified?

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**equal contribution*

ANGELA HAY

Adaptations for seed dispersal are found everywhere in nature.

Genetic Basis of Phenotypic Evolution

We use comparative approaches in two related plant species – *Cardamine hirsuta* and *Arabidopsis thaliana* – to study the genetic basis of plant development and diversity. We focus on explosive seed dispersal. This is a biomechanical trait found in *C. hirsuta,* but not *A.thaliana*. We aim to understand how this trait works and how it evolved.

EXPLOSIVE SEED DISPERSAL

Explosive fruit employ rapid movements to launch their seeds instead of relying on passive dispersal by external vectors, such as wind, water, gravity or animals. In exploding seed pods of *C. hirsuta,* the two valves coil up in an ultrafast movement, launching seeds at speeds faster than 10 m per second to spread over a metres-wide area (Figure 1). While the valves are anchored to the fruit, tension builds up, but cannot be released. Once the valve anchors break, tension is suddenly released, leading to rapid coiling of the valves and ballistic dispersal of the seeds.

To gain a comprehensive understanding of this process, we related observations at the plant scale all the way down to the cellular and genetic scales and systematically linked each scale with mathematical modelling. We found that at the organ scale, tension within the fruit valve generates the elastic energy required for explosion. This tension is produced by differential contraction of valve tissues through an active contraction of epidermal cell length. The explosive release of this tension is controlled at the cellular scale by polar lignin deposition

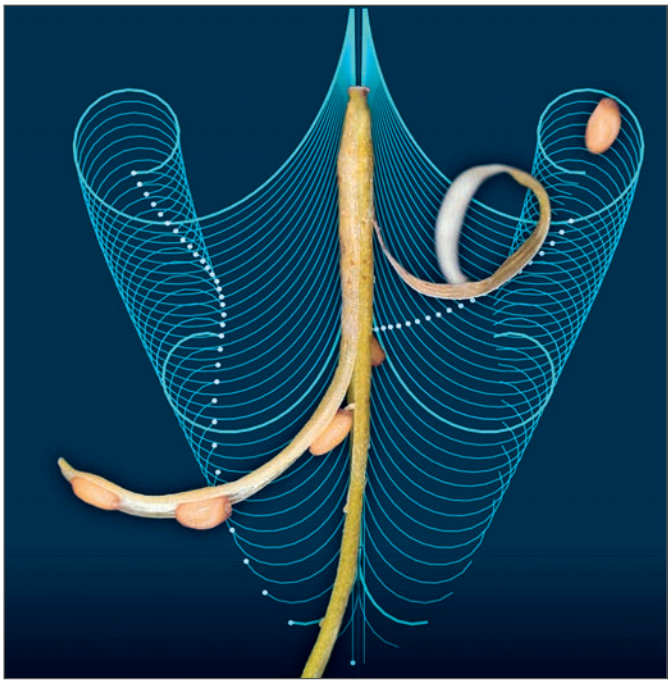

Figure 1: *The violent explosion of seed pods in the common weed bittercress (Cardamine hirsuta) is one of the fastest movements in the plant kingdom. This image shows consecutive simulations from a multi-scale model that uses interactions between cell and tissue-level processes to reproduce the explosive coiling of C. hirsuta fruit valves.*
Image credit: Angela Hay

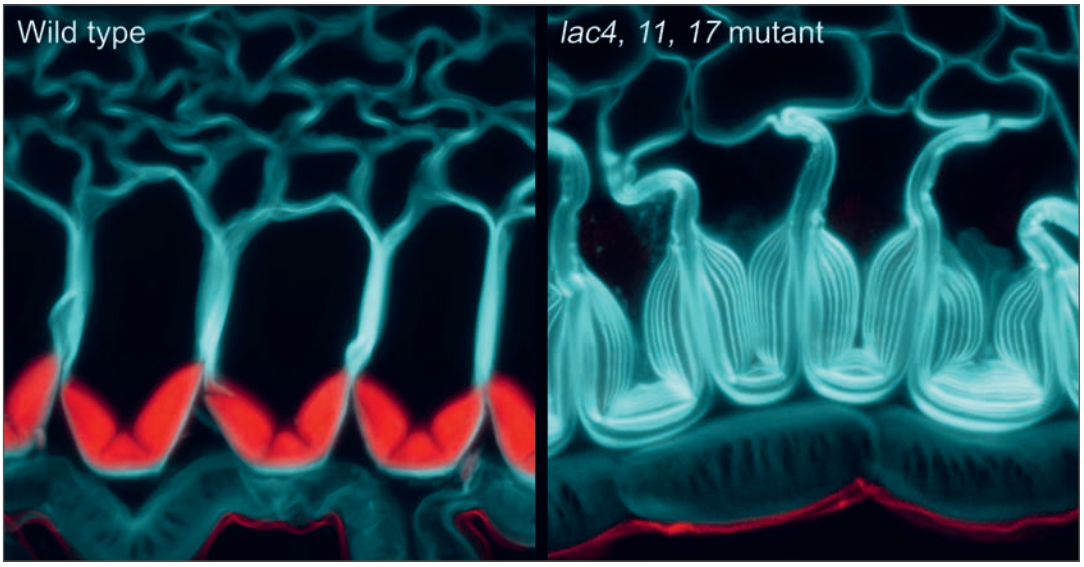

Figure 2: *C. hirsuta fruit have a unique, polar pattern of lignin deposition in their endocarp b cell walls. Three multi-copper oxidases called laccases (LAC4, 11, 17) co-localize with, and are required for, endocarp b lignification. In triple mutants that lack all three enzymes, this secondary cell wall fails to lignify. This image shows confocal images of endocarp b cells stained for lignin with basic fuchsin (red) and cellulose with calcofluor white (cyan) in wild-type and lac4, 11, 17 triple mutant fruit.* Image credit: Miguel Pérez Antón

within endocarp b cells. By bridging these different scales, we revealed an integrated mechanism for explosive seed dispersal that links evolutionary novelty with complex trait innovation.

SLAP BRACELET MECHANICS

The mechanism for explosive release works like a slap bracelet – in order to release valve tension by coiling in length, the valve must first flatten in cross-section. This is achieved via a sudden change in geometry of the lignified secondary cell wall in endocarp b cells. A lignified wall is deposited on only one side of endocarp b cells (Figure 2). This wall is very thick, but disrupted by two thin hinges that can open to flatten the valve. This unique cell wall geometry is an evolutionary novelty, associated with explosive seed dispersal in Cardamine. Genetics showed that *C. hirsuta* fruit need the endocarp b cell layer, and specifically the geometry of its lignified cell wall, in order to explode. Modeling described the mechanics by which this hinged geometry allows endocarp b cells to widen at a negligible energy cost, enabling the valve to suddenly change from a curved to a flat cross-section, causing the rapid release of tension by valve coiling.

LOCAL LIGNIN DEPOSITION

Three lignin-polymerizing enzymes called laccases (LAC4, 11, 17) co-localize with, and are required for, endocarp b lignification in *C. hirsuta* fruit (Figure 2). These oxidative enzymes activate monolignols in the cell wall into radicals that randomly couple to form the lignin polymer. The precise localization of LAC4, 11 and 17 in endocarp b cell walls, therefore, controls exactly where lignin is deposited.

Intriguingly, laccases are copper-requiring enzymes, so *C. hirsuta* plants need to accumulate sufficient amounts of copper in the fruit for lignin polymerization and explosive seed dispersal. Copper homeostasis is regulated by the transcription factor SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 7 (SPL7) throughout the green plant lineage. Loss of SPL7 in *C. hirsuta* causes a reduction in fruit copper levels and endocarp b lignification, and a consequent reduction in how far seeds are dispersed. In this way, SPL7 links mineral nutrition to efficient dispersal of the next generation.

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**equal contribution*

Giving talented young scientists from diverse backgrounds the opportunity to prove themselves as leaders of independent research groups complements and expands the focus of the departments. The groups directed by these scientists operate outside the departmental structure and can pursue their own research topics.

Currently, four independent research groups supply expertise in functional genetics of root communication (Tonni Grube Andersen), molecular basis of adaptive evolution (Angela Hancock), genetic basis of phenotypic evolution (Angela Hay), understanding how variation in gene regulation is encoded within diverse genome (Thomas Hartwig). Service groups are also independent of the departments and are headed by tenured scientists who perform research tasks, in addition to service duties which they carry out in collaboration with groups inside and outside the Institute. Ton Timmer's group manages our imaging facilities comprising a wide variety of confocal light and electron microscopic instrumentation, Hirofumi Nakagami's group provides a service on advanced protein mass spectrometry analysis, and Bruno Hüttel is head of the abovementioned Max Planck-Genome Centre Cologne (MP-GC), a core facility providing cutting edge technologies in next generation DNA- and RNA-sequence analysis.

INDEPENDENT RESEARCH GROUPS AND RESEARCH OF SERVICE GROUPS

TONNI GRUBE ANDERSEN

The underground parts of plants and their dynamic association with the environment is a treasure chest of agriculturally relevant features yet to be discovered.

Root Communication at the Single Cell Level

Because roots must provide nutrients and water for the plant while also responding to potentially harmful microbes, they continually integrate diverse signals to ensure plant survival. Not only does the plant need to elicit the right response at a cellular level but the intensity of stress also varies dramatically across different parts of the root system which makes decision making extremely complex. Although we have some understanding of how plants respond and integrate such stresses, we have yet to find out how this is coordinated at the level of individual cells. Intriguingly, certain cells in the endodermis, the boundary that separates the inner vasculature from the outer layer of the root, specifically respond to certain stress situations such as low nutrient availability. This suggests that these cells, termed "passage cells", might serve as communication hubs between the root and the outer environment (Fig 1). We are trying to elucidate the function of these passage cells and use them as a model to study development and communication between the root and their physical and biological environments. To achieve this we use state-of-the-art fluorescence-based microscopy with near-native physiological set-ups that involve precise control of nutrient and light availability. We employ this with single-cell gene expression analysis and plant-microbe community studies. Combined, these approaches allow us to investigate how specialised communication occurs between plants, the soil and microbes. We mainly work with the model plant *Arabidopsis thaliana* for which there is a highly developed genetic toolbox. However, because part of our research is focussed on how microbial associations are connected to plant transport systems, we also work with the legume *Lotus japonicus,* which forms highly specialised, mutually beneficial associations with bacteria that, in exchange for sugar, provide the plant with nitrogen.

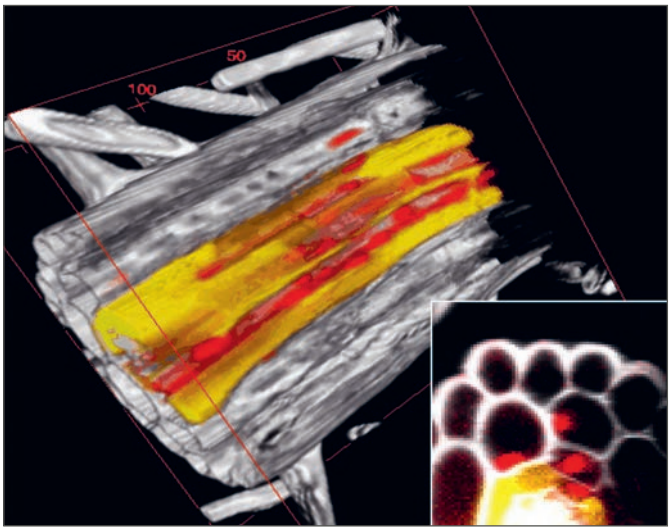

Figure 1: *An Arabidopsis root with stained cell walls (grey), endodermis (yellow), and expression of a genetic marker in passage cells (red).* Image credit: Tonni Grube Andersen

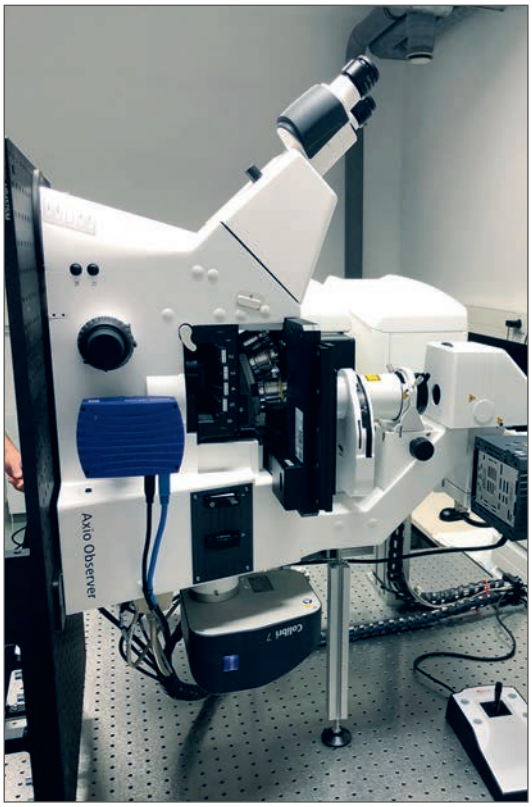

Figure 2: *Our vertically-oriented confocal microscope for the long-term high-resolution imaging of plant-microbe interactions*
Image credit: Tonni Grube Andersen

WHAT DETERMINES PASSAGE CELL IDENTITY AND FUNCTION?

We use transcriptional and translational genetic approaches as well as state-of-the-art single-cell techniques to investigate gene expression at the level of individual cells. This will allow us to gain insight into what defines the passage cells early during their differentiation from stem cells. A similar approach applied to the fully differentiated root parts is used to determine the genes expressed in established passage cells and thereby identify which function they have in the root.

A PLATFORM FOR HIGH-RESOLUTION, LONG-TERM IMAGING OF COMMUNICATION BETWEEN PLANT ROOTS AND THE ENVIRONMENT

The analysis of root behaviour and communication using standard protocols involves trade-offs that affect the ability to measure precise and minute changes. This complicates interpretation. Specifically, for microscopy analysis, plants are manipulated (e.g. moved to microscopy slides), which induces stress. This results in unpredictable cellular and developmental responses. Moreover, as roots respond to gravity, an important aspect to consider is that when plants are mounted in a typical horizontally oriented microscope, the roots will try to grow downwards and after a few hours will hinder imaging. An elegant and simple solution to overcome this is to "flip" the microscope at a 90° angle (Fig. 2) and thereby allow unrestrained growth along the vertical axis. When equipped with LED light illumination and fluidic media exchange systems, such a set-up supports long-term experiments with several days to weeks of continuous imaging. We can thus assess physiological plant responses and associations between roots and individual members of the microbiome over a hitherto unachievable spatio-temporal scale.

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Nour-Eldin H.H., Andersen T.G.*, Burow M., Madsen S.R., Jørgensen M.E., Olsen C.E., Dreyer I., Hedrich R., Geiger D., Halkier B.A.* ***NRT/PTR transporters are essential for translocation of glucosinolate defence compounds to seeds.*** *Nature 488, 531–534. (2012)*

**joint first authors*

ANGELA HANCOCK

My laboratory aims to clarify the mechanisms that underlie adaptation to challenging environments.

Molecular Basis of Adaptive Evolution

Understanding how plants adapt to extreme climatic and edaphic factors provides knowledge that can be applied toward conservation goals and to increase agricultural productivity. Our research focuses on *A. thaliana* and relatives living in extreme environments. The specific environmental selection pressures and traits we study are diverse, with environments including arid, edaphic and altitudinal extremes and traits including drought tolerance, timing of life cycle events, photosynthetic efficiency, metal transport, stature, and regulation of genome stability and gene expression.

AFRICAN *ARABIDOPSIS* GENOMES PROJECT

While *Arabidopsis thaliana* grows primarily in human-mediated environments, populations also grow naturally in some alpine environments. While 'relict' populations in Eurasia have largely been replaced by recent expansion of a weedy clade, we recently found that populations from mountain ranges in Africa and the offshore islands are native, representing ancient stable lineages (Durvasula and Fulgione *et al.,* 2017). As a next step, we teamed up with collaborators to sample new *A. thaliana*

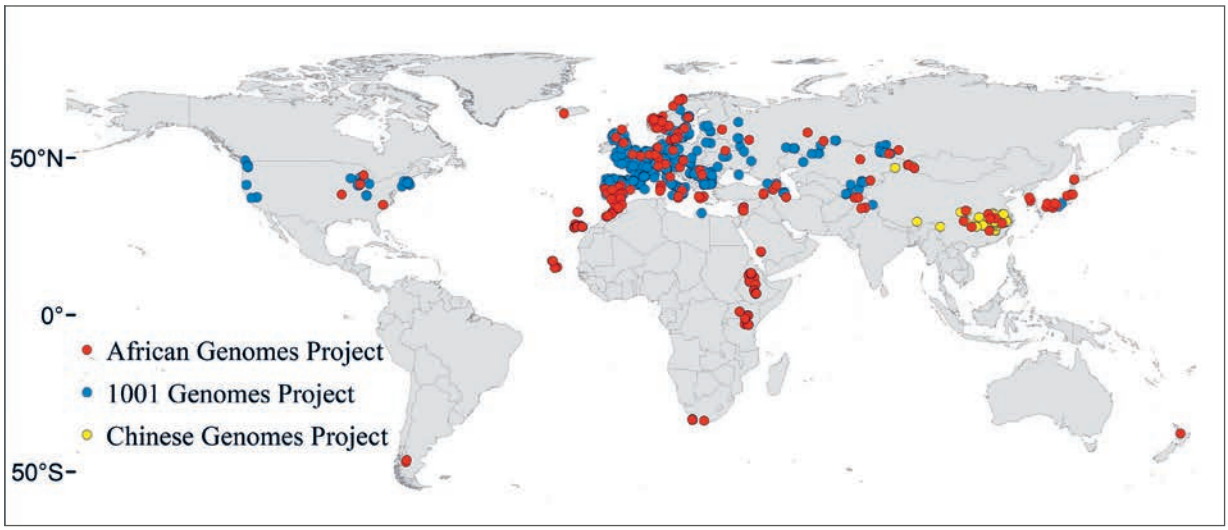

Figure 1: *Map of African Genomes Project populations (red) relative to previously sequenced A. thaliana populations (blue, yellow). Image credit: Shifa Ansari*

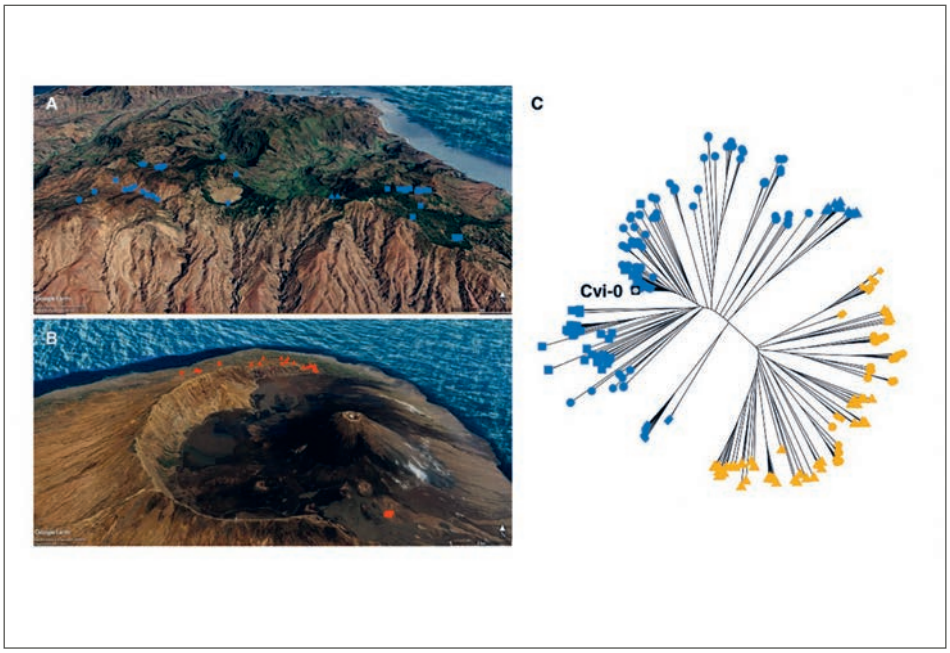

Figure 2:
Arabidopsis populations in Cape Verde
A. thaliana populations in A) Santo Antão and B) Fogo and c) a Neighbor-joining tree showing the genetic clustering of samples from the two islands.
Image credit: Célia Neto, produced from Google Earth images

populations from some of its most extreme environments, including the Cape Verde Islands, Afroalpine East Africa, the Fynbos of South Africa, Saudi Arabia, Israel and Jordan. We are leading this collaborative project to identify the genetic basis for trait variation and adaptation in a new extended set of globally distributed samples.

ADAPTATION IN CAPE VERDE ISLANDS *ARABIDOPSIS*

Cape Verde is a geographic and climatic outlier relative to Eurasian populations of *Arabidopsis* (Fulgione *et al.*, 2022). Plants in Cape Verde experience a long dry season with limited and highly variable rainfall. We collected *A. thaliana* from across its distribution on the islands Santo Antão and Fogo and have been using these accessions together with Moroccan accessions and Canary Islands accessions to reconstruct the demographic and adaptive histories of these populations (Fulgione and Neto *et al.*, 2022; Tergemina *et al.*, 2022; Elfarargi *et al.*, 2023; Neto *et al.*, 2023). This ERC-funded project aims to reconstruct broad-scale patterns of adaptive evolution as well as spatially and temporally varying selection within the islands.

ADAPTATION TO TROPICAL ALPINE ENVIRONMENTS

Plants in tropical alpine environments are faced with stress from multiple environmental factors, including cold temperatures, high UV, low CO2 partial pressure and wind. The botanist Olav Hedberg famously described the alpine tropical environment as 'summer every day and winter every night'. Because temperature varies diurnally rather than seasonally in this environment, it is an especially important selective pressure in this environment. This DFG-funded project makes use of repeated adaptive evolution across altitudinal gradients to identify the genetic basis of phenotypic convergence and to compare the genetic architecture across mountain ranges.

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THOMAS HARTWIG

Our FIND-CIS approach strives to fundamentally change how we understand and utilize gene regulation in the future.

Unravelling how Gene Regulation is encoded opens the Door for Crop Improvement

THE CHALLENGE OF UNDERSTANDING THE GENE REGULATORY GENOME

Unravelling the secrets behind how genomes encode phenotypes is one of the biggest challenges in life science. It is key to answering fundamental questions of evolution, adaptation, and also to develop climate-resilient, high-yielding crops through smart breeding. In the genomics era, genome-wide association studies (GWAS) have become to go-to tool to narrow down phenotype-determining genome regions. As such GWAS revealed that about half of the phenotype variation in crops like maize is located in the non-coding genome (Wallace et al. 2014). However, where precisely this functional regulatory variation is located in the non-coding genome is difficult to pinpoint in the absence of high-resolution maps of regulatory elements (cis-elements altogether referred to as cistrome). Current strategies to narrow down the functional parts of the non-coding genome (e.g., open chromatin analysis and transcription factor (TF) ChIP-seq) either lack the resolution to pinpoint single variants or the scalability to be employed at the population scale or under various conditions. The Hartwig Group at MPIPZ, in collaboration with the Bass laboratory at Florida State University, first developed MNase-defined cistrome Occupancy Analysis (MOA-seq, Savadel et al. 2021) to overcome these limitations. It allows genome-wide mapping of TF binding footprints in a single experiment with a high spatial resolution (~65 bp). However, MOA-seq does not provide genetic evidence for the functionality of variants, which only mutations or natural variants can provide. A worldwide consortium coordinated by the MPIPZ team, therefore, improved upon MOA-seq and conceived F1-mediated identification of non-coding cis-element-impacting SNPs (FIND-CIS). FIND-CIS allows pinpointing of putative cis-elements across a pan-genome of diverse genotypes by associating variation in genotype-specific TF-binding to epi/genetic variation across the F1 population. The novelty of using F1 hybrids ensured that epi/genetic variation could be linked to TF binding variation without trans-effects or biological/technical differences that normally challenge a quantitative analysis across a diverse population.

CONSTRUCTION OF A FIRST-GENERATION, HIGH-RESOLUTION MAP OF REGULATORY ELEMENTS

To develop the first true high-resolution map of cis-elements across a pan-genome (pan-cistrome) in plants, the team used FIND-CIS to construct a pan-cistrome of 25 maize F1 hybrids. The hybrid population, created by crossing 25 inbred lines with high-quality genome assemblies to the reference genome line B73, represents a diverse set of maize, including many of the parents of an important mapping population and several important genetic stocks. Haplotype-specific TF footprints allowed the

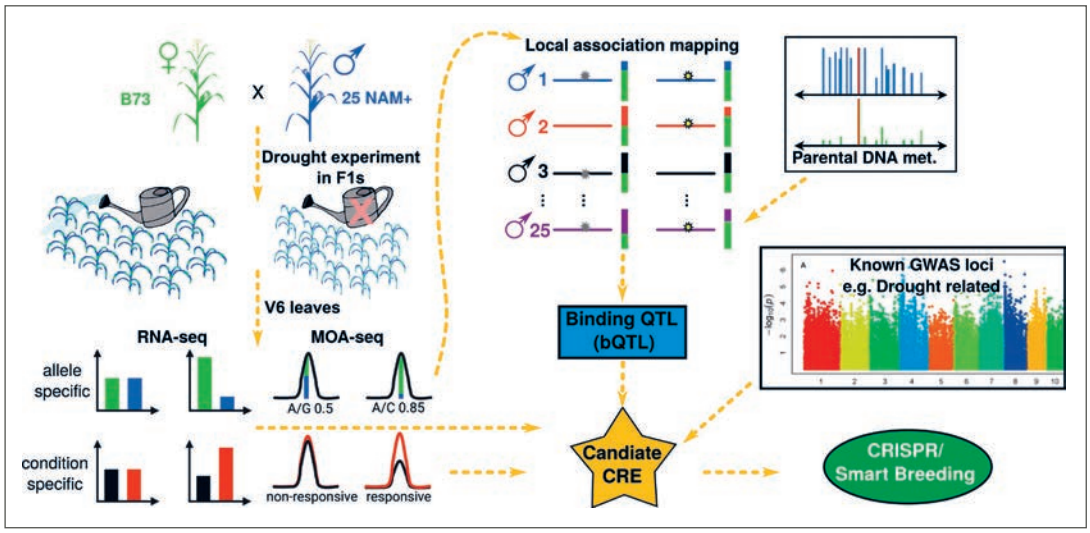

Figure 1: *Graphical FIND-CIS abstract. F1s were generated by crossing B73 with a diverse mapping population and drought-tolerant lines. A leaf pan-cistrome was constructed under drought and well-watered conditions by performing FIND-CIS, resulting in binding QTLs (bQTLs). Genetic and methylation variation was used to pinpoint variants associated with cis-element function. Integration of GWAS, condition-specific MOA-seq, and RNA-seq allows the identification of candidate cis-regulatory elements (CRE) for trait improvement, especially drought. These CRE are validated via CRISPR-based analysis.*

consortium to identify more than 200.000 variants, termed binding qualitative trait loci (bQTL), which were significantly associated with cis-element occupancy (Engelhorn *et al.*, 2024). Integration of GWAS revealed that FIND-CIS could re-discover numerous causative loci known to affect traits but with much higher accuracy than GWAS (~100 bp) (Figure 1). The association of bQTL with traits was validated by partitioning genetic variation across genomic regions. The results demonstrate that bQTL captures the majority of heritable trait variation across ~70% of the 143 tested phenotypes while comprising less than 0.05% of the maize genome (Engelhorn *et al.*, 2024).

THE POTENTIAL OF FIND-CIS TO ADDRESS CLIMATE CHALLENGES IN CROPS.

Knowledge of *cis*-regulatory variants is of particular importance for the development of stress-resilient crops. Condition-specific, fine-tuned regulation of stress-related genes could avoid disadvantages often associated with constitutive overexpression of, e.g., drought resistance genes, including reduced plant growth in non-stress conditions (Xie *et al.* 2019). Drought stress is of particular interest in the context of the climate crisis. The Hartwig Group, supported by the Deutsche Forschungsgemeinschaft (DFG), expanded their analysis to construct a drought-specific pan-cistrome and identified about 42,000 additional bQTL (DS-bQTL). Integration of the DS-bQTL with drought GWAS (Figure 1), eQTL, and haplotype/drought-specific mRNA-seq identified high-confidence drought regulation candidate variants. This again included known drought-associated variation, as well as novel variants, e.g., in the promoter and the downstream regions of ZmTINY. The Arabidopsis homolog of ZmTINY is known to confer drought tolerance but at the cost of stunted plants when overexpressed, making it a strong candidate for engineering condition-specific regulation (Xie *et al.* 2019). Together these results indicate the enormous potential of FIND-CIS to pinpoint trait-associated variation at high resolution and provide confident targets for the development of stress-resilient SMART plants as one of the core missions of CEPLAS.

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BRUNO HUETTEL

The Max Planck-Genome Centre Cologne provides advanced sequencing technologies and customized solutions for researchers within the Max Planck Society.

The Max Planck-Genome-Centre Cologne (MP-GC)

The Max Planck-Genome Centre Cologne (MP-GC), established in 2009, serves as a core facility for Next-Generation Sequencing (NGS), providing a range of sequencing services across different NGS technologies. MP-GC offers services such as DNA and RNA extraction, sample quality control, sample clean-up, fragmentation, amplicon generation, rRNA depletion, chromatin-capture (Hi-C), and library preparation for over 20 different protocols, alongside a wide array of bioinformatic services. Additionally, the facility accommodates individual requests that require either manual or automated processing.

Sequencing at MP-GC is performed on various NGS platforms, covering a broad range of samples from bacteria, fungi, plants, and animals to metagenomic and environmental samples, including water and soil. Short-read sequencing, which allows for large data generation at lower costs, is carried out on Illumina platforms, while long-read sequencing uses PacBio Revio or Nanopore technologies. Long-read sequencing is particularly beneficial for assembling genomic sequences, as it helps bridge gaps caused by repeats that hinder correct assembly with other technologies. In early 2024, MP-GC introduced methods to achieve total read lengths of 200 to 250 kb per reaction, including protocols for poly-A mRNA, single-cell mRNA, and bacterial 16S rRNA, known as “Kinnex” by PacBio. Partner MPIs have adopted these methods and the principle is also applicable to other techniques, like the TeloPrime (Lexogen) IsoSeq protocol, for enhanced full-length cDNA data.

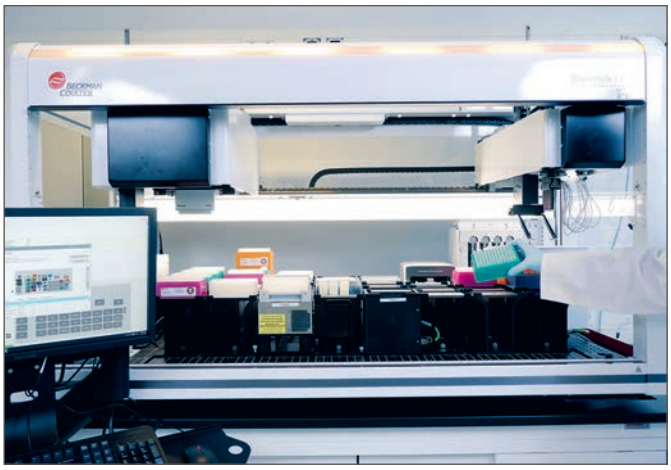

Figure 1: *Automated NGS library preparation using robotic systems. At MP-GC, high-throughput NGS library preparation is routinely conducted on a 96-well scale using robotic platforms like the Biomek i7. This approach minimizes hands-on time and reduces variability in liquid handling. MP-GC also customizes existing protocols and develops new ones as needed.*

In transcriptomics, long reads allow for full-length cDNA sequencing, aiding in detecting splicing variants. MP-GC also supports single-cell genomics and transcriptomics by combining cell sorting tools (FACSAria, BD) with microfluidics (e.g. Chromium box of 10x Genomics) to create single-cell specific sequencing libraries. MP-GC’s computing facility includes high-performance servers, data management infrastructure, an Isilon storage system, and a tape-based data archive system to handle the vast amount of data generated.

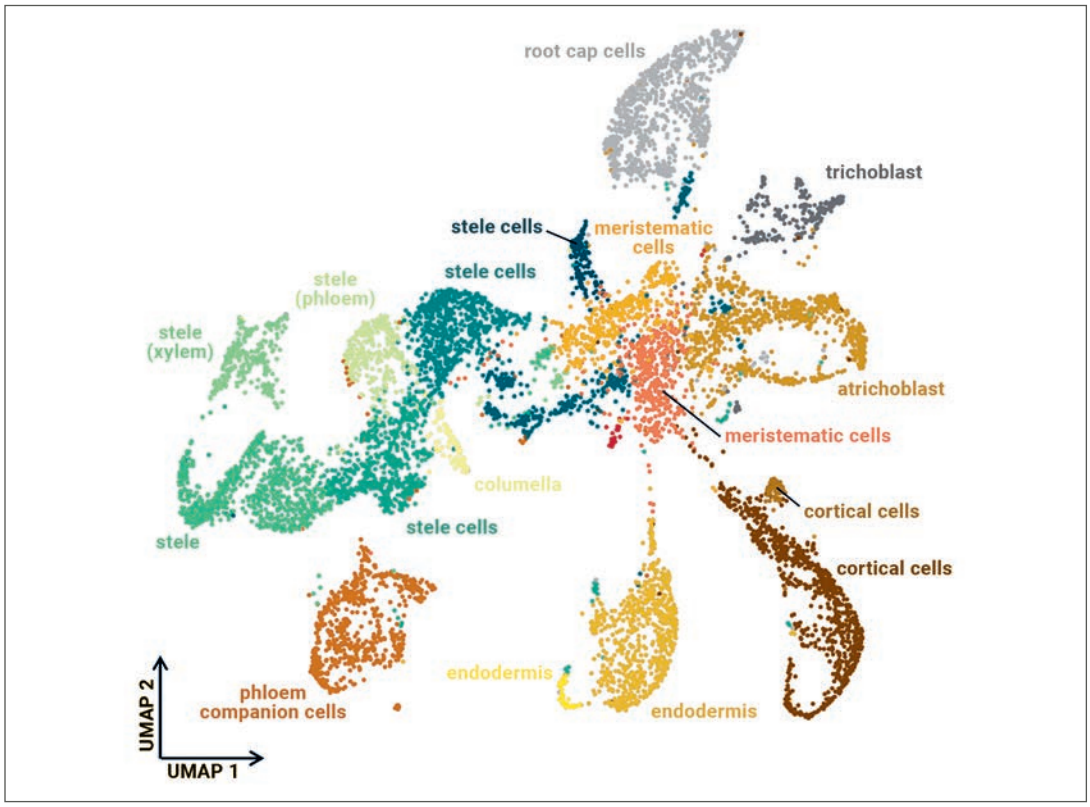

Figure 2: *Uniform Manifold Approximation and Projection (UMAP) visualization displaying cell labels and feature plots for selected marker genes in Arabidopsis thaliana. Single-cell RNA sequencing successfully identified major cell types of the targeted root tissue. This pilot work on plant cells was executed and analysed in cooperation with Singleron, Cologne.*

The facility also features a robotics section equipped with instruments for high-throughput sample processing and lab automation. Routine tasks include advanced sample pooling, automated nucleic acid extraction, and automated NGS library preparation, with the capability to automate more complex workflows upon request.

A key feature that sets MP-GC apart from commercial sequencing providers is its flexibility in planning and processing sequencing requests according to each scientist's specific needs. This includes applying the latest NGS and bioinformatics technologies, providing individualized guidance from template generation to data analysis, and performing stringent quality checks on input materials.

MP-GC also develops and adapts library preparation protocols and automation procedures to meet specific requirements, particularly for low-quality or low-quantity samples. The facility supports both small- and large-scale projects, with virtually no limits on sequencing amounts, helping scientists from various Max Planck Institutes successfully to implement their NGS projects.

MPI scientists are encouraged to visit the MP-GC to learn the necessary sample preparation methods and utilize the MP-GC's infrastructure for their research projects.

For more details, please visit our website (http://mpgc.mpipz.mpg.de).

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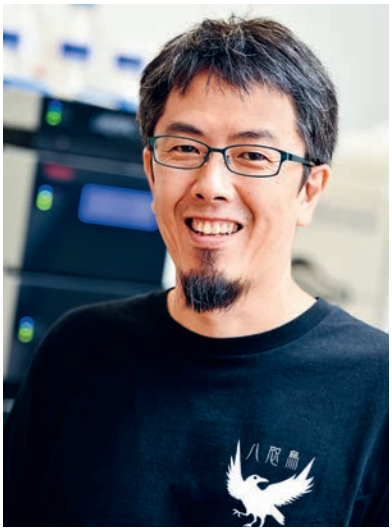
Kuo, Y.-T., Souza Câmara, A., Schubert, V., et al. ***Holocentromeres can consist of merely a few megabase-sized satellite arrays.*** *Nature Communications 14, 3502, doi: 10.1038/s41467-023-38922-7. (2023)*



HIROFUMI NAKAGAMI

Marchantia polymorpha whispers the origin and evolution of plant immunity.

Protein Mass Spectrometry Service and the Evolution of Plant Immune System

PROTEIN MASS SPECTROMETRY SERVICE

Proteotype is an influential layer to explain genotype-phenotype relationships. This is because proteins are responsible for orchestrating a whole range of cell functions. Protein levels do not necessarily correlate with transcript levels. Protein functions are also regulated by post-translational modifications and protein-protein interactions, which cannot be read from genome information. It is therefore important to determine and monitor protein abundance, proteoforms, and complex formation in order to identify regulatory components and understand the molecular mechanisms controlling plant traits.

The protein mass spectrometry service unit is equipped with state-of-the-art liquid chromatography-mass spectrometry (LC-MS) systems and has been expanding its repertoire in order to offer up-to-date service for measuring protein status. Recent research outcomes achieved together with a number of research groups confirm the power of proteomics for understanding plant systems. We are able to identify and quantify over 5000 proteins in an untargeted manner. This enables the discovery of proteins that regulate plant traits. In combination with highly efficient modified-peptide enrichment methods, we can monitor phosphorylation and ubiquitination status of thousands of proteins. We can also perform a targeted quantification, parallel reaction monitoring (PRM), which allows the sensitive detection and accurate quantification of peptides/proteins of interest in complex samples. The recent interactome analysis method using TurboID-based proximity labelling was established for plant materials. Next challenge is to establish a single cell analysis platform for plants.

ESTABLISHING THE LIVERWORT *MARCHANTIA POLYMORPHA* AS A MODEL FOR EVO-MPMI STUDY

Understanding the origin and evolution of plant immune system can give us novel ideas for developing universal plant protection technologies. The monophyletic bryophytes, comprising mosses, liverworts, and hornworts, is a sister clade to tracheophytes. The two plant lineages diverged from the

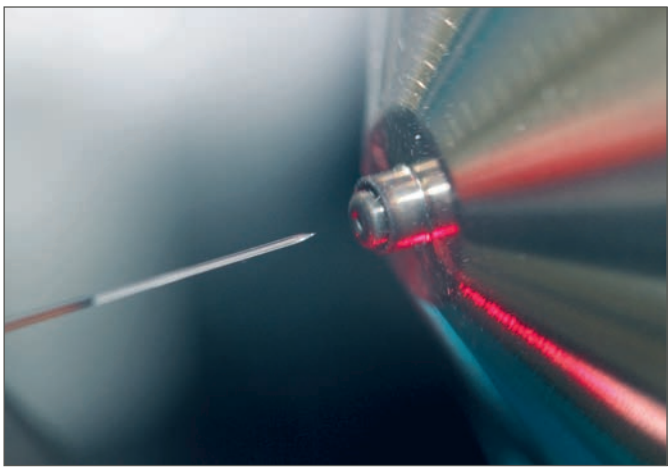


Figure 1: *LC–MS image*
Image credit: Hirofumi Nakagami

Figure 2: *Marchantia polymorpha growing in human-made environments*
Image credit: Thomas Ryohei Nakano

common ancestor of land plants, placing bryophytes in a significant position in the research of Evo-MPMI (evolutionary molecular plant-microbe interactions). The liverwort *Marchantia polymorpha,* which can be found around the human habitat, has been established as an experimental bryophyte model (Figure 1). The majority of immune-related genes characterized in angiosperms have been identified in the genome of *M. polymorpha.* Importantly, *M. polymorpha* did not undergo whole-genome duplication, with the consequence that genetic redundancy is low. The overall simplicity of gene families in this species holds advantages for genetic analysis. Studying plant-microbe interactions in *M. polymorpha* requires the establishment of proper and diverse pathosystems. We established the bioluminescence-based system to monitor growth of bacterial pathogens in *M. polymorpha,* which paved the way for discovering immunity-related components in this species.

CONSERVATION AND DIVERSIFICATION OF IMMUNE SYSTEM IN LAND PLANTS

Pattern-triggered immunity (PTI), mediated by cell-surface-localized pattern-recognition receptors (PRRs) recognizing microbe-derived molecules, serves as the first line of inducible defence in angiosperms. We discovered that *M. polymorpha* can sense fungi- and bacteria-derived molecules through LysM-type PRRs contributing to defence against fungal and bacterial pathogens. Our finding suggests that PTI was already present in the last common ancestor of all land plants. Our next goal is to understand when and how PTI was established.

Salicylic acid (SA) is a major defence-related phytohormone, which primarily induces resistance against biotrophic and hemi-biotrophic pathogens in angiosperms. In the model angiosperm *Arabidopsis thaliana,* NPR proteins function as SA receptors. AtNPR1 plays a central role in SA-induced transcriptional reprogramming whereby it positively regulates disease resistance. We discovered that the only NPR in *M. polymorpha,* MpNPR, is not the master regulator of SA-induced transcriptional reprogramming and negatively regulates bacterial resistance in this species. We found that MpNPR plays role in temperature and far-red responses. We are currently exploring the molecular function of MpNPR, aiming to shed light on the ancestral functions of NPR.

SELECTED PUBLICATIONS

Phookaew, P., Ma, Y., Suzuki, T., et al. ***Active protein ubiquitination regulates xylem vessel functionality.*** *Plant Cell, 36(9):3298-3317.(2024)*

Jeon, H.W., Iwakawa, H., Naramoto, S., et al. ***Contrasting and conserved roles of NPR pathways in diverged land plant lineages.*** *New Phytologist, 243(6):2295-2310. (2024)*

Yotsui, I., Matsui, H., Miyauchi, S., et al. ***LysM-mediated signaling in Marchantia polymorpha highlights the conservation of pattern-triggered immunity in land plants.*** *Current Biology, 33(17):3732-3746.e8. (2023)*

Melkonian, K., Stolze, S.C., Harzen, A., et al. ***miniTurbo-based interactomics of two plasma membrane-localized SNARE proteins in Marchantia polymorpha.*** *New Phytologist, 235(2):786-800. (2022)*

Pruitt, R.N., Locci, F., Wanke, F., et al. ***The EDS1-PAD4-ADR1 node mediates Arabidopsis pattern-triggered immunity.*** *Nature, 598(7881):495-499. (2021)*

TON TIMMERS

Imaging plants over many scales and as close to their native state as achievable.

Central Microscopy (CeMic)

The task of the Central Microscopy service group is to consult and advise researchers on imaging techniques as well as image processing and analysis. CeMic manages the microscope equipment of the MPIPZ and trains and supervises researchers in the operation of the instruments – either individually or in the form of practical courses and workshops on topics of general interest. The imaging requirements range from the whole plant level (with objects as large as several centimetres) to molecular details (like protein complexes at the nanoscale level). To cover this size range, the entire spectrum of imaging technologies – from a simple stereomicroscope to a sophisticated super-resolution light microscope and electron microscope – is available. CeMic also implements new sample preparation and imaging protocols to exploit the full potential that the technologies of the various microscopes provide.

FLUORESCENCE MICROSCOPY

The fluorescent tagging of proteins has revolutionised the field of live imaging. We can now visualise cellular processes in living organisms at high resolution and speed. This allows us to monitor organelle movement, gene expression and protein abundance and distribution as well as interaction with other cellular components. For this, the MPIPZ has modern fluorescence microscopes with both wide-field and confocal systems. For whole plant organ imaging,

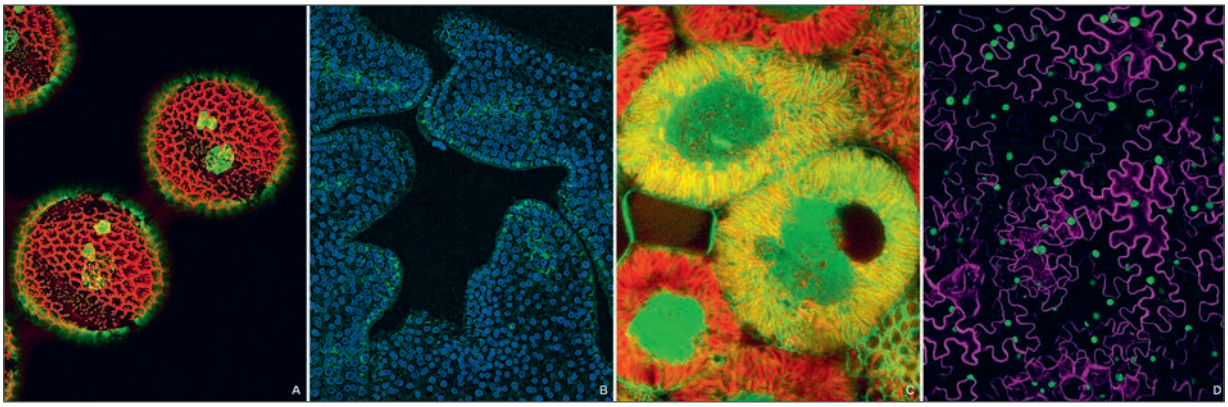


Figure 1: *Confocal laser scanning microscopy.*
A. Pollen of Brassica napus stained with a red nuclear dye.
B: Immuno-localisation of the auxin transporter PIN1 in green in Cardamine hirsuta shoots. Nuclei (blue) are stained with DAPI.
C: Live cell imaging of plasma membrane marker (green) in nodule cells of Medicago truncatula, invaded by rhizobia (red).
D. Simultaneous live cell imaging of nuclei in green and plasma membrane in magenta in leaf of Nicotiana benthamiana.
Image credit: Ton Timmers

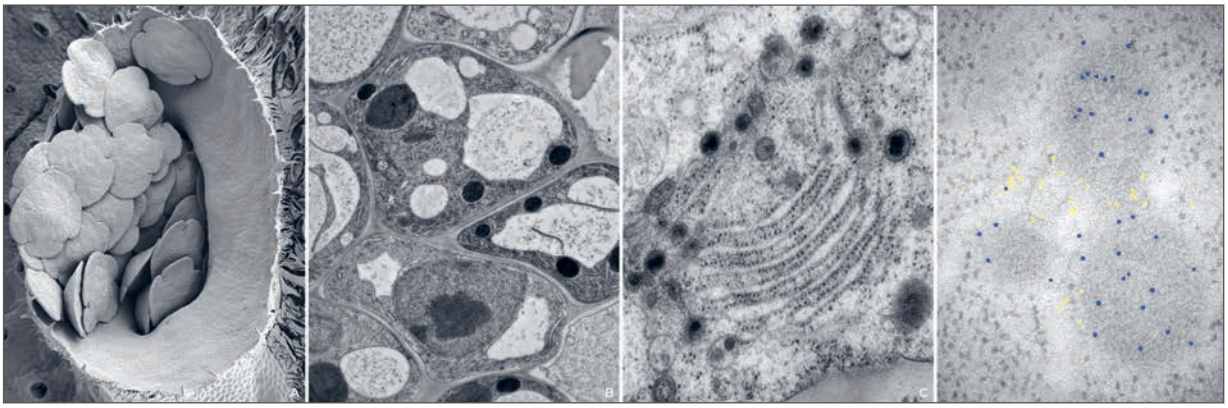


Figure 2: *Scanning and transmission electron microscopy.*
A. Thallus surface of Marchantia polymorpha with cup-shaped receptacle containing lentil-shaped units of vegetative propagation, the so-called gemmae (SEM).
B. Transmission electron micrograph of small vein cells in the valve of Cardamine hirsuta fruits processed by high-pressure freezing and freeze substitution.
C. Endoplasmic reticulum (ER) and attached vesicles in developing pollen grains (pseudomonads) of Rhynchospora pubera (TEM).
D. Double immunogold labelling of a triple ATPase (yellow pseudocolour) involved in the regulation of perennial flowering located between a small cluster of peroxisomes (blue pseudocolour) in root cells of Arabis alpina.
Image credit: Rainer Franzen and Ulla Neumann

clearing techniques are used in combination with multiphoton fluorescence microscopy and 3D imaging processing and analysis. Fast fluorescence life time (FLIM) analysis is used to differentiate between specific and non-specific fluorescence and monitor molecular interactions in vivo by measuring fluorescence resonance energy transfer (FRET).

Two technically different systems for super resolution are available at the institute: an Airy scan confocal microscope and a STED (Stimulated Emission Depletion) microscope.

ELECTRON MICROSCOPY

In microscopy, the highest magnification and resolution is achieved with transmission electron microscopy (TEM). Subtle changes in fine structure within cells or in the morphology of the cell wall can be identified and cellular constituents can be precisely localised with immuno-gold antibody labelling technology. During sample preparation, the fine cellular ultrastructure close to the native state is preserved through the use of ultra-rapid cryo-immobilization (high-pressure freezing) in combination with freeze-substitution.

Scanning electron microscopy (SEM) is used when fine detail in the morphology of plant organs needs to be analysed. The institute has an instrument that reaches a high resolution and magnification at low voltage and which can also be operated in cryo-mode.

RESEARCH

The principal research projects are conducted in collaboration with the research groups at the institute. In the framework of CEPLAS, collaborations with the groups of Alga Zuccaro and Gunther Döhlemann from the University of Cologne, investigated plant-fungal interactions at the TEM level. External collaborations include a project on nodulation in legumes with the group of Clare Gough from Toulouse in France.

SELECTED PUBLICATIONS

Shen Q., Hasegawa K., Oelerich N., et al. ***Cytoplasmic calcium influx mediated by plant MLKLs confers TNL-triggered immunity.*** *Cell Host & Microbe 32, 1-13. (2024)*

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Shen D., Wippel K., Remmel S., et al. ***The Arabidopsis SGN3/GSO1 receptor kinase integrates soil nitrogen status into shoot development.*** *EMBO Journal 43, 2468-2505. (2024)*

Amanda D., Frey F.P., Neumann U., et al. ***Auxin boosts energy generation pathways to fuel pollen maturation in barley.*** *Current Biology 32, 1798-1811. (2022)*

Viñegra de la Torre N., Vayssières A., Obeng-Hinneh E., et al. ***R2 FLOWERING REPRESSOR AAA+ ATPase 1 is a novel regulator of perennial flowering in Arabis alpina.*** *New Phytologist 236, 729-744. (2022)*

SERVICE AND FACILITIES: INTERNATIONAL MAX PLANCK RESEARCH SCHOOL (IMPRS)

PhD coordinator: Monika Schlosser

Attracting and educating early career researchers in the plant sciences is a key interest of the MPIPZ. Together with the universities in Cologne and Düsseldorf, the institute has been successfully running one of over 60 International Max Planck Research Schools (IMPRS) for over two decades. The IMPRS on Understanding Complex Plant Traits using Computational and Evolutionary Approaches recruits outstanding students from all over the world and offers various interdisciplinary and collaborative graduate projects in a stimulating environment with access to the state-of-the-art infrastructure available at all three IMPRS partner institutions.

All doctoral candidates regularly meet an advisory committee of experienced experts to constructively discuss the scientific progress made in the doctoral project. This ensures a timely completion of doctoral projects and promotes networking with the committee members that typically come from various institutions. Joint IMPRS activities such as scientific retreats further strengthen the interaction between doctoral researchers and their supervisors. The IMPRS organises training in core scientific skills such as writing, presenting, and publishing and supports doctoral researchers in attending international meetings. Upon completion of the doctorate, our early career researchers are accordingly anchored in the scientific community and equipped with the necessary skills for a successful career in the plant sciences.

The IMPRS programme also provides training in transferable skills that have become increasingly relevant in the job market. Courses and workshops organised at the MPIPZ are complemented with a large number of offerings from the partner universities. Both the University of Cologne and the Heinrich Heine University of Düsseldorf have established and professionalised cross-faculty- and more specialised graduate programmes to which all of our doctoral researchers have access. Several hundred international students, including those from high profile institutions, apply to the IMPRS programme each year, thereby demonstrating the MPIPZ's reputation as an attractive institute at which to obtain a doctorate.

SERVICE AND FACILITIES: POSTDOCTORAL OFFICE

Post-doc coordinator: Francesca Stomeo

The postdoctoral period is crucial for developing independent research skills, establishing a research niche and building professional networks in academia. With this in mind, the MPIPZ provides an ideal environment for postdoctoral researchers to advance their scientific careers, receive training in cutting-edge technologies and establish international collaborations.

The MPIPZ Postdoc Office supports MPIPZ postdocs in their onboarding, community building, career development, training and networking activities by providing a wide range of guidance and resources. New postdocs are introduced to these resources through tailored welcome sessions. Information and pipelines on Max Planck Society (Planck Academy) training opportunities, outreach activities, gender equality, well-being, contact and reporting points are shared with all new postdocs. Throughout their time at the MPIPZ, postdocs have regular annual meetings with the Postdoc Office to ensure ongoing support and guidance.

The main focus of the Postdoc Office is to provide postdocs with dedicated career development support. All MPIPZ postdocs benefit from a career development program that facilitates communication between postdocs and supervisors, enhances career awareness and soft skills, provides training opportunities, and highlights the skills necessary for future career success. During these career counselling sessions, postdocs can share their career vision, brainstorm their strengths, weaknesses and career goals, and receive advice on career planning. Another important activity of the Postdoc Office is mentoring, especially for female scientists, and career coaching by connecting postdocs with mentoring and coaching programs of the Max Planck Society. In addition, the Postdoc Office offers grant writing support in cooperation with the EU Liaison Office.

The Postdoc Office works closely with representatives of the Postdoc Initiative at MPIPZ (PIM) to understand the priorities and concerns of postdocs and to develop appropriate strategies. Regular annual events such as symposiums, career days and retreats are organised to promote networking, community building, scientific exchange, career opportunities and to increase the visibility of postdocs. Monthly events such as coffee breaks ensure ongoing interaction among postdocs and between postdocs and the Postdoc Office.

In addition, the MPIPZ co-organises the biennial CRAG-JIC-MPIPZ Early Career Researchers' Conference, demonstrating the shared commitment of the three institutes to promote and support the careers of postdocs and PhD students in their final year.

SERVICE AND FACILITIES: PHD REPRESENTATIVES AT THE MPIPZ

Once a year, the doctoral candidates at the MPIPZ elect representatives to act as spokespersons for the PhD community. This team of PhD representatives consists of an external representative and internal representatives, typically one or two internal representatives per department as well as from the associated university. The external representative is the main link between the MPIPZ and the Max Planck Society PhDNet, which is a network of all MPS doctoral candidates. The external and internal PhD representatives act at the interface between the PhD community, the administration, and the directors of the Institute. This group of doctoral candidates works closely with the PhD coordinator and is responsible for bringing issues and raising concerns, both to and from doctoral candidates. Communication between the PhD representatives of different institutes within the MPS is strongly supported by the PhDNet and MPIPZ. Within the past two years, several improvements for doctoral candidates have been implemented. These mainly concern equality of payment between stipend and contract holders. One big achievement was designing and circulating an MPIPZ-internal PhD Survey in the past two consecutive years. This allows the doctoral candidates to paint a picture of their respective situations. Among other things, the survey revealed a discrepancy in number of holiday days between different contract holders. In 2019, PhDNet successfully negotiated with the General Administration after identifying the same issue at the MPS level. This resulted in ensuring 30 days of holiday for every PhD contract holder. Just recently in early 2021, in a joint effort of the PhDNet, this increase of annual holidays was followed by a raise of MPG PhD-contracts from 50% to 65% E13 salary. Another important achievement made in close collaboration with the PhD coordinator was establishing funding possibilities for online courses and workshops, thereby providing an even greater pool of high-quality workshops beyond the ones organized on site. PhD representatives were also highly involved in organizing the first Mental Health Awareness Week at the MPIPZ. This included several engaging lectures and workshops. Parallel to scientific interests, PhD representatives also support the social aspect of PhD community life by organizing and supporting joint PhD meetings and social activities such as barbecues, Christmas parties, get-togethers, and sporting events, among others. PhD representatives have contributed to meetings, events and improving infrastructure at the MPIPZ, such as the bike shed. Sometimes scientific and social engagement of the PhD representatives go hand in hand. For instance, a new event of PhD exchange between MPIPZ and the Max Planck Institute of Molecular Plant Physiology was initiated by PhD representatives of MPIPZ and the PhD coordinators. As highlighted by these examples, the PhD representatives actively work as a team to promote the interests of the both PhD individuals and the PhD community at the MPIPZ.

SERVICE AND FACILITIES:
POST-DOC INITIATIVE AT THE MPIPZ (PIM)

The Postdoc Initiative at the MPIPZ (PIM) is a group of postdocs that represent the interests of postdocs at the institute as well as within the Max Planck Society. Postdoctoral researchers are one of the backbones of academia, conducting high-level research while on short-term temporary contracts, and searching for stability inside or outside academia. The postdocs in the PIM are not elected but are volunteers, motivated to find ways to make the postdoctoral experience and future career prospects better.

Since postdocs are already quite independent, establishing collaboration and socializing with other postdocs – particularly with those having a different scientific focus and expertise- can be challenging. One of the PIM's main goals is to offer opportunities for postdocs to grow professionally through various scientific events, with the financial support of the MPIPZ. At least once a year, supported by the Postdoc Office, the PIM organizes a large Postdoc Symposium or Retreat held at either the MPIPZ or an external site, where postdocs can discuss their research and important postdoctoral issues, receive career development advice from guests, and socialize.

Throughout the year, organized career development workshops, coffee breaks, and smaller social events are held to create a more well-rounded postdoc community. The PIM collaborates with both the John Innes Center and the Centre for Research in Agricultural Genomics to host the biennial Early Career Researchers' Conferences.

The other main goal of the PIM is to address concerns that postdocs may have regarding their working conditions, research group environment, immigration, lab environments, and general well-being. The PIM regularly meets with the Postdoc Officer & Scientific Coordinator and the Managing Director to discuss concerns and develop plans for addressing them.

In the past several years, the MPIPZ has joined the MPG PostdocNet, a network that aims to improve the working conditions and scientific development of all postdocs across the MPG. Every year the postdocs elect an External Representative who is the de facto liaison between the MPIPZ and the PostdocNet. This representative distributes relevant information from the PostdocNet to the MPIPZ postdocs and annually meets with the Steering Group and other MPG External Representatives to discuss MPG- and German-wide issues. Several postdocs at the institute have joined the PostdocNet's Working Groups and some have been elected to the Steering Group.

SERVICE AND FACILITIES: ADMINISTRATION

Manager: Karsten Schürmann

A responsible and compliant behaviour of all employees is an important factor for the Max Planck Society and its Institutes. Laws and internal regulations show the framework of the requirements. There are internal administrative functions that help to fulfill all the needs and offer service and assistance in case of questions:

HUMAN RESOURCES

- Responsible for a total of 370-400 employees (guests, interns, temporary staff, doctoral students, postdocs, non-scientific staff; ~60% of whom come from ~40 different countries),
- Offers support in the application and recruitment process,
- Assists colleagues from the 1st to the last working day at the Institute (e.g regarding contracts and amendments, social insurance issues, check salary slips),
- Helps with Job Ticket offer

ACCOUNTING

- Accounting and Payment Processing
- Asset Accounting and Administration
- Cost Performance Accounting
- Masterdata Management
- Finance and Budget Reporting
- Laws & Compliance

INTERNATIONAL OFFICE

Assistance with

- Visa applications
- Arrangement of the appointment for the registration at the home town
- Opening bank accounts
- German language courses at different levels

PURCHASE AND RECEIVING UNIT

- Offers consulting all over the purchase procedure and its specific requirements
- Executes the purchases
- Delivers incoming goods to the internal requistioner

TRAVEL OFFICE & WEDNESDAY SEMINARS

- Booking main transport & hotel
- Advanced payment of necessary business costs (i.e. conference fees)
- Reimbursement of the journey

THIRD PARTY FUNDING OFFICE

- Administrative help with third party funding applications
- Financial issues during projects' runtime (payment request, forecasts)
- Financial overviews and final administrative reports
- Cooperation with MPG headquarters Munich for tax and contract compliance

HEALTH & SAFETY

- Occupational health and safety specialist
- Biological safety officer
- Export controls – biological substances
- Authorised person according to ADR and IATA
- Chemical waste officer
- Radiation safety officer
- Company health management (Betriebliches Gesundheitsmanagement)

SERVICE AND FACILITIES:
PUBLIC RELATIONS AND OUTREACH

Mia von Scheven

The Institute's Public Relations (PR) and Outreach efforts play a crucial role in connecting our research with the public, the media, and the wider scientific community.

By effectively communicating complex plant science issues, the PR office enhances public understanding of the vital role that plants play in addressing global challenges such as food security, biodiversity loss, and climate change. A key aspect of the Institute's PR work is the dissemination of research findings through press releases to ensure that the Institute's discoveries reach a wide audience. The PR office also manages the Institute's social media platforms, sharing research updates and event details to engage with a diverse audience.

The PR and Outreach Office organises public events where researchers present their work in an accessible way. Outreach activities are important for the Institute's aim, bridging the gap between advanced scientific knowledge and society. Activities are tailored to the different audiences and provide an insight into the research conducted at the Institute, the scientific methods used as well as career opportunities in the plant sciences. The Institute holds public lectures and takes part in broader national and international science communication events, such as Girls' Day, Cologne Children's University, Pint of Science, Soapbox Science or the Fascination of Plants Day.

The Insitute's Show Garden and WissenschaftsScheune (science barn) provide an excellent platform for engaging with primary and secondary school children as well as teachers, students, associations, journalists, families and the general public through hands-on experiences, combining indoor and outdoor activities.

The aim of the WissenschaftsScheune is to arouse curiosity about plant science. It offers a wide spectrum of topics from basic research to sustainable agriculture.

Located on the neighboring farm, it offers space for presentations, exhibitions, and interactive displays with a mock laboratory area.

In the Show Garden, more than 100 cultivated and wild species are grown in small plots surrounded by biotopic structures. As well as showcasing the Institute's research, visitors will also learn how advances in plant genetics lead to practical solutions like the development of efficient breeding techniques and crop protection strategies.

The PR and Outreach Office works together with various committees and organisations such as the Kölner Wissenschaftsrunde (Cologne Science Circle), the University of Cologne, CEPLAS and the European Plant Science Organisation (EPSO).

The Institute's commitment to science communication ensures that the wider public can engage with the latest developments in plant science and understand their relevance for society.

SERVICE AND FACILITIES: LIBRARY AND INFORMATION SERVICE

Britta Hoffmann

The Library of the Max-Planck-Institute for Plant Breeding Research provides literature, electronic media and information services to its scientific staff and guests. The collection is focused on the fields of research covered by the departments and the research groups at the institute. In 2024 the library holdings comprise approximately 23,000 printed journal-volumes and 6,000 monographs. The printed holdings can be searched in the online catalogue.

The MPIPZ Library, together with the Max-Planck-Digital Library of the Max-Planck-Society, provides a selection of numerous electronic journals and other scientific information resources like e-books and databases. Currently there is access to about 17,000 E-Journals and 900,000 E-books from all areas of science. The institute pays for this service with 0.9 % of its budget. A committee of scientists gives support to the library concerning questions related to the research needs of the institute. In addition to this the library obtains all literature, which is not available on site, either electronically or as hard copy.

The library supports scientists in all questions of information retrieval and open access publishing. It is the interface to the Max Planck Digital Library, which negotiates central contracts with publishers. These contracts enable scientists of the Max Planck Society to publish free of charge in about 5,000 open access journals.

Furthermore, the library collects all institute publications for institutional self-archiving of research output on the publication repository of the Max Planck Society (MPG.PuRe) and provides all publications on the web site.

The librarian is also responsible for organising and maintaining the MPIPZ's internet and intranet.

TECHNICAL EQUIPMENT:

There are 14 PC workstations and eight additional workstations for private laptops. Two separate rooms with PCs are also available for temporary staff.

SERVICE AND FACILITIES:
IT SERVICES

Manager: Marc Thoben

The IT Services group focuses on customer-focused services and currently consists of seven IT platform and network specialists, three trainees for systems integration and the head of the group. The MPIPZ houses an extensive and diverse networked IT infrastructure, including

- A hybrid storage cluster consisting of redundant disk arrays and a robotic tape library
- A high-performance computing (HPC) cluster
- Several clusters of virtualisation servers for hosting various services:
  - Email and collaboration services
  - Customised web services
  - Fax, print and file sharing servers
  - Electronic laboratory notebooks (ELN)
  - Microscopy image archives
  - Remote access facilities

Modern high-performance microscopes come with directly attached computer workstations and large local storage systems that require a huge amount of microscopy data to be transferred to the Institute's central storage system. The microscopy workstations also require constant special technical support and maintenance. The IT group assists the central microscopy team in this.

Numerous computer-based, networked control systems are used in the buildings on the campus. These systems are operated by the facility. The IT group also works closely with the facility team, providing IT-related support, discussing further development and providing technical input into the IT requirements of new construction projects.

The IT Services group advises on the selection of computing equipment, assists with all procurement procedures and provides all levels of technical support to MPIPZ researchers and staff.

The further development of the campus IT infrastructure is planned in close cooperation with the Board of Directors, the Bioinformatics Steering Committee (BISCOM), the Sustainable Research Initiative, the Research Faculty Meeting (RFM) and the Greenhouse Group. The group is also connected to other Max Planck Institutes and is in constant exchange with them. They actively support any individual IT projects upon request. Notable examples include the Greenhouse management software for ordering space for plant trays and pots, and IT-related aspects of new high-performance microscopes and their extended storage and network requirements.

SERVICE AND FACILITIES: GREENHOUSE MANAGEMENT

Manager: Aristeidis Stamatakis

The group works in cooperation with scientists to grow plants (model plants, rice, maize, tomatoes) for scientific experiments. It also looks after the green areas associated with the Institute, including the demonstration garden and the open field trials. The team consists of ten gardeners, five assistants, two technical supervisors and the group manager. The main tasks are as follows:

- Preparing pots, sowing and transplanting
- Irrigation and nutrient management
- Sustainable plant protection
- Propagation of wild type plants
- Controlling growing conditions
- Ensuring plant quality

THE GREENHOUSE AREA HAS AS FOLLOWS:

- Greenhouses 1 and 2, with a total area of 4,000 m^2, consist of 24 8x8 cooled, 10 8x8 and 4 8x16 uncooled cabins. They are equipped with dimmable LEDs providing high uniformity of light intensity at bench level.
- Greenhouse 4, consists of four 12x9 and three 12x6. Three of them are also equiped with LEDs.
- Greenhouse 5 has three 8.4x9 cooled cabins.
- Two Saran greenhouses (total area 300 m^2) where crops can be grown under more natural conditions for a longer growing season.

There are also 70 growth chambers and 20 walk-in chambers spread in growth halls.

THE OPEN AREA UNDER CULTIVATION IS AS FOLLOWS:

- 14,000 m^2 (1.4 hectares) of arable land and consists of fruit trees and a demonstration garden of about 1,300 m^2
- Twenty-one cold frames (15 m^2 each) equipped with an automatic irrigation system.
- 33,000 m^2 of lawn.

A special greenhouse management software has been developed that uses barcodes to provide full traceability of the growing procedure and the exact position of each tray in the growing facilities.

Integrated Pest Management, a decision-making process that combines biological, cultural, physical and chemical tools to manage and reduce the risk of pests and diseases, is used in the greenhouse facilities. Frequent inspections of plants are carried out in combination with the installation of colour traps to monitor the population of harmful insects. Beneficial insects are released weekly as beneficial nematodes and B. thuringiensis is applied to the soil. Ground cork material is applied to the top of each pot to prevent insects from laying eggs. Plants such as Ricunus spp. that host beneficial insects are grown in the facilities. Spraying takes place when is necessary and always in accordance with the safety regulations for the greenhouse staff and the scientific and technical staff working in the greenhouse.

Irrigation is one of the most important components in growing healthy flowers, foliage and fruit. As each crop requires a unique irrigation management, capillary mats are used to eliminate irrigation problems.

SERVICE AND FACILITIES:
TECHNICAL SERVICES

Manager: José Luis Costa Blanco

The Technical Service is an interdisciplinary service group with 14 specialists from the sectors of construction engineering, electrical, sanitary, air conditioning and ventilation, as well as precision mechanics and facility management. This team is supplemented by additional technicians in whose responsibility is the electrical inspection of the about 13,000 electrical equipments on site.

In general, this service group takes care of the complete building set-up and the supply of essential energies. This includes corrective and preventive maintenance to ensure the operational reliability of the critical system components. In addition, this non-scientific service group is also responsible for the external cleaning and the gate services. The central building control system and administrate technical parts, e.g., distribution of chips, keys or the guest rooms are also established in this group.

A 24/7 technical emergency standby service is provided and covered by the technicians to maintain all science-related equipment in operation.

This special institute never rests and we have buildings that date back to the 1950s. Therefore, a construction coordinator at the Institute makes sure that all needed construction measures get implemented and participates in the planification for current and future construction projects.

An assistance centre for researchers, known as the “Scientific Workshop”, is also part of the Technical Services team. The colleagues take care of the individual technical needs from the scientist and offer their experience for individual programming, development or support of Lab-Automation.

THESE INCLUDE:

- Software and hardware development and support for Lab-Automation.
- Develop hardware extensions for robotic and lab devices
- Develop electronic, pneumatic and microcontroller devices (example: measuring and control sensors and actuators, light control for devices, gripper to hold a plate…)
- Technical questions and support for lab devices (example: test thermocycler (temperature and ramp time))
- Support and consulting by seeking and purchase a new lab device and software (robotic, shaker, thermocycler…)
- Technical consulting by lab projects and recommendations “for make or buy”

DIRECTIONS AND CONTACT:
HOW TO GET TO THE MPIPZ

BY CAR

- Highway A1 (north): Take the Bocklemünd exit (# 102), turn left at crossroads, follow Venloer Straße, direction Köln-Zentrum. After approx. 2 km turn right at crossroads, follow “Militärring”. After approx. 1 km turn right and follow the signs to the Max Planck Institute.
- Highway A1 (south): Take the Lövenich exit (# 103), turn right at crossroads, follow Aachener Straße, direction Köln-Zentrum.
- After about 1 km turn right towards A1 (north), A57 (north), Ossendorf, (Militärring).
- Turn left at next intersection (T crossing), take the third exit and follow the signs to the Max Planck Institute.
- If you are using your navigation system, please note that to reach the Institute from the right direction you must take the approach via “Militärring” and “Gregor Mendel Ring”. Only this route allows you to turn on Belvederestraße to reach the Institute.

BY TRAIN

- Arrival at Cologne main train station (Köln Hauptbahnhof)
- Take Underground #5 (Ossendorf) to Subbelrather Straße/Gürtel
- Then take bus #141 (Vogelsang) or bus #143 (Bocklemünd) from the stop on Subbelrather Straße (on the other side of the intersection) to stop Goldammerweg.
- Walk (for approx. 15 min.) straight on Vogelsanger Straße and Carl-von-Linné-Weg (cross railway land motorway, pass farm on the right-hand side, cross Belvederestr.).

BY PLANE

- Cologne/Bonn Airport:
  Take S-Bahn S13 or train (Regionalbahn RE8) to Cologne main station (Köln Hauptbahnhof). Proceed as described above.
- Düsseldorf Airport:
  Take S-Bahn S7 to Düsseldorf main station (Düsseldorf Hauptbahnhof), then train (IC, ICE, RE, RB) to Cologne main station. Proceed as described above.

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The MPIPZ is continually growing and evolving.
For up-to-date information please see our
website: www.mpipz.mpg.de

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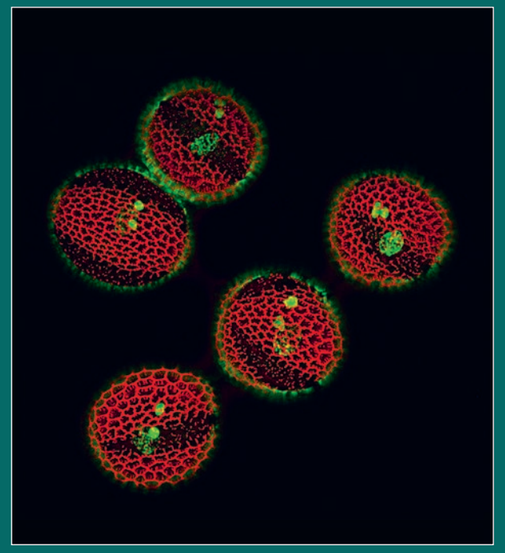

Confocal Image of *Brassica nigra* pollen grains

This high-resolution confocal image illustrates the structural components of *B. nigra* pollen, showing five mature grains (~30 µm in diameter). It is taken within the project exploring interspecific diversity in recombination frequency using single-nuclei sequencing of gametes within the Brassicaceae family.

The green fluorescence highlights three nuclei within each pollen grain:

- Two small, condensed and round sperm cells (~2.5 *µ*m each) are responsible for double fertilisation; one fertilises the egg cell to form the diploid zygote (2n), while the other fertilises two polar nuclei to produce the triploid endosperm (3n).
- A larger, irregularly shaped vegetative nucleus (~6 *µ*m), which migrates into the pollen tube to direct its growth.

The red fluorescence marks the exine, the patterned outer layer of the pollen grain, with visible apertures through which the pollen tube germinates.

The pollen grains were stained overnight with Aberrior LIVE 560, a DNA-specific fluorescent dye and imaged using a Leica STELLARIS Confocal Microscope by Samija Amar (Schneeberger Lab, Department of Chromosome Biology) in collaboration with Ton Timmers (Central Microscopy).