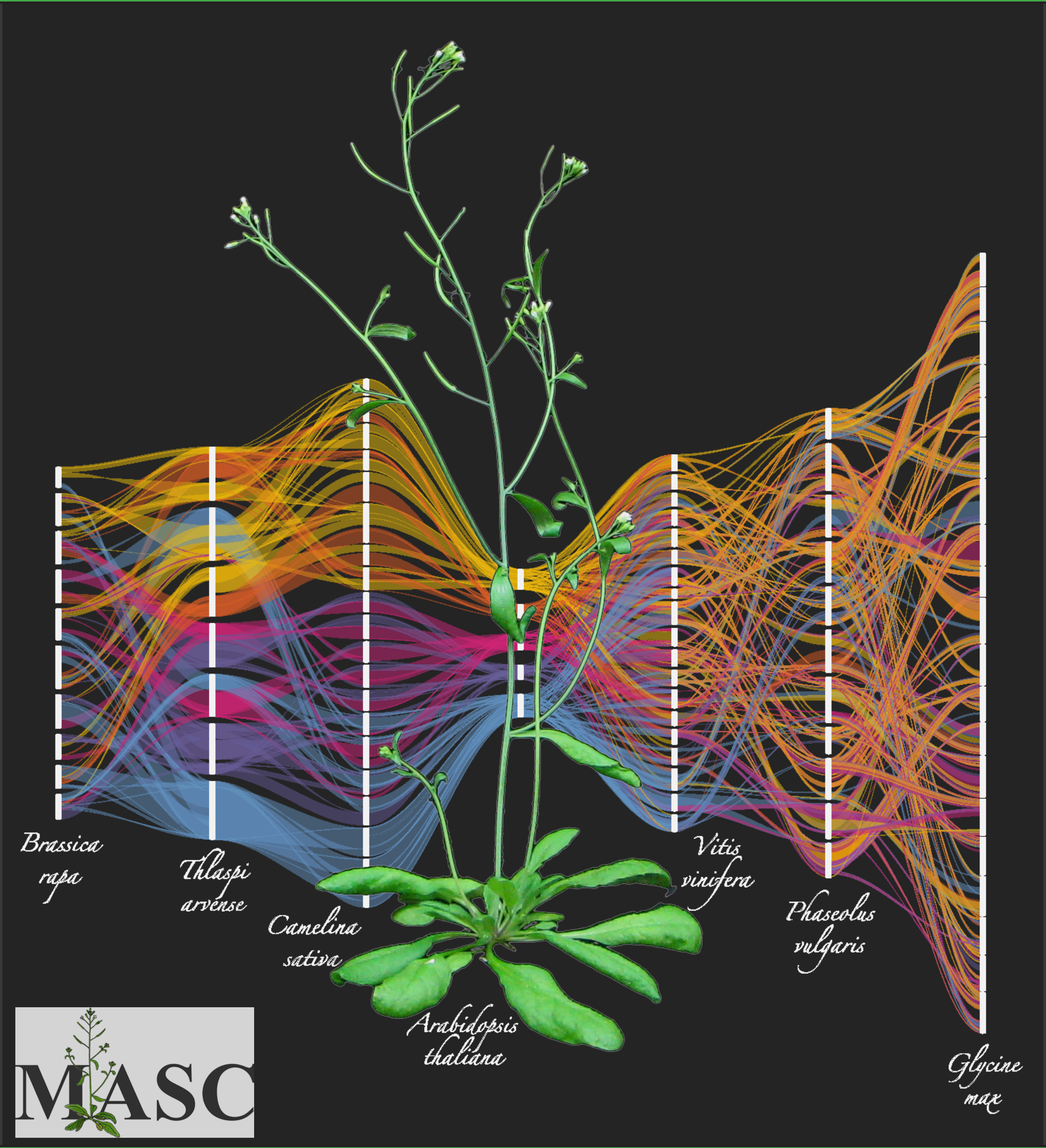
Translating the Computable Plant

Multinational Arabidopsis Steering Committee

Annual Report 2024-2025



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https://academic.oup.com/plcell/pages/translational-research

Further information about MASC can be found on the website: www.Arabidopsisresearch.org

Previous reports are also available online at:

- MASC, The Multinational Arabidopsis Steering Committee:
https://arabidopsisresearch.org/masc-publications/

- uNASC, The Nottingham Arabidopsis Stock Centre:
http://Arabidopsis.info/progreports.html

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This report has been written by the members of the MASC community including the MASC directors, subcommittee chairs and co-chairs with support of subcommittee members, country representatives, project or resource directors and the wider Arabidopsis community.

Throughout the report any references that are highlighted in **blue** include an associated figure from that open access article.

CONTENTS

The Multinational Arabidopsis Steering Committee

Annual Report 2024/2025

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Welcome from the Chair

Dear Arabidopsis community member,

I am writing to you for the first time in my capacity as chair of the multinational Arabidopsis steering committee (MASC) and would like to use this opportunity to introduce MASC briefly, provide my perspective on the state of the community and its´ future as well as invite you to become an active community member to ensure that MASC will continue to serve the community in a meaningful manner.

MASC was originally set up by a small international group of scientists, which recognized the opportunities and potential benefits of establishing Arabidopsis thaliana as a model system for plant biology. Over the subsequent decades Arabidopsis has matured into a recognized model system, comparable to Drosophila and C. elegans in the animal field, through significant investments by many organizations and contributions of scientists working on different biological questions. The combined research activity, resource development and support for the Arabidopsis model from across the globe has resulted in this “little weed” being the plant species where we probably have the most knowledge and resources currently.

Being a mature, established model system for basic science has both positive and negative consequences, which I think we need to bear in mind and address when going forward. In a world, where the need for fast solutions to pressing problems has increased, we need to communicate clearly to stakeholders the need and usefulness of a non-crop model species such as Arabidopsis. Two recent publications by Brady et al. 2025 and Roeder et al., 2025 represent this approach. I think these publications make convincing cases for the usefulness and advantages of the mature Arabidopsis model system to underpin and support translational research where, despite the arrival of novel technologies and resources, hypothesis driven, knowledge-based research is still (and will be) limited for some time to come.

These considerations bring me to the community of Arabidopsis scientists spread out across the world. We are a very diverse crowd, interested in many different biological questions and pursue our research in varying research environments against a backdrop of different (societal) challenges in daily life. MASC has focused in the past on serving the community by building resources and supporting scientific development of individuals through travel grants etc.

The question arising now is, if/how in this day and age the needs of the Arabidopsis community have changed, and MASC needs to adapt his activities accordingly. MASC has recently hosted a workshop at ICAR focused on the situations of our colleagues in Argentina and the US and is currently evaluating feasibility of different initiatives to support community members in need. Here active involvement of community members in different ways will be essential. Therefore, I would ask you to engage with us when MASC will reach out to the community over the next weeks. In parallel if you think that there are matters that MASC should address, I encourage you to directly contact your respective country representatives (listed in country sections below) or a MASC director. Your active participation is important and will ensure that MASC can continue to support the community successfully.

Looking forward to working with and for the Arabidopsis community.

Best wishes,
Thorsten Hamann, MASC Chair

ACTIVITIES OF MASC

Thanks for your interest in the latest activities of the Multinational Arabidopsis Steering Committee (MASC). As ever the first task is to thank the many contributors who have submitted pieces for this annual report. Without their input then MASC would be unable to prepare this document, which aims to track of progress and challenges of the global Arabidopsis community.

MASC Inc is incorporated as a not-for-profit in Canada. This requires official positions of President, Treasurer and Secretary. We are delighted to welcome Thorsten Hamann as the new MASC President whilst Nicholas Provart and Geraint Parry retain their positions as Treasurer and Secretary respectively. Huge thaks to Siobhan Brady for her service of President and Treasurer over the past 10 years!

Thorsten's first task was to engage the community to recruit a group of Directors. We are delighted that eight new MASC Directors joined the organising team. It is especially gratified to see the global representative amongst the MASC Directors.

- Gaby Auge (Argentina)
- Silvia Coimbra (Portugal)
- Mike Haydon (Australia)
- Rob Ingle (South Africa)
- Aashish Ranjan (India)
- Laura Ragni (Germany)
- Anna Stepanova (North America)
- Jia-Wei Wang (China)

The MASC coordinator/secretary position was established in 2002 and has been previously supported by the NSF (USA), the DFG (Germany) and by the BBSRC. From 2020 MASC has directly paid to support secretary activities, albeit for these limited roles:

- Serving as executive secretary of MASC
- Collating, writing, and editing of the annual MASC progress report with input from MASC members
- Maintaining and updating the MASC web pages to inform the global research community about various opportunities, collaborations, large-scale activities and research progress
- Organising the MASC annual meeting

From August 2020 Dr Geraint Parry has been engaged by MASC Inc to oversee its activities, which remain at a minimum level (anticipated to be a total 12 hours in 2025) to maintain the activity of the organisation. In the past preparation of the report has been aided by an early career scientist. This is something we hope to repeat in 2026 and beyond. This provides some good experience and may be undertaken by anyone who is looking for a different experience outside of their standard research activities.

MASC operates through three groups who receive input from the Arabidopsis and plant community: MASC subcommittees, Arabidopsis community projects and resources and MASC country representatives.

The MASC Subcommittees, proposed in 2002, were established to help tracking the progress and advances made by the international Arabidopsis community. This report includes contributions from four subcommittees: Bioinformatics, Epigenetics and Epigenomes, , Plant Immunity and Proteomics.

Subcommittees have certain very loose guidelines for their activities:

- Subcommittee chairs are asked to serve a 3-year minimum term to provide continuity
- Chair/co-chair should confirm and represent the interests of subcommittee members
- Submission of an annual report
- Input at MASC annual meetings

We encourage subcommittee members to take a role in the organisation of workshops at ICAR meetings. At ICAR2025 in Ghent the Bioinformatics subcommittee group organised a concurrent session on ‘**Arabidopsis Bioinformatics**’ and the Epigenetics and Epigenomics subcommittee organised a Concurrent session simply entitled ‘**Epigenetics**’.

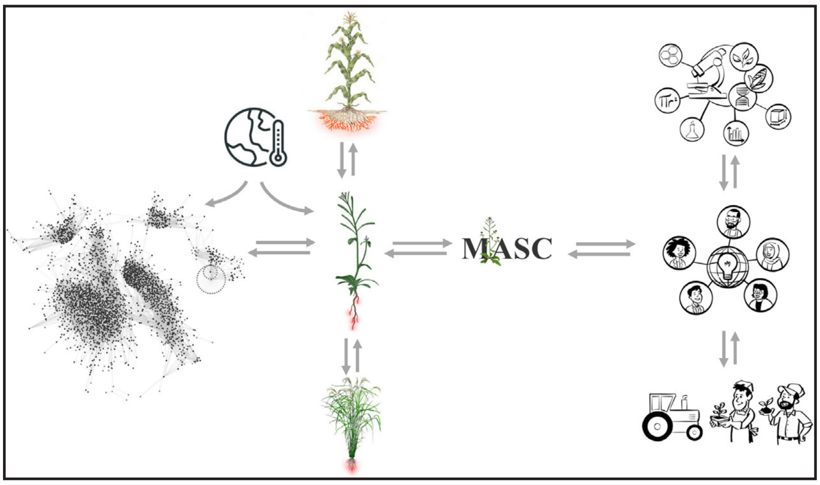
One strength of the global Arabidopsis research community comes in the form of the genomic resources and seed stocks that are available for use. This document includes reports the three major international stock centres (ABRC, NASC, RIKEN Stock Centre), from two major international phenotyping projects, from Gramene and the Global Plant Council. Finally the report includes submissions from TAIR and the BAR (Bio-Analytic Resource for Plant Biology).

Country reports provide a significant portion of the MASC report and highlight the new resources and publications that have been generated from different parts of the world. We are grateful to the Country representatives who contribute to this report.

We are extremely grateful to all representative of subcommittees, projects, or countries as they voluntarily give their time toward MASC activities.

Overall, we very much encourage Arabidopsis researchers to become involved in MASC activities, e.g. subcommittees, projects and resources or as country representatives. If this is of interest to you then please contact Geraint Parry.

Publication of the Fourth Roadmap



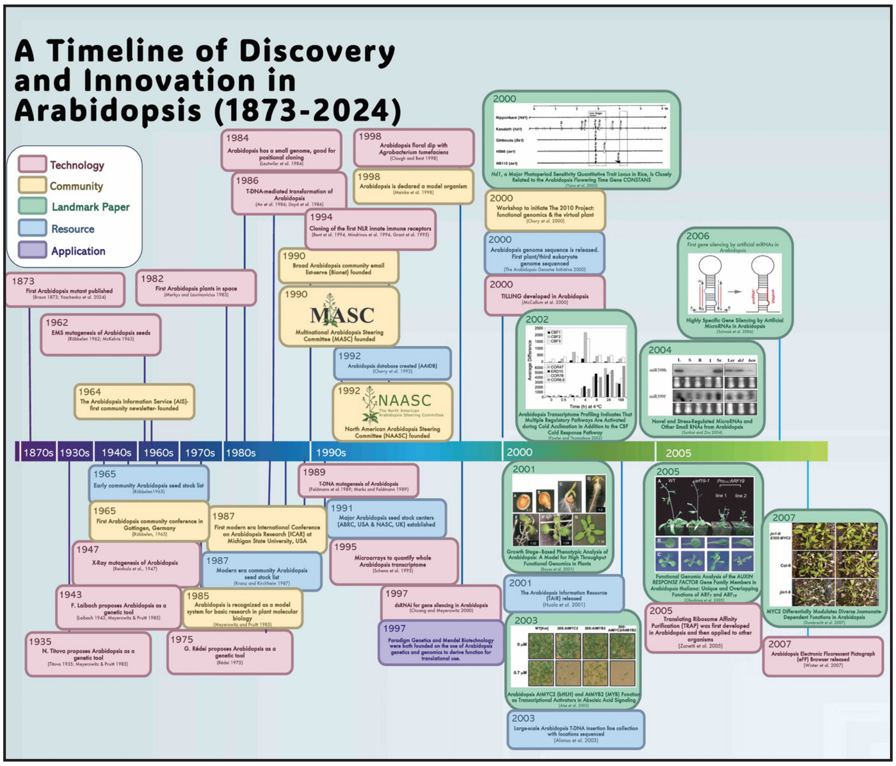
Over the past 30 years MASC has led the preparation of the series of decadal Roadmap documents that have advised on the future activities of the community.

These roadmaps were published in 1990 as '*A Long range plan for the Genome Research project*'; in 2002 as '*Beyond the Whole genome Sequence*' and in 2012 as '*From Bench to Bountiful Harvests*'.

MASC President and Secretary Siobhan Brady and Nicholas Provart were the driving force behind publication of the **Fourth Dedacal Arabipopsis Roadmap** entitled '*Arabidopsis research in 2030: Translating the computable plant*' as an #openaccess article in The Plant Journal (https://doi.org/10.1111/tpj.70047).

Incidentally the Arabidopsis Roadmap greatly complimented the publication of a focus issue of The Molecular Plant entitled "Crops2035' in which dedacal plans were published for Wheat, Maize, Barley and Soybean (https://www.cell.com/molecular-plant/issue?pii=S1674-2052(24)X0003-9).

In May 2025, The Plant Cell hosted a special issue on '**Focus on Translational Research from Arabidopsis to Crop Plants and Beyond**'. This included commentary articles entitled '*In defense of funding foundational plant science* (https://doi.org/10.1093/plcell/koaf106)' and '*A timeline of discovery and innovation in Arabidopsis'* (https://doi.org/10.1093/plcell/koaf108), which are both an outstanding summary and forward-look about the remarkable contributions and potential of Arabidopsis research.



International Conference on Arabidopsis Research (ICAR)

Over the past decade the flagship ICAR meeting has rotated though locations in Asia, North America and Europe. However, the board of directors is more than happy to consider other locations if there is a need to take the ICAR meeting to previously under-represented regions or countries.

ICAR 2025 took place in Ghent, Belgium at a meeting organised by MASC Country Representative Moritz Novack, Tom Beeckman and the Association of Applied Biologists represented by Geraint Parry. ICAR2025 was held at the Biljoke Music Centre in Gent, which had a capacity of ~600. The meeting was oversubscribed so sadly the organisers had to turn away at least 100 scientists who wanted to attend.

Delegates attended from 28 counties of whom 41% were early career professionals. Over 450 abstracts were submitted with a 50:50 gender split. ICAR2025 hosted 3 Keynote speakers, 6 Plenary and 21 Concurrent sessions, which were organised from community suggestions. These sessions provided the opportunities for 150+ oral presenters and 330+ poster presentations.

The organising committee secured over €70K funding from sponsors, which was important to mitigate unexpected costs. AAB subsidised the meeting with ~€30K so unfortunately the organisers couldn’t provide MASC with a stipend from the meeting.

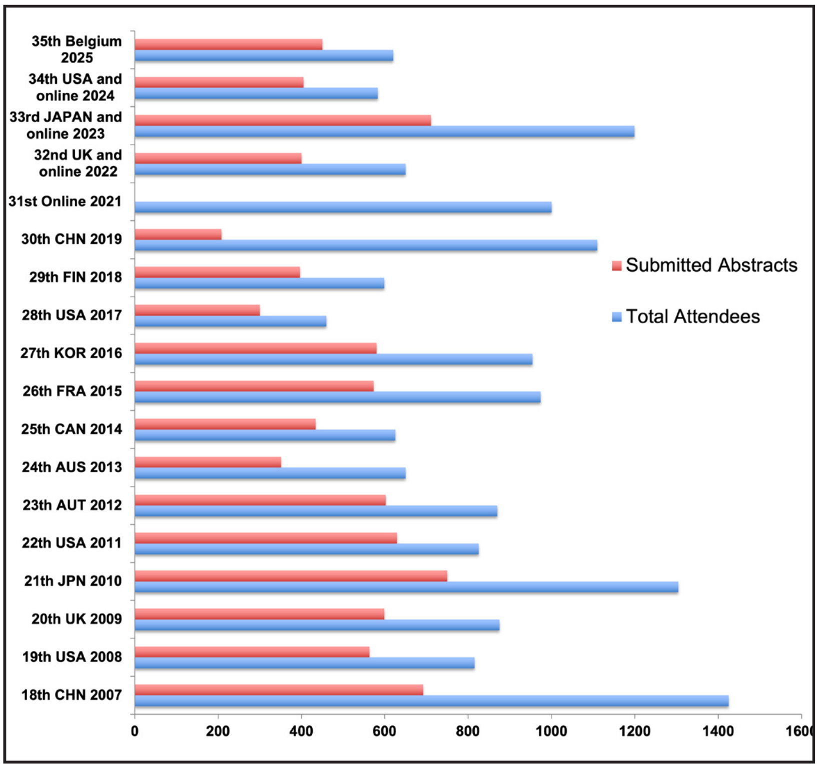
The adjacent graph shows that the number of ICAR attendees has stayed consistent over the past two decades, with higher delegate numbers at the Asian meetings.

It is gratifying to observe that the past few years has seen a higher proportion of delegates having submitted abstracts, indicating that there is a more scientifically engaged set of delegates.

For obvious reasons ICAR 2021 was online-only and engaged ~1000 delegates. The three subsequent ICARs also included a hybrid element.

However because of a decline in the number of online delegates the organisers of ICAR2025 decided to record all talks and offer access to those recordings rather than provide the option for live online participation.

Only 20 people registered for this recorded option although the talks remain available for download at www.icar2025.com



The locations for upcoming ICAR meetings:

- 36th ICAR2026, 22-26 June 2026 in Singapore.

- 37th ICAR, TBC in the Americas

- 38th ICAR in Portugal

The MASC Code of Conduct

The MASC directors in collaboration with Joanna Friesner (Executive Director of NAASC) developed a code of conduct for ICAR events. This code includes advice about appropriately dealing with harassment and unwanted reporting of conference materials. ICAR conferences will provide a safe and productive environment that promotes equal opportunity and treatment for all participants that is free of harassment and discrimination and allows the sharing of unpublished scientific findings. The code of conduct applies to all registered attendees, speakers, exhibitors, staff, contractors, volunteers, and guests; and it applies both within the ICAR conference venues and in associated events and locations where ICAR conference delegates are present.

The Code of Contact updated for ICAR2025 can be downloaded here:
https://tinyurl.com/4t4kj43u

The MASC website

http://Arabidopsisresearch.org/

The MASC website is in the process of moving to being hosted in Wordpress. This will make regular updating and maintainance a lot more straightforward and regular.

This is an information resource for previous MASC related activities.

These include:
- Abstract books from ICAR meetings going back to the 10th ICAR in 1999.
 https://arabidopsisresearch.org/icar/

- Agenda and Minutes from MASC Annual meetings since 2001.
 https://arabidopsisresearch.org/archive-documents/

- MASC Annual Reports since 1990
 https://arabidopsisresearch.org/masc-publications/

- Documents and Articles related to Roadmap activities and related surveys
https://arabidopsisresearch.org/masc-publications/

Secondly the website contains the most up-to-date information from each of the MASC Subcommittees, Project and Country reports that are published in each MASC annual report. This provides a quick reference for the latest tools and publications from each of those subcommittees, resources or countries.

ICAR2025 Reports

ICAR2025 was organised by the Asociation of Applied Biologists who provided a set of travel grants to support the travel of Early Career Scientists to the meeting. Here you can read some of their reflections from the event. Thanks to Dr Jordan Robson for collating these reports.

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The conference itself was incredibly well organised, of course we have to gloat about the boat trip!! The food was fantastic, the sessions were structured clearly, and I appreciated how each talk was grouped by subject area. This thoughtful setup made it easy to follow even those topics that were new to me.

> ***"One of the most powerful aspects of ICAR 2025 was the representation of women, especially in the plenary sessions. Seeing strong, inspiring female scientists like Prof Hailing Jin and Dr Jyothilakshmi Vadassery deliver impactful presentations made me feel seen and reminded me that I belong in this field. It gave me confidence in my future, and I could envision myself, one day, standing at the podium as a PI, sharing my own work and mentoring the next generation."***

I was also deeply inspired by the diversity of speakers, ranging from PhD students to postdocs and early-career PIs. Our passion and creativity reflected in our talks reinforced that there are many different ways to make meaningful contributions in plant science.

Attending the "Building a Diverse Community Through Effective Teaching and Mentoring" workshop was a transformative experience that deeply resonated with my own values and aspirations as an educator and community member. The workshop emphasised the importance of cultivating inclusive learning environments where we all feel seen, heard, and empowered to succeed. It provided practical strategies for culturally responsive mentorship, and fostering a sense of belonging among scientists from historically marginalised backgrounds. Equally impactful were the talks on diversity by Prof Yoselin Benitez-Alfonso and Prof Devang Mehta , which highlighted the systemic barriers that continue to affect underrepresented groups in Plant sciences research and academia and the importance of intentional efforts to dismantle those barriers. These discussions inspired me to critically reflect on my own mentoring practices and to seek out more active ways to promote diversity, equity, and inclusion in my academic and professional spaces. I came away from these experiences with a renewed commitment to being not only a more effective mentor, but also an advocate for structural change within the academic community.

When the day came for me to give my talk, I was incredibly nervous. But I'm so grateful I had the opportunity to present my work, share what we do in our lab, and represent not just myself but my community. The feedback I received was encouraging and constructive, and it gave me even more motivation to push forward in my career.

Acknowledgements

Many thanks to the conference organisers for such a wonderful experience and to Geraint for all his help throughout the process. Thank you again for providing me with these costs to cover my childcare which would have made it impossible for me to attend without your help.

Dr Huilun Sun

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ICAR2025 was an unforgettable experience both professionally and personally. When I first received the acceptance email for my session proposal, I was still a PhD candidate preparing for my dissertation. The opportunity to co-organise a session as an early-career researcher was both exciting and challenging. It gave me a valuable chance to grow, including practice email communication, collaborate with a team, and improve my project management skills. After seven months of preparation, it was a great joy to see the conference successfully held; at the same time, I had also successfully defended my doctoral dissertation. This parallel journey made the experience so meaningful, like celebrating a shared milestone of growth.

I especially loved the lively discussions in the foyer, where I reconnected with old friends and made new ones. The boat trip was another highlight, relaxing under the sunshine and enjoying the historic views of Ghent after several days of wonderful and inspiring talks. ICAR2025 showed a perfect balance between structured academic sessions and informal social interactions.

I am looking forward to attending next year's ICAR and continuing to build connections within the scientific community.

Highlights

- ICAR2025 has become a memorable event for me. I had the great honour of co-organising two concurrent sessions: Environmental Regulation of Plant Defences and Proteostasis and Protein Quality Control. This was my first time organising such an international and important event, and I learned so such from coordinating with co-chairs and invited speakers to managing session logistics and standing on stage as a host. Seeing all our efforts come together at the beautiful Bijloke Gent Music Centre was truly inspiring and rewarding.
- The diversity of sessions and the vibrant, inclusive atmosphere at ICAR2025 were deeply inspiring. In such a beautiful venue, I had the chance to attend excellent talks covering a wide range of fields and to speak with scientists at various career stages during coffee breaks and poster sessions.
- One of the most memorable moments was the informal lunch gathering with all the invited speakers and co-organisers from the Environmental Regulation of Plant Defences session. Although it was our first time meeting in person, our conversations were warm and engaging, creating a real sense of community. This session brought together professors and PhD students to discuss plant immunity in relation to environmental cues such as temperature, hypoxia, nutrition, as well as topics including biosensor, transcriptome analysis, and stomatal immunity.
- The Proteostasis and Protein Quality Control session was composed of a large and enthusiastic team of professors, post-docs, and PhD candidates. It covered diverse topics including but not limited to chloroplast degradation, oxygen-dependent proteolysis, processing body condensates, and the N-degron pathway. Despite on the final day of conference, the session attracted a large and engaged audience.

Acknowledgements

I am deeply grateful to the ICAR2025 Scientific Organising Committee for offering this wonderful opportunity to me. I would also like to thank to the Association of Applied Biologists (AAB) for providing the travel grant that made my attendance possible. Special thanks to Dr. Geraint Parry for his kind support and patient guidance throughout the process. I am also sincerely thankful to Prof. Danve Castroverde, Dr. Jorge Vicent, Dr. Alvaro Fernandez, and Dr. Hanhong Liu for being such supportive and collaborative co-organisers. Many thanks to the speakers for giving such insightful talks, and to the volunteers who helped ensure our sessions ran smoothly. Thanks as well to everyone I haven't named here, you made this experience so special. With Ghent's welcoming weather and beautiful view, I will always remember this summer.

Sourav Mukherjee

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ICAR2025 was an incredibly enriching and inspiring experience, offering numerous opportunities for professional growth and meaningful engagement. One of the most valuable aspects was the access to ECR-focused workshops, particularly the Publication Advice Clinic, which offered practical guidance on navigating academic publishing. While I was keen to attend a broad range of sessions, overlapping schedules meant I could not participate in all of them. I am grateful to the ICAR2025 organisers for providing access to session recordings, which allowed me to revisit and catch up on missed content. Balancing poster presentations, scientific talks, and networking events was demanding but ultimately rewarding, helping me maximise the benefits of the conference experience.

I sincerely thank the ICAR2025 organisers for selecting my poster and granting me the opportunity to organise a concurrent session, which significantly enriched my conference experience. I am also grateful to the AAB for awarding the Early Career Professional travel grant. Additionally, I acknowledge the support of Monash University through the 2025 School of Biological Sciences ECR National Conference Support Award, as well as the funding provided by the ICAR2025 organisers. Their collective support was instrumental in making this visit possible and highly valuable.

Some of our ECR co-organised sessions at ICAR2025: Huilun Sun's session on "Environmental Regulation of Plant Defences" (top left) & Sourav Mukherjee's session on "Temperature sensing in plants'" (top right) & networking (bottom)

Steffi Raju
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ICAR 2025 held at Ghent, Belgium was a very special experience. The meeting spanned over a period of 5 days and it had several plenary sessions, concurrent sessions, poster sessions and workshops. The event began with a very inspiring talk by Jane Parker on the TNL and how the specificity of TNLs arise in the plants upon pathogen infection. This gave a whole new perspective on how plants adopt diverse ways to evade pathogen infection at the molecular level. The subsequent days of ICAR was also very motivating and it spanned talks across diverse fields.

The major highlights of the ICAR 2025 were as below:

1. Being a student working on epigenetics and RNA biology, I am immensely benefitted by the concurrent session on epigenetics. This session covered many versatile areas of epigenomics and enabled interactions with the eminent researchers in the field. The meeting also highlighted about the upcoming conferences in the epigenetics field. The talks had very engaging discussions where I heard from eminent personalities in the field such Bob Schmitz, Keith Slotkin, Julie Law etc. The interactions from these people also gave me a broad perspective on their field of research and the post-doc opportunities as well. I am very much influenced by the student talks in this session as it was quite inspiring to see the novel research areas which they were pursuing.

2. The poster sessions has allowed me to discuss my work on a global platform and help me to get valuable suggestions on improving the work. This will help me to a greater extent in tackling the peer review process. I also gained a broader outline and perspective of studying the question in a crop like rice by gaining insights from Arabidopsis. I received a huge number of positive feedbacks on my poster which is a motivation for me to present bigger and better. I was able to explain and engage a wider community at my poster and everyone was curious about my work because it was on rice and not Arabidopsis. They were eager to know the challenges associated with working on crop plants and their transgenesis. This has given me a lot of self-assurance and confidence in my academic pursuits. My poster sessions were visited my many great scientists whose papers I have read from such as Yannick Jacob, Yujin Qi, Peter Broderson, Ari Sadanondom etc.

3. I was also excited to be part of the workshops that were organised by several key speakers. This helped me to gain perspective on the utility of specific tools in biology. The highlights on the modern microscopy techniques and spatial omics were extremely useful and could be implemented to our research as well. I also met the researchers who organized the workshop such as Tatsuya Nobori, Rituparna Goswamy who shed light into single-cell omics and spatial transcriptomics which is yet to be incorporated into the research areas at present.

The best part of the meeting was the freedom that it provided to discuss with our peers. Be it a poster session or a snack time, the conversations were always on science and some insights from the previous sessions/talks. During the break times, we have even planned how to cover maximum talks and discuss which concurrent session would be more relevant over the other. This made us to use the opportunity to the maximum and never miss anything that ICAR2025 bestowed upon us. The delegates were very warm and welcoming; I personally experienced a sense of belonging at the end of the fifth day.

I really felt the challenge was to imbibe the fact that ICAR got over so soon and I have to wait another year to meet the same people and discuss the science in an enjoyable way again. It would be great to have the meeting for 7 days and the talks being spaced apart such that the discussions or Q/A sessions would be more. I would also be eager to take part in ICAR 2026 and hoping to get more hold of the discussions and key insights in a much profound way.

Acknowledgements

I would like to extend my gratitude to Infosys Foundation and National centre for biological sciences for their support.

MASC SUBCOMMITTEE REPORTS

Bioinformatics

Prepared by

Compiled by Nicholas Provart, Leonore Reiser, Tanya Berardini and with input from MASC Bioinformatics Subcommittee members and the wider Arabidopsis community.

Recently developed Open Tools and Resources for Arabidopsis Researchers

- **TAIR:** TAIR continues to curate gene function data from the literature with an emphasis on capturing information for previously undescribed genes. Data include gene symbols, gene descriptions, mutant alleles, phenotypes, Gene Ontology and Plant Ontology annotations. Starting with the July 2025 release, TAIR has added a new data file (Locus_Allele_Phenotype_YYYMMDD.tsv) to the quarterly pipeline. In case you missed it, a nice paper by Reiser et al. (2024) describing a large update to TAIR in terms of its front end tools came out last year. It also nicely gave a snapshot of the status of the Arabidopsis genome annotation effort and described efforts to modernize the backend code that powers TAIR.

- **BAR:** The BAR celebrated 20 years of serving the community, see Sullivan et al. (Sullivan et al. 2025)! It rolled out a tool called Gaia as the primary access point for BAR datasets and tools. Gaia includes reprocessed PlantConnectome summaries (see the section after the next one for details on PlantConnectome), genetic models from 65000 papers, and easy Blast access to the BAR's eFP Browsers and ePlant tools. Two new data sets were added in the eFP-Seq Browser: Guard Cell Drought (Provart Lab) and Pollen (Misra et al., 2025) (Misra et al. 2025). Work continues on refactoring old BAR webservices into the BAR API. ThaleMine v5.1.0-20241202 was released. The BAR server hardware was updated with the purchase of a new server. The BAR also assisted with the TAIR12 genome reannotation effort, focusing on mitochondrial genes in Arabidopsis genome together with TAIR curators.

- **An Arabidopsis genome update is coming this year!** The TAIR12 Col-0 community curated genome annotation has been submitted to NCBI for inclusion as the new Arabidopsis Reference Genome. Once finalized, TAIR and other resources such as BAR and UniProt will begin the process of integration. For TAIR this will mean updating the database and all of the tools (e.g. BLAST, JBrowse etc..) that rely on current genome data. A manuscript describing the re-annotation project will be submitted later this year. See TAIR's website (https://conf.phoenixbioinformatics.org/display/COM/A.+thaliana+Col-0+v12+reannotation+effort) for updates.

- **Large-scale Data Sets and Methods of Note**: The Weirauch, Hughes, and Morris laboratories released an large catalog of RNA binding proteins in the eukaryotes, including 469 motifs for Arabidopsis RNA binding proteins (Sasse et al. 2025). The Dinesh-Kumar and Shabek groups released a TurboID-based proxitome of AKS1 and CUL1 of the SCF ubiquitin ligase in plants, with 705 and 404 proteins being considered interactors, respectively, and 120 of these being in common (Sun et al. 2024). The Schneeberger and Mercier labs published a pan-genome of 69 Arabidopsis thaliana accessions based on long-read sequencing data (Lian et al. 2024). The Mutwil Lab's effort to harness the power of ChatGPT is available at https://connectome.plant.tools. The Mutwil Lab used ChatGPT to process 51,327 abstracts and 19,809 full text articles with Arabidopsis in the abstracts to extract – in a traceable way – 4.7 million relationships between genes, molecules, compartments, organs etc. (Lim et al. 2025)!

- **Pedagogy, Policy and Outreach**: The Plant Cell Atlas continues to organize workshops on single-cell approaches in plant biology. Keep an eye on http://www.plantcellatlas.org/ for updates!

The second Gordon Research Conference on Single-Cell Approaches in Plant Biology will happen in August 2025. TAIR continues its partnership with https://www.micropublication.org/, a platform for very short peer-reviewed reports. Nicholas Provart's Plant Bioinformatics course covering 35 online tools from labs around the world on Coursera.org (https://www.coursera.org/learn/plant-bioinformatics/) was fully updated in June 2025.

Selected Publications

- Lian Q, Huettel B, Walkemeier B, Mayjonade B, Lopez-Roques C, Gil L, Roux F, Schneeberger K, and Mercier R. A pan-genome of 69 Arabidopsis thaliana accessions reveals a conserved genome structure throughout the global species range. Nat Genet. 2024:56(5):982–991. https://doi.org/10.1038/s41588-024-01715-9

- Lim SC, Itharajula M, Møller MH, Sunil RS, Fo K, Chuah YS, Foo H, Davey EE, Fullwood M, Thibault G, et al. PlantConnectome: A knowledge graph database encompassing >71,000 plant articles. Plant Cell. 2025:37(7):koaf169. https://doi.org/10.1093/plcell/koaf169

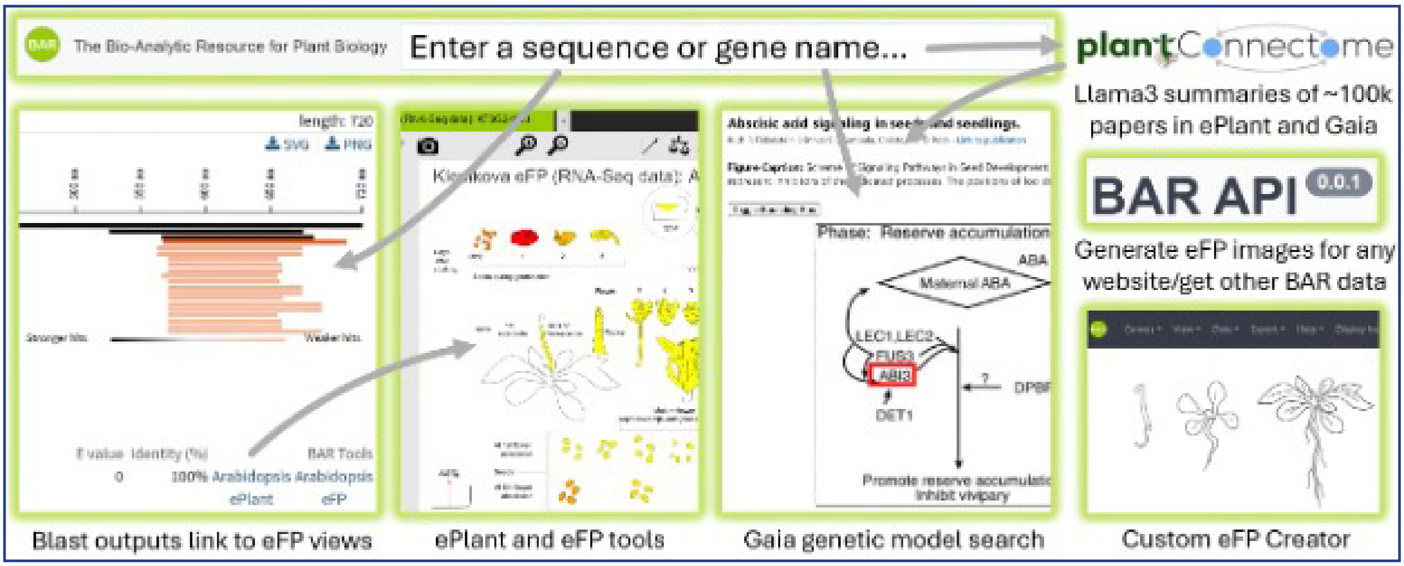
- Misra CS, Sousa AGG, Khan H, Pasha A, Provart NJ, Borg M, and Becker JD. Transcriptome dynamics in the Arabidopsis male germline during pollen–pistil interactions. Plant J. 2025:121(6):e70095. https://doi.org/10.1111/tpj.70095

- Reiser L, Bakker E, Subramaniam S, Chen X, Sawant S, Khosa K, Prithvi T, and Berardini TZ. The Arabidopsis Information Resource in 2024. Genetics. 2024:227(1):iyae027. https://doi.org/10.1093/genetics/iyae027

- Sasse A, Ray D, Laverty KU, Tam CL, Albu M, Zheng H, Levdansky Y, Lyudovyk O, Dalal T, Nie K, et al. A resource of RNA-binding protein motifs across eukaryotes reveals evolutionary dynamics and gene-regulatory function. Nat Biotechnol. 2025:1–11. https://doi.org/10.1038/s41587-025-02733-6

- Sun F, Hamada N, Montes C, Li Y, Meier ND, Walley JW, Dinesh-Kumar SP, and Shabek N. TurboID-based proteomic profiling reveals proximitome of ASK1 and CUL1 of the SCF ubiquitin ligase in plants. New Phytol. 2024:244(6):2127–2136. https://doi.org/10.1111/nph.20014

- Sullivan A, Lombardo MN, Pasha A, Lau V, Zhuang JY, Christendat A, Pereira B, Zhao T, Li Y, Wong R, et al. 20 years of the Bio-Analytic Resource for Plant Biology. Nucleic Acids Res. 2025:53(D1):D1576–D1586. https://doi.org/10.1093/nar/gkae920



Epigenetics and Epigenomics

Prepared by

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Recent or Future activities of Subcommittee members.

- International Conference on Arabidopsis Research, UCSD, USA, June, 2024
  – Epigenetics

- Keystone meeting on Plant Epigenetics and Gene Regulation, October, 2025

- Epigenetics Gordon Conference, Barcelona, Spain, August, 2025

- International Conference on Arabidopsis Research, Gent, Belgium, June, 2025
  – Epigenetics

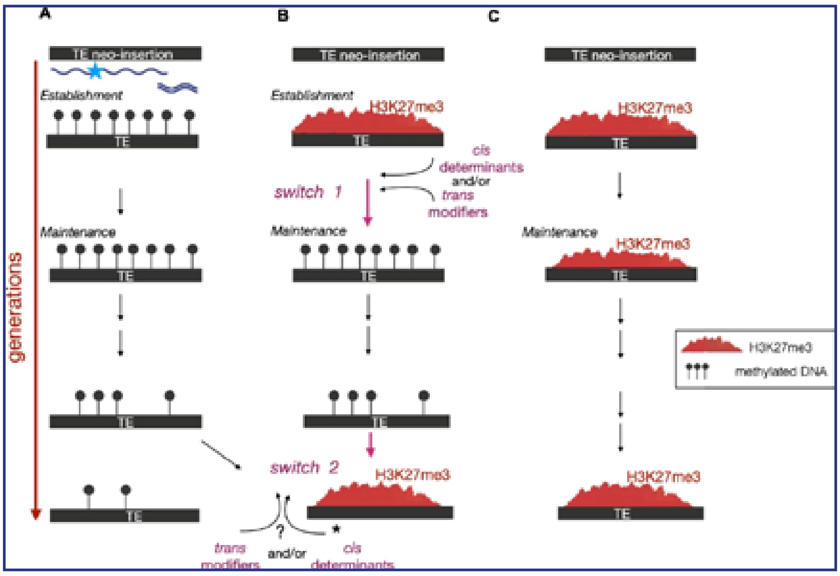
Selected Publications

- Dynamic control of H2A.Zub and H3K27me3 by ambient temperature during cell fate determination in Arabidopsis. Zhu K, Chen J, Zhao L, Lu F, Deng J, Lin X, He C, Wagner D, Xiao J. Dev Cell. 2025 Apr 16:S1534-5807(25)00204-7. doi: 10.1016/j.devcel.2025.04.002. Online ahead of print.PMID: 40267908

This study reveals how ambient temperature dynamically regulates H2A.Z ubiquitination and H3K27me3 to influence cell fate decisions during Arabidopsis development.

- Alternative silencing states of transposable elements in Arabidopsis associated with H3K27me3. Hure V, Piron-Prunier F, Yehouessi T, Vitte C, Kornienko AE, Adam G, Nordborg M, Déléris A. Genome Biol. 2025 Jan 20;26(1):11. doi: 10.1186/s13059-024-03466-6.PMID: 39833858

This study uncovers distinct epigenetic states in which transposable elements in Arabidopsis are silenced by H3K27me3, revealing an alternative mode of genome regulation beyond canonical heterochromatin pathways.



- Substrate specificity and protein stability drive the divergence of plant-specific DNA methyltransferases. Jiang J, Gwee J, Fang J, Leichter SM, Sanders D, Ji X, Song J, Zhong X. Sci Adv. 2024 Nov 8;10(45):eadr2222. doi: 10.1126/sciadv.adr2222. Epub 2024 Nov 6.PMID: 39504374

This study uncovers the key differences between two paralogous plant-specific DNA methyltransferases CMT2 and CMT3 that contribute to the diverse sub-functionalization of CHG and CHH methylation in angiosperms.

- Histone H3 lysine 4 methylation recruits DNA demethylases to enforce gene expression in Arabidopsis. Wang M, He Y, Zhong Z, Papikian A, Wang S, Gardiner J, Ghoshal B, Feng S, Jami-Alahmadi Y, Wohlschlegel JA, Jacobsen SE. Nat Plants. 2025 Feb;11(2):206-217. doi: 10.1038/s41477-025-01924-y. Epub 2025 Feb 11.PMID: 39934332

This study shows that histone H3 lysine 4 methylation (H3K4me) recruits DNA demethylases in Arabidopsis, establishing a coordinated mechanism that maintains active gene expression by preventing DNA methylation at key loci.

- Transposon-triggered epigenetic chromatin dynamics modulate EFR-related pathogen response. Mencia R, Arce AL, Houriet C, Xian W, Contreras A, Shirsekar G, Weigel D, Manavella PA. Nat Struct Mol Biol. 2025 Jan;32(1):199-211. doi: 10.1038/s41594-024-01440-1. Epub 2024 Dec 27.PMID: 39730887

This study demonstrates that transposon-derived epigenetic changes dynamically shape chromatin around immune genes in Arabidopsis, modulating EFR-mediated pathogen responses and revealing a link between genome architecture and immune regulation.

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https://arabidopsisresearch.org/subcommittees/

Plant immunity

Prepared by

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Recently developed Open Tools and Resources for Arabidopsis Researchers

- PRGminer: harnessing deep learning for the prediction of resistance genes involved in plant defense mechanisms. Duhan N, Kaundal R. Front Plant Sci. 2025 Jun 3;16:1411525. doi: 10.3389/fpls.2025.1411525. eCollection 2025. PMID: 40530297

- PRGminer is a deep learning-based tool that predicts and classifies plant resistance (R) genes from protein sequences in two phases, achieving over 95% accuracy using dipeptide composition features. It is freely available as a webserver (https://kaabil.net/prgminer/) and a standalone tool (https://github.com/usubioinfo/PRGminer).

- PHI-base - the multi-species pathogen-host interaction database in 2025. Urban M, Cuzick A, Seager J, Nonavinakere N, Sahoo J, Sahu P, Iyer VL, Khamari L, Martinez MC, Hammond-Kosack KE. Nucleic Acids Res. 2025 Jan 6;53(D1):D826-D838. doi: 10.1093/nar/gkae1084. PMID: 39588765

- PHI-base is a manually curated database of experimentally verified pathogenicity, virulence, and effector genes from diverse pathogens; its latest releases, v4.17 and v5.0, offer expanded interaction data and improved accessibility via www.phi-base.org and phi5.phi-base.org.

- FX-Cell: a method for single-cell RNA sequencing on difficult-to-digest and cryopreserved plant samples. FX-Cell and its derivatives (FXcryo-Cell, cryoFX-Cell) are optimized methods for single-cell RNA-seq in plants that enable high-quality protoplast isolation from difficult or cryopreserved tissues, broadening the applicability of scRNA-seq to diverse species and field-grown samples.

- AlphaFold 3 (by Google DeepMind and Isomorphic Labs - https://alphafoldserver.com/about)

- ACT 2.6 (Early 2025) - This upgraded version of the Arabidopsis co-expression tool (ACT) was built using WGCNA across ~3,500 array samples, resulting in 27 functional gene modules. It provides improved accuracy in identifying gene functional partners and tissue-specific expression patterns. (https://www.michalopoulos.net/act/).

- athisomiRDB (November 2024) - A comprehensive open-access database of Arabidopsis isomiRs, reporting variant miRNAs with detailed metadata. It provides a curated resource for microRNA variant analysis, facilitating studies on miRNA regulation in Arabidopsis. (http://14.139.61.8/athisomiRDB/index.html).

- Deep phenotyping platform for microscopic plant-pathogen interactions. Front Plant Sci. 2025 Feb 3;16:1462694. doi: 10.3389/fpls.2025.1462694. PMID: 39963527; PMCID: PMC11832026.

- Dot Scanner: open-source software for quantitative live-cell imaging in planta. Plant J. 2024 Jun;118(5):1689-1698. doi: 10.1111/tpj.16662. Epub 2024 Feb 4. PMID: 38310596.

- Epidermal electronic-tattoo for plant immune response monitoring. Nat Commun. 2025 Apr 4;16(1):3244. doi: 10.1038/s41467-025-58584-x. PMID: 40185801; PMCID: PMC11971386.

- TISCalling: leveraging machine learning to identify translational initiation sites in plants and viruses. Plant Mol Biol. 2025 Aug 1;115(4):102. doi: 10.1007/s11103-025-01632-3.

- EasyOmics: A graphical interface for population-scale omics data association, integration, and visualization. Plant Commun. 2025 May 12;6(5):101293. doi: 10.1016/j.xplc.2025.101293.

Recent or Future activities of Subcommittee members.

- Among the current activities, members of the subcommittee have presented their work at a range of high-profile international conferences and specialized workshops.

2024 International Plant Molecular Biology Meeting, Cairns, Australia
2025 International Plant Growth Substances Association Meeting, Fort Collins, USA
2025 IS-MPMI Congress, Cologne, Germany (July 13–17, 2025)
2025 10th Stromlo Plant Pathology Conference, Canberra, Australia (November 27–28, 2025)
2024 Fall International Conference of the Korean Society of Plant Pathology (KSPP), Seoul, Korea (October 22–25, 2024)
2024 The 66th Annual Meeting of the Japanese Society of Plant Physiologists, Kanazawa, Japan (March 15–17, 2024)

2025 Annual Meeting of the Phytopathological Society of Japan, Takamatsu, Japan (March 26–28, 2025)
2024 The 5th Korea–Japan Joint Symposium on Plant Pathology, Takamatsu, Japan (March 24–26, 2024)
EMBO Workshop – Cell Death: Friend or Foe in Animal and Plant Immunity, Sant Feliu de Guíxols, Spain (October 11–15, 2024)
EMBO Workshop – Plant Calcium Signaling, Lisbon, Portugal (July 1–4, 2024)
ICAR 2025, Ghent, Belgium
Plant and Animal Genome, San Diego, 2025.

Planned future activities include participation in the 2027 IS-MPMI Congress, Jeju, Korea (July 18–22, 2027), the Plant and Animal Genome Conference, San Diego, USA (2026), and ICAR 2026.

Selected Publications

- Nobori T, Monell A, Lee TA, Sakata Y, Shirahama S, Zhou J, Nery JR, Mine A, Ecker JR. A rare PRIMER cell state in plant immunity. Nature. 2025 Feb;638(8049):197-205. doi: 10.1038/s41586-024-08383-z. Epub 2025 Jan 8. PMID: 39779856; PMCID: PMC11798839.

Diverse cell-type-specific responses of cells in contact with, and distant from, pathogens revealed by single-cell transcriptomics.

- Miao P, Wang H, Wang W, Wang Z, Ke H, Cheng H, Ni J, Liang J, Yao YF, Wang J, Zhou JM, Lei X. A widespread plant defense compound disarms bacterial type III injectisome assembly. Science. 2025 Feb 28;387(6737):eads0377. doi: 10.1126/science.ads0377. Epub 2025 Feb 28. PMID: 40014714

This study identifies erucamide as a conserved phytoalexin that confers antibacterial immunity by binding to the T3SS component HrcC and inhibiting injectisome assembly in diverse bacterial pathogens.

- Du X, Alam M, Witek K, Milnes L, Houghton J, Lin X, Ahn HK, Zhang Y, Cui F, Sun W, Jones JDG, Guo H. Interfamily co-transfer of sensor and helper NLRs extends immune receptor functionality between angiosperms. Cell. 2025 Jun 17:S0092-8674(25)00578-1. doi: 10.1016/j.cell.2025.05.028. Online ahead of print. PMID: 40532698

This study demonstrates that co-transfer of Solanaceae sensor NLRs with NRC-type helper NLRs enables functional immune responses in diverse crop species, offering a strategy to expand disease resistance across plant families.

- Xiao Y, Sun G, Yu Q, Gao T, Zhu Q, Wang R, Huang S, Han Z, Cervone F, Yin H, Qi T, Wang Y, Chai J. A plant mechanism of hijacking pathogen virulence factors to trigger innate immunity. Science. 2024 Feb 16;383(6684):732-739. doi: 10.1126/science.adj9529. Epub 2024 Feb 15. PMID: 38359129.

An elegant mechanism by which plants can redirect pathogen effector enzymatic activity away from immunosuppressive products and towards immunoactivating products.

- Sanguankiattichai N, Chandrasekar B, Sheng Y, Hardenbrook N, Tabak WWA, Drapal M, Kaschani F, Grünwald-Gruber C, Krahn D, Buscaill P, Yamamoto S, Kato A, Nash R, Fleet G, Strasser R, Fraser PD, Kaiser M, Zhang P, Preston GM, van der Hoorn RAL. Bacterial pathogen deploys the iminosugar glycosyrin to manipulate plant glycobiology. Science. 2025 Apr 18;388(6744):297-303. doi: 10.1126/science.adp2433. Epub 2025 Apr 17. PMID: 40245141.

The mechanism by which a pathogen iminosugar virulence factor inhibits plant glycosidases to promote pathogen success was revealed by a combination of forward genetics and structural biology.

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4- Dr. Marc Nishimura, marc.nishimura@colostate.edu , Colorado State University, Fort Collins, CO, USA

Proteomics

Prepared by

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Recently developed Open Tools and Resources for Arabidopsis Researchers

- The Arabidopsis PeptideAtlas (www.peptideatlas.org/builds/arabidopsis/) is based on published MS data from the international community and collected through ProteomeXchange and reanalyzed through a uniform processing and metadata annotation pipeline. All matched MS-derived peptide data are linked to spectral, technical, and biological metadata. In the latest release of the Arabidopsis PeptideAtlas, 70 million MS/MS spectra were matched to the Araport11 annotation, identifying approximately 0.6 million unique peptides and 18,267 proteins at the highest confidence level and 3396 lower confidence proteins, together representing 78.6% of the predicted proteome. Additional identified proteins not predicted in Araport11 should be considered for the next Arabidopsis genome annotation. MS support was lacking for 21.4% (5896 proteins) of the predicted Araport11 proteome: the “dark” proteome. This dark proteome is highly enriched for E3 ligases, transcription factors, and specific signaling peptides families. This release also identified 5198 phosphorylated proteins, 668 ubiquitinated proteins, 3050 N-terminally acetylated proteins, and 864 lysine-acetylated proteins and mapped their PTM sites. PeptideAtlas is linked to TAIR, tracks in JBrowse, and other proteomics resources [1].

- The Plant PTM Viewer 2.0 (https://www.psb.ugent.be/PlantPTMViewer) provides an intuitive overview and tools to assess plant protein PTMs, including Arabidopsis. PTM Viewer 2.0 can be used for hypothesis testing and new target discovery [2].

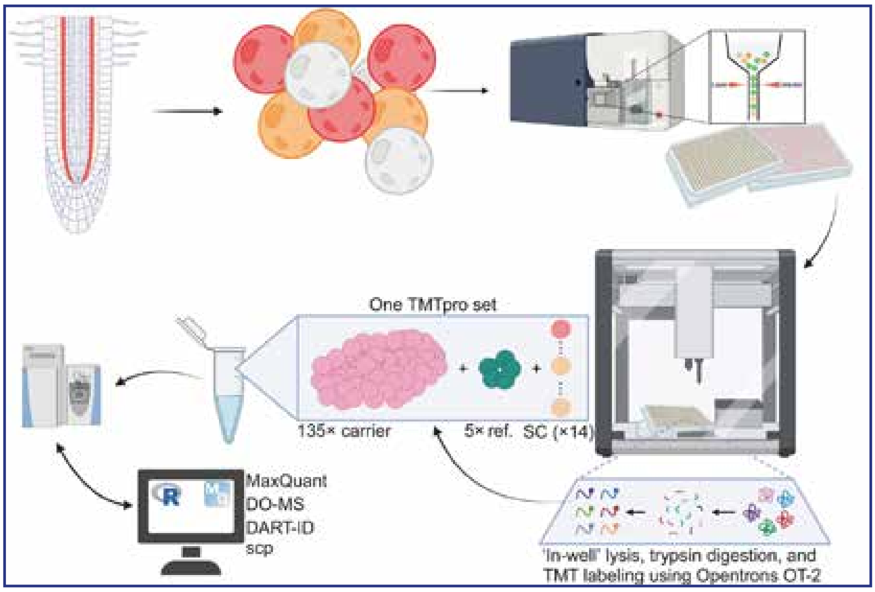
Selected Publications

- Searching (August, ‘25) PubMed with the search string: “(arabidopsis+(Proteome[Title/Abstract]+OR+proteomics)+mass+spectrometry[Title/Abstract) AND ((“2024”[Date - Publication] : “3000”[Date - Publication]))” identified some 45 publications covering a range of Arabidopsis proteome-related questions and techniques.

These included protein interactions in specific biological processes [3] [4, 5], post-translational modifications (O-GlcNAcylation, Phosphorylation, N-glycosylation, acetylation) [4-6] , the mitochondrial pollen and flower proteomes from affinity purified mitochondria [7], and several book chapters on proximity labeling in Arabidopsis [8-10], the impact of RNA editing on the plastid and mitochondrial proteomes [11, 12] and Arabidopsis developmental questions [13]. [1, 12]. An additional publication described new developments and results concerning single cell (type) proteomics in roots of Arabidopsis [14].

1. van Wijk, K.J. et al. (2024) Detection of the Arabidopsis Proteome and Its Post-translational Modifications and the Nature of the Unobserved (Dark) Proteome in PeptideAtlas. J Proteome Res 23 (1), 185-214.
2. Willems, P. et al. (2024) The Plant PTM Viewer 2.0: in-depth exploration of plant protein modification landscapes. J Exp Bot.
3. Wu, K. et al. (2025) Cytosolic WPRa4 and Plastoskeletal PMI4 Proteins Mediate Touch Response in a Model Organism Arabidopsis. Mol Cell Proteomics 24 (7), 101015.

4. Brunje, A. et al. (2024) The Plastidial Protein Acetyltransferase GNAT1 Forms a Complex With GNAT2, yet Their Interaction Is Dispensable for State Transitions. Mol Cell Proteomics 23 (11), 100850.
5. Persyn, F. et al. (2024) A Nitrogen-specific Interactome Analysis Sheds Light on the Role of the SnRK1 and TOR Kinases in Plant Nitrogen Signaling. Mol Cell Proteomics 23 (10), 100842.
6. Shrestha, R. et al. (2024) SECRET AGENT O-GlcNAcylates Hundreds of Proteins Involved in Diverse Cellular Processes in Arabidopsis. Mol Cell Proteomics 23 (4), 100732.
7. Boussardon, C. et al. (2025) The atypical proteome of mitochondria from mature pollen grains. Curr Biol 35 (4), 776-787 e5.
8. Karunadasa, S.S. et al. (2025) Detection and Quantification of Biotinylated Sites for TurboID-Based Proximity Labeling Mass Spectrometry in Arabidopsis. Methods Mol Biol 2953, 127-141.
9. Karunadasa, S.S. et al. (2025) Detection and Quantification of Biotinylated Proteins for TurboID-Based Proximity Labeling Mass Spectrometry in Arabidopsis. Methods Mol Biol 2953, 115-126.
10. Liu, C. and Moschou, P.N. (2025) Coupling Affinity Purification with Proximity Labeling in Arabidopsis: The APEAL Approach. Methods Mol Biol 2953, 143-166.
11. Rugen, N. et al. (2024) Deep proteomics reveals incorporation of unedited proteins into mitochondrial protein complexes in Arabidopsis. Plant Physiol 195 (2), 1180-1199.
12. van Wijk, K.J. et al. (2024) Detection and editing of the updated Arabidopsis plastid- and mitochondrial-encoded proteomes through PeptideAtlas. Plant Physiol 194 (3), 1411-1430.
13. Huang, A. et al. (2025) Split-YFP-coupled interaction-dependent TurboID identifies new functions of basal cell polarity in Arabidopsis. Proc Natl Acad Sci U S A 122 (32), e2502445122.
14. Montes, C. et al. (2024) Single-cell proteomics differentiates Arabidopsis root cell types. New Phytol 244 (5), 1750-1759.



Arabidopsis endodermis and cortex single-cell proteomics pipeline. Single cells (protoplasts) from plants carrying either pCASP2:GFP (endodermis; red) or pCORTEX:GFP (cortex; yellow) markers were isolated by fluorescence-activated cell sorting. Samples were processed using an Opentrons OT-2. Fifty-four multiplexed sets consisting of single-cells, reference, and carrier were analyzed by liquid chromatography coupled to tandem mass spectrometry.

PROJECTS AND RESOURCES

The Arabidopsis Biological Resource Center (ABRC)

Prepared by

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Recent activities and newly developed tools and/or resources of your project/resource.

The ABRC distributed 60,281 samples to 1,398 individuals located in 37 countries in 2024. The number of samples is approximately the same as the previous year. The number of individual recipients and the number of countries receiving stocks from the ABRC has decreased slightly from 2023. 60% of orders were shipped to researchers in the US, 12% to Japan, 5% to Canada, and 5% to Korea. Orders shipped to other countries each accounted for less than 4% of the total. In addition to orders placed directly at the ABRC website, 1,388 individual samples were provided to the European Arabidopsis Stock Center (NASC) to be distributed to their customers. The ABRC also provided bulk seed for 5,561 lines, and smaller aliquots of seed for 1,322 lines to NASC.

The ABRC received donations from researchers in the US, Canada and Iceland in 2024. The 2024 George Redei award for the largest number of stocks donated to the ABRC in a year was awarded to Liz Haswell and Ivan Radin for their donation of 124 mutant and transgenic seed stocks. The award was presented at ICAR 2025 and allows the recipient to order 75 free stocks from the ABRC. In total 259 seed stocks and 870 non-seed resources were added to the collection in 2024. These include characterized mutant and transgenic lines, natural accessions, Arabidopsis and Camelina clones.

An additional 414 seed stocks were received from the NASC, mostly T-DNA insertion lines from the GABI-Kat project. All stock information is available through the ABRC website (https://abrc.osu.edu/). In 2024 the ABRC grew 3,902 seed lines to generate additional seed for distribution and 199 seed lines for stocks with lower than 81% germination. The ABRC outreach program reached over 600 individuals in 2024 through distribution of stocks to students and educators, tours of the center, and programming at local science fairs. The ABRC also presented a joint booth with the NASC at ICAR 2025 in Ghent.

Planned future activities of your project/resource

To ensure the future of the stock centers please continue to order and donate; you may win the Redei award next year! We are particularly interested in receiving characterized mutants and new CRISPR lines. We are also happy to receive verified T-DNA insertion lines even if we already have a confirmed line in the collection.

We are very interested in receiving seeds of close relatives of Arabidopsis (e.g. A. halleri, lyrata and arenosa) and other members of the Brassicaceae. The ABRC plans to work closely with the NASC to ensure that we exchange stocks in a timely manner so that researchers around the world can benefit from resources donated to either center. Our outreach activities continue to focus on distribution of education kits and programming with local partners.

Bio-Analytic Resource for Plant Biology (BAR)

https://bar.utoronto.ca

Prepared by

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Nicholas Provart, nicholas.provart@utoronto.ca, University of Toronto

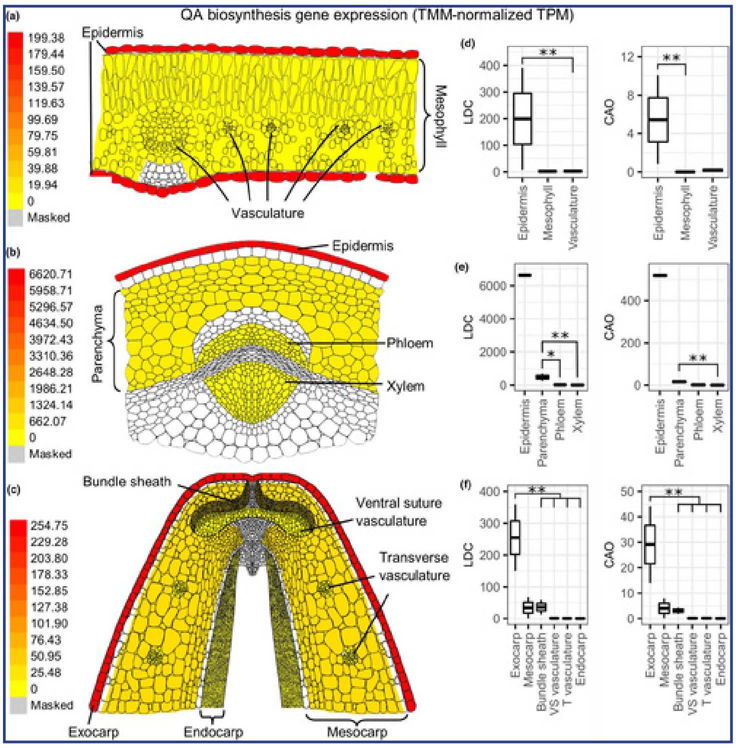
Recent activities and newly developed tools and/or resources of your project/resource.

- The BAR celebrated 20 years of serving the community, see Sullivan et al., (2025)!
- TAIR12 genome reannotation effort: the BAR worked on annotating mitochondrial genes in Arabidopsis genome together with TAIR curators.
- We upgraded the BAR server hardware, with funding from Genome Canada.
- The old BAR server was converted to the BAR's storage server.
- New data sets were added to the eFP-Seq Browser: Guard Cell Drought (Provart Lab) and Pollen (Misra et al., 2025).
- The BAR's SequenceServer was upgraded to the latest version.
- Arabidopsis Expression Browser – Klepikova data are now live for bulk queries of up to 500 genes across 79 tissues.
- Work continues on refactoring old BAR webservices into the BAR API.
- ThaleMine v5.1.0-20241202 was released.
- Annotations for around 8000 genes based on reprocessed PlantConnectome (https://plant.connectome.tools/) summaries were added to the BAR and made available in GAIA and ePlant via a BAR API endpoint.

For other species, we worked on the following.

- Developed a Canola eFP Browser (Ziegler et al., 2025).
- We rolled out around 10 views in our new eFP Sorghum Browser.
- A Lupin eFP Browser was released (Frick et al., 2025).
- We added a "Drought x Heat Stress" view to our Rice eFP Browser (Robertson et al., 2025).

- Frick, K. M., Lorensen, M. D. B. B., Micic, N., Esteban, E., Pasha, A., Schulz, A., Provart, N. J., Nour-Eldin, H. H., Bjarnholt, N., Janfelt, C., & Geu-Flores, F. (2025). The aerial epidermis is a major site of quinolizidine alkaloid biosynthesis in narrow-leafed lupin. New Phytologist, 245(5), 2052–2068. https://doi.org/10.1111/nph.20384.



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- Pahari, S., Vaid, N., Soolanayakanahally, R., Kagale, S., Pasha, A., Esteban, E., Provart, N., Stobbs, J. A., Vu, M., Meira, D., Karunakaran, C., Boda, P., Prasannakumar, M. K., Nagaraja, A., & Jain, A. K. (2024). Nutri-cereal tissue-specific transcriptome atlas during development: Functional integration of gene expression to identify mineral uptake pathways in little millet (Panicum sumatrense). The Plant Journal, 119(1), 577–594. https://doi.org/10.1111/tpj.16749.

- Robertson, S.M., Sakariyahu, S.K., Gan, E., Maqsood, O., Pasha, A., Provart, N.J. and Wilkins, O. (2025), Growth-limiting drought increases sensitivity of Asian rice (Oryza sativa) leaves to heat shock through physiological and spatially distinct transcriptomic responses. Plant J, 123: e70349. https://doi.org/10.1111/tpj.70349.

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- Ziegler, D.J., Kha, D., Kalichuk, J.L., Becker, M.G., Pasha, A., Provart, N.J., Belmonte. M.F. (2025) Plant Physiol. doi: https://doi.org/10.1093/plphys/kiaf283.

Planned future activities of your project/resource

- ThaleMine Upgrade
- BAR software upgrade (operating system, database server, software stack)
- BAR Databases update (latest datasets)
- ASPB 2025 (online)
- CSPB 2025, Halifax, NS., Canada
- GCBR 2025 in-person meeting
- New software: ePlant 3
- New eFP Browser – SUMO Map
- Several updates to existing infrastructure and BAR API

Gramene

A comparative genomics and pathways resource for plants
https://www.gramene.org

The Gramene project (also referred to as Gramene Plants) is a knowledgebase founded on stewardship of plant genomes with a focus on cross-species comparison, using a single reference assembly to anchor genomic and pathway data for model plants and major crops, aiming to support agricultural researchers.

Gramene's Pan-Genome resources for four crop species were built on the Gramene infrastructure to extend the depth of the reference genomes, linking genetic variation to agronomically important traits.

https://maize-pangenome.gramene.org/
https://oryza.gramene.org/
https://vitis.gramene.org/
https://www.sorghumbase.org/

Each of these pan-genome sites includes Arabidopsis thaliana among a small set of outgroup species to support comparative analyses and functional inference.

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Recent activities and newly developed tools and/or resources of your project/resource.

Arabidopsis thaliana continues to serve as a foundational model organism within the Gramene

Plants platform and associated crop-specific pan-genome databases maintained by Gramene. This report summarizes significant developments and enhancements made to these resources over the past year, highlighting improvements in data standardization, genomic coverage, and analytical capabilities that support the global plant research community.

- Pan-Genome Database Releases

Several major releases have expanded the genomic resources available through the Gramene platform:

Oryza Release 8 (August 2024): Enhanced rice genomic datasets with improved annotation and comparative genomic features.

Sorghum Releases 8 and 9 (October 2024 and January 2025): Consecutive updates to SorghumBase incorporating substantial genomic expansions and analytical improvements.

Maize Release 5 (March 2025): Latest iteration of Gramene Maize with enhanced pan-genomic coverage and functional annotations.

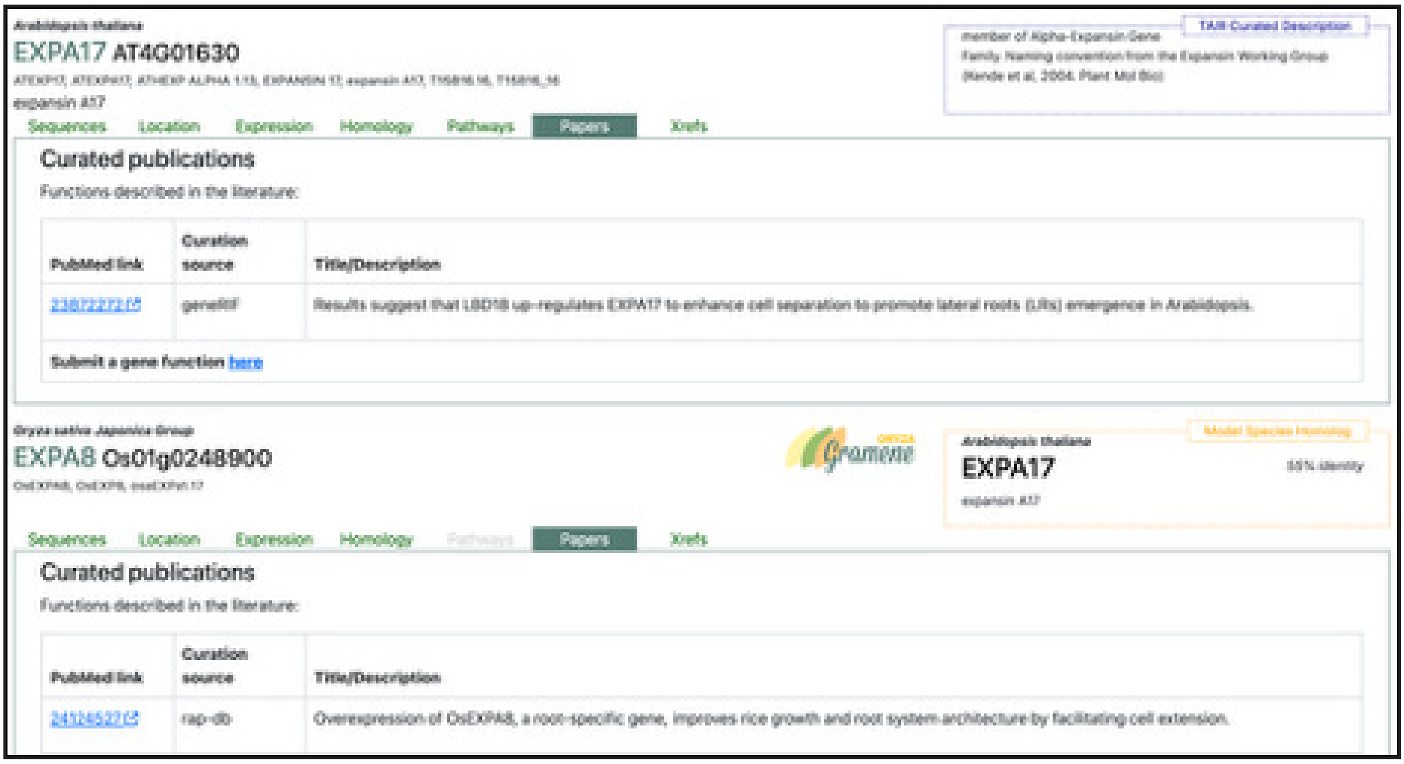
These releases collectively integrated 76 additional genomes into the platform ecosystem, with 58 genomes incorporated into SorghumBase and 18 into Gramene Maize. All newly integrated genomes include comprehensive ortholog and homeolog mapping to A. thaliana, reinforcing its central role as a reference species for comparative genomics.

- Data Standardization Initiatives

As part of ongoing efforts to improve data consistency and interoperability, over 26 million temporary SNP identifiers have been systematically updated to reference standardized SNP cluster IDs (rsIDs) for A. thaliana. This initiative significantly enhances cross-platform data integration and facilitates more robust comparative analyses across different plant species.

- Gene Family Visualization and Annotation

The Gramene search interface continues to provide sophisticated gene family visualizations that highlight the closest annotated homolog to each gene. These visualizations leverage TAIR-curated descriptions to enhance functional interpretation, providing researchers with immediate access to relevant functional context for genes of interest.



Arabidopsis thaliana

EXPA17 AT4G01630

ATEXP17, ATEXPA17, ATHEXP ALPHA 1.13, EXPANSIN 17, expansin A17, T15B16.16, T15B16_16

expansin A17

TAIR Curated Description

member of Alpha-Expansin Gene Family. Naming convention from the Expansin Working Group (Kende et al, 2004, Plant Mol Bio)

Curated publications

Functions described in the literature:

PubMed link	Curation source	Title/Description
23872272	geneRIF	Results suggest that LBD18 up-regulates EXPA17 to enhance cell separation to promote lateral roots (LRs) emergence in Arabidopsis.

Submit a gene function here

Oryza sativa Japonica Group

EXPA8 Os01g0248900

OsEXPA8, OsEXP8, osaEXPa1.17

Model Species Homolog

Arabidopsis thaliana

EXPA17

55% identity

expansin A17

Curated publications

Functions described in the literature:

PubMed link	Curation source	Title/Description
24124527	rap-db	Overexpression of OsEXPA8, a root-specific gene, improves rice growth and root system architecture by facilitating cell extension.

An example of the Papers tab in the Gramene Plant search interface of the search for the Arabidopsis gene “EXPA17 AT4G01630”, displaying the curated publication (PubMed link, Curation source and Description). The TAIR Curated Description is also given in the right corner of the search interface. The bottom panel displays the curated publication information of the rice ortholog “EXPA8

- Literature-Based Annotations

The platform maintains an extensive collection of 13,529 literature-based functional annotations sourced from authoritative databases including NCBI's GeneRIF and RAP-DB. The current distribution includes:

- 7,255 annotations for A. thaliana
- 37 annotations for A. lyrata

Recent updates show modest but consistent growth in curated Arabidopsis-related publications across platforms:

- Gramene Maize: 7,334 publications
- Gramene Oryza and SorghumBase: 7,258 publications each

- Literature Access and Community Contribution

Curated references are readily accessible through the "Papers" tab within the Gramene search interface, featuring searchable tables of PubMed-linked literature and gene annotations tagged with Trait Ontology (TO) and Plant Ontology (PO) terms. To foster community engagement and data completeness, the platform provides an embedded "Add Papers" form, particularly encouraging contributions for genes currently lacking functional annotation.

- Whole-Genome Alignments

A. thaliana maintains its crucial role as a reference species in phylogenomic analyses, gene family construction, and whole-genome alignment (WGA) comparisons. The platform currently provides WGAs between A. thaliana and 79 other species, including closely related species A. lyrata and A. halleri, accessible through Gramene Plants.

Additional comparative genomic resources include:

- A. lyrata alignments with Japonica rice, B73 maize, and Medicago
- A. halleri alignments with rice and maize

- Gene Model Quality Assessment

Through comprehensive phylogenetic analyses and alignment comparisons, the platform has identified gene model anomalies (contiguous gene split models):

- A. thaliana: 14 previously identified + 35 newly flagged in SorghumBase R9
- A. halleri: 40 identified
- A. lyrata: 43 identified

This quality assessment contributes to ongoing genome annotation refinement efforts across the platform.

Electronic Fluorescent Pictograph (eFP) Browsers

Curated gene expression data for Arabidopsis remains accessible through electronic Fluorescent Pictograph (eFP) browsers from the Bio-Analytical Resource (BAR), available across Gramene, SorghumBase, Gramene Oryza and Gramene Maize platforms. The Arabidopsis eFP browser, accessible via the Gene Expression tab, features 26 comprehensive expression maps categorized by:

- Tissue type
- Developmental stage
- Treatment conditions
- Additional experimental parameters

- Expression Atlas Integration

In collaboration with the European Bioinformatics Institute (EBI) Expression Atlas, the platform hosts baseline expression profiles for:

- A. thaliana: 18 experiments
- A. lyrata: 1 experiment

Users can access extensive differential expression datasets covering 615 Arabidopsis experiments, with 4 newly added datasets in the past year. Additionally, 14 single-cell expression (SCE) studies are available, including 1 recent addition, providing researchers with cutting-edge transcriptomic resources.

- CLIMtools portal: Advanced G×E Analysis Platform

Gramene continues to support exploration of gene-by-environment (G×E) interactions through its specialized CLIMtools portal. The latest version (v2.0) of the Arabidopsis CLIMtools (https://www.gramene.org/CLIMtools/arabidopsis_v2.0/) represents a significant advancement in climate-genomics research capabilities. The current CLIMtools platform includes:

- Data from 2,999 A. thaliana accessions
- Coverage of 473 climate variables
- Integrated analytical tools for climate GWAS, TWAS, and RiboSNitch prediction
- Five specialized R Shiny applications: AraCLIM, CLIMGeno, GenoCLIM, PhenoCLIM, and T-CLIM

These applications provide diverse visualization and analysis options for researchers investigating climate adaptation and environmental responses in plant systems.

Planned future activities of your project/resource

- **Gramene Plants Release 69**: The upcoming release will complete the replacement of temporary SNP identifiers with standardized rsIDs for A. thaliana, further enhancing data consistency and interoperability.

- **GWAS Integration:** Plans are underway to integrate genome-wide association study (GWAS) results for various traits directly into the Gramene database. This integration will enable users to browse genomic loci associated with specific phenotypes of interest, significantly enhancing the platform’s utility for trait-based research.

- **Single-Cell Expression Data:** The 14 single-cell expression studies currently available through the EBI Expression Atlas will be indexed and made directly accessible to the Gramene user community, improving the discoverability and usability of these valuable datasets.

The Nottingham Arabidopsis Stock Centre (NASC)

Prepared by

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http://arabidopsis.info/

Recent activities and newly developed tools and/or resources of your project/resource.

In the 2024 calendar year NASC users from 37 countries ordered over 44,000 stocks, with Germany (6821) taking the top spot for the first time followed by China (6810), UK (5840), and Spain (4360). At the other end of the volume scale, we saw orders from Brazil (5), Ukraine (4), and the Russian Federation (3) – remembering that every order may underpin a research or teaching project.

Thank you as always to all those generous groups continuing to donate new stocks and populations of seed (~1000 in 2024 from 10 countries). We really appreciate all new material– whether sets of lines or a single line that you have developed (if you can provide supporting data, publication is not essential). We are particularly keen to catch up on genome edited lines but will gratefully look after anything from populations (even finite ones) to ecotypes/geographical accessions.

Should you need help or advice donating or exporting your material to us, please don't hesitate to get in touch with curators@arabidopsis.info. Don't waste the valuable time of your postdocs and technicians in fulfilling seed requests from your publications– give us the seeds and the (boring) work, it is what we are here to do.

We know that it is a pain to send seeds between laboratories. We have tamed that beast and have pulled out some of the thorny distribution problems for you. So please do consider donating your stocks to the centres. Ordering seeds through NASC covers inspections, phytosanitary certificates, and inconsistent international postal regimes. If you order seeds, please use the tracking email we give you, and make sure your phone/email details at NASC are current in case the carriers need to contact you (please check your spam folders). Delays in responding to carrier emails can sometimes lead to unhelpful local storage charges, which can be expensive. We arrange the phytosanitary certificate (attached to your parcel) with correct content codes, but local requirements can vary (e.g. import documents for some countries). If in doubt, please ask your institute about any additional legal requirements– they should know.

Ghent was great, apologies that we ran out of rainbow lanyards. If you really 'need' one ask us (by email) to include one with your seed order– we have already bought a load for the ICAR in sunny Singapore.

Up-to-date details on stock donations are on the NASC site as always, please contact us at any time. If we (NASC, ABRC, RIKEN, or VASC) can help you promote your research to the community by distributing seed on your behalf, don't wait for us to find you – send an email, we can help.

RIKEN BioResource Research Center

Prepared by

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RIKEN BRC

https://epd.brc.riken.jp/en/

Recent activities and newly developed tools and/or resources of your project/resource.

- Distribution

RIKEN BRC distributed a total of 1,887 stocks to 160 laboratories across 23 countries in FY2024. Distributed stocks include 1,534 seed stocks, 223 clones/plasmids, and 127 plant cultured cell lines.

- Collection

In FY2024, RIKEN BRC collected 17,925 seed samples and 16 plasmids. The newly released materials are listed below. In total, RIKEN BRC preserves ~170k Arabidopsis mutants/transgenic lines, ~711k clones/plasmids, and 102 plant cultured cell lines.

For detailed information, please visit the Exp-Plant Catalog (https://plant.rtc.riken.jp/resource/home/index.html) and the RIKEN BRC plant cell line documentation (https://plant.rtc.riken.jp/resource/cell_line/web_documents/cell_lines/).

- M2 populations of EMS-mutagenized mutants (Col-0 background; temporally distribute to labs in Japan only)
- Binary vectors for genome editing in Marchantia polymorpha
- rpc00092: TBY2-31/ST(E), transgenic BY-2 cell line (Nicotiana tabacum L.) expressing estradiol-inducible GFP-AtSYP31 (cis-Golgi marker) and estradiol-inducible ST-mRFP (trans-Golgi marker)
- rpc00097: TBY2-31/41, transgenic BY-2 cell line (Nicotiana tabacum L.) expressing GFP-AtSYP31 and ST-mRFP
- rpc00098: topless3-GFP, transgenic BY-2 cell line (Nicotiana tabacum L.) expressing NtTPL3-GFP
- rpc00107: CrB (Catharanthus roseus L.)
- rpc00109: BY-HR, transgenic BY-2 cell line (Nicotiana tabacum L.) expressing H2B-tdTomato

Planned future activities of your project/resource

RIKEN BRC plans to receive Arabidopsis transcription factor (TF) clones prepared for Y1H/Y2H screening, as well as Arabidopsis transgenic lines expressing TF chimeric repressors or dominant activators, kindly provided by AIST. Additionally, RIKEN BRC estimates that more than 100 individual mutant or transgenic strains will be received from the Arabidopsis research community. These new materials will be released promptly following rigorous quality checks and amplification.

The Arabidopsis Information Resource (TAIR)

Prepared by

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www.arabidopsis.org

Recent activities and newly developed tools and/or resources of your project/resource.

- Data:

Genome Annotation: The TAIR12 Col-0 community curated genome annotation progressed to the next level. The different annotation tracks were finally merged into a single file (a very complex and time consuming task), quality checked and submitted to NCBI for inclusion as the new Arabidopsis Reference Genome in RefSeq. Once the submission is finalized and released to the public, TAIR and other resources such as BAR and UniProt will begin the process of integration. For TAIR this will mean updating the database and all of the tools (e.g. BLAST, JBrowse, etc.) that rely on current genome data. A publication describing the re-annotation project will be submitted.

Gene Function Annotation: We continue to curate gene function data from the primary literature with an emphasis on capturing information for previously undescribed genes. Data types include gene symbols,gene summaries, mutant alleles, phenotypes, Gene Ontology and Plant Ontology Annotations. Starting with the July 2025 release, we have added a new data file (Locus_Allele_Phenotype_YYYMMDD.tsv) to the quarterly pipeline. This file contains information about mutant alleles (names, allele types, etc.) and their associated phenotype descriptions. The Quarterly data releases are available from our website (https://www.arabidopsis.org/download/index.jsp) and public releases are mirrored at the Zenodo archive (https://doi.org/10.5281/zenodo.7843882).

Database and Tools:

Website : Following on the major replatforming in May 2024,TAIR completed an accessibility audit to assess compliance with ADA requirements and have implemented changes to ensure greater accessibility to the community. The updated VPAT (Voluntary Product Accessibility Template) document will be available on the TAIR website. Additional improvements to the new website are ongoing and we are actively responding to suggestions and feedback from the user community.

Changes to individual subscriptions/ORCID linking: Members of the community may have noticed recently implemented changes to our individual subscriptions be consistent with the usage based model. Users can connect their TAIR profiles to their ORCID profile and take advantage of the Single Sign-On and complimentary annual usage allocation.

Planned future activities of your project/resource

- Incorporation of TAIR12 genome into TAIR database and tools.

Once the TAIR12 reference genome is approved and integrated by NCBI we will update TAIR's database and tools to reflect the new genome. For the database, this means transferring annotations/data to the updated gene models (where appropriate), and incorporating new annotations. Analysis tools such as BLAST, PatMatch, JBrowse, JBrowse2, Motif Analysis, Chromosome Map Tool will be updated with the new genome. Deprecated tools such as MapViewer, Seqviewer will NOT be updated to TAIR12.

- PhyloGenes.

PhyloGenes (phylogenes.org) is our in-house tool for visualizing gene families alongside functional data to support the prediction of function for uncharacterized genes. We plan to release version 5 by the end of summer 2025 which includes major updates to the trees (based on PANTHER 19) and updated GO annotations. Future Phylogenes updates will occur after UniProt integration of TAIR12 and generation of new gene families from Panther.

- Papers.

Stay tuned, we are working on a paper for the journal Genetics for inclusion in the 2026 collection of articles on Knowledgebase and Database Resources
community. These new materials will be released promptly following rigorous quality checks and amplification.

COUNTRIES

ARGENTINA

Prepared by

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Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

- Lando et al., 2024. Immunofluorescence for Detection of TOR Kinase Activity In Situ in Photosynthetic Organisms (https://bio-protocol.org/en/bpdetail?id=5140&type=0).
An in-situ immunofluorescence method to detect TOR kinase activity via phosphorylated S6K in cells and tissues of photosynthetic organisms (Arabidopsis and Chlamydomonas), enabling non-destructive, cell-specific visualization of TOR signaling by confocal microscopy.

- Gaggion, et al. 2025. ChronoRoot 2.0: An Open AI-Powered Platform for 2D Temporal Plant Phenotyping (https://arxiv.org/abs/2504.14736).
ChronoRoot 2.0 is an open-source, low-cost platform combining affordable hardware and AI-powered image analysis for high-throughput, time-resolved phenotyping of Arabidopsis seedlings, capturing growth, tropic responses, and circadian rhythms.

Planned events for 2025 and 2026

.
- 35° Reunión Argentina de Fisiología Vegetal. August 5-8, 2025. Mar del plata.
- 53° Congreso Argentino de Genética. September 21-24, 2025. Posadas.
- 63° Reunión de la Sociedad Argentina de Investigación Bioquímica y Biología Molecular. October 27-30, 2025. Córdoba.
- 40° Jornadas Argentinas de Botánica, September 23-27, 2025. Mar del Plata.
- 31° Reunión Argentina de Ecología. October 5-10, 2025. Mendoza.
- 4° Reunión Argentina de Biología de Semillas. November 5-7, 2025. Concepción del Uruguay.
- International Conference on Agriculture and Biotechnology ICAB 2025. November 27-28, 2025. Buenos Aires.
- Plant Biology Lectures series 2026. October 2026.

Selected Publications

- Matsusaka et al., 2024 – Physiologia Plantarum (https://onlinelibrary.wiley.com/doi/full/10.1111/ppl.14145). This study identifies a novel vernalization-responsive QTL in Arabidopsis, independent of FLC, FRI, and FT, revealing alternative genetic paths to flowering adaptation.

- Rosario Pantaleno et al., 2024 – Plant, Cell & Environment (https://onlinelibrary.wiley.com/doi/10.1111/pce.15155). The study shows that mitochondrial β-cyanoalanine synthase is an important source of hydrogen sulfide for the stomatal immunity, linking organellar metabolism to defense signaling.

- Mencia et al., 2024 – Nature Structural & Molecular Biology (https://www.nature.com/articles/s41594-024-01440-1). This paper shows how a transposon-derived intergenic region fine-tunes immune receptor expression in Arabidopsis by modulating chromatin architecture and siRNA-directed methylation.

- Lehuedé et al., 2025 – New Phytologist (https://nph.onlinelibrary.wiley.com/doi/10.1111/nph.20406). This study reveals how Arabidopsis root hair cells coordinate opposing gene networks to adaptively elongate under cold and nutrient-limited conditions.

- Baulies et al., 2025 – Nature Plants (https://www.nature.com/articles/s41477-025-01922-0). This research uncovers a key role for a microRNA in coordinating root meristem regeneration, giving key insights into Arabidopsis stem cell reprogramming after injury.

Major Funding Sources

- Agencia Nacional de Promoción de la Investigación, el Desarrollo Tecnológico y la Innovación. https://www.argentina.gob.ar/jefatura/innovacion-ciencia-y-tecnologia/agencia
- Consejo Nacional de Investigaciones Científicas y Tecnológicas (CONICET). https://www.conicet.gov.ar/
- Instituto Nacional de Tecnología Agropecuaria (INTA). https://www.argentina.gob.ar/inta
- National Universities such us Universidad de Buenos Aires, Universidad Nacional de Córdoba, Universidad Nacional del Litoral, etc. https://www.cin.edu.ar/institucional/
- Fundación Williams. https://fundacionwilliams.org.ar/
- International Center for Genetic Engineering and Biotechnology (ICGEB). https://www.icgeb.org/

AUSTRALIA

Prepared by

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Planned events for 2025 and 2026

- SASPS, Australian Society of Plant Scientists Conference 24th Nov 2025 in Adelaide, South Australia.

- ASBMB, Australian Society Biochemistry and Molecular Biology 29th Sept 2025, Brisbane, Queensland.

- ComBio, Combined Biological Sciences Meeting 28th Sept 2026, Sydney, New South Wales

Selected Publications

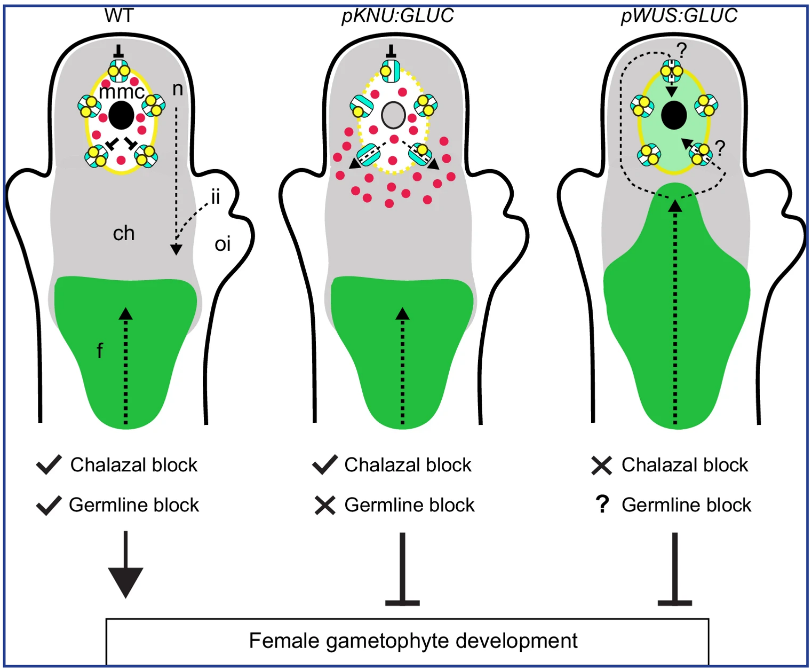
- Haywood J, Breese KJ, McDougal DP, Verdonk C, Partridge A, Lo AF, et al. Structural insights into a plant-conserved DHFR-TS reveal a selective herbicide target. Mol Plant. 2025;18(8):1294-309.

The crystal structure of a DHFR-TS (AtDHFR-TS1) from Arabidopsis thaliana shows plant-conserved architecture that suggests DHFR-TS may be a viable a herbicide target.

- Liew LC, You Y, Auroux L, Oliva M, Peirats-Llobet M, Ng S, et al. Establishment of single-cell transcriptional states during seed germination. Nat Plants. 2024;10(9):1418-34.

A temporal analysis of the germinating Arabidopsis thaliana embryo was carried out at single-cell resolution providing insight into the different regulatory mechanisms.

- Pinto SC, Leong WH, Tan H, McKee L, Prevost A, Ma C, et al. Germline β-1,3-glucan deposits are required for female gametogenesis in Arabidopsis thaliana. Nat Commun. 2024;15(1):5875.



Here authors show that increased β−1,3-glucanase delays β−1,3-glucan deposits, and halts gametogenesis.

- Wang Y, Zhang TL, Barnett EM, Sureshkumar S, Balasubramanian S, Fournier-Level A. Warm temperature perceived at the vegetative stage affects progeny seed germination in natural accessions of Arabidopsis thaliana. New Phytol. 2025;245(2):668-83.

Here the authors investigated transgenerational germination following temperature variation during the vegetative phases of natural accessions.

- Yong J, Xu W, Wu M, Zhang R, Mann CWG, Liu G, et al. Lysozyme-coated nanoparticles for active uptake and delivery of synthetic RNA and plasmid-encoded genes in plants. Nat Plants. 2025;11(1):131-44.

Lysozyme-coated nanosheets were utlised to deliver mRNA, dsRNA, siRNA and plasmid DNA into plants including Arabidopsis thaliana.

Major Funding Sources

- Fundamental and translational research can be funded by the Australian Research Council (www.arc.gov.au)
- Translational research is funded by the Grains Research Development Corporation (http://grdc.com.au)
- Industry collaborations can be funded by the Australian Research Council Linkage Programs (www.arc.gov.au)

AUSTRIA

Prepared by

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Planned events for 2025 and 2026

- Plant evolution: from origins to diversification on land, 25 – 27 November 2025, ViennaBiocenter, Austria, https://meetings.embo.org/event/25-plant-evolution

- Mendel Early Career Symposium in May 2026, Vienna BioCenter

Selected Publications

- Zhang Y, Bao Z, Smoljan A, Liu Y, Wang H, Friml J (2025) Foraging for water by MIZ1-mediated antagonism between root gravitropism and hydrotropism. Proc Natl Acad Sci U S A. 122(20):e2427315122. doi: 10.1073/pnas.2427315122.

The study find that hydrotropism is regulated by MIZU-KUSSEI 1 (MIZ1) which attenuates root gravitropism by disrupting PIN auxin transporter dynamics.

- Gallei M, Truckenbrodt S, Kreuzinger C, Inumella S, Vistunou V, Sommer C, et al. (2025) Super-resolution expansion microscopy in plant roots. Plant Cell 37(4):koaf006. doi: 10.1093/plcell/koaf006.

The study presences a method of expansion microscopy for Arabidopsis root tissues, achieving fourfold resolution enhancement.

- Julian J, Gao P, Del Chiaro A, Carlos De La Concepcion J, Armengot L, Somssich M, Duverge H, Clavel M, Grujic N, Kobylinska R, Polivka I, Besten M, Andersen TG, Dank C, Korbei B, Bachmair A, Coll NS, Minina EA, Sprakel J, Dagdas Y. (2025) ATG8ylation of vacuolar membrane protects plants against cell wall damage. Nat Plants 11(2):321-339 doi: 10.1038/s41477-025-01907-z

The study presents the involvement of a conserved turgor-pressure-dependent vacuolar integrity control system, involving V-ATPase regulated ATG8ylation to prevent cell death upon cell wall damage.

- Schoberer J, Vavra U, Shin YJ, Grünwald-Gruber C, Strasser R (2025) Elucidation of the late steps in the glycan-dependent ERAD of soluble misfolded glycoproteins. Plant J. 121(1):e17185. doi: 10.1111/tpj.17185.

The study defines distinct aspects of ER-associated degradation (ERAD) of misfolded glycoproteins that involve retrotranslocation, deglycosylation, and proteasomal degradation.

- Voichek Y, Hristova G, Mollá-Morales A, Weigel D, Magnus Nordborg M (2024) Widespread position-dependent transcriptional regulatory sequences in plants. Nat Genet 56(10):2238-46. doi: 10.1038/s41588-024-01907-3

This study reveals that, unlike animals, plant transcriptional regulation depends on position-sensitive cis-regulatory elements downstream of the transcription start site, with conserved motifs enhancing gene expression.

- Trasser M, Bohl-Villafond G, Diezma-Navas L, Loncsek L, Magnus Nordborg M, Marí-Ordóñez A (2024) PTGS is dispensable for the initiation of epigenetic silencing of an active transposon in Arabidopsis. EMBO Rep 25(12):5780-9. doi: 10.1038/s44319-024-00304-5

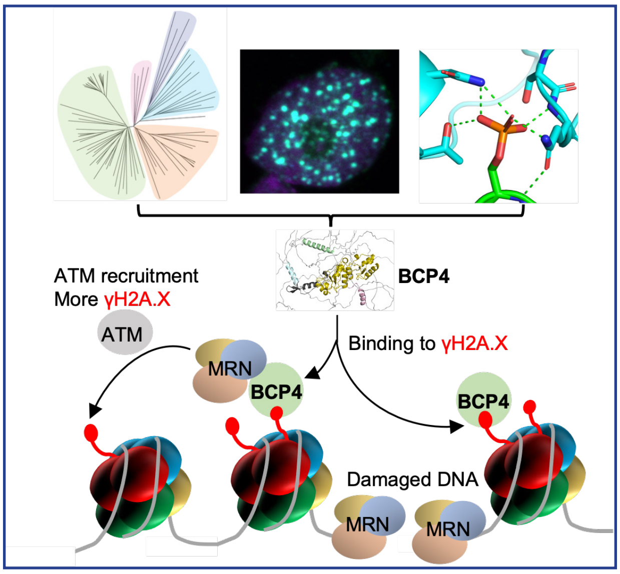
This study shows that de novo silencing of the ÉVADÉ retroelement in Arabidopsis can be achieved through RNA-directed DNA methylation (RdDM) without the need for post-transcriptional gene silencing (PTGS), suggesting PTGS is dispensable for the initiation of epigenetic silencing in plants.

- Moulinier-Anzola J, Schwihla M, Lugsteiner R, Leibrock N, Feraru MI, Tkachenko I, Luschnig C, Arcalis E, Feraru E, Lozano-Juste J, Korbei B. (2024) Modulation of abscisic acid signaling via endosomal TOL proteins. New Phytol. 243(3):1065-1081. doi: 10.1111/nph.19904.

The study uncovered that TOM1-LIKE (TOL) proteins act as plant ESCRT-0 substitutes, modulating abscisic acid (ABA) signaling by facilitating the vacuolar degradation of ubiquitinated ABA receptors and transporters, enhancing drought tolerance and ABA sensitivity without affecting plant growth and thus offering promising targets for agricultural engineering.

- Lorkovic ZJ, Klingenbrunner M, Cho CH, et al. (2024) Identification of plants' functional counterpart of the metazoan mediator of DNA Damage checkpoint 1. EMBO Rep 25(4):1936-61 doi: 10.1038/s44319-024-00107-8

This study shows that the BRCT domains containing BCP4 protein of Arabidopsis function as plant equivalents to animal damage checkpoint 1 (MDC1), binds to γH2A.X and mediate DNA damage response (DDR).



Major Funding Sources

- European Research Council	https://erc.europa.eu/
- Austrian Science Fund (FWF)	https://www.fwf.ac.at/
- Vienna Science and Technology Fund (WWTF)	https://www.wwtf.at/
- Austrian Research Promotion Agency (FFG)	https://www.ffg.at/en

BELGIUM

Prepared by

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Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

- Plant single cell RNAseq atlas
https://bioit3.irc.ugent.be/plant-sc-atlas/

- Updated collection of GoldenGate and Gateway vectors
https://gatewayvectors.vib.be/

- Centralized resource for plant post-translational modifications(PTMs)
https://www.psb.ugent.be/webtools/ptm-viewer/

- Updated versions of PLAZA
https://bioinformatics.psb.ugent.be/plaza/

Planned events for 2025 and 2026

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- SEB Annual Conference Antwerp 2025
https://www.sebiology.org/events/seb-annual-conference-antwerp-2025.html

- Agrobacterium 2025
https://www.biw.kuleuven.be/biosyst/cropbiotechnics/plant-health-and-protection-laboratory/agrobacterium-2025/under-construction

- At the forefront of Plant Research 2026
https://www.vibconferences.be/events/at-the-forefront-of-plant-research-2nd-edition

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Selected Publications

- Vukašinović N, Hsu CW, Marconi M, Li S, Zachary C, Shahan R, Szekley P, Aardening Z, Vanhoutte I, Ma Q, Pinto L, Krupař P, German N, Zhang J, Simon-Vezo C, Perez-Sancho J, Quijada PC, Zhou Q, Lee LR, Cai J, Bayer EM, Fendrych M, Truernit E, Zhou Y, Savaldi-Goldstein S, Wabnik K, Nolan TM, Russinova E. Polarity-guided uneven mitotic divisions control brassinosteroid activity in proliferating plant root cells. Cell. 2025 Apr 17;188(8):2063-2080.e24.

Brassinosteriod levels and signaling are cell-cycle regulated and guided by mother-cell polarity to ensure optimal root growth.

- Xu X, Liu H, Praat M, Pizzio GA, Jiang Z, Driever SM, Wang R, Van De Cotte B, Villers SLY, Gevaert K, Leonhardt N, Nelissen H, Kinoshita T, Vanneste S, Rodriguez PL, van Zanten M, Vu LD, De Smet I. Stomatal opening under high temperatures is controlled by the OST1-regulated TOT3-AHA1 module. Nat Plants. 2025 Jan;11(1):105-117. doi: 10.1038/s41477-024-01859-w. Epub 2024 Nov 29. PMID: 39613896.

The control of stomatal opening during heat and drought stress is integrated by TARGET OF TEMPERATURE 3 and OPEN STOMATA 1.

- Yang B, Sun Y, Minne M, Ge Y, Yue Q, Goossens V, Mor E, Callebaut B, Bevernaege K, Winne JM, Audenaert D, De Rybel B. SPL13 controls a root apical meristem phase change by triggering oriented cell divisions. Science. 2024 Nov 15;386(6723):eado4298. doi: 10.1126/science.ado4298. Epub 2024 Nov 15. PMID: 39541454; PMCID: PMC7616863.

Via a small-molecule screen, SQUAMOSA PROMOTER BINDING PROTEIN-LIKE13 (SPL13) has been shown to be involved in oriented cell division in the root apical meristem.

- Juraniec M, Goormaghtigh E, Posmyk MM, Verbruggen N. An ecotype-specific effect of osmopriming and melatonin during salt stress in Arabidopsis thaliana. BMC Plant Biol. 2024 Jul 25;24(1):707. doi: 10.1186/s12870-024-05434-5. PMID: 39054444; PMCID: PMC11270801.

Natural variation in the salt stress response suggests distinct protective mechanisms selected for as adaptation to different habitats.

- Develtere W, Decaestecker W, Rombaut D, Anders C, Clicque E, Vuylsteke M, Jacobs TB. Continual improvement of CRISPR-induced multiplex mutagenesis in Arabidopsis. Plant J. 2024 Jul;119(2):1158-1172. doi: 10.1111/tpj.16785. Epub 2024 May 7. PMID: 38713824.

Different promoters and nuclear-localization sequences have been tested to optimize expression, targeting and efficiency of Cas9-mediated generation of inheritable multiplex mutations.

Major Funding Sources

- Flanders Institute for Biotechnology (VIB; www.vib.be)
- European Union Framework Programs (cordis.europa.eu/)
- Belgian Federal Science Policy Office (www.belspo.be)
- Research Foundation – Flanders (FWO; http://www.fwo. be/en/index.aspx)
- Fonds de la Recherche Scientifique (FNRS; http://www.frs-fnrs.be)
- European Research Council (http://erc.europa.eu/)

BRAZIL

Prepared by

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Planned events for 2025 and 2026

- VI Systems Ecophysiology Symposium (VI SES) & VII International Symposium on Plant, Signaling & Behavior (VII ISPSB)
Date: 24 to 27 June 2025
Local: Hotel Brasil Tropical, Fortaleza/CE, Brazil
Organizers: Brazilian Society of Plant Physiology & Plant, Signaling & Behavior Society

- 55th Meeting of SBBq-Brazilian Society for Biochemistry and Molecular Biology
Date: 16 to 19 May 2026
Local: Hotel Majestic, Águas de Lindóia, Sao Paulo, Brazil.
Organizers: Brazilian Society for Biochemistry and Molecular Biology

- XX Brazilian Congress of Plant Physiology
Date: October 7-12, 2026.
Local: Petrolina, Pernambuco, Brazil
Organizers: Brazilian Society of Plant Physiology

- I Brazilian Conference of Plant Biotechnology
Date:06 to 10 of October 2025
Local: Campos dos Goytacazes, Universidade Estadual do Norte Fluminense - www.uenf.br

Selected Publications

- Ferreira MA, Teixeira RM, Brustolini OJB, Saia TFF, Jean-Baptiste J, Ribeiro NGA, Breves SS, Sampaio FR, Santos EGD, Leon BA, Oliveira CC, Duarte CEM, Lima LL, Oliveira LL, Ramos HJO, Reis PAB, Fontes EPB. The immune NIK1/RPL10/LIMYB signaling module regulates photosynthesis and translation under biotic and abiotic stresses. Nat Commun. 2025 May 13;16(1):4433. doi: 10.1038/s41467-025-59571-y. PMID: 40360515; PMCID: PMC12075613.

This study reveals how the immune NIK1/RPL10/LIMYB signaling module coordinates photosynthesis and protein synthesis to enhance plant resilience under both biotic and abiotic stresses.

- Vieira JGP, Duarte GT, Barrera-Rojas CH, Matiolli CC, Viana AJC, Campos RA, Canesin LED, Vicentini R, Nogueira FTS, Vincentz M. Regulation of abscisic acid receptor mRNA stability: Involvement of microRNA5628 in PYL6 transcript decay. Plant Physiol. 2024 Dec 24;197(1):kiae663. doi: 10.1093/plphys/kiae663. PMID: 39707902.

This work uncovers the role of microRNA5628 in promoting PYL6 transcript decay, revealing a novel mechanism regulating abscisic acid receptor mRNA stability.

- Ricachenevsky FK, Campos ACAL, Menguer PK, Betin FMM, Tovar J, van Dijk WFA, Guerinot ML, Salt DE, Kover PX. Comparison of linkage and association mapping in MAGIC lines identifies AtMTP3 as a new gene controlling natural variation in leaf zinc concentration in Arabidopsis. J Exp Bot. 2025 Mar 31:eraf142. doi: 10.1093/jxb/eraf142.

This study identifies AtMTP3 as a novel gene underlying natural variation in leaf zinc concentration in Arabidopsis through combined linkage and association mapping in MAGIC lines.

- Souza PVL, Alencar VTCB, Bahadar H, Silveira JAG, Daloso DM. The mitochondrial thioredoxin system regulates the TCA cycle-derived metabolic fluxes toward the GS/GOGAT cycle in illuminated leaves. J Exp Bot. 2025 Mar 24:eraf125. doi: 10.1093/jxb/eraf125.

This paper reveals that the mitochondrial thioredoxin system modulates TCA cycle–derived metabolic fluxes toward the GS/GOGAT cycle in illuminated leaves, linking redox regulation to nitrogen assimilation.

- Araújo-Lopes BG, Basso MF, Carvalho TB, Montessoro P, Carneiro AK, Silva ACD, Lima MF, Eloy NB, Silva FND, Thiebaut F, Bernado WP, Campostrini E, Engler JA, Santiago-Fernandes L, Grossi-de-Sa MF, Hemerly AS. The Multifunctional Anaphase Promoting Complex 7 (APC7) Gene Is Associated With Increased Plant Growth and Improved Resistance to DNA and RNA Viruses. Plant Cell Environ. 2025 Mar;48(3):1768-1789. doi: 10.1111/pce.15248. Epub 2024 Nov 4. PMID: 39497281.

By using a combination of genetic and biochemical approaches, this study shows that the multifunctional APC7 gene enhances plant growth while conferring improved resistance to both DNA and RNA viruses.

Major Funding Sources

- Instituto Serrapilheira (Serrapilheira is a private nonprofit institution which promotes science in Brazil.
- National Council for Scientific and Technological Development (CNPq-Brazil)
- Brazilian Federal Agency for Support and Evaluation of Graduate Education (CAPES-Brazil)
- Foundation for Research Assistance of the Sao Paulo State (FAPESP-Brazil)
- Foundation for Research Assistance of the Rio de Janeiro State (FAPERJ-Brazil)
- Foundation for Research Assistance of the Rio Grande do Sul State (FAPERGS-Brazil)
- Foundation for Research Assistance of the Minas Gerais State (FAPEMIG-Brazil)

CANADA

Prepared by

Nicholas Provart, nicholas.provart@utoronto.ca, University of Toronto

Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

The Bio-Analytic Resource for Plant Biology, the BAR at bar.utoronto.ca, is celebrating 20 years of being online, and published an update paper in NAR's Database issue in 2025, see Sullivan et al., https://doi.org/10.1093/nar/gkae920.

Updates include the Gaia search tool, which provides a convenient way to access the many data sets and tools available on the BAR, either by keyword/identifier or sequence search. Machine learning was also used for Gaia to flag genetic model figures from more than 65 000 Arabidopsis papers followed by the identification of gene names in these figures by OCR. A second addition is the use of generative AI to provide human-readable paragraphs of around 7 000 PlantConnectome network summaries. Last but not least, information was provided about the BAR's API and a Custom eFP Creator tool.

Planned events for 2025 and 2026

The 2026 Canadian Society of Plant Biology meeting will be a joint meeting with ASPB's Plant Biology conference, in Ottawa, Canada.

Eastern and Western regional CSPB meetings for 2025 have yet to be scheduled, they usually occur toward the end of the year.

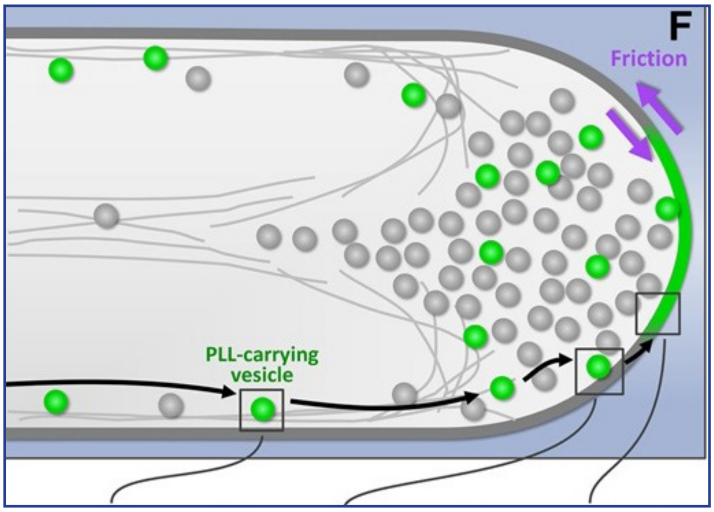
Selected Publications

- Brady, S., Auge, G., Ayalew, M., Balasubramanian, S., Hamann, T., Inze, D., Saito, K., Brychkova, G., Berardini, T.Z., Friesner, J., Ho, C.-H., Hauser, M.-T., Kobayashi, M., Lepiniec, L., Mähönen, A.P., Mutwil, M., May, S., Parry, G., Rigas, S., Stepanova, A.N., Williams, M. and Provart, N.J. (2025), Arabidopsis research in 2030: Translating the computable plant. Plant J, 121: e70047. https://dx.doi.org/10.1111/tpj.70047

This white paper outlines MASC's 4th decadal vision for Arabidopsis research, with a focus on computational approaches and translating results or methods from Arabidopsis to crop species.

- Chebli Y, Geitmann A. (2024) Pectate lyase-like lubricates the male gametophyte's path toward its mating partner. Plant Phys. 194:124-136. doi: 10.1093/plphys/kiad481.

A nice paper that identifies the role of PLL in helping the pollen tube get to where it needs to go.



- Wang, B., Bauer, A., Gómez-Felipe, A., Silveira, S. R. and Kierzkowski, D. (2025). Confocal Live Imaging of Reproductive Organs Development in Arabidopsis. Bio-protocol 15: e5177. doi: 10.21769/BioProtoc.5177.

This protocol provides a detailed pipeline the live imaging of internal reproductive floral organs of Arabidopsis including both the stamen and gynoecium, and how to capture images suitable for understanding their development.

- Mehta D, Scandola S, Kennedy C, Lummer C, Gallo MCR, Grubb LE, Tan M, Scarpella E, Uhrig RG. (2024) Twilight length alters growth and flowering time in Arabidopsis via LHY/CCA1. Sci Adv. 10:eadl3199. doi: 10.1126/sciadv.adl3199.

This paper shows that twilight length affects growth and flowering time via the LHY/CCA1 clock genes, which is important for understanding plant chronobiology from a biogeographical point of view and for identifying potential new breeding targets.

- Gonçalves Dias M, Doss B, Rawat A, Siegel KR, Mahathanthrige T, Sklenar J, Rodriguez Gallo MC, Derbyshire P, Dharmasena T, Cameron E, Uhrig RG, Zipfel C, Menke FLH, Monaghan J. (2024). New Phytol. 244:2278-94. doi:10.1111/nph.20198.

This paper describes an affinity-based proteomics approach to identify that C7 Raf-like kinases are targets of CPK28, function redundantly in stomatal opening and immunity, and possess distinct substrate specificities.

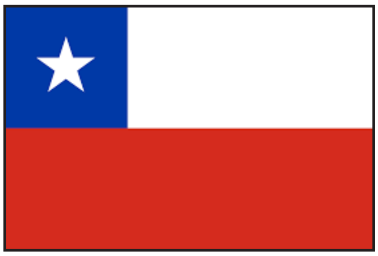
- Hoffmann N, McFarlane HE (2024) Xyloglucan side chains enable polysaccharide secretion to the plant cell wall. Dev Cell. 59:2609-25. doi: 10.1016/j.devcel.2024.06.006.

This beautiful paper using mutants, biochemistry and cell biology shows that the hemicellulose xyloglucan’s D-galactose side chains are important for its secretion, furthering our understanding of how cell walls are made.

Major Funding Sources

The Natural Sciences and Engineering Research Council of Canada (NSERC) is the main funder of Arabidopsis research.

CHILE



Prepared by

Adrian A. Moreno, adrian.moreno@unab.cl, Universidad Andres Bello

Planned events for 2025 and 2026

- XLVIII Reunión Anual 2025 Sociedad de Bioquímica y Biología Molecular de Chile (SBBMCh). October 6 – 9, 2025, La Serena, Chile.

A meeting hosted by the Chilean Society of Biochemistry and Molecular Biology. It included talks, symposiums, and poster presentations.
Organizer: Chilean Society of Biochemistry and Molecular Biology (https://www.sbbmch.cl/reunion-anual-2025/).

- XVII Annual Meeting of Chilean Society of Plant Biologists (CSPB)
November 17, 18 & 19, 2025; Valdivia, Chile.

A meeting hosted by the Chilean Society of Plant Biologists. It included talks, symposiums, and poster presentations. Examples of covered topics are Natural Variation & Plant Breeding, Plant Cell and Molecular Biology, Plant Physiology and Hormones, Cell Wall of Trees, Fruit and Vegetables, Physiological and Molecular Biology of Grains, Biosensors and Fruit Response to Stress.
Organizer: Chilean Society of Plant Biologists (https://www.biologiavegetal.cl/)

Selected Publications

- Micaela Y. Peppino; Cislaghi, Ana P.; Herrera-Vásquez, Ariel; Palomeque, Julieta R.; Bellino, Francisco; Alvarez, María; Blanco, Francisca; Cecchini, Nicolas. The Arabidopsis TNL immune receptor BNT1 localizes to the plastid envelope and is required for the flg22-induced resistance against Pseudomonas. The Plant Journal (2025) 122, e70295. (https://doi.org/10.1111/tpj.70295).

A contribution that advances our understanding of how the spatial distribution of immune receptors influences defense outputs and opens new avenues to explore the contribution of sensory plastids.

- Osorio-Navarro C, Neira-Valenzuela G, Sierra P, Adamowski M, Toledo J, Norambuena L. The configuration of the vacuole is driven by clathrin-mediated trafficking in root cells of Arabidopsis thaliana. J Exp Bot. 2025 Jul 2;76(10):2700-2714. (https://doi.org/10.1093/jxb/eraf084).

This work contributes to a long-standing debate regarding the vacuole's role in cell expansion and opens an avenue toward understanding the cellular mechanisms required for the vacuolar configuration.

Major Funding Sources

- ANID (Agencia Nacional de Investigación y Desarrollo
(https://www.anid.cl/)
- Iniciativa Científica Milenio
(http://www.iniciativamilenio.cl/)
- CORFO - Corporación de Fomento de la Producción

(https://www.corfo.cl/)

CHINA

Prepared by

Yuling Jiao, yuling.jiao@pku.edu.cn, School of Life Sciences and Center for Quantitative Biology, Peking University

Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

- TBtools-II: a Toolkit for Biologists integrating various biological data handling tools, a stand-alone software with a user-friendly interface
https://github.com/CJ-Chen/TBtools-II

- scPlant: A framework for single-cell transcriptomic data analysis in plants
https://github.com/compbioNJU/scPlant

- iCREPCP: A deep learning-based web server for identifying cis-regulatory elements within plant core promoters
http://www.hzau-hulab.com/icrepcp/

Planned events for 2025 and 2026

- 2025 Annual Meeting of the Chinese Society for Plant Biology, July 28-August 1, 2025, Harbin, Heilongjiang

- 2025 National Congress of Plant Biology, October 12-15, 2025, Changsha, Hunan (https://2025ncpb.scimeeting.cn)

Selected Publications

-Cheng T, Liu Z, Li H, Huang X, Wang W, Shi C, Zhang X, Chen H, Yao Z, Zhao P, Peng X, Sun MX (2024). Sperm- origin paternal effects on root stem cell niche differentiation. Nature 634, 220-227.

Sperm-specific TREE1/DAZ3 transcription factors paternally suppress maternal RKD2 to ensure root stem cell niche differentiation, revealing gamete genetic defects cause organ-specific developmental defects.

- Wang Y, Li S, Mokbel M, May AI, Liang Z, Zeng Y, Wang W, Zhang H, Yu F, Sporbeck K, Jiang L, Aland S, Agudo-Canalejo J, Knorr RL, Fang X (2024). Biomolecular condensates mediate bending and scission of endosome membranes. Nature 634, 1204-1210.

This study reveals a condensate-mediated membrane scission mechanism whereby FREE1 forms liquid-like condensates to drive vesicle formation via wetting-induced forces, essential for plant osmotic stress tolerance.

- Wang Z, Wang W, Zhao D, Song Y, Lin X, Shen M, Chi C, Xu B, Zhao J, Deng XW, Wang J (2024). Light-induced remodeling of phytochrome B enables signal transduction by phytochrome-interacting factor. Cell 187, 6235-6250.e19

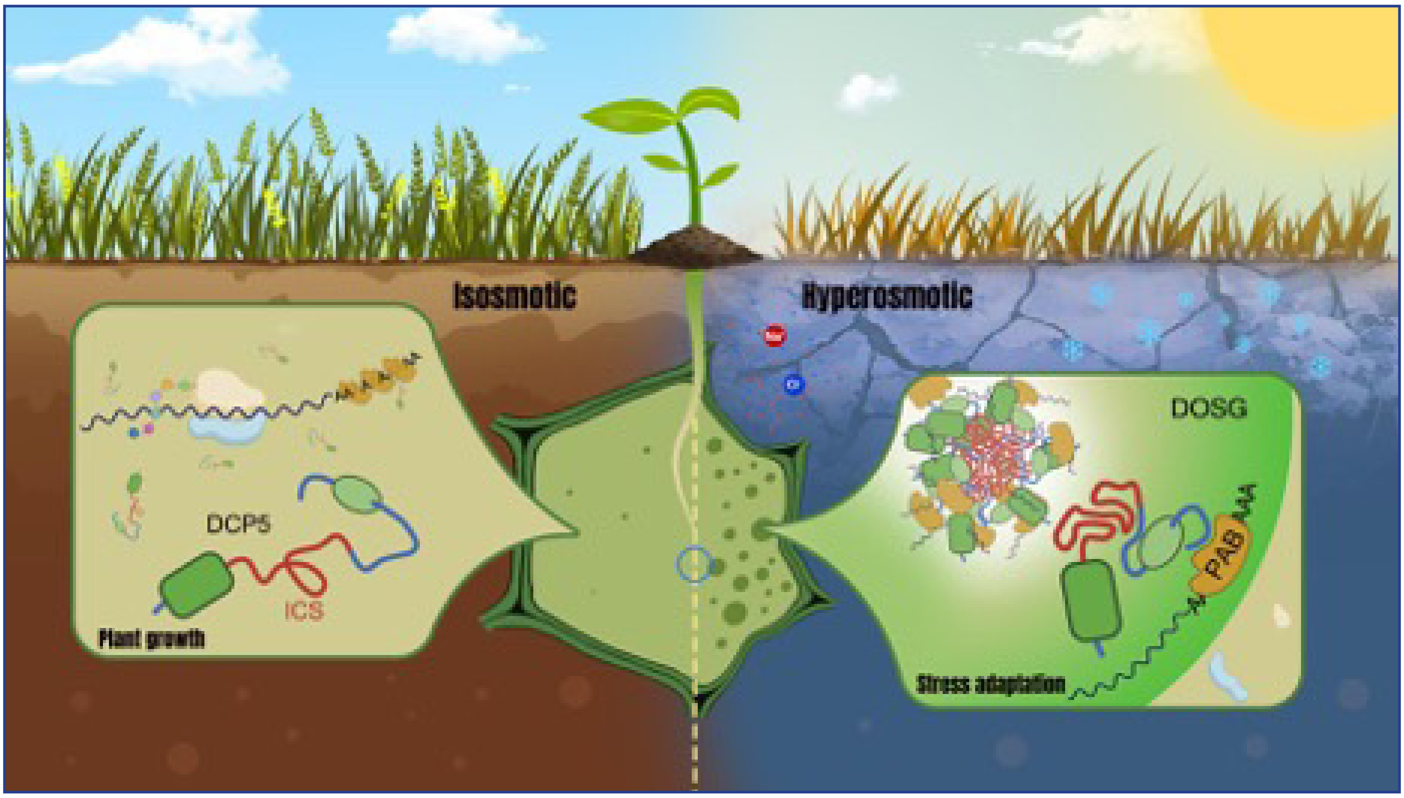
Light-induced conformational changes in phytochrome B drive formation of an asymmetric head-to-head dimer that binds PIF6, initiating photomorphogenic signal transduction.

- Yang W, Zhai H, Wu F, Deng L, Chao Y, Meng X, Chen Q, Liu C, Bie X, Sun C, Yu Y, Zhang X, Zhang X, Chang Z, Xue M, Zhao Y, Meng X, Li B, Zhang X, Zhang D, Zhao X, Gao C, Li J, Li C (2024). Peptide REF1 is a local wound signal promoting plant regeneration. Cell 187, 3024-3038.e14

This study identifies the peptide REF1 as a local wound signal that activates PORK1-WIND1 signaling to promote plant regeneration and enhance crop transformation efficiency.

- Wang Z, Yang Q, Zhang D, Lu Y, Wang Y, Pan Y, Qiu Y, Men Y, Yan W, Xiao Z, Sun R, Li W, Huang H, Guo H (2024). A cytoplasmic osmosensing mechanism mediated by molecular crowding-sensitive DCP5. Science 386, eadk9067.

DCP5 is a plant-specific osmosensor that forms stress granules via molecular crowding-triggered phase separation, sequestering mRNA and proteins to reprogram transcriptional/translational responses for osmotic stress adaptation.



Major Funding Sources

- National Natural Science Foundation (NSFC)
https://www.nsfc.gov.cn/english/site_1/index.html

CZECH REPUBLIC

Prepared by

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Charles university, Fac. of Science, Dept. of Exp. Plant Biology and Inst. of Exp. Botany, Czech Acad. Sci., Prague

Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

- Nevosád, L., Klodová, B., Rudolf, J., Raček, T., Přerovská, T., Kusová, A., Svobodová, R., Honys, D., & Procházková Schrumpfová, P. (2025). GOLEM: A tool for visualizing the distribution of Gene regulatOry eLEMents within the plant promoters with a focus on male gametophyte. The Plant journal : for cell and molecular biology, 121(5), e70037. https://doi.org/10.1111/tpj.70037

Authors introduce a freely available tool called GOLEM (Gene regulatOry eLEMents; https://golem.ncbr.muni.cz), which enables users to precisely locate any motif of interest with respect to TSS or ATG within the relevant plant genomes across the plant Tree of Life

Planned events for 2025 and 2026

- Czech Plant Nucleus Workshop 2025 is scheduled to take place in Prague on May 26-27, 2025. It will be held at Charles University in Prague. The workshop is aimed at connecting students and scientists working on plant nucleus and chromosome biology.

- Green for Good VIIth meeting 2025 – Olomouc, from 1- 4 September, Czech Republic.

Selected Publications

- Bohutínská, M., Petříková, E., Booker, T. R., Vives Cobo, C., Vlček, J., Šrámková, G., Poupětová, A., Hojka, J., Marhold, K., Yant, L., Kolář, F., & Schmickl, R. (2024). Polyploids broadly generate novel haplotypes from trans-specific variation in Arabidopsis arenosa and Arabidopsis lyrata. PLoS genetics, 20(12), e1011521. https://doi.org/10.1371/journal.pgen.1011521

Authors found that the tetraploid-characteristic haplotypes, found in genes exhibiting the most robust signals of selection, were never present in their diploid relatives; these haplotypes were made of novel 'mosaics' forged from multiple allelic sources.

- Dvořák Tomaštíková, E., Vaculíková, J., Štenclová, V., Kaduchová, K., Pobořilová, Z., Paleček, J. J., & Pecinka, A. (2024). The interplay of homology-directed repair pathways in the repair of zebularine-induced DNA-protein crosslinks in Arabidopsis. The Plant journal : for cell and molecular biology, 119(3), 1418–1432. https://doi.org/10.1111/tpj.16863

Authors show the importance of homologous recombination (HR) factor RTEL1 and microhomology-mediated end-joining (MMEJ) polymerase TEB in the repair of MET1-DPCs.

- Kubalová, M., Griffiths, J., Müller, K., Levenets, L., Tylová, E., Tarkowská, D., Jones, A. M., & Fendrych, M. (2025). Gibberellin-deactivating GA2OX enzymes act as a hub for auxin-gibberellin cross talk in Arabidopsis thaliana root growth regulation. Proceedings of the National Academy of Sciences of the United States of America, 122(30), e2425574122. https://doi.org/10.1073/pnas.2425574122

Authors show that the auxin signaling pathway steers the expression of GIBBERELLIN 2-OXIDASES (GA2OXs), key gibberellin-deactivating enzymes in the root elongation zone (EZ); GA2OXs are negative regulators of root cell elongation.

- Králová, M., Kubalová, I., Hajný, J., Kubiasová, K., Vagaská, K., Ge, Z., Gallei, M., Semerádová, H., Kuchařová, A., Hönig, M., Monzer, A., Kovačik, M., Friml, J., Novák, O., Benková, E., Ikeda, Y., & Zalabák, D. (2024). A decoy receptor derived from alternative splicing fine-tunes cytokinin signaling in Arabidopsis. Molecular plant, 17(12), 1850–1865. https://doi.org/10.1016/j.molp.2024.11.001

Alternatively spliced CRE1int7 can bind cytokinin but cannot activate the downstream cascade presenting a novel negative feedback mechanism of the cytokinin signaling pathway, facilitated by a decoy receptor that can inactivate canonical cytokinin receptors via dimerization and compete with them for ligand binding.

- Krupař, P., & Fendrych, M. (2025). When more becomes too much in acid growth. Nature plants, 11(2), 155–156. https://doi.org/10.1038/s41477-025-01919-9

New model of auxin induced acid growth suggests that excessive acidification leads to growth inhibition, which explains the biphasic response of hypocotyl to auxin.

Major Funding Sources

Both major funding agencies for basic research - Czech Science Foundation (GACR) and Ministry of Education of CR (MSMT CR) - support regularly projects based on the use of Arabidopsis as a model plant.
- Czech Science Foundation/GAČR, Prague (http://www.gacr.cz)

- Ministry of Education, Youth and Sports of Czech Republic, Prague (http://www.msmt.cz/research-and-development-1)

Both institutions support also bilateral projects with selected countries.

Targeted or applied research is since recently supported also by the Technology Agency of the Czech Republic (TACR) and Arabidopsis model is accepted as a driver for applications.

- Technology Agency of the Czech Republic (http://www.tacr.cz/english/)

- Ministry of Agriculture, National Agency for Agricultural Research (NAZV) might support projects using Arabidopsis as a driver for the applied research (http://eagri.cz/public/web/mze/poradenstvi-a-vyzkum/vyzkum-a-vyvoj/narodni-agentura-pro-zemedelsky-vyzkum/)

DENMARK

Prepared by

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Planned events for 2025 and 2026

- EMBO Workshop on Plant Membrane Biology, 18 – 22 August 2025, to take place in Helsingør, Denmark

Selected Publications

- Andersen CG, Bavnhøj L, Brag S, Bohush A, Chrenková A, Driller JH, Pedersen BP. Comparative analysis of STP6 and STP10 unravels molecular selectivity in sugar transport proteins. Proc Natl Acad Sci U S A. 2025 Apr 29;122(17):e2417370122. doi: 10.1073/pnas.2417370122.

This study reveals the structural basis of sugar selectivity in Sugar Transport Proteins (STPs) of Arabidopsis thaliana.

- Zheng S, Noack LC, Khammy O, De Meyer A, Khan GA, De Winne N, Eeckhout D, Van Damme D, Persson S. Pupylation-based proximity labeling reveals regulatory factors in cellulose biosynthesis in Arabidopsis. Nat Commun. 2025 Jan 20;16(1):872. doi: 10.1038/s41467-025-56192-3. PMID: 39833163

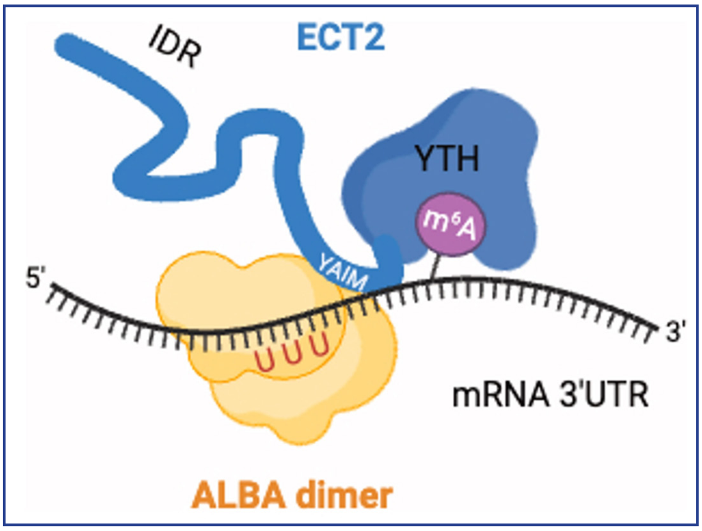
The results of this work highlight PUP-IT as a powerful proximity labeling system to identify protein interactions in plant cells.

- Bressendorff S, Sjøgaard IMZ, Prestel A, Voutsinos V, Jansson MD, Ménard P, Lund AH, Hartmann-Petersen R, Kragelund BB, Poulsen C, Brodersen P. Importance of an N-terminal structural switch in the distinction between small RNA-bound and free ARGONAUTE. Nat Struct Mol Biol. 2025 Apr;32(4):625-638. doi: 10.1038/s41594-024-01446-9.

This work elucidates the molecular basis for specific recognition and degradation of the RNA-free state of eukaryotic AGO proteins.

- Subrahmaniam HJ, Picó FX, Bataillon T, Salomonsen CL, Glasius M, Ehlers BK. Natural variation in root exudate composition in the genetically structured Arabidopsis thaliana in the Iberian Peninsula. New Phytol. 2025 Feb;245(4):1437-1449. doi: 10.1111/nph.20314.

This study provides first insights into the extent of root exudate natural variation in Arabidopsis at a regional scale.



- Reichel M, Tankmar MD, Rennie S, Arribas-Hernández L, Lewinski M, Köster T, Wang N, Millar AA, Staiger D, Brodersen P. ALBA proteins facilitate cytoplasmic YTHDF-mediated reading of m6A in Arabidopsis. EMBO J. 2024 Dec;43(24):6626-6655. doi: 10.1038/s44318-024-00312-0.

This report shows that in Arabidopsis, m6A is read not simply by YTHDF proteins, but by their complexes with the ancient RNA-binding ALBA proteins

Major Funding Sources

- Independent Research Fund Denmark, https://dff.dk/en/
- Novo Nordisk Foundation, https://novonordiskfonden.dk/en/
- Carlsberg Foundation, https://www.carlsbergfondet.dk/en

- Villum Foundation, https://villumfonden.dk/en

Planned events for 2024 and 2025

- Mendel Early Career Symposium 2024 16 - 17 May 2024 ,Vienna BioCenter, Austria, https://www.oeaw.ac.at/gmi/news-events/events/mendel-early-career-symposium-2024
- Plant Proteostasis Conference,Vienna 17 - 20 September 2024, Vienna Biocenter https://www.oeaw.ac.at/gmi/news-events/events/international-plant-proteostasis-conference-2024
- 4th International Plant Spectroscopy Conference (https://ipscvienna2024.plantspec.org/) will take place

ESTONIA

Prepared by

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Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

- University of Tartu has available custom-built gas-exchange analysis devices for measuring Arabidopsis whole-rosette photosynthesis and stomatal conductance under controlled conditions with the option to address real-time stomatal responses to changes in air CO2 concentration, air humidity, light quantity, and application of hormones. Contact: Hannes Kollist (hannes.kollist@ut.ee).

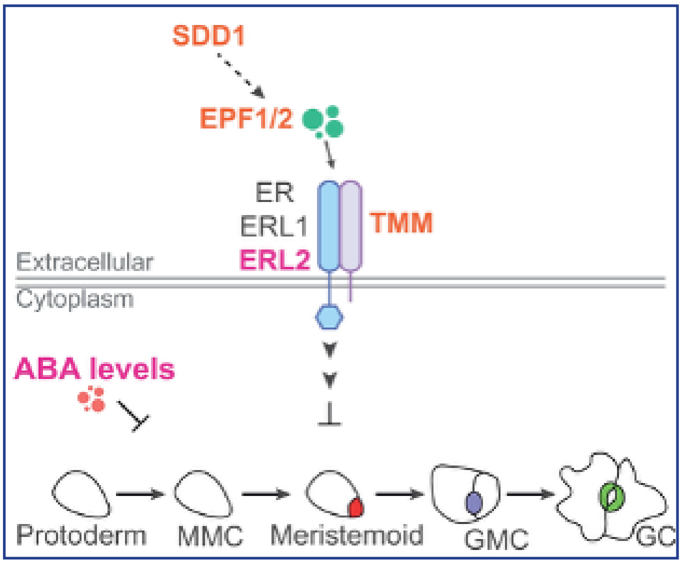
Selected Publications

- Tulva et al, 2024, https://onlinelibrary.wiley.com/doi/full/10.1111/tpj.16944

Low relative air humidity and increased stomatal density independently hamper growth in young Arabidopsis, The Plant Journal. The study shows that both low air humidity and high stomatal density impair plant growth, but the negative effect of high stomatal densities is not due to enhanced water loss. Plants also produce relatively more stomata on the adaxial (upper) leaf surface under dry air compared with control conditions.

- Jalakas et al, 2024 https://academic.oup.com/jxb/article/75/20/6476/7736051

Stomatal patterning is differently regulated in adaxial and abaxial epidermis in Arabidopsis, Journal of Experimental Botany. The study uses Arabidopsis stomatal developmental signaling mutants to address stomatal patterning in the so far little studied adaxial epidermis and shows that stomatal patterning in the adaxial and abaxial epidermis is controlled at least in part via different mechanisms.



Major Funding Sources

- Estonian Research Council, www.etag.ee

FINLAND

Prepared by

Ari Pekka Mähönen, AriPekka.Mahonen@helsinki.fi, University of Helsinki

Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

- Various promoter-RUBY lines, used to visualize plant-hormone and plant-environment interactions are deposited at NASC (see https://academic.oup.com/plphys/article/196/3/1729/7733321).

- Mobile plant phentyping platform developed by Natural Resources Institute Finland for advanced photosynthesis research in diverse environments and plant material (https://jukuri.luke.fi/items/c6394d24-44aa-454f-9aba-f5ed06b52074)./

Planned events for 2025 and 2026

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- Scandinavian Plant Physiology Society (SPPS) Congress, Helsinki, Finland, August 18-20, 2026 https://spps.se/

Selected Publications

- Eswaran G, Zhang X, Rutten JP, Han J, Iida H, López Ortiz J, Mäkilä R, Wybouw B, Planterose Jiménez B, Vainio L, Porcher A, Leal Gavarron M, Zhang J, Blomster T, Wang X, Dolan D, Smetana O, Brady SM, Kucukoglu Topcu M, ten Tusscher K, Etchells JP, Mähönen AP. (2024) Identification of cambium stem cell factors and their positioning mechanism. Science. 386: 646-653.

By combining molecular genetics and computational modelling, we show how stem cells of vascular cambium are defined in the intersection of two molecular gradients

- Lyu M, Iida H, Eekhout T, Mäkelä M, Muranen S, Ye L, Vatén A, Wybouw B, Wang X, #De Rybel B, #Mähönen AP. (2025) The dynamic and diverse nature of parenchyma cells in the Arabidopsis root during secondary growth. Nature Plants. 11: 878–890

Single cell transcriptomics and lineage tracing revealed that parenchyma cells in the secondary tissue of Arabidopsis root are dynamic and diverse

- Laihonen, L., Ranasinghe, U.T., Rantala, M., Tyystjärvi, E. and Mulo, P. (2024) Transcriptomic and proteomic analyses of distinct Arabidopsis organs reveal high PSI-NDH complex accumulation in stems. Physiologia Plantarum 176:e14227.

Arabidopsis organs show distinct transcript patterns, and Arabidopsis stem chloroplast contain thylakoids with unique organization of protein complexes.

- Bikash Baral, Saku Riihelä, Jasmin Kemppinen, Maija Sierla, Mikael Brosché, Seeing the invisible: Tools to teach and study plant transcriptional responses, Plant Physiology, Volume 196, Issue 3, November 2024, Pages 1729–1732, https://doi.org/10.1093/plphys/kiae421

Promoter-RUBY lines are an excellent tool for teaching students about plant–environment interaction, genetics, molecular biology and plant biotechnology.

- Morales, L. O., Shapiguzov, A., Rai, N., Aphalo, P. J., & Brosché, M. (2025). Protection of Photosynthesis by UVR8 and Cryptochromes in Arabidopsis Under Blue and UV Radiation. Plant, cell & environment, 48(8), 6321–6335. https://doi.org/10.1111/pce.15608

The study shows that the photoreceptors UVR8 and CRYs play partially redundant crucial roles in protecting photosynthetic apparatus in Arabidopsis from damage caused by UV-B, UV-A1, and blue light.

Major Funding Sources

- Research Council of Finland: https://www.aka.fi/en/
- Jane and Aatos Erkko Foundation: http://www.jaes.fi.
- The Ella and Georg Ehrnrooth Foundation https://www.ellageorg.fi/en
- The Finnish Cultural Foundation https://skr.fi/en

FRANCE

Prepared by

Cécile BOUSQUET-ANTONELLI, insb.das5f@cnrs.fr, CNRS, IBMP - Strasbourg & CNRS, 3 rue Michel Ange, Paris

Loïc LEPINIEC, loic.lepiniec@inrae.fr, Université Paris-Saclay, INRAE, AgroParisTech, IJPB

Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

- Arabidopsis stock center, https://publiclines.versailles.inrae.fr/

- ATOMEdb: Arabidopsis thaliana ORFeome database, http://tools.ips2.u-psud.fr/ATOMEdb

- CNRGV, Plant Genomic Center, https://cnrgv.toulouse.inra.fr/Library/Arabidopsis

- PHENOME, The French national node of EMPHASIS (a European Multi-scale Plant Phenomics and Simulation, with 11 platforms (controlled, field, omics) and shared informatics, supporting Arabidopsis and crop phenotyping. Funded under France’s “Investments for the Future” until 2024 (https://www.inrae.fr/en/research-infrastructures-inrae)

- PHENOPSIS, https://bioweb.supagro.inrae.fr/phenopsis/Accueil.php?lang=En and PHENOSCOPE (http:// www.ijpb.versailles.inra.fr/en/plateformes/ppa/index. html) , or Phenotic (https://phenotic.hub.inrae.fr/angers-plant-phenotyping-facility) are high-throughput automated phenotyping platforms at Montpellier, Versailles and Angers

- SPS tools for Functional Genomics https://eng-saclay-plant-sciences.hub.inrae.fr/infrastructures

Planned events for 2025 and 2026

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- 2025, PLant science in the ANThropocene (PLANT) Workshop, University Paris-Saclay, March 24 – April 4, Seminars are available on-line https://www.youtube.com/playlist?list=PLaT9F1eDUuN0uzR-p_X5uFxvhfCrN3UCf

- 2025, TULIP Summer School, The 13th edition of the international TULIP Summer School “Biological interactions from genes to ecosystems, June 21 – June 27. https://www.labex-tulip.fr/eng/news/tulip-summer-school-2025

- 2025, SPS (Saclay Plant Sciences) Summer School, Advanced Plant Imaging – API : From super-resolution to fluorescence lifetime imaging microscopy, June 29 – July 4, https://eng-saclay-plant-sciences.hub.inrae.fr/teaching-and-training/summer-schools/summer-school-2025

- 2025, France-Japan “Frontiers in Plant Biology” symposium, 19-21 November, Strasbourg, https://irn-fjfpb-2025.sciencesconf.org

- 2025, Symposium on Epigenetic Inheritance, celebrating V. Colot and E. Meyer, 13 & 14 Octobre, https://www.ibens.bio.ens.psl.eu/spip.php?article507

- 2025, 4th edition of the INUPRAG Symposium, Montpellier, 14 -16 of october, https://inuprag.symposium.inrae.fr

- 2026, EPIPLANT conference, June 22-24, 2026 - Nantes. https://gdr-epiplant.cnrs.fr/

Selected Publications

- Li, Z. P., et al. (2024). “Plant plasmodesmata bridges form through ER-dependent incomplete cytokinesis.” Science 386(6721): 538-545. 10.1126/science.adn4630

- Johann To Berens, P., et al. (2024). “The histone demethylase JMJ27 acts during the UV-induced modulation of H3K9me2 landscape and facilitates photodamage repair.” Nature Plants. 10.1038/s41477-024-01814-9

- Raingeval, M., et al. (2024). “Retrotransposon-driven environmental regulation of FLC leads to adaptive response to herbicide.” Nature Plants 10(11). 10.1038/s41477-024-01807-8

- Martin-Arevalillo, R., et al. (2025). “Synthetic deconvolution of an auxin-dependent transcriptional code.” Cell 188(11). 10.1016/j.cell.2025.03.028

- Perez-Sancho, J., et al. (2025). “Plasmodesmata act as unconventional membrane contact sites regulating intercellular molecular exchange in plants.” Cell 188(4). 10.1016/j.cell.2024.11.034

Gwyneth INGRAM received the Silver Medal 2025 of the CNRS.
https://www.insb.cnrs.fr/fr/personne/gwyneth-ingram-0

Major Funding Sources

- Research organizations such as CNRS, INRAE, CEA or Universities provide recurrent funding to their laboratories in addition to payment of salaries of permanent researchers and technicians. Thematic calls can also be opened by these research organizations for their research laboratories to support emerging or risky projects or to facilitate the development of interdisciplinary projects.

- The French national research agency, ANR (http:// www. agence-nationale-recherche.fr/en/about-anr/about- the- french-national-research-agency/), provides funding for project-based research

- The French Priority Research and Equipment Programme (PEPR) “Advanced Plant Selection” was launched in March 2024 (30 ME), aiming to adapt agricultural production systems to cope with climate change, while at the same time reducing phytosanitary and nutrient inputs, by supporting the development of NBT approaches.

GERMANY

Prepared by

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University of Freiburg

Planned events for 2025 and 2026

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- Botanik-Tagung (DBG International Conference)
Sep 6–10 September, 2026
Bochum
Broad plant science (often includes root/Arabidopsis topics)
https://botanik-tagung.de/general-information/outlook-2026

- MBP2026 (Molecular Biology of Plants Conference)
March 16–19, 2026
Hennef
Molecular plant biology
https://www.pflanzen-molekularbiologie.de/en/conference-molecular-biology-of-plants

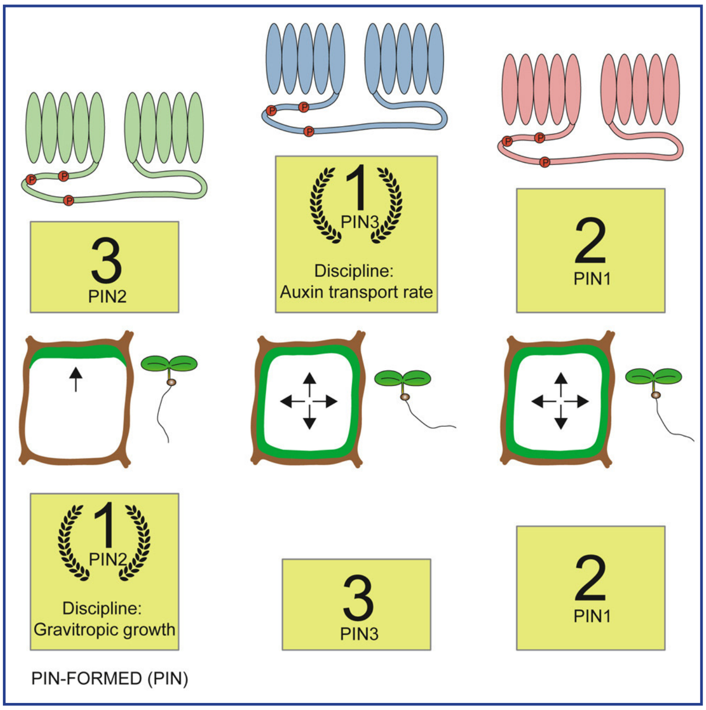
- Plant Sulphur Workshop
21–25 Sep 2025
Heidelberg
Sulphur metabolism in plants
https://conferencecentral.org/40

- Maize Genetics Meeting
Feb 26 – Mar 1, 2026
Cologne
Developmental genetics perspective
https://maizegdb.org/maize_meeting/

Selected Publications

- Transport properties of canonical PIN-FORMED proteins from Arabidopsis and the role of the loop domain in auxin transport. Dev Cell. 2024 Dec 16;59(24):3259-3271.e4. doi: 10.1016/j.devcel.2024.09.020.

The disordered cytosolic loop of the auxin efflux transporters PINs contributes to auxin transport.



PIN-FORMED (PIN)

- The temperature sensor TWA1 is required for thermotolerance in Arabidopsis Nature . 2024 May;629(8014):1126-1132. doi: 10.1038/s41586-024-07424-x.

TWA1, a predicted intrinsically disordered protein, works as a temperature-sensing transcriptional co-regulator regulating thermotolerance in Arabidopsis.

- Continental-scale associations of Arabidopsis thaliana phyllosphere members with host genotype and drought. Nat Microbiol. 2024 Oct;9(10):2748-2758. doi: 10.1038/s41564-024-01773-z. Epub 2024 Sep 6.

The leaf and soil microbiome of 267 Arabidopsis populations across Europe was compared and analyzed. Genetic variations in ACD6 gene are associated with microbiome type and drought tolerance.

- Activation and memory of the heat shock response is mediated by prion-like domains of sensory HSFs in Arabidopsis. 2025 Molecular Plant 18 (3), 457-467 DOI: 10.1016/j.molp.2025.01.007

The prior-like domains of HSFA1 are necessary for plants to respond to temperature and for thermal memory.

Major Funding Sources

- Arabidopsis research in Germany is mainly financed by the German Science Foundation (https://www.dfg.de/en) with different types of funding schemes from individual grants, research training networks (here some examples (https://rtg2498.uni-halle.de/) to big consortia, such as Collaborative Research Centers (https://www.uni-potsdam.de/en/ppp/) or excellence Cluster (not Arabidopsis-centered https://greenrobust.de/ https://www.ceplas.eu/en/home). EU-financed projects, such as ERC projects or Maria Sklodowska-Curie fellowships (https://marie-sklodowska-curie-actions.ec.europa.eu/actions/postdoctoral-fellowships), also contribute to financing Arabidopsis research in Germany. Finally, PhD/postdoc projects are also supported as fellowships by local and national foundations, such as DAAD (https://www.daad.de/en/), Alexander von Humboldt (https://www.humboldt-foundation.de/), or the Ministry of Sciences.

GREECE

Prepared by

Stamatis Rigas srigas@aua.gr
Agricultural University of Athens

Planned events for 2025 and 2026

- 74th National Conference of the Hellenic Society of Biochemistry and Molecular Biology (HSBMB),Thessaloniki 13-15 December 2024.

- Second Annual Meeting RECROP -COST Actions, Thessaloniki 13-15 May 2025

Selected Publications

- Liu C, Hatzianestis IH, Pfirrmann T, Reza SH, Minina EA, Moazzami A, Stael S, Gutierrez-Beltran E, Pitsili E, Dörmann P, D'Andrea S, Gevaert K, Romero-Campero F, Ding P, Nowack MK, Van Breusegem F, Jones JDG, Bozhkov PV, Moschou PN. 2024. Seed longevity is controlled by metacaspases. Nat Commun 15: 6748. doi: 10.1038/s41467-024-50848-2

This work uncovers a proteolytic module that modulates the accumulation of protective storage proteins during seed desiccation, thereby enhancing seed longevity.

- Liu C, Mentzelopoulou A, Hatzianestis IH, Tzagkarakis E, Skaltsogiannis V, Ma X, Michalopoulou VA, Romero-Campero FJ, Romero-Losada AB, Sarris PF, Marhavy P, Bölter B, Kanterakis A, Gutierrez-Beltran E, Moschou PN. 2024. A proxitome-RNA-capture approach reveals that processing bodies repress coregulated hub genes. Plant Cell 36: 559-584. doi: 10.1093/plcell/koad288

This paper highlights a new approach for capturing the elusive composition of membraneless compartments in plant cells.

- Balouri C, Poulios S, Tsompani D, Spyropoulou Z, Ketikoglou MC, Kaldis A, Doonan JH, Vlachonasios KE. 2024. Gibberellin Signaling through RGA Suppresses GCN5 Effects on Arabidopsis Developmental Stages. Int J Mol Sci 25: 6757. doi: 10.3390/ijms25126757

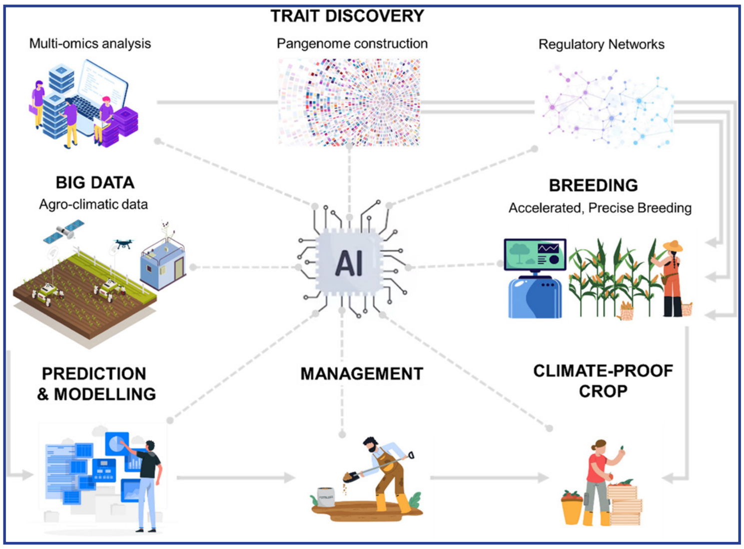
This paper describes the genetic and molecular interactions of the prototype histone acetyltransferase GCN5 with gibberellin signaling.

- Tersenidis C, Poulios S, Komis G, Panteris E, Vlachonasios K. 2024. Roles of Histone Acetylation and Deacetylation in Root Development. Plants (Basel) 13: 2760. doi: 10.3390/plants13192760

This paper highlights recent findings involving histone acetylation during root development.

- Agho C, et al 2025. Integrative approaches to enhance reproductive resilience of crops for climate-proof agriculture. Plant Stress 15: 100704. https://doi.org/10.1016/j.stress.2024.100704

This paper is an international collaboration among many MASC members involved in the RECROP-COST Action, highlighting the potential of the Greek research area in the field.



The role of Artificial Intelligence (AI) towards climate proof agriculture. Solid lines indicate the flow of information and arrows the contribution to specific aspects of science and technology related to agriculture. Dashed lines indicate how AI can collect and process all this information to develop integrated solutions for sustainable, climate-resilient agricultural systems, enabling real-time decision support, optimizing resource management, and advancing stress-tolerant crop varieties. Original vectors have been designed by Freepik (www.freepik.com) and modified.

Major Funding Sources

- General Secretariat for Research and Innovation (G.S.R.I.)
- The Hellenic Foundation for Research and Innovation (H.F.R.I.)
- European Regional Development Fund of the European Union and Greek national funds through the Operational Program Competitiveness, Entrepreneurship and Innovation, under the call RESEARCH–CREATE–INNOVATE
- ERC Consolidator Grants (CoG) 2023
- COST Actions
- AUTh Special Account for Research Funds-Research Scholarships for Post-doctoral Researchers
- Rural Development Program of Greece, Sub-Measure 16.1 ‘Cooperation’
- Fondation Santé-Supporting biomedical research in Greece

INDIA

Prepared by

Sourav Datta, IISER Bhopal

Jyothilakshmi Vadassery, NIPGR, New Delhi

Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

- athisomiRDB: A comprehensive database of Arabidopsis isomiRs (https://academic.oup.com/database/article/doi/10.1093/database/baae115/7887559)

Planned events for 2025 and 2026

- Indo-German workshop on Plant-Microbe Interactions “Implications for plant health and their interconnections” at BITS, Pilani, Rajasthan, India on October 27-28, 2025

- New Phytologist Special Workshop on ‘Molecular mechanisms of light-regulated plant development’ to be held in Bhopal from10 December to 13 December 2025.

- 6th International conference on Plant Physiology-2025 (ICPP-2025) TAMU, Coimbatore, India, December 15-18, 2025.

Selected Publications

- N Verma, D Singh, L Mittal, G Banerjee, S Noryang, AK Sinha (2024). MPK4-mediated phosphorylation of PHYTOCHROME INTERACTING FACTOR4 controls thermosensing by regulating histone variant H2A.Z deposition. The Plant Cell, doi.org/10.1093/plcell/koae223

This paper shows role of MAP kinase in phosphorylating PIF4 and thereby modulating histone deposition that affects thermomorphogenesis

- Dutta, S., Basu, R., Pal, A., Kunalika, M.H. and Chattopadhyay, S. (2024). The homeostasis of AtMYB4 is maintained by ARA4, HY5, and CAM7 during Arabidopsis seedling development. Plant Journal 120, 2515-2535.

Here the authors show that CAM7 and HY5 act as positive regulators of AtMYB4, while ARA4 acts as a negative regulator to modulate seedling development.

- Nishad, A., Gautam, J.K., Agarwal, I., and Nandi, A.K. (2025). Immune Priming Promotes Thermotolerance, Whereas Thermopriming Suppresses Systemic Acquired Resistance in Arabidopsis. Plant Cell Env 48, 3352-3363.

This paper showed an atypical interaction between stress adaptation responses against pathogen and heat. We showed that pathogen priming helps plant to tolerate more heat stress.

- Kundu P, Kumari M, Meena M.K, Mishra S and Vadassery J (2025) The Arabidopsis eATP receptor, DORN1 and CNGC19 channel act in tandem to regulate plant defense upon Spodoptera litura herbivory, Journal of Experimental Botany, eraf025,https://doi.org/10.1093/jxb/eraf025

The paper shows the crucial role of extracellular ATP as a damage signal that activates plant immunity on herbivory via its receptor DORN1 and its interaction with calcium channel, CNGC19

- Gaddam SR, Sharma A, Bhatia C, Trivedi PK (2024) A network comprising ELONGATED HYPOCOTYL 5, microRNA397b, and auxin-associated factors regulates root hair growth in Arabidopsis, Plant Physiology, 196(2), 1460–1474, https://doi.org/10.1093/plphys/kiae301

This paper reports the interplay of light and auxin signaling pathways to regulate root hair growth and development in Arabidopsis.

Major Funding Sources

- ANRF, MoE-STARS (https://stars.iisc.ac.in/), DBT (https://dbtindia.gov.in/), Council of Science and Technology, Uttar Pradesh (CSTUP)

ITALY

Prepared by

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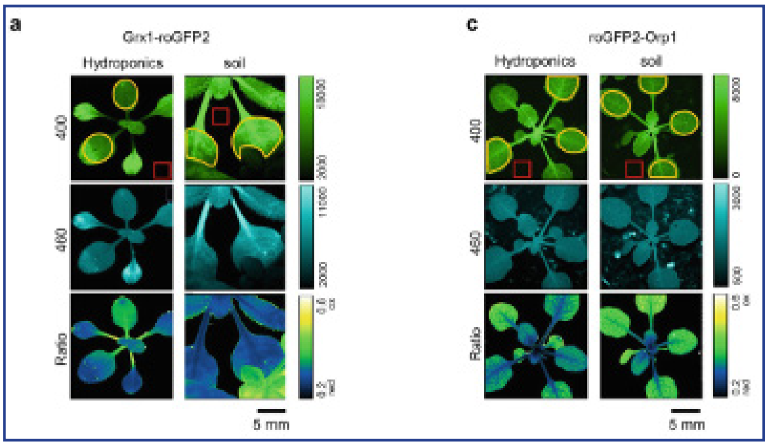
Institute of molecular biology and pathology, National Research Council

Selected Publications

- Buratti S, Grenzi M, Tortora G, Nastasi SP, Dell’Aglio E, Bassi A, Costa A. “Noninvasive In Planta Live Measurements of H2O2 and Glutathione Redox Potential with Fluorescent roGFPs-Based Sensors.” Methods Mol Biol. 2024;2798:45-64. doi: 10.1007/978-1-0716-3826-2_4.

This work presents a noninvasive in planta bioimaging protocol using genetically encoded sensors and stereo fluorescence microscopy to monitor hydrogen peroxide and glutathione redox potential in mature Arabidopsis thaliana plants grown in soil or hydroponics. This is an open access protocol.



- Pessino S, Cucinotta M, Colono C, Costantini E, Perrone D, Di Marzo M, Callizaya Terceros G, Petrella G, Mizzotti C, Azzaro C, Podio M, Marconi G, Albertini E, Dickinson H, Colombo L, Mendes MA, “Auxin response factor 10 insensitive to miR160regulation induces apospory-like phenotypes in Arabidopsis” iScience, 2024, 27-11, https://doi.org/10.1016/j.isci.2024.111115.

The commitment to the sexual germline requires spatial regulation of AUXIN RESPONSE FACTOR 10 (ARF10).

- Sessa G, Carabelli M, Sassi M “The Ins and Outs of Homeodomain-Leucine Zipper/Hormone Networks in the Regulation of Plant Development”. Int J Mol Sci 2024 May 23;25(11):5657. doi: 10.3390/ijms25115657.

This review highlights the central role of the HD-ZIP factors in the regulation of plant development through the interaction with hormone networks

- Pagano, P., Bertoncini, A., Pagano, A., Nisa, M.-U., Raynaud, C., Balestrazzi, A. and Macovei, A. (2024), Exposure of Arabidopsis thaliana Mutants to Genotoxic Stress Provides New Insights for the Involvement of TDP1α and TDP1β genes in DNA-Damage Response. Plant, Cell & Environment, 47: 5483-5497. https://doi.org/10.1111/pce.15128

The study investigates the involvement of TDP1 genes in DDR-related processes by using Arabidopsis thaliana mutants treated with genotoxic agents.

- Lorrai L, Erguvan O, Raggi S, Jonsson K, Široká J, Tarkowská D, Novák O, Griffiths J, Jones AM, Verger S, Robert R, Ferrari S (2024) “Cell wall integrity modulates HOOKLESS1 and PHYTOCHROME INTERACTING FACTOR4 expression controlling apical hook formation” Plant Physiology 196(2): 1562–1578. https://doi.org/10.1093/plphys/kiae370

Loss of cell wall integrity suppresses gibberellic acid accumulation and HOOKLESS1 and PHYTOCHROME INTERACTING FACTOR4 expression, ultimately repressing apical hook formation in Arabidopsis.

Major Funding Sources

- European Union, scheme Next-Generation EU and HORIZON-MSCA
- Ministero dell’Università e della Ricerca (MUR), scheme PRIN2022
- Università degli studi di Milano
- Sapienza University of Rome

JAPAN

Prepared by

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Satoshi Iuchi, satoshi.iuchi@riken.jp, RIKEN BRC
Taiji Kawakatsu, taiji.kawakatsu@riken.jp, RIKEN BRC

Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

- RIKEN Center for Sustainable Resource Science (CSRS) (https://csrs.riken.jp/en/)
    - Platform for RIKEN Metabolomics (http://prime.psc.riken.jp/)
    - RIKEN Arabidopsis Genome Encyclopedia (http://rarge-v2.psc.riken.jp/)

- RIKEN BioResource Research Center (BRC) (https://epd.brc.riken.jp/en/)
    - Seed Catalog (https://epd.brc.riken.jp/en/seed)
    - Plant DNA Catalog (https://epd.brc.riken.jp/en/pdna)
    - Plant Cells (https://epd.brc.riken.jp/en/pcellc)

- Kazusa DNA Research Institute (http://www.kazusa.or.jp/e/)
    - MassBase: a plant metabolome database (https://webs2.kazusa-db.jp/massbase/)
    - Plant GARDEN Plant Genome And Resource Database Entry (https://plantgarden.jp)
    - Kazusa Genome Atlas (https://genome.kazusa.or.jp/home/)

- National Institute for Basic Biology (http://www.nibb.ac.jp/en/)
    - ChaetoBase (Gene annotation database for Chaetoceros gracilis) (https://chaetoceros.nibb.ac.jp/)
    - The Plant Organelles Database 3 (http://podb.nibb.ac.jp/Organellome/)

Planned events for 2025 and 2026

- Oct. 28-31, 2024: International Symposium on plant phenology and climate feedbacks mediated by BVOCs (PCF2024), Nagaragawa Convention Center, Gifu, Japan (https://www.plant-climate-feedback.com/international-conference-2024)

- Mar. 14-16, 2025: 66th Annual Meeting of Japanese Society of Plant Physiologists. Kanazawa University, Kanazawa, Japan (https://jspp.org/annualmeeting/66/e_greeting.php)

- May. 18-22, 2025: Plant Reproductive Development and Genomics. Awaji Yumebutai Conference Center, Hyogo, JAPAN (https://www.csh-asia.org/?content/2653)

- Sep. 18-20, 2025: 89th Annual Meeting of the Botanical Society of Japan. Fukuoka Convention Center, Fukuoka, Japan (https://taikai89.bsj.or.jp)

Selected Publications

- Kamiyama, Y., Katagiri, S., Li, Y., Yamashita, K., Takase, H., and Umezawa, T. Hyperosmolarity-induced suppression of group B1 Raf-like protein kinases modulates drought-growth trade-off in Arabidopsis. Proc. Natl. Acad. Sci. USA, 121, e2419204121 (2024) https://www.pnas.org/doi/10.1073/pnas.2419204121

This study reveals that under hyperosmotic stress, suppression of group B1 Raf-like protein kinases (Raf13 and Raf15) by PP2A-mediated dephosphorylation modulates the trade-off between drought tolerance and growth in Arabidopsis.

- Maeda, A.E., Matsuo, H., Muranaka, T., and Nakamichi, N. Cold-induced degradation of core clock proteins implements temperature compensation in the Arabidopsis circadian clock. Sci. Adv., 10, eadq0187 (2024) https://www.science.org/doi/10.1126/sciadv.adq0187

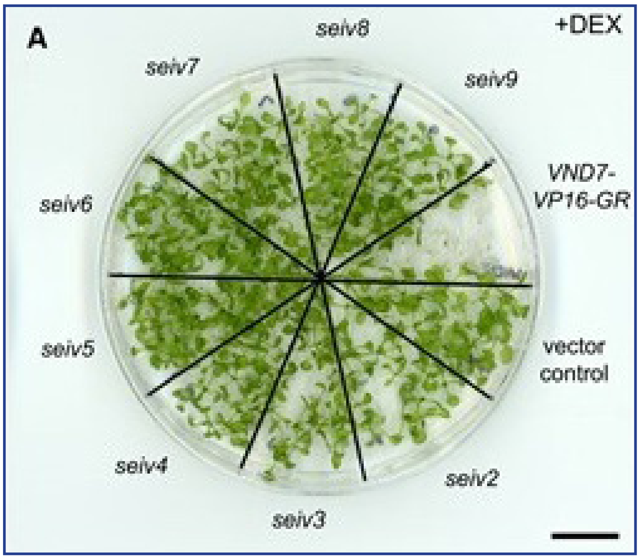
This study shows that exposure to cold promotes LKP2-dependent ubiquitination and degradation of the core clock proteins TOC1 and PRR5 in Arabidopsis, thereby enabling temperature compensation and stabilizing the circadian clock's ~24-hour period across varying temperatures.

- Kobayashi, R., Ohkubo, Y., Izumi, M., Ota, R., Yamada, K., Hayashi, Y., Yamashita, Y., Noda, S., Ogawa-Ohnishi, M., and Matsubayashi, Y. Integration of shoot-derived polypeptide signals by root TGA transcription factors is essential for survival under fluctuating nitrogen environments. Nature Commun., 15, 6903 (2024) https://www.nature.com/articles/s41467-024-51091-5

This study reveals that the transcription factors TGA1 and TGA4 serve as central regulators integrating shoot-derived nitrogen deficiency and sufficiency signals to modulate root nitrate uptake, enabling Arabidopsis to adapt and grow under fluctuating nitrogen conditions.

- Phookaew, P., Ma, Y., Suzuki, T., Stolze, S.C., Harzen, A., Sano, R., Nakagami, H., Demura, T., and Ohtani, M. Active protein ubiquitination regulates xylem vessel functionality. Plant Cell, 36, 3298–3317 (2024) https://academic.oup.com/plcell/article/36/9/3298/7725539?login=true

This study demonstrates that the activity of the master regulator VND7 in xylem vessel differentiation is controlled by specific ubiquitination-related factors (PUB46, PUB36, and UBP1), and that ubiquitination of the lysine residue K94 is particularly important for VND7's transcriptional activity, highlighting the central role of protein ubiquitination in regulating xylem vessel formation.



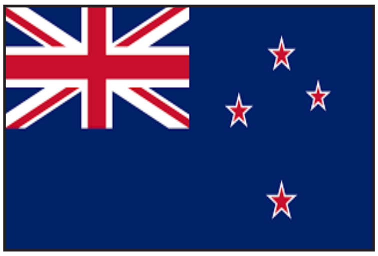
- Yabe, K., Kamio, A., Oya, S., Kakutani, T., Hirayama, M., Tanaka, Y., and Inagaki, S. H3K9 methylation regulates heterochromatin silencing through incoherent feedforward loops. Sci. Adv., 9, eadn4149 (2024) https://www.science.org/doi/10.1126/sciadv.adn4149

This study demonstrates that H3K9me2 not only facilitates but orchestrates silencing by actuating antagonistic silencing and anti-silencing pathways, providing insights into the molecular basis underlying proper partitioning of chromatin domains and the creation of metastable epigenetic variation.

Major Funding Sources

-RIKEN and National Institute of Basic Biology are supported by MEXT.
- Kazusa projects are supported by Chiba-Prefecture.
- Grants-in-Aid for Science from MEXT (https://www.jsps.go.jp/english/e-grants/)
- CREST of Japan Science and Technology Corporation (https://www.jst.go.jp/kisoken/crest/en/)
- ERATO of Japan Science and Technology Corporation (https://www.jst.go.jp/erato/en/index.html)
- PRESTO of Japan Science and Technology Corporation (https://www.jst.go.jp/kisoken/presto/en/index.html)
- ACT-X of Japan Science and Technology Corporation (https://www.jst.go.jp/kisoken/act-x/en/index.html)
- FOREST of Japan Science and Technology Corporation (https://www.jst.go.jp/souhatsu/en/index.html)
- MIRAI Program of Japan Science and Technology Corporation (https://www.jst.go.jp/mirai/en/)
- Strategic International Cooperative Program (SICORP) of Japan Science and Technology Corporation (https://www.jst.go.jp/inter/english/program_e/structure_e/general.html)
- Moonshot Research and Development Program (https://www8.cao.go.jp/cstp/english/moonshot/top.html)
- ASPIRE of Japan Science and Technology Corporation (https://www.jst.go.jp/aspire/en/)
- GteX of Japan Science and Technology Corporation (https://www.jst.go.jp/gtex/en/)
- ALCA-Next of Japan Science and Technology Corporation (https://www.jst.go.jp/alca/en/index.html)

NEW ZEALAND



Prepared by

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Planned events for 2025 and 2026

- New Zealand Plant Protection Society Conference, 10 – 13 August 2026, Napier

- Queenstown Research Week (2026, date TBA)

Selected Publications

- Valmonte-Cortes, G.R.; Higgins, C.M.; MacDiarmid, R.M. Arabidopsis Calcium Dependent Protein Kinase 3, and Its Orthologues OsCPK1, OsCPK15, and AcCPK16, Are Involved in Biotic and Abiotic Stresses. Plants 2025, 14, 294. https://doi.org/10.3390/plants14020294

An excellent collaborative paper between researchers from AUT, University of Auckland and Plant and Food Research with conserved effects in kiwifruit.

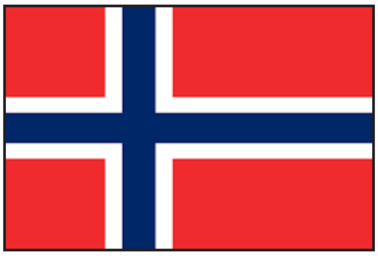
- Mayo-Smith, M., Poulet, A., Zhang, L. et al. Medicago Mting1 Mting2 double knockout mutants are extremely dwarfed and never flower implicating essential MtING functions in growth and flowering. BMC Plant Biol 25, 410 (2025). https://doi.org/10.1186/s12870-025-06432-x

This paper focuses on important Medicago flowering time genes and make use of Arabidopsis data to decipher the activity of MtING proteins in gene expression regulation.

Major Funding Sources

- Marsden Fund for fundamental/blue sky research
https://www.royalsociety.org.nz/what-we-do/funds-and-opportunities/marsden/
- Aotearoa New Zealand Tāwhia te Mana Research Fellowships
https://www.royalsociety.org.nz/what-we-do/funds-and-opportunities/tawhia-te-mana/
- Primary Sector Growth Fund
https://www.mpi.govt.nz/funding-rural-support/primary-sector-growth-fund

NORWAY



Prepared by

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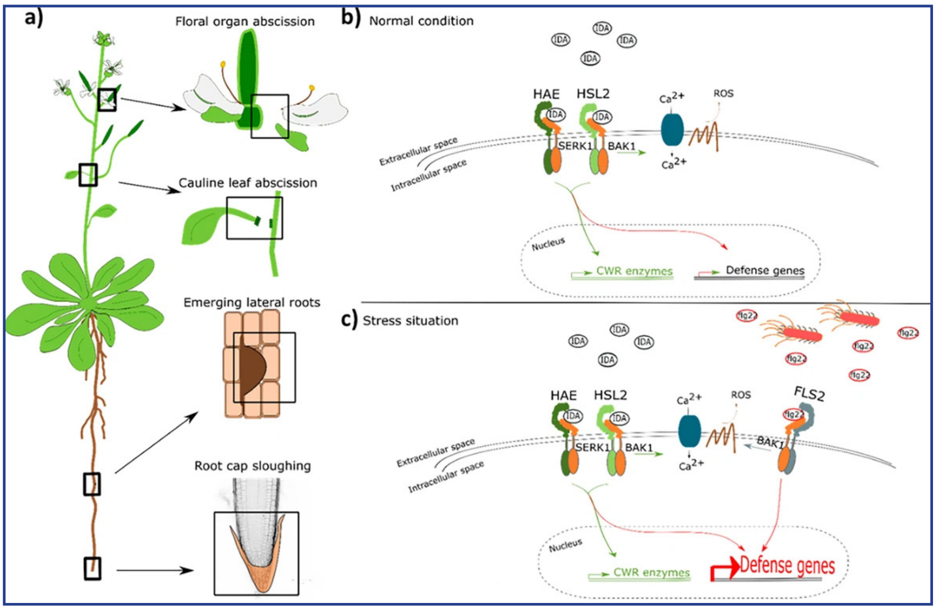
Selected Publications

- Galindo-Trigo S, Khandare V, Roosjen M, Adams J, Wangler AM, Bayer M, Borst JW, Smakowska-Luzan E, Butenko MA A multifaceted kinase axis regulates plant organ abscission through conserved signaling mechanisms.Curr Biol, 34(13):3020-3030.e7, 24 Jun 2024 https://doi.org/10.1016/j.cub.2024.05.057



- Lalun VO, Breiden M, Galindo-Trigo S, Smakowska-Luzan E, Simon RGW, Butenko MA A dual function of the IDA peptide in regulating cell separation and modulating plant immunity at the molecular level. Elife 12:RP87912 https://doi.org/10.7554/elife.87912 2024.

- Amanda K Broz,Daniel B Sloan,Iain G Johnston. Stochastic organelle genome segregation through Arabidopsis development and reproduction. New Phytol 241(2):896-910. doi: 10.1111/nph.19288 2024.

- Uflewski M, Rindfleisch T, Korkmaz K, Tietz E, Mielke S, Correa Galvis V, Dünschede B, Luzarowski M, Skirycz A, Schwarzländer M, Strand DD, Hertle AP, Schünemann D, Walther D, Thalhammer A, Wolff M, Armbruster U. The thylakoid proton antiporter KEA3 regulates photosynthesis in response to the chloroplast energy status. Nat Commun. 15(1):2792. doi: 10.1038/s41467-024-47151-5 2024 2024.

- Buscaill P, Sanguankiattichai N, Kaschani F, Huang J, Mooney BC, Li Y, Lyu J, Sueldo D, Kaiser M, van der Hoorn RAL. Subtilase SBT5.2 inactivates flagellin immunogenicity in the plant apoplast. Nat Commun. 15(1):10431. doi: 10.1038/s41467-024-54790-1 2024.

Major Funding Sources

- Norwegian Research Council, forskningsradet.no
- ERC, erc.eu

POLAND

Prepared by

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Institute of Plant Genetics of the Polish Academy of Sciences

Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

On May 6, 2025, the University of Life Sciences in Lublin officially opened Poland's first plant phenomics and imaging center. This state-of-the-art facility will concentrate on investigating plant responses to environmental stresses, particularly drought, in both model and agricultural species.

https://up.lublin.pl/en/blog/scientific-precision-at-the-leaf-level-groundbreaking-research-technology-already-in-operation-in-lublin/

Planned events for 2025 and 2026

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- 9-12 September, Warszawa. XII Meeting of the Polish Society of Experimental Plant Biology https://ptber.org.pl/default/en/12th-psepb-conference-announcement/

- 02-03 July 2026, Kraków. The European Congress of Life Sciences EUROBIOTECH https://eurobiotech.krakow.pl/

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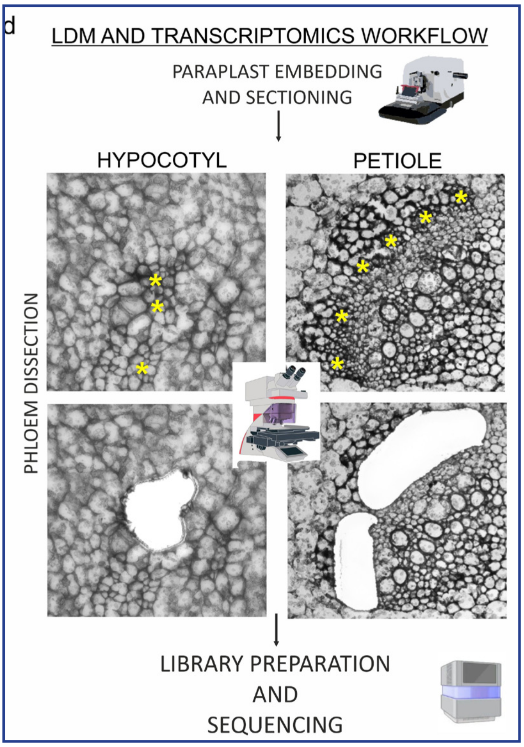
Selected Publications

- Kbiri, N., Fernández-Jiménez, N., Dziegielewski, W., Sáez-Zárate, E., Pelé, A., Mata-Villanueva, A., Dluzewska, J., Santos, Juan L., Pradillo, M., and Ziolkowski, Piotr A. (2025). Genetic dissection of MutL complexes in Arabidopsis meiosis. Nucleic Acids Research 53.

The work offers new insights into the role of MutLγ complex factors MLH1 and MHL3 in regulating the crossover pathway.

- Blicharz, S., Stefanowicz, K., Truman, W., Basińska-Barczak, A., Singh, D., Kasprzewska, A., de Diego, N., Vrobel, O., Ćavar Zeljković, S., Tarkowski, P., et al. (2025). Laser dissection-assisted phloem transcriptomics highlights the metabolic and physiological changes accompanying clubroot disease progression in oilseed rape. The Plant Journal 121, e17156

This study underscores the critical role of long-distance phloem-mediated coordination in the responses of plants to clubroot disease.



- Silveira, S.R., Collet, L., Haque, S.M., Lapierre, L., Bagniewska-Zadworna, A., Smith, R.S., Gosselin, F.P., Routier-Kierzkowska, A.-L., and Kierzkowski, D. (2025). Mechanical interactions between tissue layers underlie plant morphogenesis. Nature Plants 11, 909-923.

The study explores the mechanical interactions between cellular layers and their significant influence on the final morphology of organs. This research enhances our understanding of developmental biology and the factors that contribute to organ shaping.

- Złotkowska, E., Wlazło, A., Kiełkiewicz, M., Misztal, K., Dziosa, P., Soja, K., Barczak-Brzyżek, A., and Filipecki, M. (2024). Automated imaging coupled with AI-powered analysis accelerates the assessment of plant resistance to Tetranychus urticae. Scientific Reports 14, 8020.

Description of an automated and AI-assisted method for identifying spider mite tolerant forms of Arabidopsis thaliana.

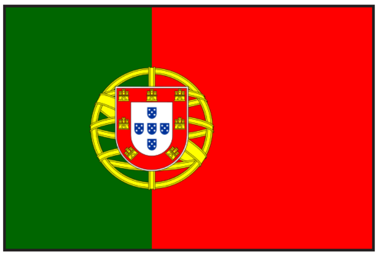
- Adamowski, M., Randuch, M., Matijević, I., Narasimhan, M., and Friml, J. (2024). SH3Ps recruit auxilin-like vesicle uncoating factors for clathrin-mediated endocytosis. Cell Reports 43, 114195.

The research paper examines the role of the SH3Ps protein in clathrin-mediated endocytosis, highlighting its significance in this cellular process.

Major Funding Sources

- Arabidopsis thaliana serves as a key model organism in plant research, and the primary source of funding for studies involving this species is the National Science Centre of Poland. This support underscores the significance of Arabidopsis thaliana in advancing our understanding of plant biology. https://www.ncn.gov.pl/en

PORTUGAL



Prepared by

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University of Porto

Planned events for 2025 and 2026

- Youth Research Meeting (IJUP) 2025 and 2026, in May, Porto, Portugal

- XVII Plant Cell Wall Meeting will be held in Porto, Portugal 15-16 June 2026
https://cellwall2026.org/

- Auxin 2026, Vidamar Hotel Albufeira, Algarve
www.auxin2026.org

Selected Publications

- Pinto SC, Leong WH, Tan H, McKee L, Prevost A, Ma C, Shirley NJ, Petrella R, Yang X, Koltunow AM, Bulone V, Kanaoka MM, Higashyiama T, Coimbra S and Tucker MR. 2024. Germline β-1,3-glucan deposits are required for female gametogenesis in Arabidopsis thaliana. Nature Communications 15: 5875. DOI: https://doi.org/10.1038/s41467-024-50143-0.

Our findings indicate that germline B-1,3-glucan fulfils a functional role in the ovule by insulating the primary germline cell, and thereby determines the success of downstream female gametogenesis.

- Ferreira, MJ, Silva, J, Takeuchi, H, Suzuki, T, Higashiyama, T, Coimbra, S. 2024. Transcriptomic landscape 1 of seedstick in Arabidopsis thaliana funiculus after fertilisation. BMC Plant Biol 24, 771. https://doi.org/10.1186/s12870-024-05489-4.

Overall, the analysis performed in this study allowed delving into the STK-network established in Arabidopsis funiculus, fulfilling a literature gap. Simultaneously, our findings reinforced the reliability of the transcriptome, making it a valuable resource for candidate genes selection for functional genetic studies in the funiculus.

- Manrique S, Cavalleri A, Guazzotti A, Villarino G, Simonini S, Bombarely A, Higashiyama T, Grossniklaus U, Mizzotti C, Pereira AM, Coimbra S, Onelli E, Masiero S, Franks R, Colombo L. 2024. HISTONE DEACETYLASE 19 regulates shot MERISTEMLESS expression in the carpel margin meristem contributing to ovule number determination and transmitting tract differentiation. Plant Physiology DOI: 10.1093/plphys/kiad629

Chromatin immunoprecipitation assays indicated that STM is a direct target of HDA19 during pistil development and that the transcription factor SEEDSTICK is also required to regulate STM via histone acetylation. Thus, we identified factors required for the downregulation of STM in the CMM, which is necessary for organogenesis and tissue differentiation.

- Moreira D, Kaur D, Fourbert-Mendes S, Showalter AM, Coimbra S, Pereira AM. 2024. Eight hydroxyproline-O-galactosyltransferases play essential roles in female reproductive development. Submitted to Plant Science, 112231. https://doi.org/10.1016/j.plantsci.2024.112231.

This study revealed that at least three more enzymes exhibit Hyp-O-GALT activity in Arabidopsis (GALT3, 4 and 6), and reinforces the crucial importance of AGP carbohydrates in carrying out the biological functions of AGPs during plant reproduction.

- Foubert-Mendes S, Silva J, Ferreira MJ, Pereira L, Coimbra S. 2025. A review on the function of arabinogalactan-proteins during pollen grain development. Plant Reproduction 38:8 https://doi.org/10.1007/s00497-024-00515-9

Understanding the intricate interplay between AGPs and PG development sheds light on the underlying mechanisms that drive reproductive success and highlights the indispensable role of AGPs in ensuring the integrity and functionality of PGs.

Major Funding Sources

- Fundação para a Ciência e Tecnologia (FCT) - https://www.fct.pt/
- Fundação “La Caixa” - https://fundacaolacaixa.pt/
- European funding – Marie Curie actions - https://marie-sklodowska-curie-actions.ec.europa.eu/
- Research Organizations such as LAQV Requimte (https://laqv.requimte.pt/), GreenUP (https://www.fc.up.pt/GreenUPorto/pt/), CIBIO(https://cibio.up.pt/en/), GULBENKIAN (https://gulbenkian.pt/fundacao/apresentacao/), ITQB (https://www.itqb.unl.pt/),…and many others, provide recurrent funding to their laboratories.

SINGAPORE

Prepared by

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Planned events for 2025 and 2026

- Plant Biomolecular Condensation and Signalling, Singapore Bioscience Symposium, 10-12 December, 2025, Nanyang Technological University, Singapore. https://www.ntu.edu.sg/sbs/symposium/sbs-2025

- International Conference on Arabidopsis Research (ICAR) 2026, 22-26 June, 2026, National University of Singapore, Singapore.

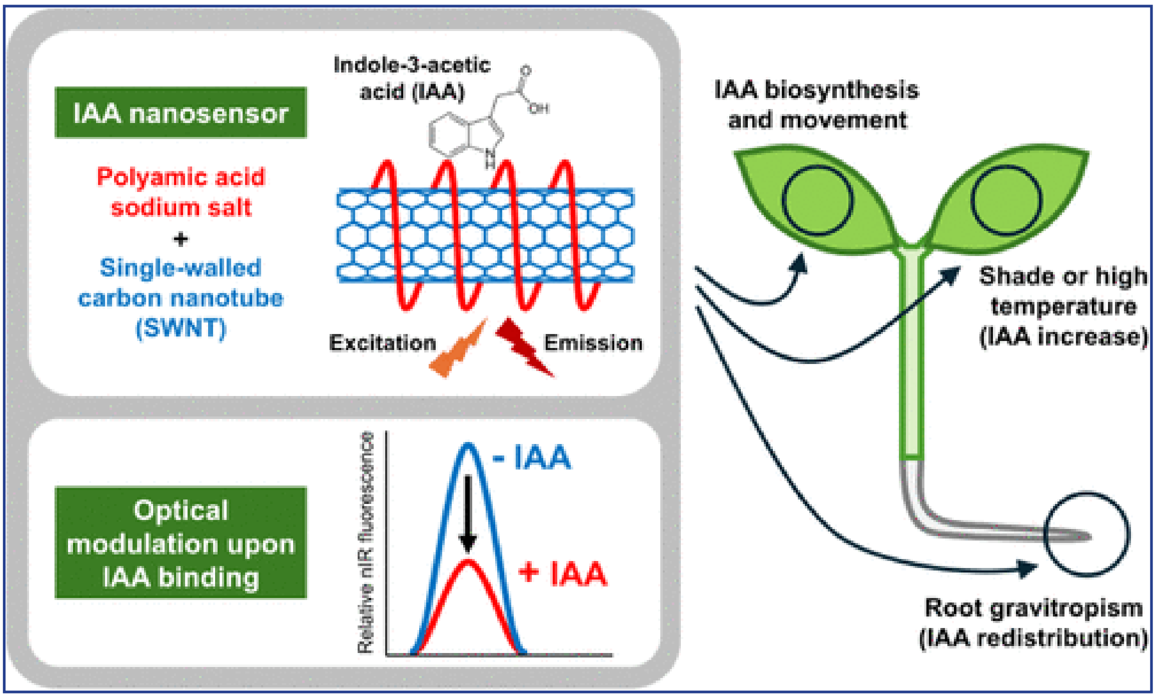
Selected Publications

- Huang X, Ma Z, He D, Han X, Liu X, Dong Q, Tan C, Yu B, Sun T, Nordenskiold L, et al. 2025. Molecular condensation of the CO/NF-YB/NF-YC/FT complex gates floral transition in Arabidopsis. The EMBO Journal 44(1): 225-250.

This study reveals that the floral regulator CONSTANS undergoes light-dependent condensation with NF-YB, NF-YC, and FT to form dynamic macromolecular complexes that activate FT transcription and gate floral transition in Arabidopsis.

- Khong DT, Vu KV, Sng BJR, Choi IKY, Porter TK, Cui J, Gong X, Wang S, Nguyen NH, Ang MC, et al. 2025. A Near-Infrared Fluorescent Nanosensor for Direct and Real-Time Measurement of Indole-3-Acetic Acid in Plants. ACS Nano 19(16): 15302-15321.

This research develops an IAA (indole-3-acetic acid) nanosensor used for qualitative and quantitative mapping of IAA induction and spatial movement in plants undergoing environmental or stress response.



- Low PM, Kong Q, Blaschek L, Ma Z, Lim PK, Yang Y, Quek T, Lim CJR, Singh SK, Crocoll C, et al. 2025. ZINC FINGER PROTEIN2 suppresses funiculus lignification to ensure seed loading efficiency in Arabidopsis. Developmental cell 60(12): 1719-1729 e1716.

This study identifies ZINC FINGER PROTEIN2 as a key transcriptional repressor that suppresses ectopic secondary cell wall formation in the Arabidopsis funiculus by directly targeting NST1, thereby maintaining funiculus flexibility and ensuring efficient nutrient loading into seeds.

- Shao Y, Ma J, Zhang S, Xu Y, Yu H. 2025. NERD-dependent m(6)A modification of the nascent FLC transcript regulates flowering time in Arabidopsis. Nature Plants 11(3): 468-482.

This study uncovers a novel regulatory paradigm in which m6A RNA modification regulates gene transcription in plants.

- Wan WL, Kim G, Kim N, Tan YY, Watari M, Charoennit N, Lee RRQ, Phang IRK, Wang J, Liew YY, et al. 2025. Structural determinants of DANGEROUS MIX 3, an alpha/beta hydrolase that triggers NLR-mediated genetic incompatibility in plants. Mol Cell 85(14): 2776-2795 e2778.

This study uncovers the structural mechanism by which polymorphisms in the Arabidopsis alpha/beta hydrolase DM3 destabilize its dimer interface, thereby activating the NLR DM2h and triggering autoimmune genetic incompatibility in hybrid plants.

Major Funding Sources

- Ministry of Education, Singapore. https://www.moe.gov.sg/
- National Research Foundation, Singapore. https://www.nrf.gov.sg/

SOUTH AFRICA

Prepared by

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Planned events for 2025 and 2026

- No meetings scheduled in 2026, next relevant meeting is the South African Society of Biochemistry and Molecular Biology conference, Cape Town, September 2027

Selected Publications

The Arabidopsis community in South Africa is tiny, with only a handful of labs using this model plant as their primary system to study plant biology, but we are clinging on! Publications during this period were:

- Plasma membrane CYBDOM proteins catalyse apoplastic AsA regeneration and interact with RbohD to activate autophagy and drought tolerance in plants. Xiuxiu et al. (2025) Nature Plants DOI: 10.1038/s41477-025-02057-y.

Demonstrated that heterologous expression of CYDOM proteins from Arabidopsis and the resurrection plant Boea hygrometrica increased autophagy and drought tolerance in transgenic Arabidopsis lines. (one author based at the University of Stellenbosch)

- The role of the jasmonate signalling transcription factors MYC2/3/4 in circadian clock-mediated regulation of immunity in Arabidopsis. Joseph et al. (2025) Philosophical Transactions of the Royal Society B: Biological Sciences DOI: 10.1098/rstb.2023.0338.

Demonstrated that MYC2, MYC3 and MYC4 function redundantly in circadian clock-mediated regulation of immunity to the necrotrophic pathogen Botrytis cinerea. (all authors based at the University of Cape Town)

- Proteome profiling of lumichrome-treated Arabidopsis thaliana suggests that various regulatory mechanisms mediate enhanced photosynthesis and plant growth. Pholo-Tait et al. (2025). South African Journal of Botany DOI: 10.1016/j.sajb.2024.07.036.

Demonstrated that the plant growth promoting properties of the bacterial molecule lumichrome may results from delayed leaf senescence. (6/9 authors based at the University of Stellenbosch)

- An Arabidopsis pentatricopeptide repeat Is a moonlighting protein with cross-talking in vitro adenylyl cyclase and kinase activities. Dikobe et al. (2024). Plant Molecular Biology Reporter DOI: 10.1007/s11105-023-01401-w.

First report of bi-functional activity of a plant PRR protein. (all authors based at North-West University)

Major Funding Sources

- National Research Foundation (https://www.nrf.ac.za/funding/)

SPAIN

Prepared by

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https://ferrandizlab.webs.upv.es

Planned events for 2025 and 2026

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- XVII Reunión de Biología Molecular de Plantas, Bilbao. July 1-3, 2026.
- “Evolutionary Strategies in Plant Biotechnology: From Natural Selection to Synthetic Innovation”. IV Conference Severo Ochoa. Valencia, June 18-19 sebbm.es/actividades-sebbm/conferencias-severo-ochoa/

Selected Publications

- Cisneros AE, Alarcia A, Llorens-Gomez JJ, Puertes A, Juarez-Molina M, Primo A, Carbonell A. Syn-tasiR-VIGS: virus-based targeted RNAi in plants by synthetic trans-acting small interfering RNAs derived from minimal precursors. Nucleic Acids Res. 2025 53:gkaf183.

Describes an exciting new tool based on syn-tasiRNAs precursors coupled to VIGS, able to produce highly efficient tasiRNAs to silence desired targets, and thus representing a versatile, scalable, and nontransgenic platform for precision RNA interference and antiviral vaccination in plants.

- Ruiz-Solani N, Alonso-Diaz A, Capellades M, Serrano-Ron L, Ferro-Costa M, Sanchez-Corrionero A, Rabissi A, Argueso CT, Rubio-Somoza I, Laromaine A, Moreno-Risueno MA, Coll NS. Exogenous bacterial cellulose induces plant tissue regeneration through the regulation of cytokinin and defense networks. Sci Adv. 2025 11:eadr1509.

This study uncovers how bacterial cellulose triggers a transcriptional response that induces plant regeneration in non-meristematic tissues, a discovery with both fundamental and applied implications.

- Daniel-Mozo M, Rombola-Caldentey B, Mendoza I, Ragel P, De Luca A, Carranco R, Alcaide AM, Ausili A, Cubero B, Schumacher K, Quintero FJ, Albert A, Pardo JM. The vacuolar K(+)/H(+) exchangers and calmodulin-like CML18 constitute a pH-sensing module that regulates K(+) status in Arabidopsis. Sci Adv. 2024 10:eadp7658.

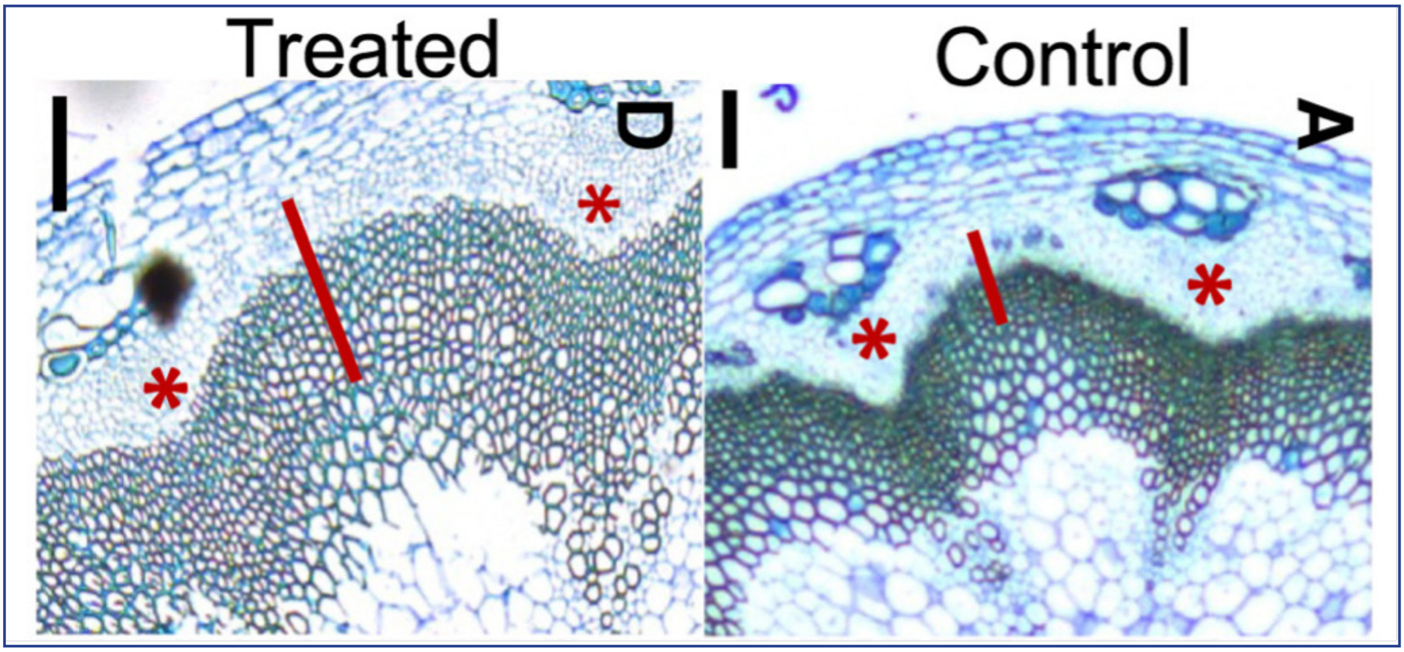
A great example of how structural biology coupled with biochemistry can provide new insights on the regulation of ion homeostasis in plants.

- de Los Reyes P, Serrano-Bueno G, Romero-Campero FJ, Gao H, Romero JM, Valverde F. CONSTANS alters the circadian clock in Arabidopsis thaliana. Mol Plant. 2024 17:1204-1220.

While CONSTANS is well-known for its role in photoperiodic flowering, this research highlights a previously uncharacterized interaction between CONSTANS and the circadian clock, providing new insights into the complex regulatory networks that synchronize environmental cues with internal plant processes.

- Carrio-Segui A, Brunot-Garau P, Urbez C, Miskolczi P, Vera-Sirera F, Tuominen H, Agusti J. Weight-induced radial growth in plant stems depends on PIN3. Curr Biol. 2024 34(18):4285-4293.

An elegant work that explores how mechanical stimuli, such as weight, influence radial growth in plant stems. Understanding this mechanism is crucial as it sheds light on how plants physically adapt to environmental pressures and mechanical loads, both essential for their structural integrity and survival.



Major Funding Sources

- In Spain, Arabidopsis research is mainly funded by the State Research Agency (AEI) in competitive calls launched every year (https://www.aei.gob.es/en/). In 2024, around 90 projects to individual laboratories were granted, which representa a small increase in respect to previous years. Additional national calls and regional funding also support other initiatives.

- European funding for basic plant research is usually scarce, but several MSCA actions (IF, RISE, or DN) have been awarded to Spanish fellows to work in Arabidopsis. In addition, ERC funding is also financing grants in different schemes, i.e CoG to Clara Sánchez-Rodriguez (CBGP), StG to Ivan Reyna-Llorens (CRAG) and Ainhoa Martínez-Medina (CSIC).

SWEDEN

Prepared by

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UPSC, Umeå University

Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

-Fonseca, A. & Rosa, S. in Methods for Plant Nucleus and Chromatin Studies: Methods and Protocols (eds Célia Baroux & Christophe Tatout) 187-203 (Springer US, 2025).

- Han, Y. et al. EasyOmics: A graphical interface for population-scale omics data association, integration, and visualization. Plant Communications 6, 101293 (2025). https://doi.org/https://doi.org/10.1016/j.xplc.2025.101293

Planned events for 2025 and 2026

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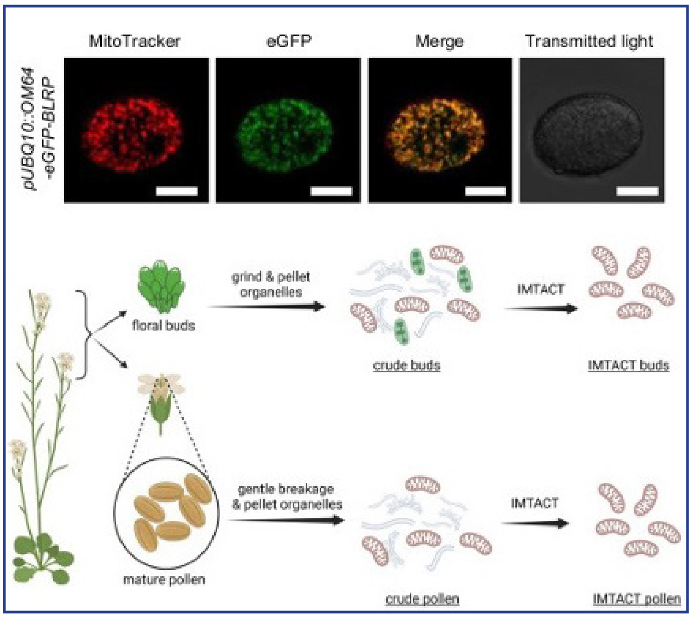
- Swedish Oikos Meeting 4-5 February, 2025, Stockholm, Sweden
- 14th Conference of the European Foundation for Plant Pathology 2-5 June, 2025, Uppsala, Sweden
- Agri4D 2025, 23-25 September, Uppsala, Sweden
- cryoNET Symposium 2025, 1-2 October, Umeå, Sweden
- The Swedish National Plant Protection Conference, 12-13 November, 2025, Alnarp, Sweden.

This year's theme is "Forestry, horticulture and agriculture in a changing climate - innovative thinking for a sustainable future". The conference is held mostly in Swedish.

Selected Publications

- Boussardon, C. et al. The atypical proteome of mitochondria from mature pollen grains.Current Biology 35, 776-787.e775 (2025). https://doi.org/https://doi.org/10.1016/j.cub.2024.12.037

This work uses a novel isolation of mitochondria tagged in specific cell-type (IMTACT) strategy to show that mature pollen grains have lost many proteins required for general transcription and translation machinery, but a relatively high level of those proteins associated with energy metabolism and Ca2+ maintain. Thus, revealing that the proteome of mitochondria genome and metabolism are differently regulated in pollen as they mature.



-Kokla, A. et al. A long-distance inhibitory system regulates haustoria numbers in parasitic plants. Proceedings of the National Academy of Sciences 122, e2424557122 (2025). https://doi.org/10.1073/pnas.2424557122

This study explores hormonal regulation of haustoria formation of parasitic plants, and show that cytokinins and a generated long-distance signal precedes haustoria establishment and apparently control haustoria numbers and nutrient harvesting from the host.

- Meena, S. K. et al. Antisense transcription from stress-responsive transcription factors fine-tunes the cold response in Arabidopsis. The Plant Cell 36, 3467-3482 (2024). https://doi.org/10.1093/plcell/koae160

Here analysis of antisense transcription initiating close to the poly(A) signal of genes (PAS genes) in Arabidopsis, pinpoints role of antisense transcripts in cold response of B-BOX DOMAIN PROTEIN28 (BBX28) and C2H2-TYPE ZINC FINGER FAMILY PROTEIN5 (ZAT5) genes.

- Nair, A. et al. ELF3 coordinates temperature and photoperiodic control of seasonal growth in hybrid aspen. Current Biology 35, 1484-1494.e1482 (2025). https://doi.org/https://doi.org/10.1016/j.cub.2025.02.027

This study draws on previous studies in the annual Arabidopsis and expands them to a perennial species – addressing the role of EARLY FLOWERING 3 (ELF3), in seasonal adaptation of Populus trees. ELF3 was found to function in photoperiodic regulation as well as in coordination of low temperature responses of growth cessation, essential for seasonal regulation of growth

Major Funding Sources

Swedish governmental agencies and foundations such as;
- The Swedish Research Council (VR); VR supports researcher-initiated, basic research

- The Swedish Foundation for Strategic Research; Supports strategic research in natural science, engineering and medicine
- The Swedish Agency for Innovation Systems (VINNOVA); Promotes sustainable growth by funding needs-driven research and the development of effective innovation systems
- The Swedish Research Council Formas; Supports research (rather applied) and need-driven research in the areas Environment, Agricultural Sciences and Spatial Planning
- The Swedish Foundation for International Cooperation in Research and Higher Education (STINT); Supports research and teaching exchanges with a rather broad scope. For instance, it supports postdoctoral stays outside the EU/EFTA (incl. the United Kingdom).

There are many foundations that support basic research devoted to plant sciences and many of the grantees use Arabidopsis as their main model system, for instance:

- The Wallenberg Foundations;
Private foundations supporting research initiated basic research as well as larger centers of excellence devoted to functional genomics and other strategic areas
- SciLifeLab & Wallenberg National Program for Data-Driven Life Science
- Carl Trygger's Foundation for Scientific Research;
A private foundation supporting research within the areas of agriculture, forestry, biology, chemistry and physics
- The Kempe Foundations;
Private foundations devoted to support scientific research
- The Magnus Bergvall Foundation
A private foundation supporting basic science
- Stiftelsen Olle Engkvist Byggmästare;
A private foundation supporting basic science

SWITZERLAND

Prepared by

Reiko Akiyama, reiko.akiyama@ieu.uzh.ch, University of Zurich
Manuela Dahinden mdahinden@ethz.ch, Zurich-Basel Plant Science Center
Kentaro Shimizu, kentaro.shimizu@uzh.ch, University of Zurich

Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

- Priya Ramakrishna, Francisco M. Gámez-Arjona, Etienne Bellani, Cristina Martin-Olmos, Stéphane Escrig, Damien De Bellis, Anna De Luca, José M. Pardo, Francisco J. Quintero, Christel Genoud, Clara Sánchez-Rodriguez, Niko Geldner, Anders Meibom (2025) Elemental cryo-imaging reveals SOS1-dependent vacuolar sodium accumulation, Nature, 637: 1228–1233. https://www.nature.com/articles/s41586-024-08403-y

- Simon Snoeck, Hyun Kyung Lee, Marc W. Schmid, Kyle W. Bender, Matthias J. Neeracher, Alvaro D. Fernández-Fernández, Julia Santiago, Cyril Zipfel (2024) Leveraging coevolutionary insights and AI-based structural modeling to unravel receptor–peptide ligand-binding mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 121(33): e2400862121. https://www.pnas.org/doi/10.1073/pnas.2400862121

Planned events for 2025 and 2026

- 13th Plant Peptide Receptor Meeting, September 8-10, 2025, Edinburgh, UK (https://pprm2025.events.kdmeventsportal.co.uk/)
- 14th Cold Spring Harbor Laboratory Meeting ‘Plant Genomes, Systems Biology & Engineering, December 3-6, 2025, Cold Spring Harbor Laboratory, USA (https://meetings.cshl.edu/meetings.aspx?meet=PLANTS)
- 7th international symposium on Plant Apoplastic Diffusion Barriers (PADiBa2026), August 31-September 3, 2026, Lausanne, Switzerland
- PSC (Zurich-Basel Plant Science Center) Symposium, autumn 2026, Zurich, Switzerland

- Upcoming events:
https://www.plantsciences.uzh.ch/en/rssnews.html

- Outreach activities:
https://www.plantsciences.uzh.ch/en/Outreach.html

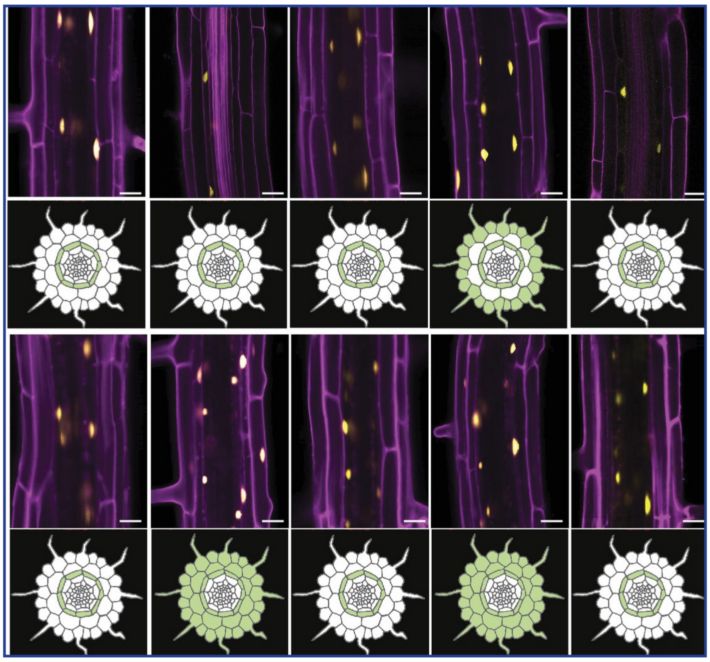
Selected Publications

- Lena Hyvärinen, Christelle Fuchs, Anne Utz-Pugin, Kay Gully, Christian Megies, Julia Holbein, Mayumi Iwasaki, Lara Demonsais, Maria Beatriz Capitão, Marie Barberon, Rochus B. Franke, Christiane Nawrath, Sylvain Loubéry, Luis Lopez-Molina (2025) Temperature-dependent polar lignification of a seed coat suberin layer promoting dormancy in Arabidopsis thaliana. Proceedings of the National Academy of Sciences of the United States of America, 122 (6): e2413627122. https://www.pnas.org/doi/10.1073/pnas.2413627122

This paper uncovers how cold temperatures during seed development in the mother plant influence seed dormancy through apoplastic modifications in the Arabidopsis thaliana seed coat.

- Jens Westermann, Thanvi Srikant, Adrián Gonzalo, Hui San Tan, Kirsten Bomblies (2024) Defective pollen tube tip growth induces neo-polyploid infertility. Science, 383 (6686): eadh0755. https://doi.org/10.1126/science.adh0755

This paper reports that a severe fertility-compromising defect in pollen tube tip growth arises in new polyploids of Arabidopsis arenosa, while these phenotypes recover in evolved polyploids, showing that pollen tube tip growth as an important fertility challenge for neo-polyploid plants.



- Kay Gully, Alice Berhin, Damien De Bellis, Cornelia Herrfurth, Ivo Feussner, Christiane Nawrath (2025) The GPAT4/6/8 clade functions in Arabidopsis root suberization nonredundantly with the GPAT5/7 clade required for suberin lamellae. Proceedings of the National Academy of Sciences of the United States of America, 121 (21): e2314570121. https://doi.org/10.1073/pnas.2314570121

This paper reports that both the GPAT4/6/8 and GPAT5/7 clades of glycerol-3-phosphate acyltransferases (GPATs) contribute to suberin formation in Arabidopsis roots.

- Yasuhiro Sato, Rie Shimizu-Inatsugi, Kazuya Takeda, Bernhard Schmid, Atsushi J. Nagano & Kentaro K. Shimizu (2024) Reducing herbivory in mixed planting by genomic prediction of neighbor effects in the field. Nature Communications, 15: 8467. https://www.nature.com/articles/s41467-024-52374-7

This paper identifies key genotype pairs responsible for associational resistance to herbivory using the genome-wide polymorphism data of Arabidopsis thaliana incorporating the method “Neighbor GWAS”.

- Andreas Keppler, Michelle Roulier, Sebastian Pfeilmeier, Gabriella C. Petti, Anna Sintsova, Benjamin A. Maier, Miriam Bortfeld-Miller, Shinichi Sunagawa, Cyril Zipfel, Julia A. Vorholt (2024) Plant microbiota feedbacks through dose-responsive expression of general non-self response genes. Nature Plants 11: 74–89. https://www.nature.com/articles/s41477-024-01856-z#Sec8

This paper shows that general non-self response (GNSR) components of Arabidopsis thaliana conversely impact leaf microbiota composition.

Highly cited researchers 2024 (members of the Zurich-Basel Plant Science Center):
- Niko Geldner, Plant and Animal Science
- Cyril Zipfel, Plant and Animal Science

Major Funding Sources

- Swiss National Science Foundation (SNSF) http://www.snf.ch/en/Pages/default.aspx

UNITED KINGDOM

Prepared by

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arabidopsiseventsuk@gmail.com

Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

- Hypoxia-activated fluorescent probes
Perri M, Khan MS, Wallabregue ALD, Voloboeva V, Ridgway AM, Smith EN, Bolland H, Hammond EM, Conway SJ, Weits DA, Flashman E. Hypoxia-activated fluorescent probes as markers of oxygen levels in plant cells and tissues. New Phytol. 2025 May 8. doi: 10.1111/nph.70202.

- A computer-automated micro-extensometer
Trozzi N, Wodniok W, Kelly-Bellow R, Meraviglia A, Chételat A, Adkins N, Lane B, Smith RS, Kwiatkowska D, Majda M. Camelot: a computer-automated micro-extensometer with low-cost optical tracking. BMC Biol. 2025 Apr 28;23(1):112. doi: 10.1186/s12915-025-02216-9.

- Measurement tool for CO2 assimilation
Brazel AJ, Manoj NS, Turck F, Ó'Maoiléidigh DS. Measuring CO2 assimilation of Arabidopsis thaliana whole plants and seedlings. Plant Sci. 2025 Jan;350:112295. doi: 10.1016/j.plantsci.2024.112295.

- Cas9 and Cas12a mutagenesis toolkit
Lawrenson T, Clarke M, Kirby R, Forner M, Steuernagel B, Brown JKM, Harwood W. An optimised CRISPR Cas9 and Cas12a mutagenesis toolkit for Barley and Wheat. Plant Methods. 2024 Aug 13;20(1):123. doi: 10.1186/s13007-024-01234-y.

Planned events for 2025 and 2026

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- BSPP Plant Pathology Meeting
9-11 September 2025, Nottingham, UK

- Journal of Experimental Botany (JXB) 75th Anniversary Symposium
17-19 September 2025, Edinburgh, UK
https://www.sebiology.org/events/journal-of-experimental-botany-symposium.html

- Plant proteins: functions, regulation, production and utility
21 - 23rd October, Leeds UK
https://www.eventsforce.net/biochemsoc/frontend/reg/thome.csp?pageID=130758&eventID=241&traceRedir=2

- Black in Plant Science (BiPS) Conference
24th October, Leeds UK
blackinplantscience.org/bips-conference-2025/

- Advances in Nematology
4th December 2025, London UK
https://www.aab.org.uk/events/

- International Conference on Photosynthesis Research 2026 (ICPR26)
26th-30th July 2026, Liverpool, UK
https://photosynthesis2026.com//

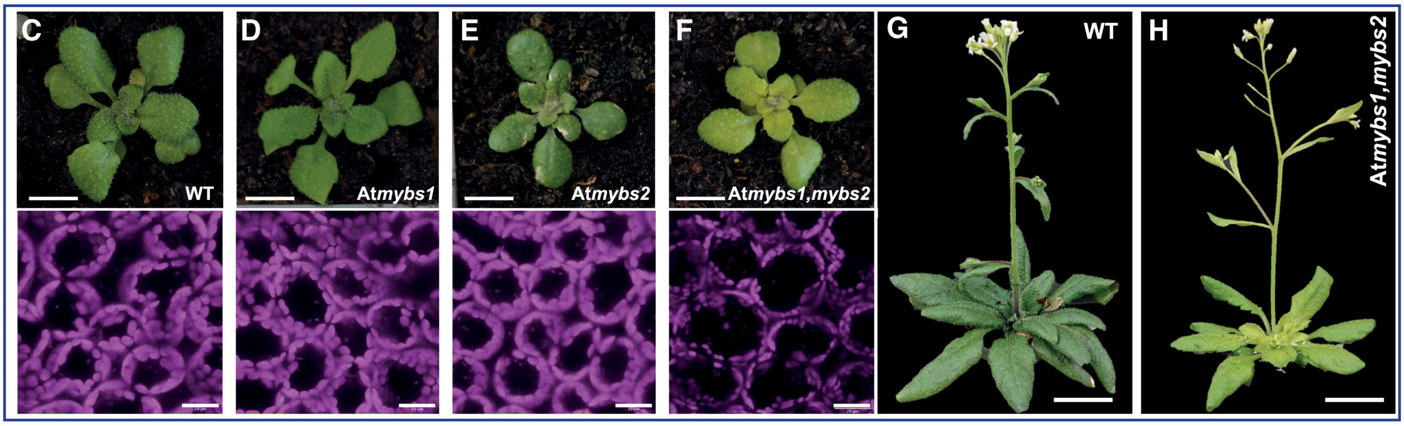
Selected Publications

- Bian C, Demirer GS, Oz MT, Cai YM, Witham S, Mason GA, Di Z, Deligne F, Zhang P, Shen R, Gaudinier A, Brady SM, Patron NJ. Conservation and divergence of regulatory architecture in nitrate-responsive plant gene circuits. Plant Cell. 2025 Jun 4;37(6):koaf124. doi: 10.1093/plcell/koaf124.

Plant roots dynamically respond to nitrogen availability by executing a signaling and transcriptional cascade resulting in altered plant growth that is optimized for nutrient uptake. This paper dissects a known sub-circuit upstream of NLP6 and NLP7 in Arabidopsis, which was predicted to contain multiple multi-node feedforward loops suggestive of an optimized design principle of nitrogen transcriptional regulation. Conservation and divergence of this circuit and its influence on nitrogen-dependent root system architecture were similarly assessed in tomato (Solanum lycopersicum). The resulting models were genetically validated in varying concentrations of available nitrate by measuring the transcriptional output of the network revealing rewiring of nitrogen regulation across distinct plant lineages.

- Frangedakis E, Yelina NE, Billakurthi K, Hua L, Schreier T, Dickinson PJ, Tomaselli M, Haseloff J, Hibberd JM. MYB-related transcription factors control chloroplast biogenesis. Cell. 2024 Sep 5;187(18):4859-4876.e22. doi: 10.1016/j.cell.2024.06.039.

Chloroplast biogenesis is dependent on master regulators from the GOLDEN2-LIKE (GLK) family of transcription factors. This paper identifies MYB-related transcription factors as regulators of chloroplast biogenesis in the liverwort Marchantia polymorpha and angiosperm Arabidopsis thaliana. They conclude that MYB-related and GLK transcription factors orchestrate chloroplast development in land plants.



- Mateo-Bonmatí E, Montez M, Maple R, Fiedler M, Fang X, Saalbach G, Passmore LA, Dean C. A CPF-like phosphatase module links transcription termination to chromatin silencing. Mol Cell. 2024 Jun 20;84(12):2272-2286.e7. doi: 10.1016/j.molcel.2024.05.016.

The interconnections between co-transcriptional regulation, chromatin environment, and transcriptional output remain poorly understood. This paper investigates the mechanism underlying RNA 3’ processing-mediated Polycomb silencing of Arabidopsis FLOWERING LOCUS C (FLC).

- Lopes FL, Formosa-Jordan P, Malivert A, Margalha L, Confraria A, Feil R, Lunn JE, Jönsson H, Landrein B, Baena-González E. Sugar signaling modulates SHOOT MERISTEMLESS expression and meristem function in Arabidopsis. Proc Natl Acad Sci U S A. 2024 Sep 10;121(37):e2408699121. doi: 10.1073/pnas.2408699121.

This paper shows that sugar signals influence SAM function by altering the protein levels of SHOOT MERISTEMLESS (STM), a key regulator of meristem maintenance. STM is less abundant in inflorescence meristems with lower sugar content, resulting from plants being grown or treated under limiting light conditions. Additionally, sucrose but not light is sufficient to sustain STM accumulation in excised inflorescences.

- Osborne R, Labandera AM, Ryder AJ, Kanali A, Xu T, Akintewe O, Schwarze MA, Morgan CD, Hartman S, Kaiserli E, Gibbs DJ. VRN2-PRC2 facilitates light-triggered repression of PIF signaling to coordinate growth in Arabidopsis. Dev Cell. 2025 Aug 4;60(15):2046-2060.e5. doi: 10.1016/j.devcel.2025.03.001.

VERNALIZATION2 (VRN2) is a flowering plant-specific subunit of the polycomb-repressive complex 2 (PRC2), a conserved eukaryotic holoenzyme that represses gene expression by depositing the histone H3 lysine 27 trimethylation (H3K27me3) mark in chromatin. This paper shows that VRN2 is enriched in the hypoxic shoot apex and emerging leaves of Arabidopsis where it negatively regulates growth by establishing a stable and conditionally repressed chromatin state in key PHYTOCHROME INTERACTING FACTOR (PIF)-regulated genes that promote cell expansion.

Major Funding Sources

- Biotechnology and Biological Research Council (BBSRC) http://www.bbsrc.ac.uk/
- British Society of Plant Pathology https://www.bspp.org.uk/
- The Gatsby Charitable Foundation http://www.gatsby.org.uk/
- European Research Council http://ec.europa.eu/research/era/index_en.htm
- Natural Environment Research Council http://www.nerc.ac.uk
- The Gates Foundation http://www.gatesfoundation.org/
- The Leverhulme Trust: https://www.leverhulme.ac.uk/
- The Newton Fund https://www.newtonfund.ac.uk/

UNITED STATES and North American Arabidopsis Steering Committee (NAASC)

Prepared by

Joanna Friesner, Coordinator & Executive Director NAASC (arabidopsisconference@gmail.com)

Additional NAASC members contributing to this report:
Faculty (elected for 5-year terms)
- Cris Argueso, Colorado State University, USA
- Adrienne Roeder, Cornell University, USA
- Dior Kelley, Iowa State University, USA
- Gloria Muday, Wake Forest University, USA
- Mentewab Ayalew, Spelman College, USA
- Liang Song, University of British Columbia, CANADA
- Mary Gehring, Whitehead Institute for Biomedical Research, MIT, USA
- Sharon Kessler, Purdue University, USA
- Zachary Nimchuk, University of North Carolina, Chapel Hill, USA
- Arif Ashraf, University of British Columbia, CANADA
- Wolfgang Busch, The Salk Institute, USA

Early Career Scholars (elected for a 1-year term: Oct. 2024-Oct 2025)
- Mingyuan Zhu, Duke University, USA
- Vincent Cerbantez-Bueno, University of California, Riverside, USA
- Catherine Freed, University of Wisconsin, Madison, USA

Please describe any new or updated experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2024 or early 2025.

- Best practices in plant fluorescence imaging and reporting: A primer. Kirk J Czymmek, Yoselin Benitez-Alfonso, Tessa Burch-Smith, et al. The Plant Cell, July 2025. This is a primer article describing best practices for fluorescent microscopy in plants. https://doi.org/10.1093/plcell/koaf143

- A rare PRIMER cell state in plant immunity. Nobori, T., Monell, A., Lee, T.A. et al. Nature, January 2025. The article describes a cell population to emerge at the nexus of immune-active hotspots in bacteria-infected Arabidopsis leaves; the cells feature expression of a previously uncharacterized transcription factor, GT-3A, which contributes to immunity. https://doi.org/10.1038/s41586-024-08383-z

- Recruitment, rewiring and deep conservation in flowering plant gene regulation. Baumgart, L.A., Greenblum, S.I., Morales-Cruz, A. et al. Nat. Plants, July 2025. The article presents a scalable TFBS assay that was leveraged to create an atlas of nearly 3,000 genome-wide binding site maps for 360 TFs in ten species spanning 150 million years of flowering plant evolution; the plants included Arabidopsis thaliana, Arabidopsis lyrata, Capsella rubella, Brassica oleracea (wild cabbage); Solanum lycopersicum (tomato), Solanum tuberosum (potato), Fragaria vesca (wild strawberry), Populus trichocarpa (black cotton- wood); and two monocots grasses: Oryza sativa (rice) and Sorghum bicolor (sorghum). https://doi.org/10.1038/s41477-025-02047-0

Planned events for 2025 and 2026

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Upcoming in 2025: Three webinars featuring the 2025 NAASC Arabidopsis Community Awardees (times/dates tba; tentative: 1 each in October, November, December)
Register to receive updates: https://www.arabidopsiscommunity.org/rsvp-awards-sessions
- 2025 Philip N. Benfey Arabidopsis Community Lifetime Achievement Awardees: Mark Estelle, USA; Maarten Koornneef, The Netherlands; Detlef Weigel, Germany.
- 2025 NAASC Arabidopsis Community Impact Awardees: Early Career Category: Jade Bleau, Scotland; Later Career Category: José Dinneny, USA; Joanna Friesner, USA.
- 2025 NAASC Dissemination of Arabidopsis Knowledge Awardees: Early Career Category: Natanella Illouz-Eliaz, USA; Later Career Category: Dawn Nagel, USA; Nicholas Provart, Canada; Anna Stepanova, USA.

Earlier in 2025:
- Lab Launchpad: The New PI’s Guide to Starting Your Own Lab (Webinar). Featuring Dr. Rachel Shahan (UCLA), Dr. Kevin Cox (WUSTL/Danforth Plant Science Center), and Dr. Monika Fischer (University of British Columbia). Organized by the NAASC Early Career Scholars Subcommittee. Recording: https://youtu.be/B9CyhxuOTPg
- My Plant Biology Story (Webinar). Featuring Dr. Nayelli Marsch, Dr. Stefan De Folter, and Dr. Stewart Gillmor, CINVESTAV-Irapuato, Mexico. Organized by the NAASC Inclusivity Scholars Program Subcommittee. Recording: https://youtu.be/lOok5cb2FZw
- Morphogenic Regulator-Assisted Plant Transformation. Featuring Dr. Jianqiang Shen, (UC Berkeley), Dr. Juan Debernardi (UC Davis) and Dr.Greg Goralogia, (Oregon State University). Organized by PMEX (Plant Methods EXchange, founded by former elected NAASC early career scholars). Recording: https://youtu.be/ErHXIPcHW-U

Upcoming in 2025: NAASC election for faculty, students & postdocs that conduct Arabidopsis research in the US, Canada, and Mexico (nominations accepted Sept. 2025)
- Consult this URL for details on how to nominate yourself, or a community-minded colleague: www.arabidopsiscommunity.org/naasc-election
- Are you interested in being on the ballot and serving on NAASC to support the community?
- Are in the US, Canada, or Mexico AND a faculty member, student, or postdoc that conducts research using Arabidopsis?
- The upcoming annual NAASC election cycle starts with nominations in September 2025 (self-nominations are accepted).

Additional activities
- 2 NAASC-led publications in The Plant Cell; listed in the publications section, below.
- MNC (Mentored Networking Cohort) at ICAR 2025-Ghent (5 students & postdocs)
- US Scholar Travel Awards to ICAR 2025-Ghent (6 students, postdocs, pre-tenure faculty)

Join as a member: Arabidopsis Community Group, supported by NAASC.
Support the NAASC Arabidopsis Community group by becoming a member! Membership is open to Arabidopsis aficionados from all geographic locations. Annual memberships begin at just $10 USD; if the fee is a barrier, you may request a membership waiver at the URL below. Membership benefits: www.arabidopsiscommunity.org/join-ac.

- Arabidopsis Community Awards- nominations for 2026 start this fall

Please consider nominating deserving members of the community! The 2026 awards cycle will open in fall 2025. Updates will be sent to members (www.arabidopsiscommunity.org/join-ac) & posted at: www.arabidopsiscommunity.org/nominations-community-awards

- Philip N. Benfey Arabidopsis Community Lifetime Achievement Awards (PACLA) for excellence in Arabidopsis research, impactful and positive mentoring, and community service. This award has been named after Philip Benfey who exhibited all these qualities.
Award Blog: www.arabidopsiscommunity.org/news-events/pacla-2025

The 2025 award cycle recipients:
Dr. Mark Estelle, University of California, San Diego, USA
Dr. Maarten Koornneef, retired, The Netherlands
Dr. Detlef Weigel, Max Planck Institute for Biology, Tübingen, Germany

- NAASC Arabidopsis Community Impact Awards for demonstrated commitment to supporting the Arabidopsis community and making positive impacts on it.
Award Blog: www.arabidopsiscommunity.org/news-events/2025-community-impact
The 2025 award cycle recipients:
Dr. Jade Bleau, University of Dundee, Scotland. Early Career Category.
Dr. José Dinneny, Stanford University, USA. Later Career Category.
Dr. Joanna Friesner, NAASC, USA. Later Career Category.

- NAASC Dissemination of Arabidopsis Knowledge Awards for innovative teaching, outreach activities/initiatives, and/or communication for Arabidopsis & plant biology.
Award Blog: www.arabidopsiscommunity.org/news-events/2025-knowledge-dissemination
The 2025 award cycle recipients:
Dr. Natanella Illouz-Eliaz, Salk Institute for Biological Studies, USA. Early Career Category.
Dr. Dawn Nagel, University of California, Riverside, USA. Later Career Category.
Dr. Nicholas Provart, University of Toronto, Canada. Later Career Category.
Dr. Anna Stepanova, North Carolina State University (NCSU), USA. Later Career Category.

- George Redei Seed Stock Award for the researcher that donates the most seeds to the Arabidopsis Biological Resource Center (ABRC); Award co-sponsored with ABRC.
The 2025 co-awardees:
Dr. Ivan Radin, University of Minnesota, St. Paul, USA & Dr. Elizabeth Haswell, USA, for donating 131 Arabidopsis thaliana stocks in 2024. www.arabidopsiscommunity.org/redei-award

- Plant Method Exchange (PMEX) platform

The NAASC Early Career Scholars Subcommittee (ECSS) is working to build the Plant Method Exchange (PMEX) platform. The ECSS aims to build a platform in connection with the plant biology research community to efficiently share their protocols and easily discuss potential optimizations. We also expect such a platform to promote the standardization of the common experimental set-up. We hope the future success of this platform, powered by NAASC, will be of a strong testimonial for the broader impacts of NAASC and increase the inclusiveness of plant biology research. The PMEX website was created (https://plant-methods.owlstown.net/). We are calling for submissions for more protocols and recruiting volunteers for review. We hope to build a comprehensive, curated, and free open-access protocol sharing platform in five years.
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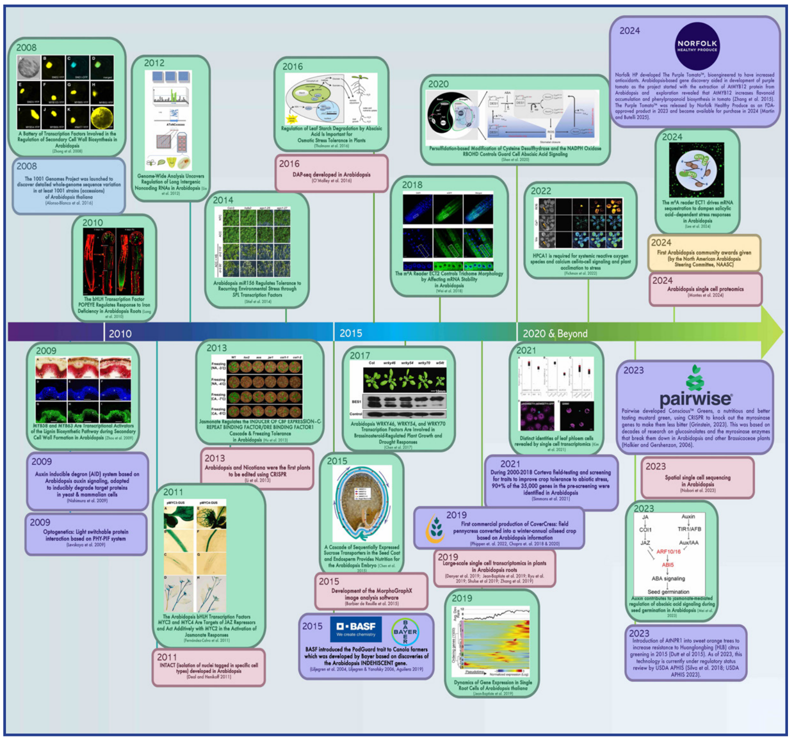
Selected Publications



-NAASC HIGHLIGHT: In defense of funding foundational plant science. Joanna Friesner, Cris Argueso, Wolfgang Busch, Thorsten Hamann, Lucia Strader, Mary Williams, Shuang Wu, Adrienne H. K. Roeder. May 2025. The Plant Cell. A timely commentary that lays out a vigorous defense of foundational, i.e. “basic,” plant science research; describes that often, Arabidopsis is preferable to working directly in crops; highlights several transformative applications generated from basic plant research; and makes the argument that plant science is vital to the survival of humanity. https://doi.org/10.1093/plcell/koaf106

- NAASC HIGHLIGHT: A Timeline of Discovery and Innovation in Arabidopsis. Catherine Freed, Arif Ashraf, Nancy A Eckardt, Adrienne H K Roeder, Joanna Friesner. May 2025. The Plant Cell. A timeline focusing on the history and importance of Arabidopsis with emphasis on the last 20 years. https://doi.org/10.1093/plcell/koaf108

- Unlocking expanded flagellin perception through rational receptor engineering. Li, T., Jarquin Bolaños, E., Stevens, D.M. et al. July 2025. Nat. Plants.

This paper used principles elucidated in Arabidopsis to engineer new versions of receptors that detect pathogen molecules. https://doi.org/10.1038/s41477-025-02049-y

- Canalization of flower production across thermal environments requires Florigen and CLAVATA signaling. Smith ES, John A, Willoughby AC, Jones DS, Galvão VC, Fankhauser C, Nimchuk ZL. July 2025. Curr Biol. https://doi.org/10.1016/j.cub.2025.06.001

Brassinosteriod levels and signaling are cell-cycle regulated and guided by mother-cell polarity to ensure optimal root growth.

Major Funding Sources

- In 2025, NAASC members (PI Dior Kelley, Co-PI Joanna Friesner) secured funding to support 13 U.S. scientists to participate in ICAR 2025-Gent via NSF Award #2516566.
- Currently, US federal funding for most areas of scientific research- including plant biology- is facing severe challenges due to proposed (and some already-imposed) cuts and scale-backs at all levels of the scientific endeavor.
- At ICAR 2025-Gent, Joanna Friesner, NAASC Coordinator, was asked to provide some perspectives on the current state of research funding in the US. The outlook for US science funding is not positive, though it is currently unclear to what extent future programs and funding will be affected and by how much.
- That presentation can be viewed here: https://bit.ly/462rXzZ
- US Arabidopsis Research has primarily been supported by funding through the Federal Government via the National Science Foundation (NSF): http://www.nsf.gov/
- Additional support for some projects that use Arabidopsis have come from:
    - US Department of Agriculture (USDA): http://www.usda.gov/
    - US Department of Energy (DOE): http://energy.gov/
    - National Institutes of Health (NIH): http://www.nih.gov/
    - National Aeronautics and Space Administration (NASA): http://www.nasa.gov/