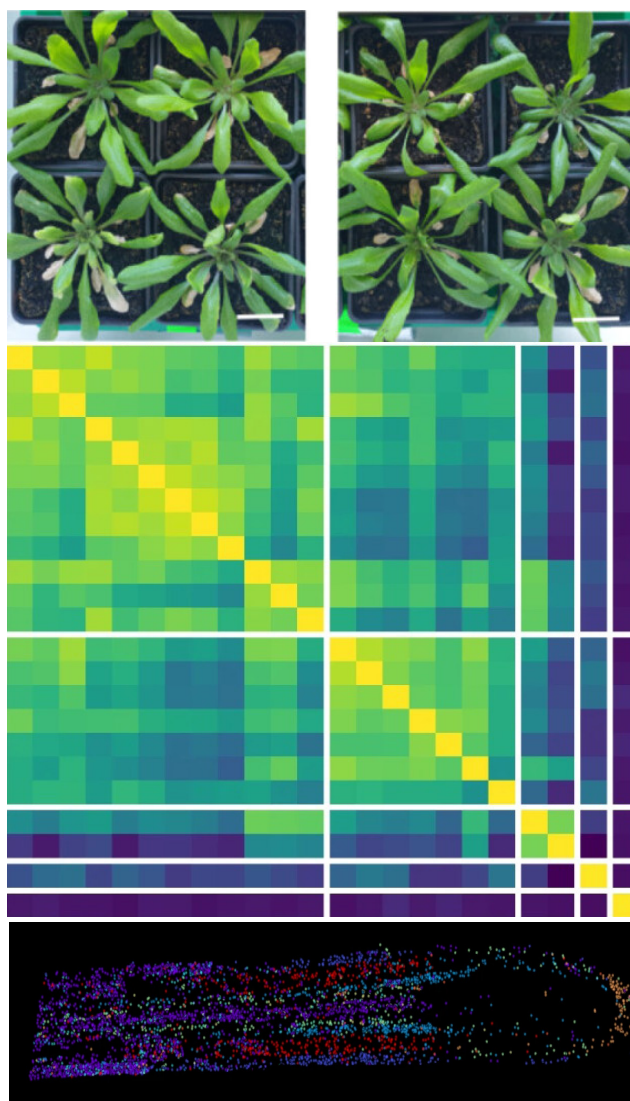


Translating the Computable Plant

Multinational Arabidopsis Steering Committee

Annual Report 2023-2024



**MIASC**



Design and editing

Geraint Parry

MASC Secretary, Arabidopsis Events UK

<https://www.arabidopsisevents.uk/>

arabidopsisventsuk@gmail.com

Cover images taken from Open Access publications

Top: Ochoa *et al* (2023) Natural variation in Arabidopsis responses to Plasmodiophora brassicae reveals an essential role for Resistance to Plasmodiophora brassicae 1 (RPB1)

<https://onlinelibrary.wiley.com/doi/full/10.1111/tpj.16438>

Middle: Li *et al* (2023) Nature Communications 14 (1), 2600, 5/5/2023

<https://www.nature.com/articles/s41467-023-38096-2>

Bottom: Nobori *et al* (2023) Multiplexed single-cell 3D spatial gene expression analysis in plant tissue using PHYTOmap.

<https://www.nature.com/articles/s41477-023-01439-4>

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

Previous reports are also available online at:

- MASC, The Multinational Arabidopsis Steering Committee:

<https://arabidopsisresearch.org/index.php/en/publications>

- uNASC, The Nottingham Arabidopsis Stock Centre:

<http://Arabidopsis.info/progreports.html>

Published by the Multinational Arabidopsis Steering Committee (MASC) August 2024

MASC Inc is registered as a not-for-profit corporation in Canada under Corporatation Number 960778-1, subject to the regulations of the Canada Not-for-profit Corporations Act

Acknowledgements

MASC is grateful to all authors for their contribution to the MASC annual report 2023-4

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 green include an associated figure from that open access article.

Contents

Members of MASC	01
Activities of MASC	04
Tribute to Phil Benfey	11
MASC Subcommittee Reports	12
MASC Project Reports	23
MASC Country Reports	33

The Multinational Arabidopsis Steering Committee

Annual Report 2023/2024

MASC interim President

Siobhan Brady

sbrady@ucdavis.edu

MASC Treasurer

Nicholas Provart

nicholas.provart@utoronto.ca

MASC Secretary

Geraint Parry

arabidopsiseventsuk@gmail.com

MASC Directors

Shahid Mukhtar

mshahid@clemson.edu

Yuling Jiao

yuling.jiao@pku.edu.cn

MASC Subcommittee Contacts

Bioinformatics

Nicholas Provart

nicholas.provart@utoronto.ca

Epigenetics and Epigenomes

Robert Schmitz

schmitz@uga.edu

Xuehua Zhong

xuehua.zhong@wisc.edu

Metabolomics

Wolfram Weckwerth

wolfram.weckwerth@univie.ac.at

Takayuki Tohge

tohge@bs.naist.jp

Natural Variation and Comparative Genomics

J. Chris Pires

chris.pires@colostate.edu

Ya-Long Guo

yalong.guo@ibcas.ac.cn

Plant Immunity

Shahid Mukhtar

mshahid@clemson.edu

Proteomics

Klaas van Wijk

kv35@cornell.edu

Systems and Synthetic Biology

Siobhan Brady

sbrady@ucdavis.edu

MASC Project Resource Contacts

ABRC

David Somers

somers.24@osu.edu

Emma Knee

knee.2@osu.edu

BAR

Nicholas Provart

nicholas.provart@utoronto.ca

Global Plant Council

Isabel Mendoza

isabel@globalplantcouncil.org

Gramene

Marcela Karey Tello-Ruiz

telloruiz@cshl.edu

NASC

Sean May

sean@Arabidopsis.org.uk

Phenotyping Resources

Roland Pieruschka

r.pieruschka@fz-juelich.de

RIKEN

Masatomo Kobayashi

kobayasi@rtc.riken.jp

TAIR

Leonore Reiser
lreiser@phoenixbioinformatics.org

**MASC Country/ Region
Representatives****Argentina**

Gabriela Auge
auge.gabriela@inta.gob.ar

Australia

Monika Murcha
monika.murcha@uwa.edu.au

Austria

Marie-Theres Hauser
marie-theres.hauser@boku.ac.at

Belgium

Moritz K. Nowack
moritz.nowack@vib.be

Brazil

Wagner Araújo
wlaraujo@ufv.br
Adriano Nunes-Nesi
nunesnesi@ufv.br

Canada

Dario Bonetta
dario.bonetta@uoit.ca
Nicholas Provart
nicholas.provart@utoronto.ca

Chile

Adrian A. Moreno
adrian.moreno@unab.cl

China

Yuling Jiao
yuling.jiao@pku.edu.cn

Czech Republic

Viktor Žárský
viktor@natur.cuni.cz

Denmark

Michael Palmgren
palmgren@plen.ku.dk

Estonia

Hanna Hõrak
hanna.horak@ut.ee

Finland

Ari Pekka Mahonen
aripekka.mahonen@helsinki.fi

France

Loic Lepiniec
Loic.Lepiniec@versailles.inra.fr
Cécile Bousquet-Antonelli
insb.das5f@cnrs.fr

Germany

Klaus Harter
klaus.harter@zmbp.uni-tuebingen.de

Greece

Stamatis Rigas
srigas@aua.gr

India

Jyothilakshmi Vadassery
jyothi.v@nipgr.ac.in
Sourav Datta
sdatta@iiserb.ac.in

Ireland

Charles Spillane
charles.spillane@nuigalway.ie

Israel

Assaf Mosquna
assaf.mosquna@mail.huji.ac.il

Italy

Alice Pajoro
alice.pajoro@cnr.it

Japan

Masatomo Kobayashi
kobayasi@rtc.riken.jp
Minami Matsui
minami@riken.jp
Motoaki Seki
motoaki.seki@riken.jp

New Zealand

Rowan Herridge
Rowan.Herridge@otago.ac.nz

Norway

Thorsten Hamann
thorsten.hamann@ntnu.no

Poland

Robert Malinowski
rma1@igr.poznan.pl

Saudi Arabia

Yunhe Jiang
yunhe.jiang@kaust.edu.sa

Singapore

Eunyoung Chae
dbsce@nus.edu.sg

South Korea

Inhwan Hwang
ihhwang@postech.ac.kr

Spain

Cristina Ferrandiz
cferrandiz@ibmcp.upv.es

Sweden

Maria E. Eriksson
maria.erikson@plantphys.umu.se

Switzerland

Misako Yamazaki
misako.yamazaki@ieu.uzh.ch
Kentaro K. Shimizu
kentaro.shimizu@ieu.uzh.ch

Taiwan

Cheng-Hsun Ho
zcybele3@sinica.edu.tw

Turkey

Baris Uzilday
baris.uzilday@ege.edu.tr

United Kingdom

Geraint Parry
arabidopsiseventsuk@gmail.com

United States of America

Joanna D. Friesner
jdfriesner@danforth.edu

Activities of MASC

Thanks for being interested in the latest activities of the Multinational Arabidopsis Steering Committee (MASC). 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 the official positions of President, Treasurer and Secretary of which the current incumbents are Siobhan Brady, Nicholas Provart and Geraint Parry respectively. These people have been in post since MASC Inc was incorporated in 2017. In the next year, we will seek a new President and update members of our Executive Board. We remain very much open to new ideas that will inform the future activities of MASC.

The recent launch of the 'Arabidopsis Community supported by NAASC' has provided a new exciting resource for the global community (<https://www.arabidopsiscommunity.org/>) This organisation has arise from the activities of NAASC (the North America Arabidopsis Steering Committee), is organised from the USA and are initiating many important activities that lower the boundaries to entry to ICAR (and other) meetings.

MASC looks forward to interacting where relevant with the 'Arabidopsis Community' to take a more global view with regard Arabidopsis research and researchers. This role for MASC is exemplified both through the publication of this document and in the upcoming publication of the '4th Decadal Vision: Arabidopsis Research in 2030: Translating the Computable Plant' and through oversight of the ICAR meetings.

In 2017 eight MASC Directors were elected for a range of term lengths. These directors officially took up their positions at the MASC annual meeting that took place at ICAR2018 in Turku, Finland. However over the past few years we have been unable to recruit new directors so at the end of 2024 there won't be any current directors. Therefore MASC need to elect new directors and the leadership team will make a renewed push to recruit both from existing MASC participants and/or anyone currently 'outside' the organisation.

If you are interested in becoming a MASC Director please contact Geraint Parry (arabidopsiseventsuk@gmail.com). These roles are VERY light-touch, requiring very little work!

This is a current list of the MASC board of directors and the end of their term. You will see that Shahid and Yuling will soon leave so we are looking to recruit a completely new set of Directors.

- 2020-2024: Shahid Mukhtar (United States of America), Yuling Jiao (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 the minimum level (anticipated to be a total 12 hours in 2024) to maintain the activity of the organisation. In 2022 and 2023 preparation of the report has been aided by a UK-based PhD student. This is something we hope to repeat in 2025 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 continuous input from the entire 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 five subcommittees: Bioinformatics, Epigenetics and Epigenomes, Natural Variation and Comparative Genomics, Plant Immunity and Systems and Synthetic Biology.

Subcommittees have certain loose guidelines for their activities:

- Subcommittee chairs are usually required for 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 ICAR2024 in San Diego the Bioinformatics subcommittee group organised a concurrent session on '**Our Community Effort to Reannotate the Arabidopsis Genome**' 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 the bulk 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 contributed to this report.

We are extremely grateful to all representative of subcommittees, projects, or countries as they voluntarily give their time toward MASC activities. All MASC contributors are invited to attend the remote MASC annual meeting that will take place on September 12th at 2pm GMT.

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. The future of the Arabidopsis community is up to us. We encourage you to attend our annual meeting and to consider becoming one of our directors or a member of our leadership.

International Conference on Arabidopsis Research (ICAR)

Over the past decade the flagship ICAR meeting has rotated through locations in Asia, North America and Europe. However, the board of directors are 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 2024 took place in San Diego, USA at a meeting organised by Joanna Friesner and NAASC. 538 in-person and 45 online delegates attended the meeting, which is an excellent number considering the competition from other global plant science meetings occurring in late June 2024 (IPMB in Cairns Australia and ASPB in Hawaii). 47% of ICAR2024 attendees were early career students (including 18 undergraduates!). Alongside the 4 Keynote speakers, 6 Plenary sessions there were a remarkable 37 Concurrent sessions that were organised thanks to community suggestions. These sessions provided the opportunity for 310 oral presenters in addition to 250 poster presentations.

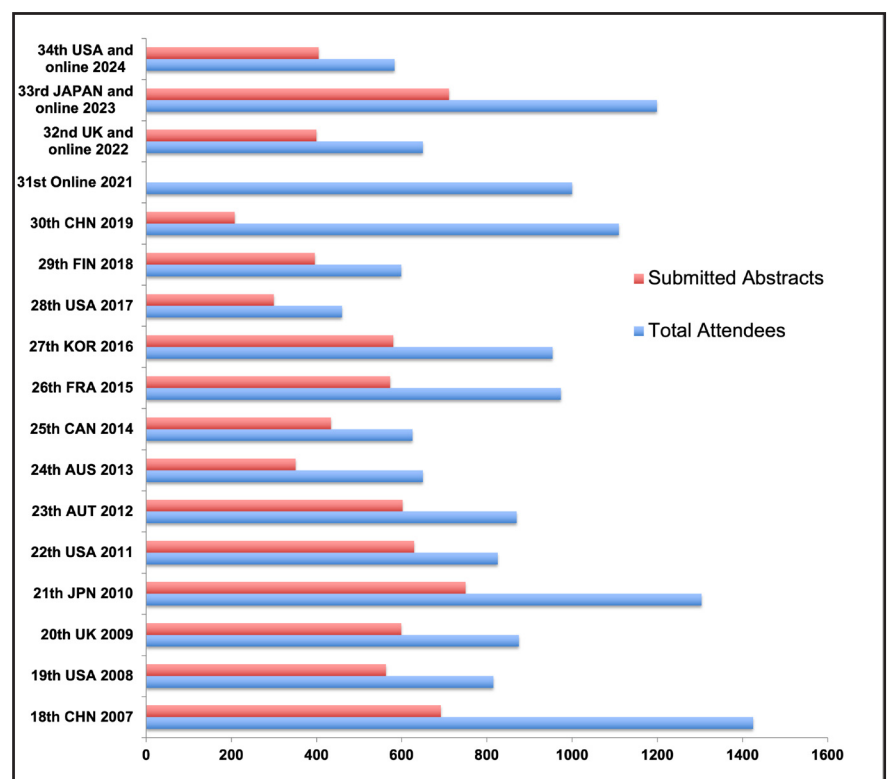
NAASC was able to secure some excellent funding primarily from the US National Science Foundation, but also from several additional sponsors, that supported the attendance of 86 early career and/or global South scientists with free registration. Three Global South attendees were also provided free campus accommodation to enable their participation.

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 (2023 JAPAN, 2019 CHINA, 2016 KOREA).

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 subsequent ICARs have also included a hybrid element. However the number of online delegates have declined over the past 3 years. (~200 in 2022, 55 in 2023, 45 in 2024).

In 2023 both online and in-person registrations were a similar price but in 2022 and 2024 the online price was much lower than the in-person price. Organising a good quality hybrid meeting has significant costs so future ICAR organisers will need to carefully consider both economic and access reasons when organising a hybrid meeting. NAASC reports that the hybrid cost component of ICAR 2024 was \$22,000+ whereas virtual attendee revenue was slightly under \$10,000. On the positive side, when several speakers canceled at the last minute due to illness or travel challenges, they were able to be quickly converted to virtual speakers.



Organisation of ICAR meetings relies upon a committed local organising committee who might engage a conference management company to deal with the meeting details. Unlike most major international meetings there is limited seed funding available from MASC to help with the organisational costs of ICARs.

The locations for upcoming ICAR meetings:

- 35th ICAR, Ghent, Belgium. June 16th-20th 2025. www.icar2025.com
- 36th ICAR, TBC in Asia
- 37th ICAR, TBC in The Americas

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 ICAR2024 can be read here:
<https://icar2024.weebly.com/advocacyconduct-code.html>

The MASC website

<http://Arabidopsisresearch.org/>

The MASC website is hosted in Canada by Hostpapa, maintained by Geraint Parry and Nick Provart.

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.

<http://Arabidopsisresearch.org/index.php/en/icar>

- Agenda and Minutes from MASC Annual meetings since 2001.

<http://Arabidopsisresearch.org/index.php/en/archive>

- MASC Annual Reports since 1990

<http://Arabidopsisresearch.org/index.php/en/publications>

- Documents and Articles related to Roadmap activities and related surveys

<http://Arabidopsisresearch.org/index.php/en/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.

Publication of the Fourth Roadmap

Over the past 30 years MASC has led in 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'.

The 4th Decadal Roadmap document has been recently prepared by Elizabeth Haswell, Nicholas Provart and other members of MASC. This document is titled 'Arabidopsis Research in 2030: Translating the Computable Plant' and will be soon submitted for publication in a peer-reviewed journal.

The topics promoted in this document were synthesised following a workshop session at ICAR2023 and a 2024 survey in which respondents were asked, among other questions, to identify which of the 100 important questions for plant biology from Larson *et al.* (2023, *New Phytol.* <https://doi.org/10.1111/nph.18663>) Arabidopsis researchers should focus on.

The Roadmap covers 8 broad topics:

- Increasing computational approaches
- Supporting research and training
- Translating from Arabidopsis to crops – or “back-translating” into Arabidopsis to elucidate mechanisms in other plants
- Promoting accessibility and diversity at conferences
- Coordinating research efforts
- Understanding/mitigating climate change and plant stress
- Sustainably producing food, materials, and fuel
- Emphasizing the importance of fundamental research

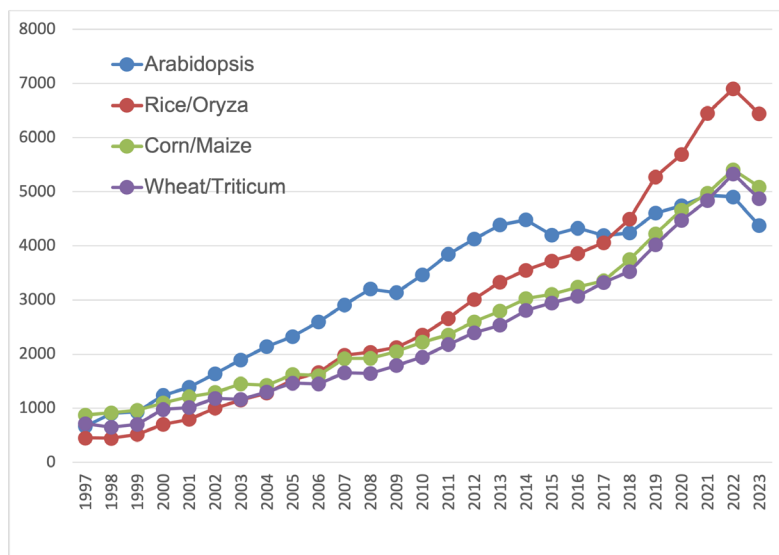
Once the document is published MASC looks forward to receiving community feedback.

Update on Arabidopsis Publications

Over the past decade the MASC report has performed a simple analysis of the number of Arabidopsis publications as assessed through the PubMed database.

Global Analysis

In the 2018 report we reported that the number of Arabidopsis publications had for the first time dipped below the number of publications that include 'Rice/ Orzya'. Over the past years this difference has increased and indeed the number of publications on Maize/Corn and Wheat/Triticum have now overtaken those that feature Arabidopsis. Of course there are many reasons for this but there is little doubt that incredible technical breakthroughs and increase in knowledge has allowed for an increase in research publications in food crops.

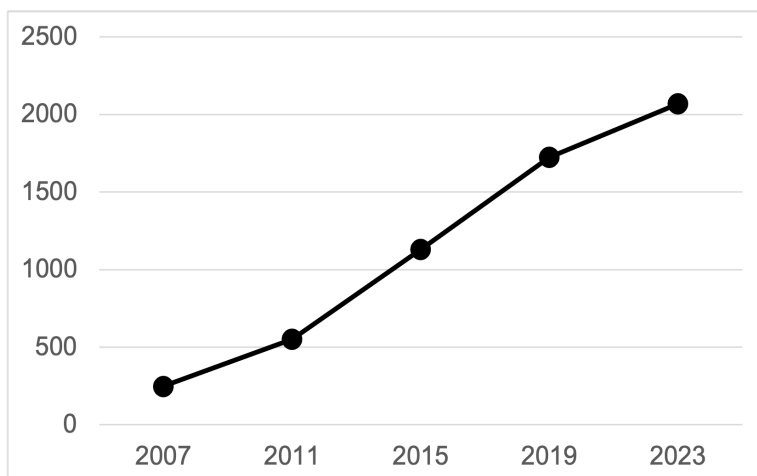


Number of Publications that feature different plant species. PubMed search using the following terms: ARABIDOPSIS [Title/Abstract] AND (“journal article”[Publication Type] OR “review”[Publication Type]) AND 20XX[DP], Rice [Title/Abstract] OR “Orzya” [Title/Abstract], Maize [Title/Abstract] OR “Corn” [Title/Abstract], Wheat [Title/Abstract] OR “Triticum” [Title/Abstract].

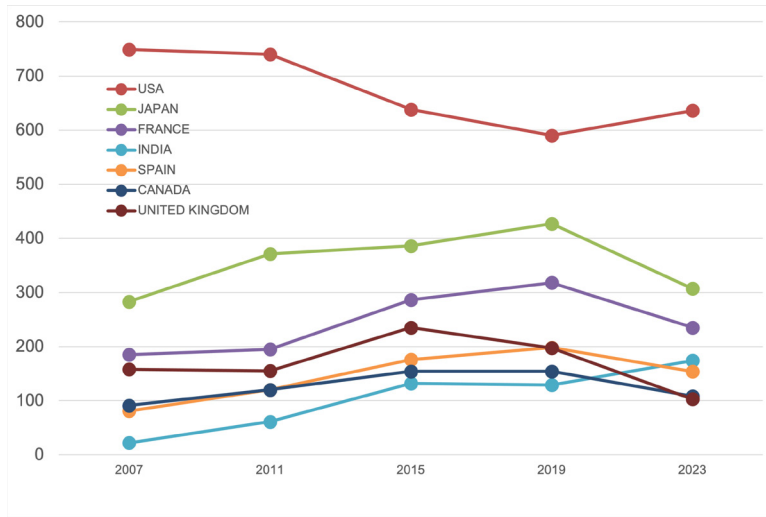
Country Analysis

The growth in Arabidopsis publications over the last thirty years was first driven by the ‘Western World’ and over the past 15 years by China. The number of publications from Chinese researchers is still increasing and in 2023 represents over half the total number of global Arabidopsis publications. Elsewhere across the globe the number of Arabidopsis publications in each country have flat-lined or are in decline. This is clearest in the United Kingdom where the number of Arabidopsis publications has almost halved from 2019-2023 (incidentally over this time-period the number of rice, corn or wheat publications have slightly declined).

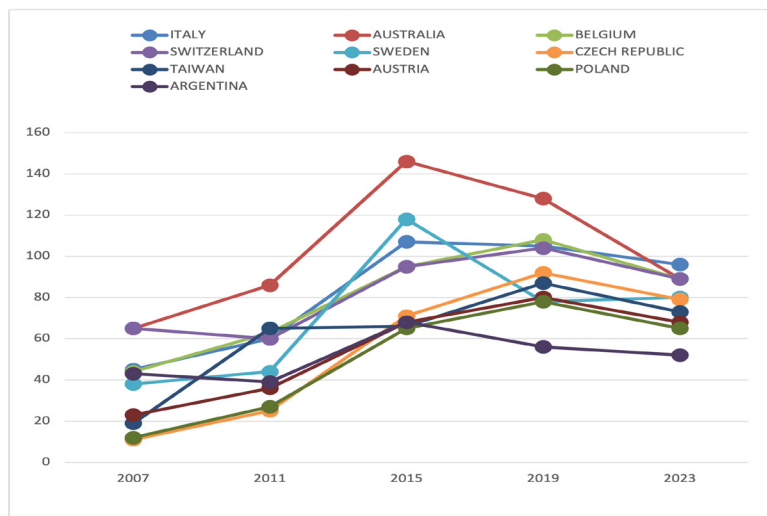
India and Singapore are the only other countries with sustained increases in publications over the past decade, albeit from low numbers. We might expect to continue to observe this increase over coming years as funders in these countries understand the importance of Arabidopsis research to provide a base of fundamental discoveries that can then be applied to the large number of economically important crops.



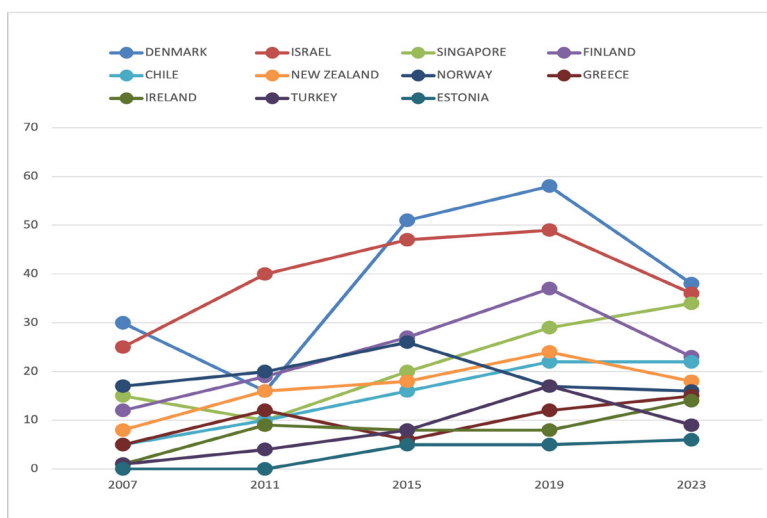
Number of publications that include Arabidopsis research from China since 2007. This search term was used in Pubmed: ARABIDOPSIS [Title/Abstract] AND CHINA AND (“journal article”[Publication Type] OR “review”[Publication Type]) AND 20XX[DP].



Number of publications that include Arabidopsis research from countries with over 100 publications in 2023. This search term was used in Pubmed: ARABIDOPSIS [Title/Abstract] AND COUNTRY AND (“journal article”[Publication Type] OR “review”[Publication Type]) AND 20XX[DP].



Number of Publications that include Arabidopsis research from countries with between 50-100 publication in 2023. This search term was used in Pubmed: ARABIDOPSIS [Title/Abstract] AND COUNTRY AND (“journal article”[Publication Type] OR “review”[Publication Type]) AND 20XX[DP].



Number of Publications that include Arabidopsis research from countries with fewer than 50-publications in 2023. This search term was used in Pubmed: ARABIDOPSIS [Title/Abstract] AND COUNTRY AND (“journal article”[Publication Type] OR “review”[Publication Type]) AND 20XX[DP].

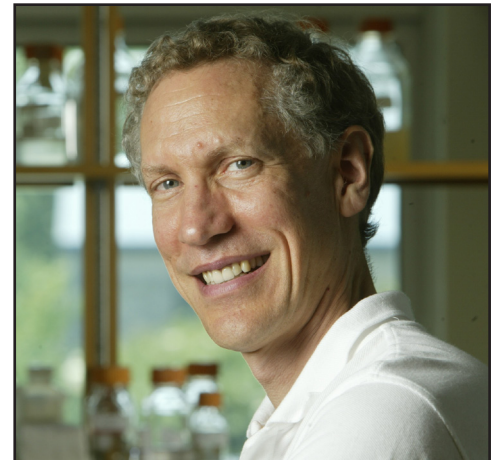
A Tribute to Philip N. Benfey, a Luminary in the Field of Plant Biology

SM Brady, GM Coruzzi.

On September 26, 2023, the Arabidopsis research community lost a visionary - Philip N. Benfey, Paul Kramer Professor at Duke University.

Philip made critical advancements in our understanding of root developmental biology and in the generation of cell type and single cell-resolution resources. This work culminated in The Root Cell Atlas - a pointillist view of the expression profile of every gene within the root.

In addition to his extraordinary science, Philip was a leader in the Arabidopsis community. He served as president of the Multinational Arabidopsis Steering Committee in 2005 and 2006, as well as a member of the North American Arabidopsis Steering Committee from 2003-2007. He enabled functional genomics research as the chair of the Multinational Coordinated Arabidopsis thaliana Functional Genomics Project.



Philip was recognized for his research achievements as a Member of the United States National Academy of Sciences and as a Howard Hughes Medical Institute Investigator, a Pioneer of the ASPB, amongst many other accolades. Importantly, Philip was an exceptional mentor, colleague and friend. His untimely passing leaves a gaping hole in our plant community. We encourage all to learn more about Philip Benfey's legacy in the following tributes.

References and Links:

Remembering Philip N. Benfey: A visionary in plant biology and mentor extraordinaire.

N. Raikhel, JR Ecker, G Coruzzi. PNAS. 120(45), e2317677120

Philip N. Benfey (1953-2023): A "ring" master of plant development and cellular genomics.

GM Coruzzi, KD Birnbaum. Science. 382(6675): 1127.

Philip N. Benfey (1953-2023).

MJ Bennett, SM Brady, JR Dinneny, Y Helariutta, R. Sozzani. Developmental Cell. 58(22):2413-2415.

Arabidopsis Lifetime Achievement Award:

<https://www.arabidopsiscommunity.org/news-events/benfey-arabidopsis-community-lifetime-achievement-award>

ASPB Pioneer:

<https://aspb.org/membership/aspb-pioneer-members/pioneer-philip-benfey/#testimonials>

ASPB Members Remember Philip Benfey

<https://blog.aspb.org/aspb-remembers-philip-benfey/>

NYU Genome Symposium Tribute to Philip Benfey:

<https://as.nyu.edu/departments/biology/events-news/news/philip-benfey.html> (Video link)

MASC Philip Benfey Lifetime Achievement Awards

<https://youtu.be/QCx1rPPg-Pw>

Philip N. Benfey Memorial Symposium

<https://youtu.be/QCx1rPPg-Pw>

MASC Subcommittee Reports

Bioinformatics	13
Natural Variation and Comparative Genomics	15
Epigenetics and Epigenomics	17
Plant immunity	19
Systems and Synthetic Biology	21

MASC Bioinformatics Subcommittee Report

Prepared by

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

TAIR: TAIR continues to add new gene function data on a weekly basis. This past year 1222 new/updated locus summaries, 499 new/updated gene symbols, 1766 articles linked to 3677 genes, 14301 experimental Gene Ontology (GO) and Plant Ontology (PO) annotations, 131 new/updated alleles, and 232 phenotypes linked to germplasms were curated. TAIR regularly updates InterPro domain mapping for the Arabidopsis proteins using bimonthly updates data from UniProt. TAIR also released a new version of its website in May 2024. The redesigned website is easier-to-navigate, more accessible, and is mobile friendly. Also, in terms of modernizing code, TAIR rolled out an instance of JBrowse2 for browsing Arabidopsis genomic data sets in a track-based manner. Most of the tracks from TAIR's still-operational JBrowse instance have been ported over. One of the enhancements in JBrowse2 is being able to visualize synteny, such as that between the Arabidopsis thaliana and Arabidopsis lyrata genomes. A paper by Reiser et al. (2024) describing these updates to TAIR came out earlier this year. It also nicely gives a snapshot of the status of the Arabidopsis genome annotation effort and describes efforts to modernize the backend code that powers TAIR.

BAR: The Bio-Analytic Resource for Plant Biology was designated a “global core biodata resource” last year by the Global Biodata Coalition, one of just 52 such databases worldwide (<https://globalbiodata.org/what-we-do/global-core-biodata-resources/>). The BAR contains data from not just Arabidopsis, but also Medicago truncatula, rice, wheat, barley and 27 other plant species (with data for 3 others to be released soon). These data include nucleotide and protein sequence data, gene expression data, protein-protein and protein-DNA interactions, protein structures, subcellular localizations, and polymorphisms. The data are stored in more than 200 relational databases holding 186 GB of data and are presented to the user via web apps. These web apps provide data analysis and visualization tools that are hosted on the BAR. Some of the most popular tools are eFP (“electronic fluorescent pictograph”) Browsers, ePlants, and ThaleMine (an Arabidopsis-specific instance of InterMine). The BAR upgraded Thalemine to the current version (v5.1.0-20230710) based on the InterMine 5.1.0 release, with data updates from many sources from mid-2023. The BAR released a high-resolution gynoeceium view for its Arabidopsis eFP Browser (Luna-García et al. 2024).

An Arabidopsis genome update is coming this year! In October 2022, Tanya Berardini of TAIR and Nicholas Provar of the BAR organized a conference call for members of the Arabidopsis genome sequencing and annotation community to develop a plan for producing a new structural annotation of the *A. thaliana* Col-0 genome, to update the Araport11 version, released in June 2016. NCBI ran their annotation pipeline on a new consensus “telomere-to-telomere” assembly last year (https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_028009825.2/). TAIR has coordinated this effort with NCBI and with volunteers from labs around the world who are adding/updating NORs, rDNAs and tandem repeats, and who are expertly curating of protein coding genes, transposable elements, and lncRNAs. See TAIR's website (<https://conf.phoenixbioinformatics.org/display/COM/A.+thaliana+Col-0+v12+reannotation+effort>) for updates. The genome annotations will be submitted to NCBI following completion of manual verification and quality checks later this summer. All participants in the effort are working on a manuscript together.

Large-scale Data Sets and Methods of Note: Peleke et al. (2024) used deep learning to unravel the cis-regulatory code of several model plant species, including Arabidopsis. 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 101,341 Arabidopsis publications to extract – in a traceable way – 387,777 relationships between

genes, molecules, compartments, organs etc. Check out the preprint by Fo et al. (2023)! ggPlantMap was developed by Jo and Kajala (2024) for “eFP” representations that can be generated with an open-source R package. The eFP Browser representation also made its way into a nice toolkit called TBtools, with more than 130 functions for working with high-throughput data (Chen et al. 2020, 2023).

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! An inaugural Gordon Research Conference on Single-Cell Approaches in Plant Biology kicked off last August to positive reviews from attendees. TAIR continues its partnership with <https://www.micropublication.org/>, a platform for very short peer-reviewed reports. Nicholas Provart’s Plant Bioinformatics course covering 33 online tools from labs around the world on Coursera.org (<https://www.coursera.org/learn/plant-bioinformatics/>) was fully updated in June 2024.

References

Chen C, Chen H, Zhang Y, Thomas HR, Frank MH, He Y, and Xia R. TBtools: An Integrative Toolkit Developed for Interactive Analyses of Big Biological Data. *Mol Plant*. 2020;13(8):1194–1202. <https://doi.org/10.1016/j.molp.2020.06.009>

Chen C, Wu Y, Li J, Wang X, Zeng Z, Xu J, Liu Y, Feng J, Chen H, He Y, et al. TBtools-II: A “one for all, all for one” bioinformatics platform for biological big-data mining. *Mol Plant*. 2023;16(11):1733–1742. <https://doi.org/10.1016/j.molp.2023.09.010>

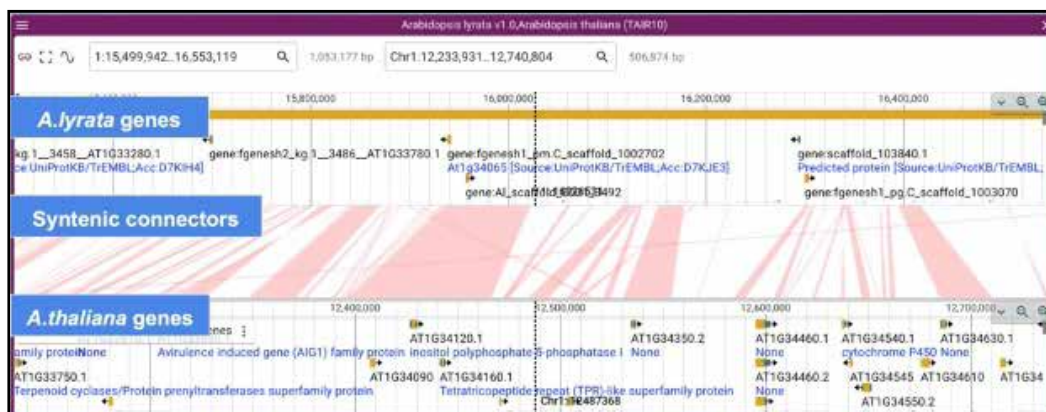
Fo K, Chuah YS, Foo H, Davey EE, Fullwood M, Thibault G, and Mutwil M. PlantConnectome: knowledge networks encompassing >100,000 plant article abstracts. 2023;2023.07.11.548541. <https://doi.org/10.1101/2023.07.11.548541>

Jo L and Kajala K. ggPlantmap: an open-source R package for the creation of informative and quantitative ggplot maps derived from plant images. *J Exp Bot*. 2024;erae043. <https://doi.org/10.1093/jxb/erae043>

Luna-García V, Bernal Gallardo JJ, Rethoret-Pasty M, Pasha A, Provart NJ, and de Folter S. A high-resolution gene expression map of the medial and lateral domains of the gynoecium of *Arabidopsis*. *Plant Physiol*. 2024;195(1):410–429. <https://doi.org/10.1093/plphys/kiad658>

Peleke FF, Zumkeller SM, Gültas M, Schmitt A, and Szymański J. Deep learning the cis-regulatory code for gene expression in selected model plants. *Nat Commun*. 2024;15(1):3488. <https://doi.org/10.1038/s41467-024-47744-0>

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>



Natural Variation and Comparative Genomics Subcommittee Report

Prepared by

J. Chris Pires (Chair)

jchrispires@gmail.com, Colorado State University

Ya-Long Guo (Co-Chair)

yalong.guo@ibcas.ac.cn, Institute of Botany, Chinese Academy of Sciences

Recently developed Open Tools and Resources for Arabidopsis Researchers

Many new genomic resources have been produced in the Brassicaceae, see selected publications below for examples.

Recent or Future activities of Subcommittee members.

Lots of species of the Brassicaceae family have been sequenced and studied in diverse aspects. In particular, natural variation of the model species *Arabidopsis* produced many fascinating results. Subcommittee members jointly organized the XX International Botanical Congress will be hold from 21-27 July 2024.

Selected Publications

Hendriks, K.P., Kiefer, C., Al-Shehbaz, I.A., Bailey, C.D., Hooft van Huysduynen, A., Nikolov, L.A., Nauheimer, L., Zuntini, A.R., German, D.A., Franzke, A., Koch, M.A., Lysak, M.A., Toro-Nunez, O., Ozudogru, B., Invernón, V.R., Walden, N., Maurin, O., Hay, N.M., Shushkov, P., Mandakova, T., Schranz, M.E., Thulin, M., Windham, M.D., Resetnik, I., Spaniel, S., Ly, E., Pires, J.C., Harkess, A., Neuffer, B., Vogt, R., Brauchler, C., Rainer, H., Janssens, S.B., Schnull, M., Forrest, A., Guggisberg, A., Zmarzty, S., Lepschi, B.J., Scarlett, N., Stauffer, F.W., Schonberger, I., Heenan, P., Baker, W.J., Forest, F., Mummenhoff, K., and Lens, F. 2023. Global Brassicaceae phylogeny based on filtering of 1,000-gene dataset. *Curr Biol* 33, 4052-4068.

This study involves a worldwide community of thousands of researchers working on Brassicaceae and its diverse members, which reveals a new genus-level family phylogeny, and will be an indispensable tool for studies on biodiversity and plant biology.

Lan, Z., Song, Z., Wang, Z., Li, L., Liu, Y., Zhi, S., Wang, R., Wang, J., Li, Q., Bleckmann, A., Zhang, L., Dresselhaus, T., Dong, J., Gu, H., Zhong, S., and Qu, L.J. (2023). Antagonistic RALF peptides control an intergeneric hybridization barrier on Brassicaceae stigmas. *Cell* 186, 4773-4787.

This study uncover a “lock-and-key” system governing the hybridization breadth of interspecific/intergeneric crosses in Brassicaceae. Manipulating this system holds promise for facilitating broad hybridization in crops.

Jiang, J., Xu, Y.C., Zhang, Z.Q., Chen, J.F., Niu, X.M., Hou, X.H., Li, X.T., Wang, L., Zhang, Y., Ge, S., and Guo, Y.L. (2024). Forces driving transposable element load variation during *Arabidopsis* range expansion. *Plant Cell* 36, 840-862.

This study reveals the variation in TE genetic load during *Arabidopsis* expansion and highlights the causes of TE load variation from the perspectives of both population genetics and quantitative genetics.

Wlodzimierz, P., Rabanal, F.A., Burns, R., Naish, M., Primetis, E., Scott, A., Mandakova, T., Gorringer, N., Tock, A.J., Holland, D., Fritschi, K., Habring, A., Lanz, C., Patel, C., Schlegel, T., Collenberg, M., Mielke, M., Nordborg, M., Roux, F., Shirsekar, G., Alonso-Blanco, C., Lysak, M.A., Novikova, P.Y., Bousios, A., Weigel, D., and Henderson, I.R. (2023). Cycles of satellite and transposon evolution in Arabidopsis centromeres. *Nature* 618, 557-565.

This study identified rapid cycles of transposon invasion and purging through satellite homogenization, which drive centromere evolution and ultimately contribute to speciation.

Lian, Q., Huettel, B., Walkemeier, B., Mayjonade, B., Lopez-Roques, C., Gil, L., Roux, F., Schneeberger, K., and Mercier, R. (2024). A pan-genome of 69 *Arabidopsis thaliana* accessions reveals a conserved genome structure throughout the global species range. *Nat Genet* 56, 982-991.

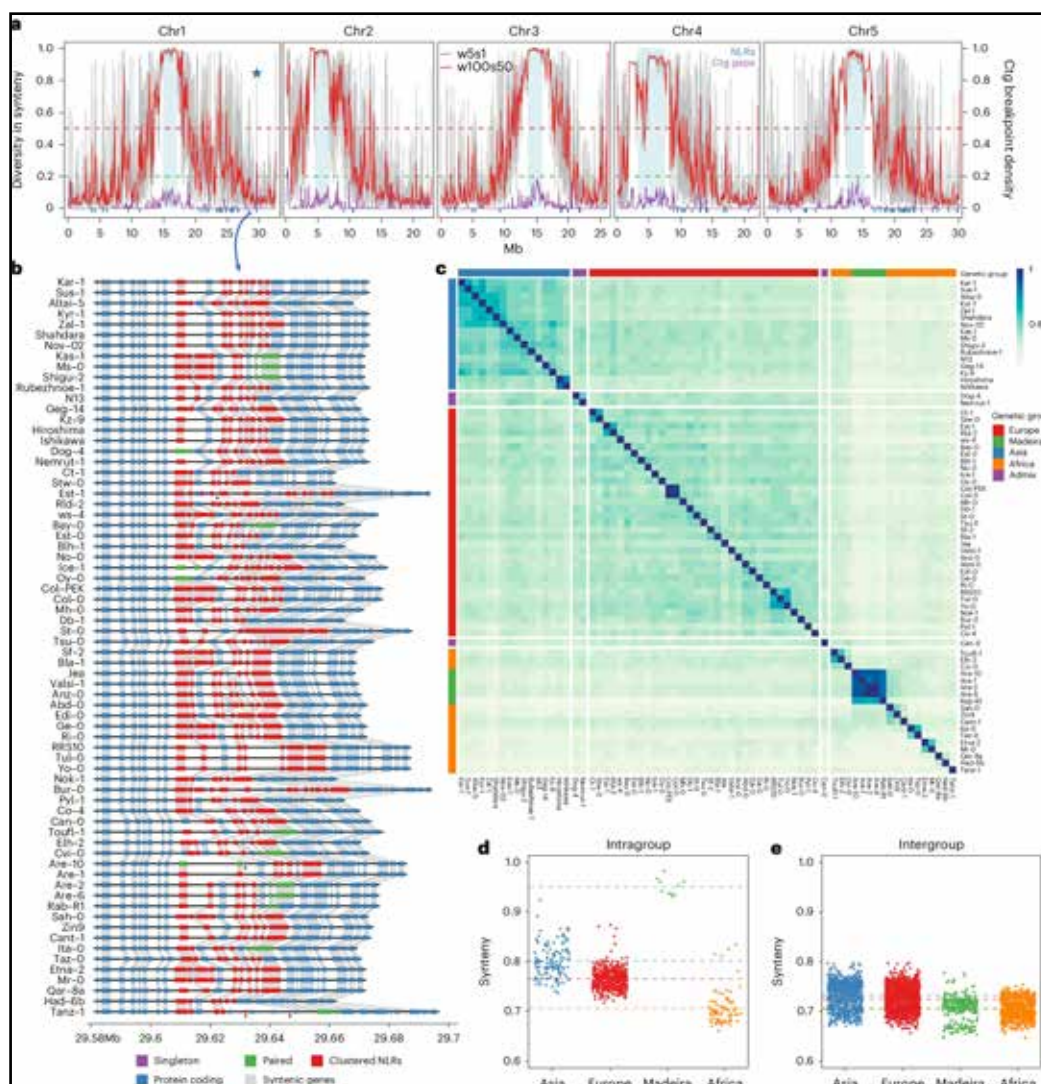
This study present chromosome-level genome assemblies of 69 accessions from a global species range, these 69 new *Arabidopsis* genome assemblies will empower future genetic research.

Members of the subcommittee

Sureshkumar Balasubramanian sureshkumar.balasubramanian@monash.edu

Wolfgang Busch wbusch@salk.edu

Patrick Edger edgerpat@msu.edu



Epigenetics and Epigenomics Subcommittee Report

Prepared by

Robert Schmitz, schmitz@uga.edu, University of Georgia

Xuehua Zhong, xuehuazhong@wustl.edu, Washington University in St. Louis

Recent or Future activities of Subcommittee members.

2024

International Conference on Arabidopsis Research, San Diego, CA, July, 2024

- Epigenetics
- Epigenome and Epitranscriptome in Environmental Stress Signaling and Memory
- Chromatin at Single-cell and Single-molecule Resolution

Plant Epigenetics - EpiPlant – Clermont-Ferrand, France, July, 2024

International Plant Molecular Biology (IPMB) Congress, Queensland, Australia, June 2024

- Epigenetics
- Transposable Elements
- Transcriptional and Post-transcriptional Regulation

2025

Keystone meeting on Plant Epigenetics and Gene Regulation, 2025

International Conference on Arabidopsis Research, Gent, Belgium, June, 2025

- Epigenetics

Selected Publications

Epiallelic variation of non-coding RNA genes and their phenotypic consequences.

Liu J, Zhong X. Nat Commun. 2024 Feb 14;15(1):1375. doi: 10.1038/s41467-024-45771-5.

Sequence and epigenetic landscapes of active and silent nucleolus organizer regions in Arabidopsis.

Fultz D, McKinlay A, Enganti R, Pikaard CS. Sci Adv. 2023 Nov 3;9(44):eadj4509. doi: 10.1126/sciadv.adj4509.

An evolutionary epigenetic clock in plants.

Yao N, Zhang Z, Yu L, Hazarika R, Yu C, Jang H, Smith LM, Ton J, Liu L, Stachowicz JJ, Reusch TBH, Schmitz RJ, Johannes F. Science. 2023 Sep 29;381(6665):1440-1445. doi: 10.1126/science.adh9443.

Chromatin remodeling of histone H3 variants by DDM1 underlies epigenetic inheritance of DNA methylation.

Lee SC, Adams DW, Ipsaro JJ, Cahn J, Lynn J, Kim HS, Berube B, Major V, Calarco JP, LeBlanc C, Bhattacharjee S, Ramu U, Grimanelli D, Jacob Y, Voigt P, Joshua-Tor L, Martienssen RA. Cell. 2023 Sep 14;186(19):4100-4116.e15. doi: 10.1016/j.cell.2023.08.001.

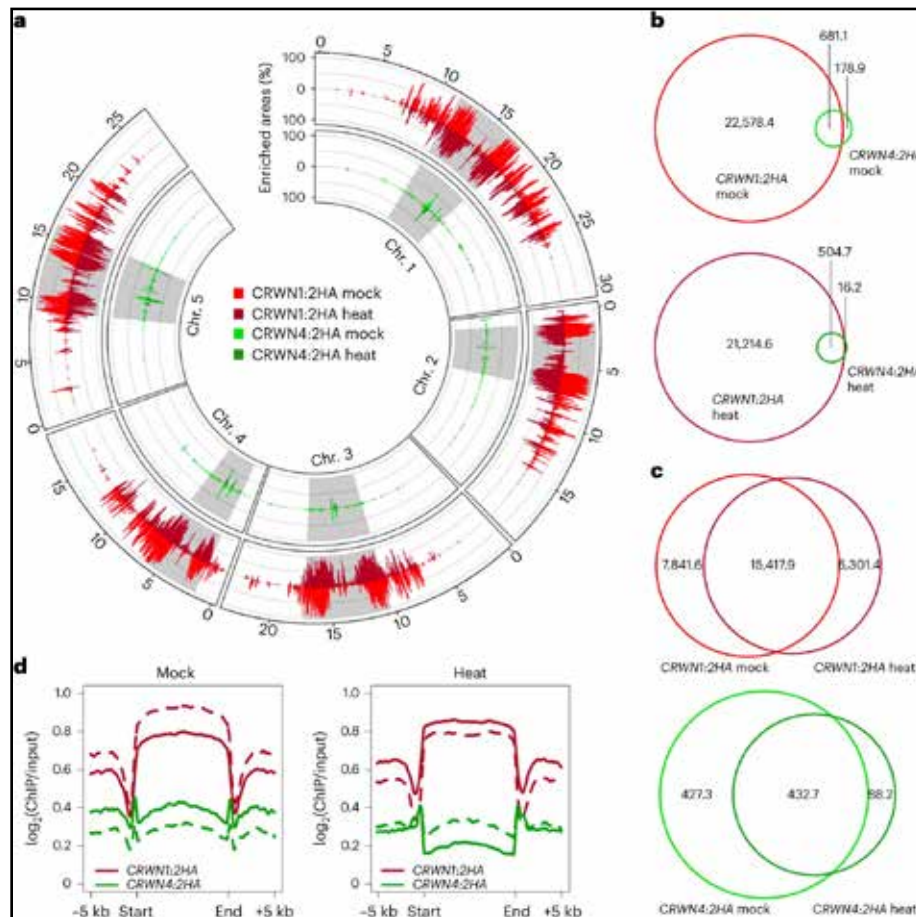
The plant nuclear lamina disassembles to regulate genome folding in stress conditions

Wang N, Wang Z, Tzourtzou S, Wang X, Bi X, Leimeister J, Xu L, Sakamoto T, Matsunaga S, Schaller A, Jiang H, Liu C. Nat Plants. 2023 Jul;9(7):1081-1093. doi: 10.1038/s41477-023-01457-2.

Members of the subcommittee

Robert Schmitz, schmitz@uga.edu, University of Georgia

Xuehua Zhong, xuehuazhong@wustl.edu, Washington University in St. Louis



Plant Immunity Subcommittee Report

Prepared by

Chair, **Shahid Mukhtar**
Clemson University
mshahid@clemson.edu

Members:

- 1- Dr. Yasuhiro Kadota, yasuhiro.kadota@riken.jp, RIKEN Center for Sustainable Resource Science (CSRS), Yokohama, Japan
- 2- Dr. Karolina Mukhtar kmukhta@clemson.edu Clemson University, SC, USA
- 3- Dr. Farid El Kasmi, farid.el-kasmi@zmbp.uni-tuebingen.de, ZMBP – Center for Plant Molecular Biology, University of Tuebingen, Tuebingen, Germany
- 4- Dr. Marc Nishimura, marc.nishimura@colostate.edu, Colorado State University, Fort Collins, CO, USA
3. Recently developed Open Tools and Resources for Arabidopsis Researchers

Please provide a list of resources that have been developed over the past 12 months that are relevant to your subcommittee's research area.

1. AlphaFold3; <https://deepmind.google/technologies/alphafold/>
2. AraPathogen2.0: An Improved Prediction of Plant–Pathogen Protein–Protein Interactions Empowered by the Natural Language Processing Technique. <http://zzdlab.com/arapathogen2/index.php>
3. PPIntegrator: semantic integrative system for protein–protein interaction and application for host–pathogen datasets. <https://github.com/YasCoMa/ppintegrator>
4. Arabidopsis Developmental Atlas Viewer: <http://neomorph.salk.edu:9000/#about>
5. Deep-HPI-pred: An R-Shiny applet for network-based classification and prediction of Host-Pathogen protein-protein interactions. <https://github.com/tahirulqamar/Deep-HPI-pred>

Recent or Future activities of Subcommittee members.

The 33rd International Conference on Arabidopsis Research held in Makuhari, Japan.
2023 Fall international conference of Korean Society of Plant Pathology (KSPP)
2023 Brazilian Symposium on Plant Molecular Genetics; Florianopolis, Brazil (5/30-6/2)
2023 The Plant & Animal Genome, Australia
2023 IS-MPMI Congress; Providence, RI, USA (7/16-7/20)
2024 The Plant & Animal Genome, San Diego, USA
2024 IPMB; Cairnes, Australia (6/24-6/28)
2025 IS-MPMI Congress; Cologne, Germany (7/13-7/17)
2025 The Plant & Animal Genome, San Diego, USA

Selected Publications

Saarenpää S, Shalev O, Ashkenazy H, Carlos V, Lundberg DS, Weigel D, Giacomello S. Spatial metatranscriptomics resolves host-bacteria-fungi interactomes. *Nature Biotechnology*. 2023 Nov 20. doi: 10.1038/s41587-023-01979-2.

This article introduced spatial metatranscriptomics (SmT), a sequencing technique that utilizes 16S/18S/ITS/poly-d(T) multimodal arrays to simultaneously characterize both the host transcriptome and the microbiome within tissues, achieving a resolution of 55 µm

Nomura K, Andrezza F, Cheng J, Dong K, Zhou P, He SY. Bacterial pathogens deliver water- and solute-permeable channels to plant cells. *Nature*. 2023 Sep;621(7979):586-591. doi: 10.1038/s41586-023-06531-5.

AlphaFold2-enabled discovery that bacterial virulence proteins use a porin-like mechanism to release water from host cells, hydrating the apoplast and generating the classic “water soaking” phenotype to promote pathogen success.

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.

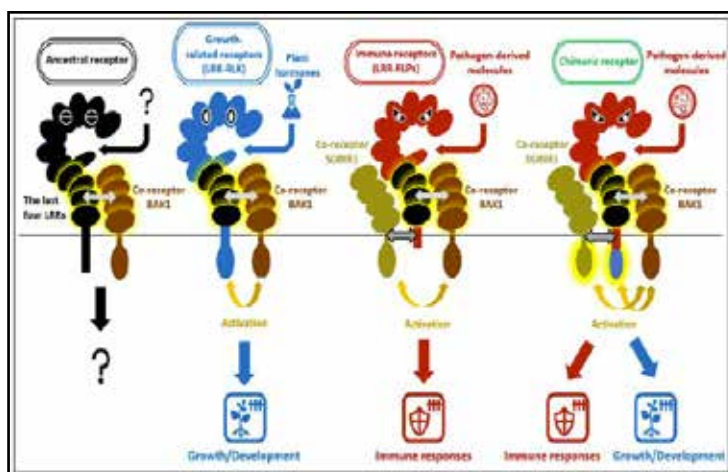
Structural biology reveals that a plant polygalacturonase inhibitor protein functions by altering pathogen polygalacturonase catalysis, creating a mixed-organism enzyme complex that produces immune-activating products rather than inhibiting immunity.

Tang B, Feng L, Hulin MT, Ding P, Ma W. Cell-type-specific responses to fungal infection in plants revealed by single-cell transcriptomics. *Cell Host Microbe*. 2023 Oct 11;31(10):1732-1747.e5. doi: 10.1016/j.chom.2023.08.019.

By creating an atlas of 95,040 *Arabidopsis thaliana* leaf cells infected by *Colletotrichum higginsianum*, this work reveals cell-type-specific gene expression, with vasculature cells showing enriched intracellular immune receptors and trajectory analysis highlighting varying interactions with the fungus.

Ngou BPM, Wyler M, Schmid MW, Kadota Y, Shirasu K. Evolutionary trajectory of pattern recognition receptors in plants. *Nat Commun*. 2024 Feb 1;15(1):308. doi: 10.1038/s41467-023-44408-3.

This work reveals that cell-surface receptors involved in immunity and development share a common origin. After diversification, their ectodomains, juxtamembrane, transmembrane, and cytosolic regions have either diversified or stabilised to recognise diverse ligands and activate differential downstream responses.



Members of the subcommittee

Chair, Dr. Shahid Mukhtar mshahid@clemson.edu Clemson University, SC, USA

Members:

- 1- Dr. Yasuhiro Kadota, yasuhiro.kadota@riken.jp, RIKEN Center for Sustainable Resource Science (CSRS), Yokohama, Japan
- 2- Dr. Karolina Mukhtar kmukhta@clemson.edu Clemson University, SC, USA
- 3- Dr. Farid El Kasmi, farid.el-kasmi@zmbp.uni-tuebingen.de, ZMBP – Center for Plant Molecular Biology, University of Tuebingen, Tuebingen, Germany
- 4- Dr. Marc Nishimura, marc.nishimura@colostate.edu, Colorado State University, Fort Collins, CO, USA

Systems and Synthetic Biology Subcommittee Report

Prepared by

Siobhan Brady, sbrady@ucdavis.edu, UC Davis

Recently developed Open Tools and Resources for Arabidopsis Researchers

Next-Gen GWAS: full 2D epistatic interaction maps retrieve part of missing heritability and improve phenotypic prediction C Carré, JB Carluer, C Chaux, C Estoup-Streiff, N Roche, E Hosy, A Mas, ...
Genome Biology 25 (1), 76

PHYTOMap: (<https://www.nature.com/articles/s41477-023-01439-4>)

ggPlantmap: (<https://pubmed.ncbi.nlm.nih.gov/38329371/>)

ccPlantDB: <https://academic.oup.com/nar/article/52/D1/D1629/7252671>

Recent or Future activities of Subcommittee members.

- 1- Planning of the International Plant Systems Biology Meeting 2025 in Venice Italy.
- 2- Synthetic Biology UK 2024 27-28 November, Hinxton Hall, Cambridge, UK.
- 3- Plant SynBio Hackathon, August 2024

Selected Publications

The trans-regulatory landscape of gene networks in plants

NFC Hummel, A Zhou, B Li, K Markel, IJ Ornelas... - Cell Systems, June 2023

[https://www.cell.com/cell-systems/pdf/S2405-4712\(23\)00146-1.pdf](https://www.cell.com/cell-systems/pdf/S2405-4712(23)00146-1.pdf)

Hummel et al. characterize the activity of more than 400 transcriptional effector domains from Arabidopsis and annotate effector activity in a gene regulatory network to elucidate novel targets for engineering in synthetic biology.

Double DAP-seq uncovered synergistic DNA binding of interacting bZIP transcription factors

M Li, T Yao, W Lin, WE Hinckley, M Galli, W Muchero, A Gallavotti, Jin-Gui Shen and Shao-shao Carol Huang Nature Communications 14 (1), 2600, 5/5/2023

This paper presents the double DNA Affinity Purification-sequencing (dDAP-seq) technique that maps heterodimer binding sites on endogenous genomic DNA which is key for combinatorial gene regulation, the next frontier in gene regulatory networks.

Jores T, Tonnie J, Mueth NA, Romanowski A, Fields S, Cuperus JT, Queitsch C. Plant enhancers exhibit both cooperative and additive interactions among their functional elements. Plant Cell. 2024 Mar 21:koae088. doi: 10.1093/plcell/koae088.

Experimental evidence that plant enhancers exhibit cooperative and additive interactions.

Guiziou S, Maranas CJ, Chu JC, Nemhauser JL. An integrase toolbox to record gene-expression during plant development. *Nat Commun.* 2023 Apr 3;14(1):1844. doi: 10.1038/s41467-023-37607-5.

Demonstration of history-dependent circuits for decoding the order of expression during organogenesis.

SHR and SCR coordinate root patterning and growth early in the cell cycle

CM Winter, P Szekely, V Popov, H Belcher, R Carter, M Jones, SE Fraser, ...

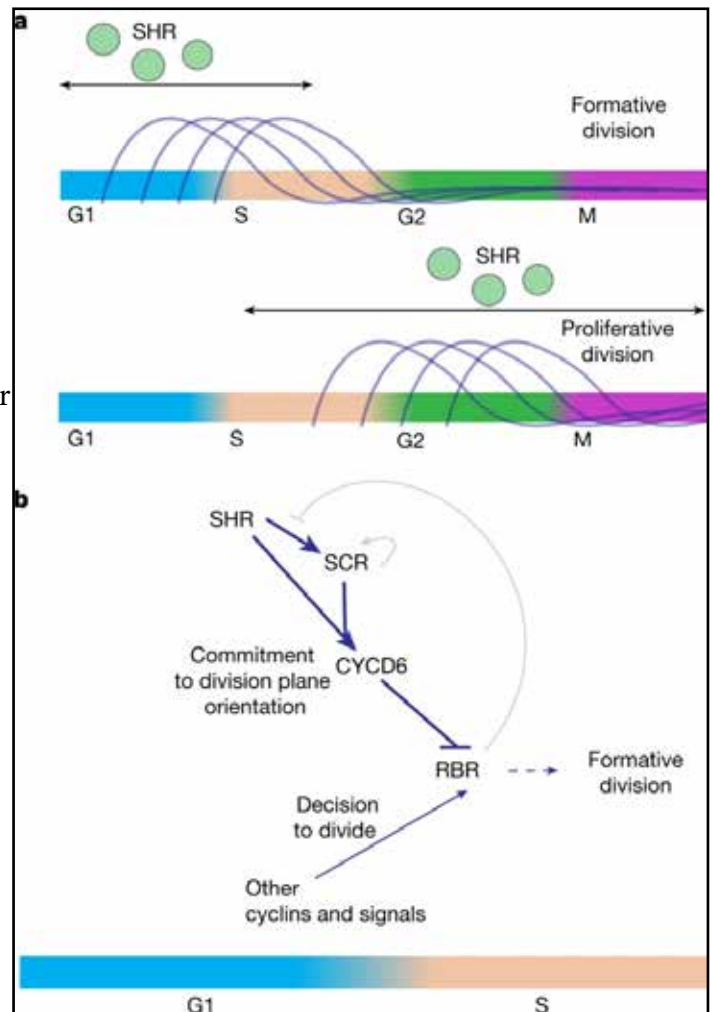
Nature 626 (7999), 611-616

<https://www.nature.com/articles/s41586-023-06971-z>

Using light sheet microscopy, the Benfey lab shows that levels of short root and scarecrow transcription factors early in the cell cycle determine the orientation of the division plane, resulting in either formative or proliferative cell division, revealing an uncharacterized mechanism by which developmental regulators directly coordinate patterning and growth.

Members of the subcommittee

Siobhan Brady
Gloria Coruzzi
Gabriel Krouk
Shahid Mukhtar
Nicola Patron



Projects and Resources

Arabidopsis Biological Resource Center	24
Bio-Analytic Resource for Plant Biology	25
Gramene: A comparative genomics and pathways resource for plants	27
The Nottingham Arabidopsis Stock Centre	29
RIKEN BioResource Research Center	30
The Arabidopsis Information Resource (TAIR)	31



Prepared by

Emma Knee, knee.2@osu.edu

David Somers, somers.24@osu.edu, The Ohio State University

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

ABRC distributed 62,669 samples to 1,594 individuals located in 43 countries in 2023. This represents a decrease in samples from the previous year which can be attributed to fewer large sets of seed stocks being ordered. The number of researchers receiving samples is slightly higher and the number of countries represented is approximately the same as the previous year. 59% of orders were shipped to researchers in the US, 13% to Japan, 6% to Canada, and 5% to Korea. Other countries each accounted for less than 4% of total orders. In addition to orders placed directly at the ABRC website, 1,608 individual samples were requested by the European Arabidopsis Stock Center (NASC) to be distributed to their customers. ABRC also provided to NASC bulk seed for 2,270 lines, and smaller aliquots of seed for 1,597 lines.

ABRC received donations of 263 seed stocks from the research community over the past year. These included characterized mutant and transgenic lines as well as natural variants and close relatives of Arabidopsis. 20 non-seed resources were also added to the collection including multi-knock CRISPR libraries, Arabidopsis clones, and cloning vectors. The majority of donations were received from the US. Donations were also received from China, Hong Kong, and Israel. All stock information is available through ABRC website (<https://abrc.osu.edu/>). ABRC no longer uploads stock data to TAIR but has made select stock data available via an API allowing query by stock name or AGI. Contact ABRC to request API access.

The seed collection now numbers over 530,000 stocks. ABRC has ceased distribution of some non-seed stocks that were no longer ordered, so that the collection of non-seed stocks has decreased by 58% to just over 189,000 stocks. The center also operates with a smaller staff than in previous years and has streamlined operations. Quality control testing is mostly focused on monitoring seed germination rates and targets 2000 to 3000 stocks per year. New seed lots are generated for stocks with lower than 81% germination.

The ABRC outreach program reached over 1000 individuals in 2023. Activities included tours of the center, presentations at local science fairs, and distribution of education kits and other stocks to students and educators. Publications Planned future activities of your project/resource ABRC continues to seek additional sources of funding in order to keep stock prices as low as possible. Stock distribution is projected to continue at the current level and donations are projected to increase in the coming year based on communications we have received from potential donors. Please consider donating any Arabidopsis resources your laboratory has generated. We are particularly interested in receiving characterized mutants, especially lines with multiply stacked mutations. We are happy to receive verified T-DNA insertion lines even if we already have a confirmed line in the collection. We are also happy to receive seeds of close relatives of Arabidopsis and other Brassicaceae. ABRC will continue to provide stocks to NASC and a reciprocal receipt of stocks from NASC is hoped to resume following an extended hiatus.

Outreach activities will continue to focus on distribution of education kits and programming with local partners. ABRC and NASC will staff a joint booth at ICAR 2024 in San Diego.

Bio-Analytic Resource for Plant Biology (BAR)

<https://bar.utoronto.ca>



Prepared by

Nicholas Provart (director) nicholas.provart@utoronto.ca
BAR bioinformatics technician **Asher Pasha**, University of Toronto.

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

- eFP Arabidopsis Gynoecium view is added in collaboration with Stefan de Folter's Lab
- BAR is designated one of just 52 Global Core Biodata Resources
- BAR FAIR-sharing page was created: <https://fairsharing.org/FAIRsharing.8c6779>
- BAR API is a new API to access data in BAR databases
- ThaleMine is updated to v5.1.0-20230710 with the latest datasets
- 400+ interactions determined by TurboID using BIN2 were added to the Arabidopsis Interactions Viewer/AIV2 database
- ASPB Plant Biology 2023 conference talk and booth in Savannah, GA, USA
- ICAR Conference 2023 in Chiba, Japan
- ASPB Plant Biology 2024 conference talk and booth in Honolulu, HI, USA
- ePlant Barley is released as two separate apps. ePlant Barley legacy and ePlant Barley with version 3 gene IDs for the "seed atlas" dataset from the Pecinka Lab
- eFP Mangosteen is a new eFP Browser on the BAR, together with the Goh Lab
- eFP Wheat abiotic stress data are added, in collaboration with the Kagale Lab
- eFP Sorghum is updated with new views in collaboration with the Ware Lab at CSHL
- ePlant Medicago LCM data are added, in collaboration with the Frugoli Lab
- ePlant Eucalyptus is published, in collaboration with Jin Zhang's Lab
- eFP Little Millet is published, in collaboration with the Soolanayakanahally Lab
- eFP Cacao with the Guiltinan Lab in online as of July 2024
- The BAR's SequenceServer (Blast server) is updated with Mangosteen and Euphorbia sequences
- eFP Arabidopsis Gynoecium view is added in collaboration with Stefan de Folter's Lab
- BAR is designated one of just 52 Global Core Biodata Resources
- BAR FAIR-sharing page was created: <https://fairsharing.org/FAIRsharing.8c6779>
- BAR API is a new API to access data in BAR databases
- ThaleMine is updated to v5.1.0-20230710 with the latest datasets
- 400+ interactions determined by TurboID using BIN2 were added to the Arabidopsis Interactions Viewer/AIV2 database
- ASPB Plant Biology 2023 conference talk and booth in Savannah, GA, USA
- ICAR Conference 2023 in Chiba, Japan
- ASPB Plant Biology 2024 conference talk and booth in Honolulu, HI, USA
- ePlant Barley is released as two separate apps. ePlant Barley legacy and ePlant Barley with version 3 gene IDs for the "seed atlas" dataset from the Pecinka Lab
- eFP Mangosteen is a new eFP Browser on the BAR, together with the Goh Lab
- eFP Wheat abiotic stress data are added, in collaboration with the Kagale Lab
- eFP Sorghum is updated with new views in collaboration with the Ware Lab at CSHL
- ePlant Medicago LCM data are added, in collaboration with the Frugoli Lab
- ePlant Eucalyptus is published, in collaboration with Jin Zhang's Lab
- eFP Little Millet is published, in collaboration with the Soolanayakanahally Lab
- eFP Cacao with the Guiltinan Lab in online as of July 2024
- The BAR's SequenceServer (Blast server) is updated with Mangosteen and Euphorbia sequences

Publications

Jiang, Y., N'Diaye, A., Koh, C. S., Quilichini, T. D., Shunmugam, A. S. K., Kirzinger, M. W., Konkin, D., Bekkaoui, Y., Sari, E., Pasha, A., Esteban, E., Provart, N. J., Higgins, J. D., Rozwadowski, K., Sharpe, A. G., Pozniak, C. J., & Kagale, S. (2023). The coordinated regulation of early meiotic stages is dominated by non-coding RNAs and stage-specific transcription in wheat. *Plant Journal*, 114(1), 209–224. <https://doi.org/10.1111/tpj.16125>

Luna-García, V., Gallardo, J. J. B., Rethoret-Pasty, M., Pasha, A., Provart, N. J., & De Folter, S. (2023). A high-resolution gene expression map of the medial and lateral domains of the gynoecium of *Arabidopsis*. *Plant Physiology*, 195(1), 410–429. <https://doi.org/10.1093/plphys/kiad658>

Schnabel, E., Thomas, J., El-Hawaz, R., Gao, Y., Poehlman, W. L., Chavan, S., Pasha, A., Esteban, E., Provart, N., Feltus, F. A., & Frugoli, J. (2023). Laser Capture Microdissection Transcriptome Reveals Spatiotemporal Tissue Gene Expression Patterns of *Medicago truncatula* Roots Responding to Rhizobia. *Molecular Plant-microbe Interactions*, 36(12), 805–820. <https://doi.org/10.1094/mpmi-03-23-0029-r>

Wee, C., Pasha, A., Provart, N. J., Muhammad, N. a. N., Subbiah, V. K., Arita, M., & Goh, H. (2024). An eFP reference gene expression atlas for mangosteen. *Scientia Horticulturae*, 327, 112846. <https://doi.org/10.1016/j.scienta.2024.112846>

Fan, C., Lyu, M., Zeng, B., He, Q., Wang, X., Lu, M., Liu, B., Liu, J., Esteban, E., Pasha, A., Provart, N. J., Wang, H., & Zhang, J. (2024). Profiling of the gene expression and alternative splicing landscapes of *Eucalyptus grandis*. *Plant, Cell & Environment/Plant, Cell and Environment*, 47(4), 1363–1378. <https://doi.org/10.1111/pce.14814>

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*). *Plant Journal*. <https://doi.org/10.1111/tpj.16749>

Kovacik, M., Nowicka, A., Zwyrtková, J., Strejčková, B., Vardanega, I., Esteban, E., Pasha, A., Kaduchová, K., Krautsova, M., Červenková, M., Šafář, J., Provart, N. J., Simon, R., & Pecinka, A. (2024). The transcriptome landscape of developing barley seeds. *the Plant Cell*. <https://doi.org/10.1093/plcell/koae095>

Planned future activities of your project/resource

- Arabidopsis guard cell data under drought in eFP-Seq Browser
- ThaleMine data upgrade
- BAR server upgrade. We will move to new Dell PowerEdge R760 server in summer 2024
- New eFP Sorghum datasets with CSHL
- Collaborate with TAIR on MtDNA in Chromosome 2 of *Arabidopsis* for the Col-CC12/TAIR12 genome reannotation effort

Gramene: A comparative genomics and pathways resource for plants



<https://www.gramene.org>

The Gramene project –rebranded Gramene Plants– (www.gramene.org) 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/>

<http://www.sorghumbase.org/>

Prepared by

Marcela Karey Tello-Ruiz, telloruiz@cshl.edu, Cold Spring Harbor Laboratory (CSHL)

Reviewed by **Doreen Ware**, ware@cshl.edu, doreen.ware@usda.gov, USDA ARS, CSHL; **Andrew Olson**, olson@cshl.edu, CSHL; and **Sunita Kumari**, kumari@cshl.edu CSHL

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

Arabidopsis serves as one of the central model research organisms for Gramene Plants and Gramene’s crop-specific pan-genome databases. Over the past year, we released two updates for Gramene (R67 in August 2023; R68 in November 2023) and five updates for the pan-genome resources: Oryza (R7 in August 2023), Sorghum (R6 in June 2023 and R7 in March 2024), Grape (R3 in February 2024), and Maize (R4 in February 2024). In total, 35 new genomes were added across the platforms: 22 in Gramene Plants, 1 in SorghumBase, 11 in Gramene Vitis, and 1 in Gramene Maize, with orthologs/homeologs assigned to *A. thaliana*.

For genes in family trees, the Gramene search interface now displays the closest annotated homolog with a TAIR-curated description, thereby providing access to curated gene functions. Our collection of gene functional annotations from the literature, sourced from NCBI’s GeneRIF and RAP-DB, has grown to a total of 13,529 with 7,255 annotations for *A. thaliana* (an increase of 71 compared to the prior year) and 37 new annotations for *A. lyrata* (see Figure 1).

Access to these curated annotations is deployed in the “Papers” tab of the Gramene search interface. This tab presents a table of PubMed-linked publications associated with a given gene, and its annotations, utilizing Trait Ontology (TO) or Plant Ontology (PO) terms, which are searchable. Additionally, users can now submit additional gene functions through an embedded form in this tab, labeled “Add Papers” if no prior functional annotations were linked to curated publications (see Figure 1).

Arabidopsis thaliana is one of the plant outgroups included in phylogenetic analyses performed to sculpt gene family trees. It continues to be used as one of the reference dicot species for pairwise whole-genome alignments (WGAs) and synteny maps. Synteny maps with *A. thaliana* were created for the 11 new

grapevine assemblies in Gramene Vitis, as well as for teosinte Til11 in Gramene Maize (see Figure 2). WGAs between *A. thaliana* and 79 plant species (including *A. lyrata* and *A. halleri*) are available in Gramene Plants, along with three additional WGAs for *A. lyrata* with Japonica rice, B73 maize, and Medicago, and two more for *A. halleri* against rice and maize. Using the trees and WGAs, putative gene annotation artifacts (also known as contiguous gene split models) calculated for Gramene R68 based on the corresponding Gene Tree database, revealed 14 such putative split models in *A. thaliana* (31 in SorghumBase R6), 40 in *A. halleri*, and 43 in *A. lyrata*.

The electronic Fluorescent Pictograph (eFP) browsers from the Bio-Analytical Resources (BAR) were added to support curated RNA-seq-based gene expression data for Arabidopsis, sorghum, soybean, and maize genes in the latest released versions of Gramene, SorghumBase, and Gramene Maize. Arabidopsis eFPs are only available from the Gene Expression tab of the search interface in Gramene and SorghumBase. There are 26 eFP images based on the published studies of Arabidopsis which are categorized based on tissue type, growth and development, biological condition, chemical treatment, etc.

Gramene and its pan-genome sites continue to provide gene expression profiles for 18 baseline experiments for *A. thaliana* and 1 for *A. lyrata*, curated in collaboration with the EBI Expression Atlas. In addition, differential expression data for 611 experiments in Arabidopsis spp. and 13 single-cell experimental (SCE) studies in *A. thaliana*, also curated by Gramene in collaboration with the Expression Atlas are offered directly from the EBI Expression Atlas website.

We continue to host a CLIMtools portal where users can explore Genome x Environment (G x E) associations for Arabidopsis and rice. In its version 2.0, the Arabidopsis CLIMtools portal (https://www.gramene.org/CLIMtools/arabidopsis_v2.0/) encompasses 473 climate variables in 2,999 Arabidopsis accessions, RiboSNitch predictions, climate GWAS and TWAS, and hosts five R Shiny apps that provide distinct views of the data: AraCLIM, CLIMGeno, GenoCLIM, PhenoCLIM, and T-CLIM. Publications Planned future activities of your project/resource In the next year, Gramene Plants will replace temporary SNP identifiers with standard reference SNP cluster IDs (rsIDs) for *A. thaliana*. In addition, we intend to integrate GWAS results for various traits into the Gramene database. This will allow users to browse genomic loci associated with phenotypes of interest.

The 13 SCE studies in the EBI Expression Atlas will be indexed and made available to the Gramene user community in the future.

The Nottingham Arabidopsis Stock Centre (NASC)

<http://arabidopsis.info/>

Prepared by

Sean May, Director Sean.May@nottingham.ac.uk

Marcos Castellanos-Uribe, Operations Manager.



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

Orders sent from NASC increased a little to 62,892 stocks total for the 2023 calendar year (compared to ~60K for 2022). Community use has stabilised after the dip to 48K we saw in 2021 but has not yet returned to pre-covid levels (>100K).

We know that it has become increasingly difficult in recent years to send seeds between laboratories. We were ahead of that curve and have come through the painful birth of a much more complicated service on our side. For you, ordering seeds through NASC can make this process a lot easier for your laboratory – we take care of the inspections, phytosanitary certificates, and bewilderingly variable international postal regimes. So please consider donating your stocks to the centres, it may make your lives a lot easier to pass this frustrating work from your postdocs and technicians onto us.

Thank you to all those generous groups continuing to donate new stocks and populations of seed (>3200 in 2023 – more than 8 a day). We really appreciate every contact. Again, if you need help or advice donating or exporting stocks to us, please don't hesitate to get in touch with curators@arabidopsis.info.

For recipients, we send a tracking email with your order so please use this, and check that your phone/email details at NASC are current just in case DHL need to contact you (please check your spam folders). Delays in responding to emails can sometimes lead to local storage charges, which are often many times the (low) import costs. We apply for the phytosanitary certificate attached to your order and allocate the correct content codes, but local requirements beyond that can vary (especially if you need import documents). If in doubt, please check for any additional legal requirements at your local entry point/institute.

We are looking forward to the ICAR in sunny San Diego, with a new 'crop' of 'thank you' goodies to you, the community, at our booth. Come see us - but if you miss out, just look at our twitter photos: <https://twitter.com/NascArabidopsis> and ask for specific conference goodies to be included in your seed order (assuming we still have some left by then).

For up-to-date details on stock donations or anything else that you wish to know, please visit the NASC site, or contact us at any time. If we (NASC, ABRC, and RIKEN) can help you or promote your research to the community by distributing seed on your behalf, then please don't wait for us to find you – send an email, we can help.

Prepared by

Masatomo Kobayashi (masatomo.kobayashi@riken.jp)

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

Together with RIKEN CSRS, RIKEN BRC sponsored 3 Keynotes and MASC Workshop in the ICAR2023 that was held in Japan in June 2023. We intended to support face-to-face discussion among the attendees on “Arabidopsis for SDGs/4th Decadal Vision”.

The Exp-Plant Catalog (<https://plant.rtc.riken.jp/resource/home/index.html>) provides the information of plant resources provided from RIKEN BRC.

Following resources have been added to the Catalog during the past 12 months.

1. We released following three callus cell lines established from suspension cell lines. Since the original suspension cell lines are not suitable for overseas transport, we decided to provide the callus cell cultures that are stably maintained on solid culture media for overseas users. Suspension cell cultures can be easily induced from the callus cell cultures.

- rpc00110: Grape YU-1-c
- rpc00111: Arabidopsis YG1-c
- rpc00112: Arabidopsis At tom-c

2. The Exp-Plant Catalog now includes 85 lines of Arabidopsis mutant and transgenic seeds that have been newly deposited from Japanese scientists. Now the Catalog provides information of 524 individual lines in total.

3. The 201 F2 seed stocks established by crossing Arabidopsis natural accessions with Col and Ler are now available from RIKEN BRC. These natural accessions include the group IDs, gr1 and gr2. Publications Planned future activities of your project/resource The RIKEN BRC intends to support the research compatible with an increasingly inclusive and sustainable global society. For use in the studies on abiotic stress responses, Experimental Plant Division has distributed the seeds of natural accessions and their F2 progenies after crossing with Col and Ler. Now we start digging the value of natural accessions by genotype and phenotype characterization. We will establish a new database and disseminate such information to the international research community.

The Arabidopsis Information Resource

www.arabidopsis.org

Prepared by

Leonore Reiser, lreiser@arabidopsis.org, Phoenix Bioinformatics

Tanya Berardini, tberardi@arabidopsis.org, Phoenix Bioinformatics



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

Data: Genome Annotation

Tanya Berardini (TAIR) and Nick Provarit (BAR) initiated the reannotation project via Zoom in October 2022, enlisting the support of NCBI to run their annotation pipeline on a new consensus telomere to telomere assembly (https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_028009825.2/). TAIR has been coordinating the effort with a dedicated group of volunteers who have contributed a high quality, gapless reference genome including the NORs, tandem repeats and expert curation of protein coding genes, transposable elements, lncRNAs, and rDNAs. Regular updates are being provided on the TAIR website (<https://conf.phoenixbioinformatics.org/display/COM/A.+thaliana+Col-0+v12+reannotation+effort>). The genome annotations will be submitted to NCBI following completion of manual verification and quality checks. All of the participants in the effort are working on a manuscript together.

Gene Function Annotation

We continue to add new gene function data on a weekly basis including: 1222 new/updated locus summaries, 499 new/updated gene symbols, 1766 articles linked to 3677 genes, 14301 experimental Gene Ontology (GO) and Plant Ontology (PO) annotations, 131 new/updated alleles, and 232 phenotypes linked to germplasms. We regularly update InterPro domain mapping for the Arabidopsis proteins using the bimonthly updates data from UniProt.

We especially wish to acknowledge the contributions of individual authors who submitted their annotations via our Generic Ontology Annotation Tool (GOAT: goat.phoenixbioinformatics.org). TAIR gene function data and more is included in our quarterly data releases that are available from our website (<https://www.arabidopsis.org/download/index.jsp>) and Zenodo archive (<https://doi.org/10.5281/zenodo.7843882>).

Software/Tools:

TAIR website update

After over a year of development and a short period of beta testing, we released a new version of the TAIR website on May 6, 2024. The website (frontend) update follows a complete rewrite of the 'backend' to a more modern technical platform. These changes were necessary as the legacy software was becoming increasingly difficult and costly to maintain. The changes to the backend improved reliability and speed. The redesigned website is more responsive, accessible, and mobile friendly. The updated searches include new functionalities such as embedding the bulk search/ download capabilities into the Gene and Protein searches. We are continuing to iterate on the design and functionality of the TAIR website.

JBrowse2: We also installed an instance of the open source genome browser JBrowse2; a significant rewrite of the original JBrowse. Most of the tracks from JBrowse have been ported over. One of the enhancements in JBrowse2 is visualization of syntenic datasets which we plan to add over time. We are also working with the JBrowse2 community to include some favorite features of the Seqviewer nucleotide sequence view into JBrowse2.

Conferences:

TAIR hosted an update on the V12 genome annotation at the Arabidopsis Informatics workshop at PAG31 in San Diego (January 2024) and will present more updates at Plant Biology 2024 in the AgBioData Plant Bioinformatics Workshop Session (June 2024) and the Community Annotation workshop at ICAR (July 2024).

Publications:

Leonore Reiser, Erica Bakker, Sabarinath Subramaniam, Xingguo Chen, Swapnil Sawant, Kartik Khosa, Trilok Prithvi, Tanya Z. Berardini (2024) The Arabidopsis Information Resource in 2024, *Genetics*, <https://doi.org/10.1093/genetics/iyae027>

Planned future activities of your project/resource

Data: We plan to submit the V12 genome annotation to NCBI and integrate the new version into TAIR's database and tools. We will continue to maintain an Apollo instance for refining gene models. For data curation, we will continue to emphasize capturing information about new gene functions and are investigating integration of large language models into our curation pipeline.

Tools: We will continue to update and modify the design and functionality of the TAIR website based on user feedback. We encourage community members to reach out to us via email (curator@arabidopsis.org) to share their ideas/concerns/questions.

Thanks

In 2024 TAIR celebrates our 25th anniversary (est. Nov 1999). We are grateful to have had the privilege of serving the plant science community for all of these years and thank everyone for their continued support.

Countries

ARGENTINA	34
AUSTRALIA	36
AUSTRIA	38
BELGIUM	40
BRAZIL	42
CHILE	44
CHINA	45
CZECH REPUBLIC	47
ESTONIA	49
FINLAND	50
FRANCE	51
GREECE	53
ITALY	54
JAPAN	56
NEW ZEALAND	58
NORWAY	59
POLAND	60
PORTUGAL	61
SPAIN	63
SWEDEN	65
SWITZERLAND	67
UNITED KINGDOM	69
UNITED STATES and NAASC	72

ARGENTINA

Prepared by

Gabriela Auge, auge.gabriela@inta.gob.ar, Instituto de Agrobiotecnología y Biología Molecular (IABIMO) INTA-CONICET. Hurlingham, Argentina.



Rocío Tognacca, rtognacca@agro.uba.ar, Instituto de Fisiología, Biología Molecular y Neurociencias (IFIBYNE) UBA-CONICET. Buenos Aires, Argentina.

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 2023 or early 2024.

Moretti, B., Rodriguez Alvarez, S.N. & Grecco, H.E. Nfinder: automatic inference of cell neighborhood in 2D and 3D using nuclear markers. *BMC Bioinformatics* 24, 230 (2023). <https://doi.org/10.1186/s12859-023-05284-2>

Nfinder enhances pipelines for tracking cell interactions and studying tissue-level spatiotemporal correlations.

Planned events for 2024 and 2025

- XIX Congreso Latinoamericano de Genética, Congreso Nacional de Genética 2024 de la Sociedad Mexicana de Genética, LII Congreso Argentino de Genética, LVII Reunión Anual de la Sociedad de Genética de Chile, II Congreso Paraguayo de Genética, IX Congreso de la Sociedad Uruguaya de Genética, V Congreso de La Red Latinoamericana de Genética Humana-RELAGH. October 21-24, 2024. Guadalajara, Mexico.
- Plant Biology Lectures Series 2024. 16-18 October 2024, Rosario, Argentina.
- LX Reunión Anual de la Sociedad Argentina de Investigación Bioquímica y Biología Molecular (SAIB). November 5-8, 2024. Córdoba, Argentina.
- 2° Congreso Argentino de Semillas. November 28-29, 2024, Córdoba, Argentina.
- XXXV Reunión Argentina de Fisiología Vegetal. September, 2025. Mar del Plata, Argentina.
- XL Jornadas Argentinas de Botánica, September, 2025. Mar del Plata, Argentina.
- 4° Reunión Argentina de Biología de Semillas (RABioS), November, 2025. Concepción del Uruguay, Argentina.
- 31° Reunión Argentina de Ecología. October, 2025.

Selected Publications

Leonardo A Arias, Sebastián D'Ippolito, Jéscica Frik, Natalia L Amigo, Fernanda Marchetti, Claudia A Casalongué, Gabriela C Pagnussat, Diego F Fiol, The DC1 Domain Protein BINUCLEATE POLLEN is Required for POLLEN Development in *Arabidopsis thaliana*, *Plant and Cell Physiology*, Volume 63, Issue 12, December 2022, Pages 1994–2007, <https://doi.org/10.1093/pcp/pcac122>

This study identified BNP, a gene coding for a DC1 domain protein, which is required for pollen development and germination by interacting with VOZ1 and VOZ2.

Torres, J. R., Botto, J. F., & Sanchez, D. H. (2024). Canonical transcriptional gene silencing may contribute to long-term heat response and recovery through MOM1. *Plant, Cell & Environment*, 47(1), 372-382. <https://doi.org/10.1111/pce.14722>

This study led by an early-career researcher shows that a canonical TGS factor may play a role in plant acclimation and recovery from prolonged heat stress, despite the induced epigenetic disturbances.

Pereyra, M. E., Costigliolo Rojas, C., Jarrell, A. F., Hovland, A. S., Snipes, S. A., Nagpal, P., ... & Casal, J. J. (2023). PIF4 enhances the expression of SAUR genes to promote growth in response to nitrate. *Proceedings of the National Academy of Sciences*, 120(39), e2304513120. <https://doi.org/10.1073/pnas.2304513120>

This work from a group with proved tracking record of publications sheds light on a novel mechanism that integrates nutrient and growth pathways during the promotion of plant stature, offering insights for genetically modifying plant height without reducing nitrogen use efficiency.

Mammarella, M. F., Lucero, L., Hussain, N., Muñoz-Lopez, A., Huang, Y., Ferrero, L., ... & Ariel, F. (2023). Long noncoding RNA-mediated epigenetic regulation of auxin-related genes controls shade avoidance syndrome in *Arabidopsis*. *The EMBO Journal*, 42(24), e113941. <https://doi.org/10.15252/embj.2023113941>

Another excellent paper from a highly prolific and highly collaborative group on the role of the lncRNA APOLO on the regulation of SAS by modulating auxin signaling in response to far-red light, highlighting its potential as a bioactive molecule for agricultural applications.

Canal, María Victoria, Natanael Mansilla, Diana E. Gras, Agustín Ibarra, Carlos M. Figueroa, Daniel H. Gonzalez, and Elina Welchen. "Cytochrome c levels affect the TOR pathway to regulate growth and metabolism under energy-deficient conditions." *New Phytologist* 241, no. 5 (2024): 2039-2058. <https://doi.org/10.1111/nph.19506>

This work led by an outstanding female researcher shows that CYTc-deficient plants adjust growth by reducing the TOR-pathway activation as a preventive signal to adjust growth in anticipation of energy exhaustion.

Huynh, S. D., Melonek, J., Colas des Francs-Small, C., Bond, C. S., & Small, I. (2023). A unique C-terminal domain contributes to the molecular function of Restorer-of-fertility proteins in plant mitochondria. *New Phytol*, 240(2), 830-845. <https://doi.org/10.1111/nph.19166>

Khan, M. A., Herring, G., Zhu, J. Y., Oliva, M., Fourie, E., Johnston, B., Zhang, Z., Potter, J., Pineda, L., Pflueger, J., Swain, T., Pflueger, C., Lloyd, J. P. B., Secco, D., Small, I., Kidd, B. N., & Lister, R. (2024). CRISPRi-based circuits to control gene expression in plants. *Nat Biotechnol*. <https://doi.org/10.1038/s41587-024-02236-w>

Pinto, S. C., Leong, W. H., Tan, H., McKee, L., Prevost, A., Ma, C., Shirley, N. J., Petrella, R., Yang, X., Koltunow, A. M., Bulone, V., Kanaoka, M. M., Higashiyama, T., Coimbra, S., & Tucker, M. R. (2024). Germline beta-1,3-glucan deposits are required for female gametogenesis in *Arabidopsis thaliana*. *Nat Commun*, 15(1), 5875. <https://doi.org/10.1038/s41467-024-50143-0>

Sureshkumar, S., Bandaranayake, C., Lv, J., Dent, C. I., Bhagat, P. K., Mukherjee, S., Sarwade, R., Atri, C., York, H. M., Tamizhselvan, P., Shamaya, N., Folini, G., Bergey, B. G., Yadav, A. S., Kumar, S., Grummisch, O. S., Saini, P., Yadav, R. K., Arumugam, S., . . . Balasubramanian, S. (2024). SUMO protease FUG1, histone reader AL3 and chromodomain protein LHP1 are integral to repeat expansion-induced gene silencing in *Arabidopsis thaliana*. *Nat Plants*, 10(5), 749-759. <https://doi.org/10.1038/s41477-024-01672-5>

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

Marie-Theres Hauser, marie-theres.hauser@boku.ac.at , University of Natural Resources and Life Sciences, Vienna (BOKU)

J. Matthew Watson, james.watson@gmi.oeaw.ac.at, Gregor Mendel Institute of Molecular Plant Biology



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 24.-27.09.2024 in Vienna at BOKU
- Plant Chromosome Biology (<https://plantcyto2025.univie.ac.at/>) will take place 15.-17. 2025 Vienna BioCenter, AUSTRIA
- EMBO conference Plant Evolution: From Origins to Diversification on Land will take place 25-27.11.25 at the Gregor Mendel Institute of Molecular Plant Biology (GMI) in Vienna, AUSTRIA <https://coming-soon.embo.org/w25-18>

Selected Publications

Gabriele Bradamante, Vu Hoang Nguyen, Marco Incarbone, Zohar Meir, Heinrich Bente, Mattia Donà, Nicole Lettner, Ortrun Mittelsten Scheid, Ruben Gutzat (2024) Two ARGONAUTE proteins loaded with transposon-derived small RNAs are associated with the reproductive cell lineage in Arabidopsis. *Plant Cell*. 36(4):863-880. doi: 10.1093/plcell/koad295.

This publication reports that ARGONAUTE proteins AGO5 and AGO9, which carry small RNAs from highly methylated transposons, mark sexually reproductive cells in Arabidopsis, indicating an early segregating germline similar to animals.

Marco Incarbone Gabriele Bradamante, Florian Pruckner, Tobias Wegscheider, Wilfried Rozhon, Vu Nguyen, Ruben Gutzat, Zsuzsanna Mérai, Thomas Lendl, Stuart MacFarlane, Michael Nodine, Ortrun Mittelsten Scheid (2023) Salicylic acid and RNA interference mediate antiviral immunity of plant stem cells.*Proc Natl Acad Sci U S A*. 120(42):e2302069120. doi: 10.1073/pnas.2302069120.

This study shows that, RNA interference (RNAi) amplified by an RNA-dependent RNA polymerase activated by salicylic acid prevents viral proliferation in stem cells, providing a crucial mechanism for stem cell immunity against several RNA viruses, despite their ability to suppress RNAi in other plant tissues.

Benjamin Jaegle, Rahul Pisupati, Luz Mayela Soto-Jiménez, Robin Burns, Fernando A Rabanal, Magnus Nordborg (2023) Extensive sequence duplication in Arabidopsis revealed by pseudo-heterozygosity. *Genome Biol*. 24(1):44.doi: 10.1186/s13059-023-02875-3.

The study found that most heterozygous SNP calls in Arabidopsis are artifacts, emphasizes caution with short-read sequencing SNP data, and highlights that significant copy-number variation in genes suggests future analyses with independently assembled genomes.

Bhagyshree Jamge, Zdravko J Lorković, Elin Axelsson, Akihisa Osakabe, Vikas Shukla, Ramesh Yelagandula, Svetlana Akimcheva, Annika Luisa Kuehn, Frédéric Berger (2023) Histone variants shape chromatin states in Arabidopsis. *Elife*:12:RP87714. doi: 10.7554/eLife.87714.

This study reveals that histone variants, particularly H2A variants, play a crucial role in organizing chromatin states in Arabidopsis by interacting with histone modifications, and that the chromatin remodeler DDM1 is essential for the exchange of histone variants, affecting chromatin state distribution.

Lorenzo Picchianti, Víctor Sánchez de Medina Hernández, Ni Zhan, Nicholas At Irwin, Roan Groh, Madlen Stephani, Harald Hornegger, Rebecca Beveridge, Justyna Sawa-Makarska, Thomas Lendl, Nenad Grujic, Christin Naumann, Sascha Martens, Thomas A Richards, Tim Clausen, Silvia Ramundo, G Elif Karagöz, Yasin Dagdas (2023)

Shuffled ATG8 interacting motifs form an ancestral bridge between UFMylation and autophagy. *EMBO J.* 42(10):e112053. doi: 10.15252/embj.2022112053. Epub 2023 Feb 10.

This study reveals that UFMylation by UFM1 is crucial for ER homeostasis by triggering C53-mediated autophagy in response to stalled translation and highlights the evolutionary conservation across eukaryotes, excluding fungi and some algae.

Mattia Donà, Gabriele Bradamante, Zorana Bogojevic, Ruben Gutzat, Susanna Streubel, Magdalena Mosiolek, Liam Dolan, Ortrun Mittelsten Scheid (2023) A versatile CRISPR-based system for lineage tracing in living plants *Plant J.* 115:1169-1184. doi: 10.1111/tj.16378.

This publication uses CRISPR to trace cell lineages in living plants by correcting a frameshift mutation to restore fluorescent protein expression, with Cas9 activity controlled by tissue-specific and inducible promoters..

Jakob Weiszmann, Dirk Walther, Pieter Clauw, Georg Back, Joanna Gunis, Ilka Reichardt, Stefanie Koemeda, Jakub Jez, Magnus Nordborg, Jana Schwarzerova, Iro Pierides, Thomas Nägele, Wolfram Weckwerth (2023) Metabolome plasticity in 241 Arabidopsis thaliana accessions reveals evolutionary cold adaptation processes. *Plant Physiol.* 193(2):980-1000. doi: 10.1093/plphys/kiad298.

The study used natural accessions and two temperatures to determine with machine learning tool the predictive power of natural metabolic variation among accessions. They report that the plasticity of metabolic regulation is predictable from the genome and epigenome and driven evolutionarily by growth habitats.

Ivan Kulich, Julia Schmid, Anastasia Teplova, Linlin Qi, Jiří Friml (2024) Rapid translocation of NGR proteins driving polarization of PIN-activating D6 protein kinase during root gravitropism. *Elife*:12:RP91523. doi: 10.7554/eLife.91523.

The study found that localization of the NEGATIVE GRAVITROPIC RESPONSE OF ROOTS 1 (NGR1) on the statolith surface and plasma membrane (PM) domains is indispensable for NGR1 functionality. A rapid, NGR-dependent translocation of PIN-activating AGCVIII kinase D6PK towards lower PMs of gravity-perceiving cells might be the reason for the rapid redirection of auxin fluxes following gravistimulation.

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

Moritz K. Nowack moritz.nowack@vib.be VIB-UGent Center for Plant Systems
Biology, Ghent, Belgium



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 2023 or early 2024.

- 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 2024 and 2025

35th ICAR, Ghent, Belgium. June 16th-20th 2025. www.icar2025.com

Selected Publications

Schoenaers S, Lee HK, Gonneau M, Faucher E, Levasseur T, Akary E, Claeijs N, Moussu S, Broyart C, Balcerowicz D, AbdElgawad H, Bassi A, Damineli DSC, Costa A, Feijó JA, Moreau C, Bonnin E, Cathala B, Santiago J, Höfte H, Vissenberg K."Rapid alkalization factor 22 has a structural and signalling role in root hair cell wall assembly." *Nat Plants*. 2024 Mar;10(3):494-511. doi: 10.1038/s41477-024-01637-8.

This study reveals the dual role of the peptide RAF22 in controlling root tip growth by functioning as a structural component organizing cell wall architecture and as a feedback signalling molecule that regulates this process depending on its interaction partners.

Morales-Herrera S, Jourquin J, Coppé F, Lopez-Galvis L, De Smet T, Safi A, Njo M, Griffiths CA, Sidda JD, Mccullagh JSO, Xue X, Davis BG, Van der Eycken J, Paul MJ, Van Dijck P, Beeckman T. "Trehalose-6-phosphate signaling regulates lateral root formation in *Arabidopsis thaliana*." *Proc Natl Acad Sci U S A*. 2023 Oct 3;120(40):e2302996120. doi: 10.1073/pnas.2302996120.

This work uncovers a tissue-specific network during the early phase of LR formation that balances energy status with auxin signaling using trehalose 6-phosphate as a signaling molecule.

Safi A, Smagghe W, Gonçalves A, Wang Q, Xu K, Fernandez AI, Cappe B, Riquet FB, Mylle E, Eeckhout D, De Winne N, Van De Slijke E, Persyn F, Persiau G, Van Damme D, Geelen D, De Jaeger G, Beeckman T, Van Leene J, Vanneste S. “Phase separation-based visualization of protein-protein interactions and kinase activities in plants.” *Plant Cell*. 2023 Sep 1;35(9):3280-3302. doi: 10.1093/plcell/koad188.

This article presents the SYnthetic Multivalency in PLants (SYMPL)-vector set as a tool to assay protein–protein interactions and kinase activity in planta based on phase separation.

Wang Y, Perez-Sancho J, Platre MP, Callebaut B, Smokvarska M, Ferrer K, Luo Y, Nolan TM, Sato T, Busch W, Benfey PN, Kvasnica M, Winne JM, Bayer EM, Vukašinović N, Russinova E. “Plasmodesmata mediate cell-to-cell transport of brassinosteroid hormones.” *Nat Chem Biol*. 2023 Nov;19(11):1331-1341. doi: 10.1038/s41589-023-01346-x.

This study demonstrates that plasmodesmata are responsible for short-distance transport of brassinosteroid phytohormones between neighboring cells, and that brassinosteroids can autoregulate their own motility by modulating the permeability of plasmodesmata.

Nguyen TH, Thiers L, Van Moerkercke A, Bai Y, Fernández-Calvo P, Minne M, Depuydt T, Colinas M, Verstaen K, Van Isterdael G, Nützmänn HW, Osbourn A, Saeys Y, De Rybel B, Vandepoele K, Ritter A, Goossens A. “A redundant transcription factor network steers spatiotemporal Arabidopsis triterpene synthesis.” *Nat Plants*. 2023 Jun;9(6):926-937. doi: 10.1038/s41477-023-01419-8.

This paper describes the gene regulatory network in *Arabidopsis thaliana* that regulates cell-specific biosynthesis of triterpenes, a class of specialized metabolites that modulate developmental and ecological functions and comprise many therapeutic and other high-value compounds

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

Wagner L. Araújo

Departamento de Biologia Vegetal Universidade Federal de Viçosa 36570-900
Viçosa, MG, Brazil wlaraujo@ufv.br

Adriano Nunes Nesi

Departamento de Biologia Vegetal Universidade Federal de Viçosa 36570-900 Viçosa, MG, Brazil nunesnesi@ufv.br



Planned events for 2024 and 2025

XIX Brazilian Congress of Plant Physiology,
Viçosa, Minas Gerais, Brazil, from October 7 to 12, 2024.

Selected Publications

Romero JM, Serrano-Bueno G, Camacho-Fernández C, Vicente MH, Ruiz MT, Pérez-Castiñeira JR, Pérez-Hormaeche J, Nogueira FTS, Valverde F. CONSTANS, a HUB for all seasons: How photoperiod pervades plant physiology regulatory circuits. *Plant Cell*. 2024 May 29;36(6):2086-2102. doi: 10.1093/plcell/koae090. PMID: 38513610; PMCID: PMC11132886.

This review is dedicated to the functions of the protein CONSTANS (CO) other than photoperiodic flowering in different plant species, further providing relevant ideas about CO protein structure and function, and in the evolution of photoperiodic sensing. Finally, the authors also discuss recent advances in agricultural and biotechnological applications of CONSTANS and its structural homologs, the CONSTANS-like (COL) genes.

Kfoury B, Rodrigues WFC, Kim SJ, Brandizzi F, Del-Bem LE. Multiple horizontal gene transfer events have shaped plant glycosyl hydrolase diversity and function. *New Phytol*. 2024 Apr;242(2):809-824. doi: 10.1111/nph.19595. Epub 2024 Feb 28. PMID: 38417454

This work sheds light on the macroevolutionary processes that have shaped the glycosyl hydrolases (GHs) repertoire in plants, highlighting the acquisition of GH families through horizontal transfer and the role of GHs in plant adaptation and defense mechanisms.

Pougy KC, Sachetto-Martins G, Almeida FCL, Pinheiro AS. 1 H, 15 N, and 13 C backbone and side chain resonance assignments of the cold shock domain of the *Arabidopsis thaliana* glycine-rich protein AtGRP2. *Biomol NMR Assign*. 2023 Jun;17(1):143-149. doi: 10.1007/s12104-023-10133-7. Epub 2023 May 5. PMID: 37145295.

This study investigate the mechanisms by which AtGRP2 (*Arabidopsis thaliana* glycine-rich protein 2), a 19-kDa RNA-binding glycine-rich protein that regulates key processes in *A. thaliana*, specifically binds its RNA targets. The authors were able to report here the sequence-specific resonance assignments of AtGRP2-CSD as a first step toward its structural, dynamics, and RNA binding characterization by NMR.

Souza PVL, Hou LY, Sun H, Poeker L, Lehman M, Bahadar H, Domingues-Junior AP, Dard A, Bariat L, Reichheld JP, Silveira JAG, Fernie AR, Timm S, Geigenberger P, Daloso DM. Plant NADPH-dependent thioredoxin reductases are crucial for the metabolism of sink leaves and plant acclimation to elevated CO₂. *Plant Cell Environ.* 2023 Aug;46(8):2337-2357. doi: 10.1111/pce.14631. Epub 2023 Jun 2. PMID: 37267089.

This study revealed that a previously unknown role of the NADPH-thioredoxin reductases (NTR) system in regulating sink leaf metabolism and plant acclimation to high CO₂ conditions

Barros JAS, Cavalcanti JHF, Pimentel KG, Magen S, Soroka Y, Weiss S, Medeiros DB, Nunes-Nesi A, Fernie AR, Avin-Wittenberg T, Araújo WL. The interplay between autophagy and chloroplast vesiculation pathways under dark-induced senescence. *Plant Cell Environ.* 2023 Dec;46(12):3721-3736. doi: 10.1111/pce.14701. Epub 2023 Aug 24. PMID: 37615309.

By using a combination of genetic and biochemical approaches, this study revealed the significance of the chloroplast vesiculation pathway on the metabolic responses to induced senescence

Major Funding Sources

- 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)

CHILE



Prepared by

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

Planned events for 2024 and 2025

- XLVII Reunión Anual 2024 Sociedad de Bioquímica y Biología Molecular de Chile (SBBMCh). La Serena, Chile, 30 sep – 4 Oct. 2024.

A meeting hosted by the Chilean Society of Biochemistry and Molecular Biology. It included talks, symposiums, and poster presentations. This year the society celebrates 50th years.

Organizer: Chilean Society of Biochemistry and Molecular Biology (<https://www.sbbmch.cl/annual-meeting-2024/>)

Selected Publications

Shanks CM, Rothkegel K, Brooks MD, Cheng CY, Alvarez JM, Ruffel S, Krouk G, Gutiérrez RA, Coruzzi GM. Nitrogen sensing and regulatory networks: it's about time and space. *Plant Cell*. 2024 May 1;36(5):1482-1503. doi: 10.1093/plcell/koae038. PMID: 38366121; PMCID: PMC11062454. (<https://academic.oup.com/plcell/article/36/5/1482/7608181>)

Up to date review on N nutrition.

Ibeas MA, Salinas-Grenet H, Johnson NR, Pérez-Díaz J, Vidal EA, Alvarez JM, Estevez JM. Filling the gaps on root hair development under salt stress and phosphate starvation using current evidence coupled with a meta-analysis approach. *Plant Physiol*. 2024 Jun 26:kiae346. doi: 10.1093/plphys/kiae346. Epub ahead of print. PMID: 38918899. (<https://academic.oup.com/plphys/advance-article/doi/10.1093/plphys/kiae346/7699132>)

A meta-analysis on existing evidence related to plant response to multiple combined stresses using as model Pi deficiency and salt stress.

Major Funding Sources

ANID (Agencia Nacional de Investigación y Desarrollo
(<https://www.anid.cl/>)

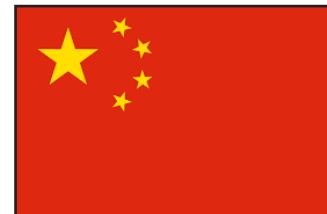
Iniciativa Científica Milenio
(<http://www.iniciativamilenio.cl/>)

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 2023 or early 2024.

- 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>
- RLKdb: A curated database of plant receptor-like kinase families <https://biotec.njau.edu.cn/rlkdb/>
- 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 2024 and 2025

- 2024 International Conference on Molecular Plant Sciences, August 8-12, 2024, Shanghai (<http://www.molplant.org.cn/icmps2024>)
- 2024 Annual Meeting of the Chinese Society for Plant Biology, August 25-29, 2024, Chengdu, Sichuan
- 2024 National Congress of Plant Biology, November 16-19, 2023, Guangzhou, Guangdong (<http://ncpb.net/>)

Selected Publications

Chen JY, Yu RB, Li N, Deng ZG, Zhang XX, Zhao YR, Qu CF, Yuan YF, Pan ZX, Zhou YY, Li KL, Wang JJ, Chen ZR, Wang XY, Wang XL, He SN, Dong J, Deng XW, Chen HD (2023). Amyloplast sedimentation re-polarizes LAZYs to achieve gravity sensing in plants. *Cell* 186, 4788-4802.

This study identifies a molecular mechanism for gravity sensing in plants involving LAZY protein phosphorylation and interaction with chloroplast translocons, leading to asymmetrical auxin distribution and root growth.

Huang F, Luo X, Ou Y, Gao ZX, Tang QM, Chu ZZ, Zhu XG, He YH (2023). Control of histone demethylation by nuclear-localized α -ketoglutarate dehydrogenase. *Science* 381, eadf8822.

This study discovered that the mitochondrial enzyme KGDH, which normally participates in the respiratory tricarboxylic acid cycle, can also inhibit histone demethylases in the nucleus, thereby affecting gene expression by altering histone methylation.

Lan ZJ, Song ZH, Wang ZJ, Li L, Liu YQ, Zhi SH, Wang RH, Wang JZ, Li QY, Bleckmann A, Zhang L, Dresselhaus T, Dong J, Gu HY, Zhong S, Qu LJ (2023). Antagonistic RALF peptides control an inter-generic hybridization barrier on Brassicaceae stigmas. *Cell* 186, 4773-4787.

This study reveals a “lock-and-key” system involving receptor-like kinases and cell wall proteins interacting with stigmatic peptides, which controls pollen tube penetration and can be manipulated to facilitate broad hybridization in crops.

Meng JG, Xu YJ, Wang WQ, Yang F, Chen SY, Jia PF, Yang WC, Li HJ (2023). Central-cell-produced attractants control fertilization recovery. *Cell* 186, 3593-3605.

This study reveals a female gamete-attraction system involving the secretion of peptides SALVAGER1 and SALVAGER2, which enhance fertilization recovery and reproductive assurance when initial pollen tube attraction fails.

Yu YQ, Tang WX, Lin WW, Li W, Zhou X, Li Y, Chen R, Zheng R, Qin GC, Cao WH, Pérez-Henríquez P, Huang RF, Ma J, Qiu QQ, Xu ZW, Zou AL, Lin JC, Jiang LW, Xu TD, Yang ZB (2023). ABLs and TMKs are co-receptors for extracellular auxin. *Cell* 186, 5457-5471.

This study identifies ABL1 and ABL2 as new auxin-binding proteins that function as co-receptors with TMKs and ABP1, providing a clearer understanding of extracellular auxin perception in plants.

Zhao Y, Shi H, Pan Y, Lyu MH, Yang ZX, Kou XX, Deng XW, Zhong SW (2023). Sensory circuitry controls cytosolic calcium-mediated phytochrome B phototransduction. *Cell* 186, 1230-1243.

Red light induces a rapid increase in cytosolic Ca²⁺, which is crucial for the nuclear translocation of phytochrome B, thereby facilitating the cotyledon opening and expansion of etiolated Arabidopsis seedlings during the transition from darkness to light.

Major Funding Sources

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

CZECH REPUBLIC

Prepared by

Viktor Žárský viktor@natur.cuni.cz

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 2023 or early 2024.

Authors from the lab of Kamil Růžička (Inst. Of Exp. Bot., Czech Acad. Of Sci.) in this paper - Timofeyenko K, Kanavalau D, Alexiou P, Kalyna M, Růžička K. 2023. Catsnap: a user-friendly algorithm for determining the conservation of protein variants reveals extensive parallelisms in the evolution of alternative splicing. *New Phytologist* 238(4):1722-1732. DOI: 10.1111/nph.18799

Describe a new tool they developed to search for the conservation of protein variants – CATSNAP at <https://catsnap.cesnet.cz/>.

Planned events for 2024 and 2025

- SEB/Soc. Of Exp. Biol. Conference 2024 – Prague, 2 – 5 July, Czech Republic
- EMBO workshop – Plant genome stability and change 2024 – Olomouc, 16 – 19 June, Czech republic (organizer Aleš Pečinka – Inst. Of Exp. Bot., Czech Acad. Of Sci.)
- European Plant Cytoskeletal Club/EPCC meeting 2024 Prague, from 27–28 June 2024, Prague, Czech Republic (organizer Kateřina Schwarzerová, Dept. of Exp. Bot., Fac. Of Science, Charles university, Prague)
- Green for Good VIIth meeting 2025 – Olomouc, from 1- 4 September, Czech republic. **Selected**

Publications

Serre, N. B. C., Wernerová, D., Vittal, P., Dubey, S. M., Medvecká, E., Jelínková, A., Petrášek, J., Grossmann, G., & Fendrych, M. (2023). The AUX1-AFB1-CNGC14 module establishes a longitudinal root surface pH profile. *eLife*, 12, e85193. <https://doi.org/10.7554/eLife.85193>

Using new probe details of pH profile dynamics related to root growth and gravitropic response is described.

Crhak Khaitova, L., Mikulkova, P., Pecinkova, J., Kalidass, M., Heckmann, S., Lermontova, I., & Riha, K. (2024). Heat stress impairs centromere structure and segregation of meiotic chromosomes in Arabidopsis. *eLife*, 12, RP90253. <https://doi.org/10.7554/eLife.90253>

Meiotic centromeres in Arabidopsis are highly sensitive to heat stress, and suggest that centromeres and kinetochores may represent a critical bottleneck in plant adaptation to increasing temperatures.

Martinek, J., Cifrová, P., Vosolsobě, S., García-González, J., Malínská, K., Mauzerová, Z., Jelínková, B., Krtková, J., Sikorová, L., Leaves, I., Sparkes, I., & Schwarzerová, K. (2023). ARP2/3 complex associates with peroxisomes to participate in pexophagy in plants. *Nature plants*, 9(11), 1874–1889. <https://doi.org/10.1038/s41477-023-01542-6>

Participation of ARP2/3 complex is uncovered.

Huebbers, J. W., Caldarescu, G. A., Kubátová, Z., Sabol, P., Levecque, S. C. J., Kuhn, H., Kulich, I., Reinstädler, A., Büttgen, K., Manga-Robles, A., Mérida, H., Pauly, M., Panstruga, R., & Žárský, V. (2024). Interplay of EXO70 and MLO proteins modulates trichome cell wall composition and susceptibility to powdery mildew. *The Plant cell*, 36(4), 1007–1035. <https://doi.org/10.1093/plcell/koad319>

Functional interaction between exocyst complex and MLOs in plant exocytosis is uncovered.

Fulneček, J., Klimentová, E., Cairo, A., Bukovcakova, S. V., Alexiou, P., Prokop, Z., & Riha, K. (2023). The SAP domain of Ku facilitates its efficient loading onto DNA ends. *Nucleic acids research*, 51(21), 11706–11716. <https://doi.org/10.1093/nar/gkad850>

That speed of conserved DNA repair Ku is not the decisive factor in stabilizing telomere or double-strand break DNA structures

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.

1. Czech Science Foundation/GAČR, Prague (<http://www.gacr.cz>)

2. 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.

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

4. 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/>)

ESTONIA

Prepared by

Hanna Hõrak, hanna.horak@ut.ee, Institute of Technology, University of Tartu,
Nooruse 1, 50411, Tartu, Estonia



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 2023 or early 2024.

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

Yeh et al, 2023, MPK12 in stomatal CO₂ signaling: function beyond its kinase activity, *New Phytologist*

The study shows that the function of MPK12, a key kinase involved in mediating stomatal CO₂ signalling, does not depend on its kinase activity.

Koolmeister et al, 2024, Stomatal CO₂ responses at sub- and above-ambient CO₂ levels employ different pathways in Arabidopsis, *Plant Physiology*

The study shows that different guard cell signalling components mediate stomatal CO₂ responses under sub- and above-ambient CO₂ concentration ranges.

Tulva et al, 2023, Plants lacking OST1 show conditional stomatal closure and wildtype-like growth sensitivity at high VPD, *Physiologia Plantarum*

The study shows that normally high VPD-insensitive plants that lack OST1, a key kinase involved in stomatal VPD responses, acquire stomatal sensitivity to high VPD when grown under reduced soil water content.

Major Funding Sources

Estonian Research Council, www.etag.ee

FINLAND



Prepared by

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

Planned events for 2024 and 2025

Centre of Excellence in Tree Biology, located in University of Helsinki, is organizing a conference called Plants in a Changing World, 25-27th September 2024

<https://www.helsinki.fi/en/researchgroups/viikki-plant-science-centre/plants-in-a-changing-world-2024>

Selected Publications

Ivanauskaite, A., Rantala, M., Laihonen, L., Konert, M., Schwenner N., Mühlenbeck, J., Finkemeier, I. and Mulo, P. (2023) Loss of chloroplast GNAT acetyltransferases results in distinct metabolic phenotypes in Arabidopsis. *Plant and Cell Physiology* 64, 549-563.

Chloroplast acetyltransferases have an impact on the accumulation of metabolites in plant leaves.

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.

The photosynthetic machinery of Arabidopsis stems differs from that of other green tissues, and each Arabidopsis organ possesses unique transcript profile.

Waszczak C, Yarmolinsky D, Leal Gavarrón M, Vahisalu T, Sierla M, Zamora O, Carter R, Puukko T, Sipari N, Lamminmäki A, Durner J, Ernst D, Winkler JB, Paulin L, Auvinen P, Fleming AJ, Andersson MX, Kollist H, Kangasjärvi J. (2024) Synthesis and import of GDP-L-fucose into the Golgi affect plant–water relations. *New Phytologist* 241:747–763

Blocking the synthesis of GDP-L-fucose, or its import into the Golgi apparatus, leads to uncontrolled transpiration of water from leaf tissues.

Bourdon M, Lyczakowski JJ, Cresswell R, Amsbury S, Vilaplana F, Le Guen MJ, Follain N, Wightman R, Su C, Alatorre-Cobos F, Ritter M, Liszka A, Terrett OM, Yadav SR, Vatén A, Nieminen K, Eswaran G, Alonso-Serra J, Müller KH, Iuga D, Miskolczi PC, Kalmbach L, Otero S, Mähönen AP, Bhalerao R, Bulone V, Mansfield SD, Hill S, Burgert I, Beaugrand J, Benitez-Alfonso Y, Dupree R, Dupree P, Helariutta Y. (2023) Ectopic callose deposition into woody biomass modulates the nano-architecture of microfibrils. *Nat Plants*. 9:1530-1546.

Overproduction of callose in wood leads to altered wood composition both in Arabidopsis and poplar.

Major Funding Sources

Research Council of Finland: <https://www.aka.fi/en/>

Jane and Aatos Erkkö Foundation: <http://www.jaes.fi>.

The Ella and Georg Ehrnrooth Foundation <https://www.ellageorg.fi/en>

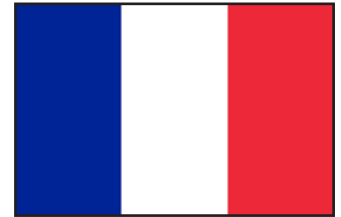
The Finnish Cultural Foundation <https://skr.fi/en>

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 2023 or early 2024.

- Arabidopsis stock center, <https://publiclines.versailles.inrae.fr/>
- ATOMEdb: Arabidopsis thaliana ORFeome database, <http://tools.ips2.u-psud.fr/ATOMEdb>
- <https://cnrgv.toulouse.inra.fr/Library/Arabidopsis>
- PHENOPSIS, <https://bioweb.supagro.inrae.fr/phenopsis/Accueil.php?lang=En> and PHENOSCOPE (<http://www.ijpb.versailles.inra.fr/en/plateformes/ppa/index.html>) are high-throughput automated phenotyping platforms at Montpellier and Versailles
- SPS tools for Functional Genomics <https://eng-saclay-plant-sciences.hub.inrae.fr/infrastructures>

Planned events for 2024 and 2025

- PLANT SCIENCES IN THE ANTHROPOCENE, from March 24 to April 04, 2025, at Université Paris-Saclay, France - The objective of this workshop is to address key challenges for the international plant science community, from basic sciences to socio-economic and environmental aspects including climate change. <https://www.institut-pascal.universite-paris-saclay.fr/en/scientific-programs/plant-sciences-anthropocene>
- PERSPECTIVES ON PROTEIN NETWORKS IN PLANTS, Ibmp-cnrs, Strasbourg, France, September 19 - 20, 2024. <https://pnp2024.sciencesconf.org>
- Post-transcriptional Gene Regulations in Plants (PGRP), September 3-5, 2024, Banyuls/mer, France. <https://pgrp2024.sciencesconf.org>
- 13TH INTERNATIONAL PLANT COLD HARDINESS SEMINAR (IPCHS), Clermont-Ferrand, France, August 26 - 30, 2024? <https://ipchs13.seminaire.inrae.fr>
- EPIPLANT/SEB 2024 the conference will start Wednesday, 10th-12th of July 2024 at Clermont Ferrand, France. <https://www.sebiology.org/events/epiplant-seb-2024.html>
- 5TH EPICATCH MEETING Bordeaux university, France, July 10 - 12, 2024 <https://epicatch5.sciencesconf.org>
- 14th International Conference of the French Society of Plant Biology 12 to 14 of June 2024, Bordeaux. <https://sciences-environnement.u-bordeaux.fr/evenements/14th-international-conference-french-society-plant-biology>
- The 16th International Conference on Reactive Oxygen and Nitrogen Species in Plants will take place in Antibes, France, on 29,-31 May 2024. <https://www.alphavisa.com/pog/2024/index.php>
- IJPB SYMPOSIUM 2024 - PLANT MODELING: OPPORTUNITIES AND CHALLENGES, 13-15 may 2024 / IJPB for Plant Sciences, Versailles-Saclay, <https://ijpb-plant-sciences.symposium.inrae.fr/>

Selected Publications

Steven Moussu et al. Plant cell wall patterning and expansion mediated by protein-peptide polysaccharide interaction. *Science* 382, 719-725 (2023). DOI:10.1126/science.adi4720

Huy Cuong Tran et al. An mTRAN-mRNA interaction mediates mitochondrial translation initiation in plants. *Science*, 381, eadg0995 (2023). DOI:10.1126/science.adg0995

Lian, Q., et al. A pan-genome of 69 *Arabidopsis thaliana* accessions reveals a conserved genome structure throughout the global species range. *Nat Genet* 56, 982–991 (2024). Doi :10.1038/s41588-024-01715-9

Arrivé, M. et al. A tRNA-modifying enzyme facilitates RNase P activity in *Arabidopsis* nuclei. *Nat. Plants* 9, 2031–2041 (2023). DOI : 10.1038/s41477-023-01564-0

Vrielynck, et al. SCEP1 and SCEP2 are two new components of the synaptonemal complex central element. *Nat. Plants* 9, 2016–2030 (2023). DOI : 10.1038/s41477-023-01558-y

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/](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.

GREECE



Prepared by

Stamatis Rigas srigas@aua.gr Agricultural University of Athens

Selected Publications

Isaioglou I, Podia V, Velentzas AD, Kapolas G, Beri D, Karampelias M, Plitsi PK, Chatzopoulos D, Samakovli D, Roussis A, Merzaban J, Milioni D, Stravopodis DJ, Haralampidis K. 2024. APRF1 interactome reveals HSP90 as a new player in the complex that epigenetically regulates flowering time in *Arabidopsis thaliana*. *Int. J. Mol. Sci.* 25, 1313.

The interactome of APRF1 includes proteins that are localized in several subcellular compartments and are implicated in multiple biological processes.

Liu C, Mentzelopoulou A, Muhammad A, Volkov A, Weijers D, Gutierrez-Beltran E, Moschou PN. 2023. An actin remodeling role for *Arabidopsis* processing bodies revealed by their proximity interactome. *EMBO Journal* 42, e111885.

In this work, the authors describe the link between condensates with a plasma membrane-localized complex. They used proximity biotinylation approaches to characterize a condensate. This approach enabled to link condensates, previously called “membrane-less organelles”, with membranes.

Liu C, Mentzelopoulou A, Papagavriil F, Ramachandran P, Perraki A, Claus L, Barg S, Dormann P, Jaillais Y, Johnen P, Russinova E, Gizeli E, Schaaf G, Moschou PN. 2023. SEC14-like condensate phase transitions at plasma membranes regulate root growth in *Arabidopsis*. *PLoS Biol* 21, e3002305.

In this work, the authors identified a membrane-associated protein that forms condensates and can undergo phase transitions: from liquid to more solid states. This transition depends on a well-conserved protease. They also identified these transitions as components of auxin signaling.

Liu C, Mentzelopoulou A, Hatzianestis IH, Tzagkarakis E, Skaltsogiannis V, Ma X, Michalopoulou VA, Romero-Campero FJ, Romero-Losada AB, Sarris PF, Marhavy P, Bolter 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.

In this work, the authors repurpose proximity biotinylation approaches to capture the RNAs that localize in condensates. They surprisingly identify that RNAs can localize in condensates together with their encoded proteins. They also identify the pathway of ethylene as a converging point of RNA-protein interactions.

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
- Rural Development Program of Greece, Sub-Measure 16.1 ‘Cooperation’

ITALY

Prepared by

Alice Pajoro Alice.pajoro@cnr.it Institute of Molecular Biology and Pathology,
National Research Council c/o , Sapienza, Pl. Aldo Moro 5, 00185 Rome, Italy



Planned events for 2024 and 2025

- Workshop on Plant Biology 2024 21st-23rd February 2024 Bertinoro
- “Fascination of Plants Day” FoPD 2024 (<https://plantday18may.org>) May 2024, all around Italy
- Workshop on Molecular Mechanisms Controlling Flowering 16th-20th June 2024, Palermo
- Congress of the Italian Society of Agricultural Genetics SIGA 10th-13th September 2024, Bologna
- International Plant Science Conference (IPSC) 11th-13th September 2024, Teramo
- XVII Edition of the Congress of the Italian Federation of Life Sciences (FISV), September 18th-20th, 2024. Padova
- SBI Summer School “New Genomic Techniques in plant science”, 24th-26th September 2024, Torino
- Practical Course “Seeds of innovation: Genomic sequencing and GWAS in Agriculture”, 24th-27th September 2024
- Integration and Regulation of Plant Proteolytic Pathways Gordon Research Conference, January 19 - 24, 2025. Barga (Lucca)
- Congress of the Italian Society of Agricultural Genetics SIGA September 2025.
- International Plant Science Conference (IPSC) September 2025
- Congress of the Italian Federation of Life Sciences (FISV), September 2025.

Selected Publications

Gradogna A, Lagostena L, Beltrami S, Tosato E, Picco C, Scholz-Starke J, Sparla F, Trost P, Carpaneto A. (2023) Tonoplast cytochrome b561 is a transmembrane ascorbate-dependent monodehydroascorbate reductase: functional characterization of electron currents in plant vacuoles. *New Phytologist* 238(5):1957-1971. doi: 10.1111/nph.18823.

Measuring electron currents in isolated *Arabidopsis* vacuoles is not an easy task. Here the technique is successfully used to show that ascorbate-dependent currents in mesophyll vacuoles are entirely due to cytochrome b-561 isoform A.

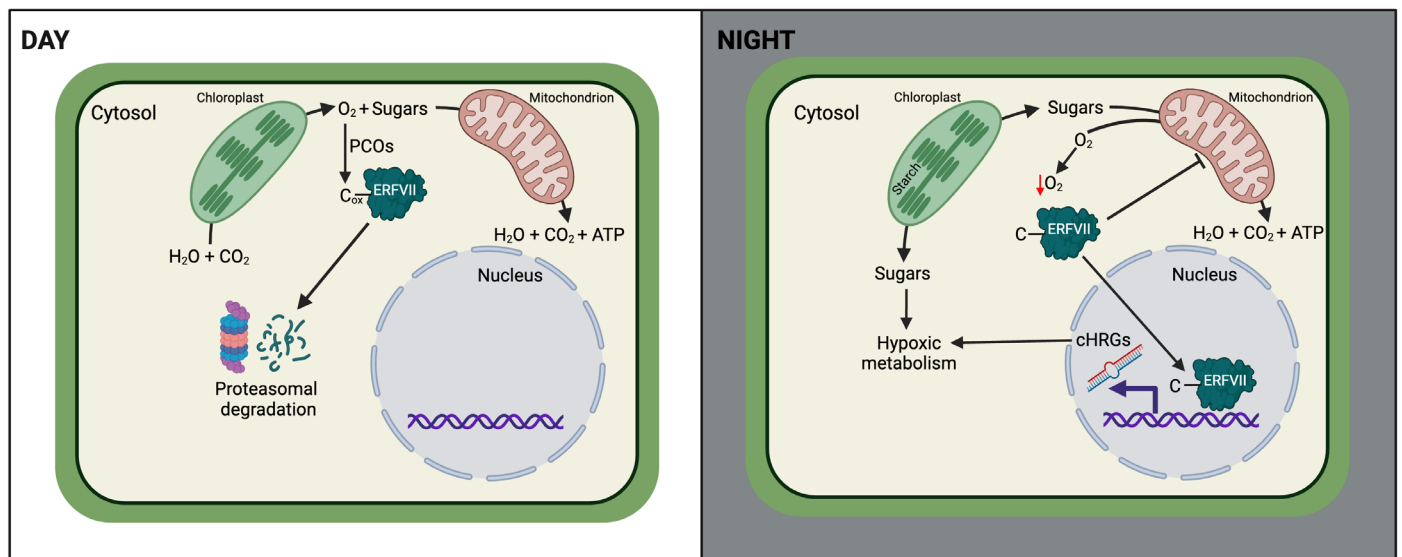
Russo G, Capitanio S, Trasoletti M, Morabito C, Krukowski P, Visentin I, Genre A, Schubert A, Cardinale F (2023) Strigolactones promote the localization of the ABA exporter ABCG25 at the plasma membrane in root epidermal cells of *Arabidopsis thaliana*. *Journal Experimental Botany* 74(18):5881-5895 doi: 10.1093/jxb/erad298.

We propose a new mechanism for ABA homeostasis regulation in the context of osmotic stress acclimation: the fine-tuning by strigolactones of ABCG25 localization in root cells

Coculo D, Del Corpo D, Ozáez Martínez M, Vera P, Piro G, De Caroli M, Lionetti, V. (2023) *Arabidopsis* subtilases promote defense-related pectin methylesterase activity and robust immune responses to botrytis infection. *Plant Physiology and Biochemistry*, Volume 201,2023,107865, <https://doi.org/10.1016/j.plaphy.2023.107865>

The manuscript highlights the role of subtilases (SBTs) SBT3.3 and SBT3.5 as modulators of PME activity in *Arabidopsis* against *Botrytis* to promptly boost immunity limiting the growth-defense trade-off.

Triozzi PM, Brunello L, Novi G, Ferri G, Cardarelli F, Loreti E, Perales M, and Perata P. (2024). Spatiotemporal oxygen dynamics in young leaves reveal cyclic hypoxia in plants. *Molecular Plant*. 17, 377–394 <https://doi.org/10.1016/j.molp.2024.01.006>



We demonstrate that cyclic fluctuations in internal oxygen levels occur in young emerging leaves of *Arabidopsis* plants. Cyclic hypoxia in plants is based on a mechanism requiring the ETHYLENE RESPONSE FACTORS type VII (ERFVII). The ERFVII-dependent mechanism allows precise adjustment of leaf growth in response to carbon status and oxygen availability within plant cells.

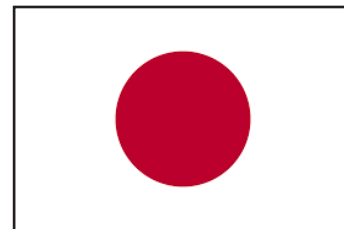
Possenti M, Sessa G, Alfé A, Turchi L, Ruzza V, Sassi M, Morelli G, Ruberti I (2024). HD-Zip II transcription factors control distal stem cell fate in *Arabidopsis* roots by linking auxin signaling to the FEZ/SOMBRERO pathway. *Development* 151 (8): dev202586 <https://doi.org/10.1242/dev.202586>

This article shows that HD-Zip II transcription factors regulate root stem cells activity by counteracting the auxin-induced columella differentiation downstream of the FEZ/SMB proliferative module.

Major Funding Sources

- Italian Ministry of Education, University and Research (MUR) (<https://www.mur.gov.it/it>)
- Program PRIN2020, PRIN2022, PRIN2022-PNRR
- Agritech National Research Center, European Union Next-Generation EU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR) – MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4 – D.D. 1032 17/06/2022, CN00000022). <https://agritechcenter.it/>
- National Biodiversity Future Center NBFC, European Union Next-Generation EU PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR), Missione 4 Componente 2, “Dalla ricerca all’impresa”, Investimento 1.4, Project CN00000033.
- Rome Technopole” <https://www.rometechnopole.it/> European Union “NextGenerationEU” program
- PhD training programme PON ricerca e Innovazione 2014-2020. Asse IV Istruzione e ricerca per il recupero-”React-EU”. Azione IV.5, Dottorati su tematiche Green
- Sapienza University of Rome
- University of Milan, Department of Biosciences
- National Research Council Co-founded International Exchange Program CNR-Royal Society

JAPAN



Prepared by

Motoaki Seki, motoaki.seki@riken.jp, RIKEN CSRS

Masatomo Kobayashi, masatomo.kobayashi@riken.jp, RIKEN BRC

Shinya Hagihara, hagi@riken.jp, RIKEN CSRS

Masanori Okamoto, okamo@riken.jp, RIKEN CSRS

Yuki Nakamura, yuki.nakamura.yf@riken.jp, RIKEN CSRS

Satoshi Iuchi, satoshi.iuchi@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 2023 or early 2024.

RIKEN Center for Sustainable Resource Science (CSRS) (<http://www.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/>)

- We have added the information of 85 mutant and transgenic lines of Arabidopsis to the Exp-Plant Catalog (https://plant.rtc.riken.jp/resource/psi/psi_list2.html). Now 524 mutant and transgenic lines deposited from Japanese scientists are on the Catalog.
- We have released three callus cell lines established from suspension cell lines of Arabidopsis and grape, since original suspension cell lines are not suitable for overseas transport (<https://epd.brc.riken.jp/en/archives/5762>).

Kazusa DNA Research Institute (<http://www.kazusa.or.jp/e/>)

- MassBase: a plant metabolome database (<http://bit.ly/1Rlf9Dd>)
- Plant GARDEN Plant Genome And Resource Database ENtry (<https://plantgarden.jp>)
- Kusaki DB: a database to assess existence and completeness of orthogroups in plant species (<http://pgdbj.snp.kazusa.or.jp/app/kusakidb>) (<https://hub.docker.com/r/ghelfi/kusakidb>)

National Institute for Basic Biology (<http://www.nibb.ac.jp>)

= ChaetoBase (Gene annotation database for *Chaetoceros gracilis*) (<https://chaetoceros.nibb.ac.jp/>)

Planned events for 2024 and 2025

- Mar. 17-19, 2024: 65th Annual Meeting of Japanese Society of Plant Physiologists. Kobe International Conference Center, Kobe, Japan (https://jspp.org/annualmeeting/65/e_greeting.php).

- Jul. 9-12, 2024: EMBO COB Workshop “Plant Tropisms”. National Institute for Basic Biology, Okazaki, Japan (<https://meetings.embo.org/event/24-plant-tropisms>).

- Sep. 13-16, 2024: 88th Annual Meeting of the Botanical Society of Japan. Utsunomiya University, Utsunomiya, Japan (<https://bsj88.org/en/en-meeting/>).

Selected Publications

Ngou, B.P.M., Wyler, M., Schmid, M.W., Kadota, Y., Shirasu, K. Evolutionary Trajectory of Pattern Recognition Receptors in Plants. *Nature Communications*. (2024) 15: 308. <https://doi.org/10.1038/s41467-023-44408-3>.

This research has advanced our understanding of the origins and evolution of plant immunity and has enabled the rapid and accurate prediction of genes that function as immune receptors.

Isono K, Nakamura K, Hanada K, Shirai K, Ueki M, Tanaka K, Tsuchimatsu T, Iuchi S, Kobayashi M, Yotsui I, Sakata Y, Taji T. LHT1/MAC7 contributes to proper alternative splicing under long-term heat stress and mediates variation in the heat tolerance of Arabidopsis. *PNAS Nexus*. (2023) 2(11):pgad348. doi: 10.1093/pnasnexus/pgad348. PMID: 38024403; PMCID: PMC10644991.

Authors identified Arabidopsis LHT1/MAC7 that encodes a putative RNA helicase involved in mRNA splicing as a responsible gene for the variation in long-term heat tolerance between Ms-0 and Col-0 accessions.

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, (<http://www.jsps.go.jp/english/e-grants/>)

CREST of Japan Science and Technology Corporation (<http://bit.ly/22I8avZ>)

ERATO of Japan Science and Technology Corporation (<https://www.jst.go.jp/erato/en/index.html>)

MIRAI Program of Japan Science and Technology Corporation (<http://www.jst.go.jp/mirai/jp/about/index.html>)

Strategic International Cooperative Program (SICORP), JST-NSF Joint Research Project. (<http://www.jst.go.jp/inter/english/sicorp/index.html>)

“Impulsing Paradigm Change through Disruptive Technologies” (ImPACT) (<http://www.jst.go.jp/impact/en/outline.html>)

MEXT “Cross-ministerial Strategic Innovation Promotion Program” (SIP) in 2014. (<http://www.mext.go.jp/english/topics/1345957.htm>)

PRESTO of Japan Science and Technology Corporation (<https://www.jst.go.jp/kisoken/presto/en/index.html>)

Moonshot Research and Development Program

(<https://www8.cao.go.jp/cstp/english/moonshot/top.html>)

JST ACT-X

(<https://www.jst.go.jp/kisoken/act-x/index.html>)

JST ASPIRE

(<https://www.jst.go.jp/aspire/en/>)

JSY GteX

(<https://www.jst.go.jp/gtex/en/>)

NEW ZEALAND



Prepared by

Rowan Herridge, University of Otago (rowan.herridge@otago.ac.nz)

Planned events for 2024 and 2025

- Queenstown Research Week, 31st August-5 September 2024 (<https://www.queenstownresearchweek.org/>)
- NZSPB Hybrid Hub Conference, Lincoln/Auckland/Palmerston North, 28-29th November, 2024 (contact nick.albert@plantandfood.co.nz)

Selected Publications

Dong, Y.; Gupta, S.; Wargent, J.J.; Putterill, J.; Macknight, R.C.; Gechev, T.S.; Mueller-Roeber, B.; Dijkwel, P.P. Comparative Transcriptomics of Multi-Stress Responses in *Pachycladon cheesemanii* and *Arabidopsis thaliana*. *Int. J. Mol. Sci.* 2023, 24, 11323. <https://doi.org/10.3390/ijms241411323>

This article led by researchers at Massey University, with contributions from Otago and Auckland shows how *Arabidopsis* can respond to stress and contrasts this with the stress-tolerant species *P. cheesemanii*.

Kim, H., Kim, J., Choi, D. S., Kim, M. S., Deslandes, L., Jayaraman, J., & Sohn, K. H. (2024). Molecular basis for the interference of the *Arabidopsis* WRKY54-mediated immune response by two sequence-unrelated bacterial effectors. *The Plant Journal*, 118(3), 839-855.

This article led by researchers from Seoul National University and Plant and Food Research in New Zealand identifies WRKY54 as a target of two bacterial effectors AvrRp4 and PopP2.

Major Funding Sources

Marsden Fund, Royal Society Te Aparangi (<https://www.royalsociety.org.nz/what-we-do/funds-and-opportunities/marsden>)

MBIE Endeavor Fund (<https://www.mbie.govt.nz/science-and-technology/science-and-innovation/funding-information-and-opportunities/investment-funds/endeavour-fund>)

NORWAY

Prepared by

Thorsten Hamann, Thorsten.hamann@ntnu.no, Norwegian University of Science and Technology



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 2023 or early 2024.

The national graduate school in Plant Biology (Photosyntech <https://photosyntech.no/>) is now fully active and bringing together all stakeholders from across the plant science community.

Planned events for 2024 and 2025

- Norwegian Plant Biology conference organized in association with the National Norwegian PhD school in Plant Biology, 20-22.3.2024 Oslo
- Fascination of Plants day 2024 and 2025 <https://plantday18may.org> organized by the Norwegian University of Life Sciences.

Selected Publications

Structural evidence for MADS-box type I family expansion seen in new assemblies of *Arabidopsis arenosa* and *A. lyrata*. Bramsiepe J, Krabberød AK, Bjerkan KN, Alling RM, Johannessen IM, Hornslien KS, Miller JR, Brysting AK, Grini PE. *Plant J.* 2023; 116(3):942-961. doi: 10.1111/tpj.16401.

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

Adaptive protein evolution through length variation of short tandem repeats in *Arabidopsis*. Reinar WB, Greulich A, Stø IM, Knutsen JB, Reitan T, Tørresen OK, Jentoft S, Butenko MA, Jakobsen KS. *Sci Adv.* 2023; 9(12):eadd6960. doi: 10.1126/sciadv.add6960.

Responsiveness to long days for flowering is reduced in *Arabidopsis* by yearly variation in growing season temperatures. Kinmonth-Schultz H, Sønstebø JH, Croneberger AJ, Johnsen SS, Leder E, Lewandowska-Sabat A, Imaizumi T, Rognli OA, Vinje H, Ward JK, Fjellheim S. *Plant Cell Environ.* 2023; 46(11):3337-3352. doi: 10.1111/pce.14632.

Major Funding Sources

Norwegian Research Council, forskingsradet.no
ERC, erc.eu

POLAND

Prepared by

Robert Malinowski, rmal@igr.poznan.pl, Institute of Plant Genetics Polish Academy of Sciences, Poznan, Poland



Selected Publications

Dluzewska, J., Dziegielewski, W., Szymanska-Lejman, M., Gazecka, M., Henderson, I.R., Higgins, J.D. and Ziolkowski, P.A. (2023) MSH2 stimulates interfering and inhibits non-interfering crossovers in response to genetic polymorphism. *Nat Commun*, 14, 6716.

Work provides the data that confirms central role of the MSH2 in a regulator of meiotic DSB repair in *Arabidopsis*

Ochoa, J.C., Mukhopadhyay, S., Bieluszewski, T., Jędrzycka, M., Malinowski, R. and Truman, W. (2023) Natural variation in *Arabidopsis* responses to *Plasmodiophora brassicae* reveals an essential role for Resistance to *Plasmodiophora brassicae* 1 (RPB1). *The Plant Journal*, 116, 1421-1440.

The discovery of a single dominating resistance gene to clubroot disease in *Arabidopsis thaliana*.

Sarnowska, E., Kubala, S., Cwiek, P., Sacharowski, S., Oksinska, P., Steciuk, J., Zaborowska, M., Szurmak, J.M., Dubianski, R., Maassen, A., Stachowiak, M., Huettel, B., Ciesla, M., Nowicka, K., Rolicka, A.T., Alseekh, S., Bucior, E., Franzen, R., Skoneczna, A., Domagalska, M.A., Amar, S., Hajirezaei, M.-R., Siedlecki, J.A., Fernie, A.R., Davis, S.J. and Sarnowski, T.J. (2023) A non-canonical function of *Arabidopsis* ERECTA proteins and a role of the SWI3B subunit of the SWI/SNF chromatin remodeling complex in gibberellin signaling. *The Plant Journal*, 115, 788-802.

This work describes the role of SWI3B-containing SWI/SNF CRCs in gibberellin signaling

Major Funding Sources

National Science Centre Poland [<https://www.ncn.gov.pl/en>]

PORTUGAL

Prepared by

Sílvia Vieira de Almeida Coimbra scoimbra@fc.up.pt University of Porto



Planned events for 2024 and 2025

- Iberian Plant Biology 2023. Braga Portugal 9-12 July
- Youth Research Meeting (IJUP) 2023, in Porto, Portugal

Selected Publications

Figueiredo, R, Costa, M, Moreira, D, Moreira, M, Noble, J, Pereira, LG, Melo, P, Palanivelu, R, Coimbra, S, Pereira, AM. 2024. JAGGER localization and function is dependent on GPI anchor addition. *Plant Reproduction* DOI: 10.1007/s00497-024-00495-w

Different JAGGER proteins with deletions in predicted ω -site regions and GAS (GPI attachment signal) domain, expected to compromise the addition of the GPI anchor, led to disruption of JAGGER localization in the cell periphery. All JAGGER proteins with disrupted localization were also not able to rescue the polytubey phenotype, pointing to the importance of GPI-anchor addition to in vivo function of the JAGGER protein.

Moreira, D, Kaur, D, Pereira, AM, Held, MA, Showalter, AM, Coimbra, S. 2023. Type II arabinogalactans initiated by hydroxyproline O-galactosyltransferases play important roles in pollen–pistil interactions. *The Plant Journal*. DOI: 10.1111/tpj.16141

The present work demonstrates the functional importance of the carbohydrate moieties of AGPs in ovule development and pollen–pistil interactions.

Figueiredo, R, Lopes, AL, Pereira, AM, Moreira, D, Silva, J, Ferreira, MJ, Pereira, LG, Coimbra, S. 2023. The biology of arabinogalactan proteins in plant abiotic stress and reproduction. In: Geitmann A (ed) *Plant Cell Walls – Research Milestones and Conceptual Insights*. CRC Press, Taylor & Francis Group. DOI: 10.1201/9781003178309-16

In this review, we present an overview of the accumulated knowledge on AGP involvement in abiotic stress tolerance and in plant reproduction, as these two physiological processes are essential for plant growth and seed yield, and consequently for sustainable food security.

Ferreira, MJ, Silva, J, Pinto, SC, Coimbra, S. 2023. I Choose you: Selecting accurate reference genes for qPCR expression analysis in reproductive tissues in *Arabidopsis thaliana*. *Biomolecules*. DOI: 10.3390/biom13030463

Our results showed that RCE1, SAC52 and TUA2 had the most stable expression in different flower developmental stages while YLS8, HIS3.3 and ACT7 were the top-ranking reference genes for normalisation in mutant studies. Furthermore, we validated our results by analysing the expression pattern of genes involved in reproduction and examining the expression of these genes in published mutant backgrounds. Overall, we provided a pool of appropriate reference genes for expression studies in reproductive tissues of *A. thaliana*.

Lopes, AL, Moreira, D, Pereira, AM, Ferraz, R, Mendes, S, Pereira, LG, Colombo, L, Coimbra, S. 2023. AGPs as molecular determinants of reproductive development. *Annals of Botany*. DOI: 10.1093/aob/mcad046

These findings reveal distinct AGP distribution patterns in different developmental mutants related to the female reproductive unit in *Arabidopsis*. The value of the immunofluorescence labelling technique is highlighted in this study as an invaluable tool to dissect the remodelling nature of the cell wall in developmental processes.

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 Requite (<https://laqv.requite.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/>)

SPAIN

Prepared by

Cristina Ferrandiz cferrandiz@ibmcp.upv.es Instituto de Biología Molecular y Celular de Plantas, CSIC-UPV www.ibmcp.upv.es/FerrandizLab



Planned events for 2024 and 2025

- 6th International Symposium on Plant Apoplastic Diffusion Barriers (PADiBa) Girona, 02-05 September 2024
- EMBO Workshop “Cell death: friend or foe in animal and plant immunity” Sant Feliu de Guixols, 11-15 November, 2024
- PlantAct Workshop, Madrid, April 2025. www.plant-act.org/es/blog
- Workshop “Plants under environmental stress: overcoming current climate changes. Baeza, 5-7 Noviembre, 2024.

Selected Publications

Sánchez-Vicente I, Albertos P, Sanz C, Wybouw B, De Rybel B, Begara-Morales JC, Chaki M, Mata-Pérez C, Barroso JB, Lorenzo O. Reversible S-nitrosylation of bZIP67 by peroxiredoxin IIE activity and nitro-fatty acids regulates the plant lipid profile. *Cell Rep.* 2024; 43(4):114091.

This work uncovers a new role of nitric oxide in controlling seed lipid storage and the importance of post-translational modification of transcription factors influenced by NO signaling.

Tremblay BJM, Santini CP, Cheng Y, Zhang X, Rosa S, Qüesta JI. Interplay between coding and non-coding regulation drives the Arabidopsis seed-to-seedling transition. *Nat Commun.* 2024;15(1):1724.

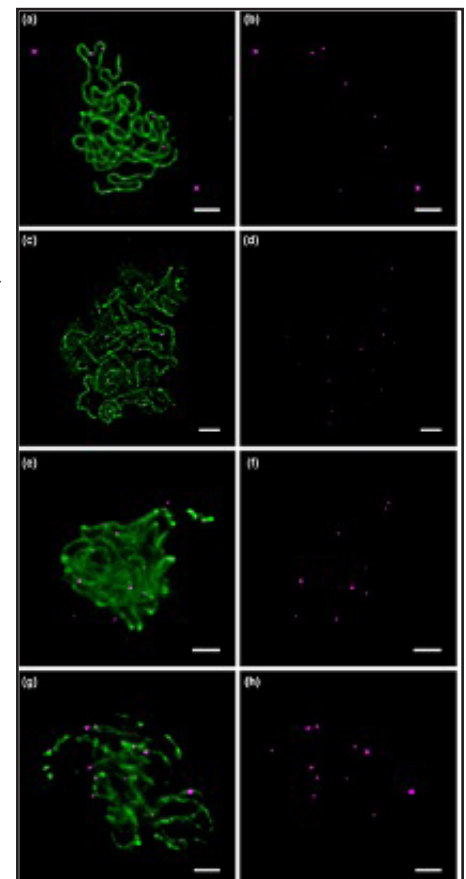
A comprehensive study of different levels of regulation of transcriptional events at the seed-to-seedling transition. Exciting results composing a broad view of germination.

Martínez-Pérez M, Aparicio F, Arribas-Hernández L, Tankmar MD, Rennie S, von Bülow S, Lindorff-Larsen K, Brodersen P, Pallas V. Plant YTHDF proteins are direct effectors of antiviral immunity against an N6-methyladenosine-containing RNA virus. *EMBO J.* 2023 42(18):e113378.

This elegant study provides new insights on the mechanism of plant basal antiviral immunity based on demethylation of viral RNA.

- **Parra-Nunez P, Fernández-Jiménez N, Pachon-Penalba M, Sanchez-Moran E, Pradillo M, Santos JL. Synthetically induced Arabidopsis thaliana autotetraploids provide insights into the analysis of meiotic mutants with altered crossover frequency. *New Phytol.* 2024 241(1):197-208.**

A clever strategy provides exciting new results to better understand the meiosis and chromosome recombination in polyploids made in Arabidopsis.



Perez-Garcia P, Pucciariello O, Sanchez-Corrionero A, Cabrera J, Del Barrio C, Del Pozo JC, Perales M, Wabnik K, Moreno-Risueno MA. The cold-induced factor CBF3 mediates root stem cell activity, regeneration, and developmental responses to cold. *Plant Commun.* 2023 Nov 13;4(6):100737.

A close view on the impact of environmental factors in stem cell behavior and responses made in *Arabidopsis* roots exposed to cold.

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 2023, around 80 projects to individual laboratories were granted, which is in line with 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. AdG to Crisanto Gutiérrez (CBM), CoG to Clara Sánchez-Rodríguez (CBGP), StG to Ivan Reyna-Llorens (CRAG) and Ainhoa Martínez-Medina (CSIC) or PoCG to Ana Caño-Delgado (CRAG).

SWEDEN

Prepared by

Maria E. Eriksson, maria.eriksson@umu.se, UPSC, Umeå University



Planned events for 2024 and 2025

- 30th Scandinavian Plant Physiology Society (SPPS) Conference, August 27-29, 2024, Copenhagen, Denmark

Plant Energy Management, Molecular Mechanisms and Signalling

- August 26-30, 2024, Umeå, Sweden

14th Conference of the European Foundation for Plant Pathology

2nd -5th June, 2025, Uppsala, Sweden

Selected Publications

Tran, H.C. et al. (2023) An mTRAN-mRNA interaction mediates mitochondrial translation initiation in plants. *Science*, 381 (6661) <https://doi.1126/science.adg0995>

Using *Arabidopsis* as a model system and characterization of mTRAN1 and mTRAN2, exclusively found inside mitochondria and found essential for development/ growth. This work provides novel details on translation initiation in specifically mitochondrial translation mechanisms that evolved from a common bacterial ancestor.

Saarenpää, S. et al. (2023) Spatial metatranscriptomics resolves host-bacteria-fungi interactomes. *Nature Biotechnology*, <https://doi.org/10.1038/s41587-023-01979-2>

This work offers advancement on understanding of multiple species interactions' as they occur using spatial metatranscriptomics of leaves from *Arabidopsis* grown outdoors. It shows tissue hotspots for interactions of bacteria, fungi and *Arabidopsis* in leaf tissues.

Hoffmann, G. et al. (2023) Cauliflower mosaic virus disease spectrum uncovers novel susceptibility factor NCED9 in *Arabidopsis thaliana*. *Journal of Experimental Botany* 74 (15), <https://doi.org/10.1093/jxb/erad204>

Abcisic acid (ABA) is an important stress evoked plant hormone. This genome-wide association study pinpoints variability in the 9-CIS-EPOXYCAROTENOID DIOXYGENASE 9 (NCED9) locus as an important susceptibility factor for Cauliflower mosaic virus (CaMV), as infection is nearly abolished in the *nced9* mutant. The importance of ABA homeostasis during CaMV infection was further underlined by their findings.

Derba-Maceluch, M. et al. (2023) Xylan glucuronic acid side chains fix suberin-like aliphatic compounds to wood cell walls. *New Phytologist* 238 (1) <https://nph.onlinelibrary.wiley.com/doi/full/10.1111/nph.18712>

By expressing fungus enzyme in wood as an enzymatic tool of wood composition, this work casts a light on hemicellulose composition and structure using *Arabidopsis* and *Populus* sp. tree cell walls as model systems. They focus on xylan glucuronosylation, which affects the plant secondary cell wall properties, and processibility of wood going further.

Zou, Y. et al., (2024) Thermoprotection by a cell membrane-localized metacaspase in a green alga *Plant Cell* 36 (3) <https://doi.org/10.1093/plcell/koad289>

The role of metacaspases (MCAs) in plants and algae are still not fully understood. This work adds knowledge about their functions, important for future studies and applications in adaptation of plants to variable temperatures.

Major Funding Sources

More general such as Human Frontiers <https://www.hfsp.org/funding/hfsp-funding/research-grants>,
EMBO <https://www.embo.org/funding/>,
ERC <https://erc.europa.eu/>,
EU <https://www.mariecuriealumni.eu/news/european-funding-opportunities-10-websites-you-need-know>

Nordic sources like Novo Nordisk Foundation <https://novonordiskfonden.dk/en/grants/>,
Nordforsk <https://www.nordforsk.org/>

Swedish governmental agencies and foundations such as;

- The Swedish Research Council (VR); <http://www.vr.se>
VR supports researcher-initiated, basic research
- The Swedish Foundation for Strategic Research; <http://www.stratresearch.se>
Supports strategic research in natural science, engineering and medicine
- The Swedish Agency for Innovation Systems (VINNOVA); <http://www.vinnova.se>
Promotes sustainable growth by funding needs-driven research and the development of effective innovation systems
- The Swedish Research Council Formas; <http://www.formas.se>
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) <https://www.stint.se/en/our-programmes/>
Supports research and teaching exchanges with a rather broad scope. For instance, it supports postdoctoral stays outside the EU/EFTA (incl. the United Kingdom).

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 2023 or early 2024.

PlantServation, a method incorporating robust image-acquisition hardware and deep learning-based software that extracts leaf color by detecting plant individuals automatically.

Akiyama R, Goto T, Tameshige T, Sugisaka J, Kuroki K, Sun J, Akita J, Hatakeyama M, Kudoh H, Kenta T, Tonouchi A, Shimahara Y, Sese J, Kutsuna N, Shimizu-Inatsugi R, Shimizu KK (2023) Seasonal pigment fluctuation in diploid and polyploid Arabidopsis revealed by machine learning-based phenotyping method PlantServation. Nature Communications 14: 5792. <https://doi.org/10.1038/s41467-023-41260-3>
PlantServation_demo_set.zip <https://zenodo.org/records/7321725>

Planned events for 2024 and 2026 Conferences, symposiums

- PSC Symposium 2024, 5 December, 2024 “Response to society and policy needs through plant, food and energy sciences”, ETH Zürich
- SwissPLANT symposium 2025, 15 - 17 January 2025, Les Diablerets
- Biology 25, early 2025, Zurich

Outreach activities

- Outreach in general: <https://www.plantsciences.uzh.ch/en/Outreach.html>

Upcoming events

<https://www.plantsciences.uzh.ch/en/rssnews.html>

Selected Publications

Yew CL, Tsuchimatsu T, Shimizu-Inatsugi R, Yasuda S, Hatakeyama M, Kakui H, Ohta T, Suwabe K, Watanabe M, Takayama S, Shimizu KK. (2023) Dominance in self-compatibility between subgenomes of allopolyploid Arabidopsis kamchatica shown by transgenic restoration of self-incompatibility. Nature Communications: 14: 7618. <https://doi.org/10.1038/s41467-023-43275-2>

Using the transgenic plants of the model polyploid species Arabidopsis kamchatica, the authors showed the importance of dominance of self-incompatibility between two subgenomes in allopolyploid evolution.

Yang H, Kim X, Sklenar J, Aubourg S, Sancho-Andrés G, Stahl E, Guillou MC, Gigli-Bisceglia N, Tran Van Canh L, Bender KW, Stintzi A, Reymond P, Sanchez-Rodriguez C, Testerink C, Renou JP, Menke FLH, Schaller A, Rhodes J and Zipfel C (2023) Subtilase-mediated biogenesis of the expanded family of SERINE RICH ENDOGENOUS PEPTIDES. *Nature Plants* 9: 2085–2094. <https://doi.org/10.1038/s41477-023-01583-x>

In this paper, the authors defined the large divergent family of SCOOP secreted signaling peptides, and characterized by cleavage by related subtilases.

Nawkar GM, Legris M, Goyal A, Schmid-Siegert E, Fleury J, Mucciolo A, De Bellis D, Trevisan M, Schueler A, and Fankhauser C (2023). Air channels create a directional light signal to regulate hypocotyl phototropism. *Science* 382, 935–940. <https://www.science.org/doi/10.1126/science.adh9384>

This study reveals the importance of inter-cellular air channels for the establishment of light gradients across a photosensitive tissue and a robust phototropic response.

Simonini S, Bencivenga S, Grossniklaus U (2024) A paternal signal induces endosperm proliferation upon fertilization in *Arabidopsis*. *Science* 383 (6683): 646–653. <https://doi.org/10.1126/science.adj4996>

This paper shows that a sperm-derived signal induces the proliferation of a female gamete, the central cell, precisely upon fertilization.

Moussu S, Lee HK, Haas KT, Broyart C, Rathgeb U, De Bellis D, Lévassieur T, Schoenaers S, Fernandez GS, Grossniklaus U, Bonnin E, Hosy E, Vissenberg K, Geldner N, Cathala B, Höfte H, Santiago J (2023) Plant cell wall patterning and expansion mediated by protein-peptide-polysaccharide interaction. *Science* 382: 719–725. <https://doi:10.1126/science.adi4720>

This paper reports a dual structural and signaling role for the complex of RAPID ALKALINIZATION FACTOR 4 (RALF4) in pollen tube growth and in the assembly of complex extracellular polymers.

Highly cited researchers 2023 (members of the Plant Science Center):

Klaus Schläppi, Cross-field
Marcel van der Heijden, Microbiology
Cyril Zipfel, Plant and Animal Science

Major Funding Sources

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

- European Research Council (ERC), <https://erc.europa.eu/>
- University Research Priority Program of Evolution in Action: From Genomes to Ecosystems (directors: Ueli Grossniklaus, Kentaro K. Shimizu, University of Zurich), <http://www.evolution.uzh.ch/en.html>
- University Research Priority Program of Global Change and Biodiversity (directors: Norman Backhaus, Owen Petchey, Maria J. Santos, University of Zurich), <https://www.gcb.uzh.ch/en.html>

UNITED KINGDOM



Prepared by

Geraint Parry, Arabidopsis Events UK 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 2023 or early 2024.

Tuning Plant Promoters

Cai YM, Witham S, Patron NJ. Tuning Plant Promoters Using a Simple Split Luciferase Method to Assess Transcription Factor-DNA Interactions. *ACS Synth Biol.* 2023 Nov 17;12(11):3482-3486. doi: 10.1021/acssynbio.3c00094.

<https://pubs.acs.org/doi/10.1021/acssynbio.3c00094?goto=supporting-info>

Program for analysis of genomic repeats

Wlodzimierz P, Hong M, Henderson IR. TRASH: Tandem Repeat Annotation and Structural Hierarchy. *Bioinformatics.* 2023 May 4;39(5):btad308. doi: 10.1093/bioinformatics/btad308.

Molecular cartography: a high-throughput quantitative in situ hybridization

Perico C, Zaidem M, Sedelnikova O, Bhattacharya S, Korfhage C, Langdale JA. Multiplexed in situ hybridization reveals distinct lineage identities for major and minor vein initiation during maize leaf development. *Proc Natl Acad Sci U S A.* 2024 Jul 9;121(28):e2402514121. doi: 10.1073/pnas.2402514121.

Planned events for 2024 and 2025

Empowering Research for Community Impact - OED Symposium 2024

10-11 September 2024, London, UK

<https://www.sebiology.org/events/oed-symposium-2024.html>

BSPP Plant Pathology Meeting

10-13 September 2024, Oxford, UK

<https://bspp.bookingmanager.website/conference/ppath2024/>

Advances in Nematology

5th December 2024, London UK

<https://www.aab.org.uk/events/>

Plant Biology Education: Creating a Vision for the Future

7-8 January 2025, Lancaster University, UK

<https://cvent.me/LB9K1D>

Genetics Society: Seed Plant SIG

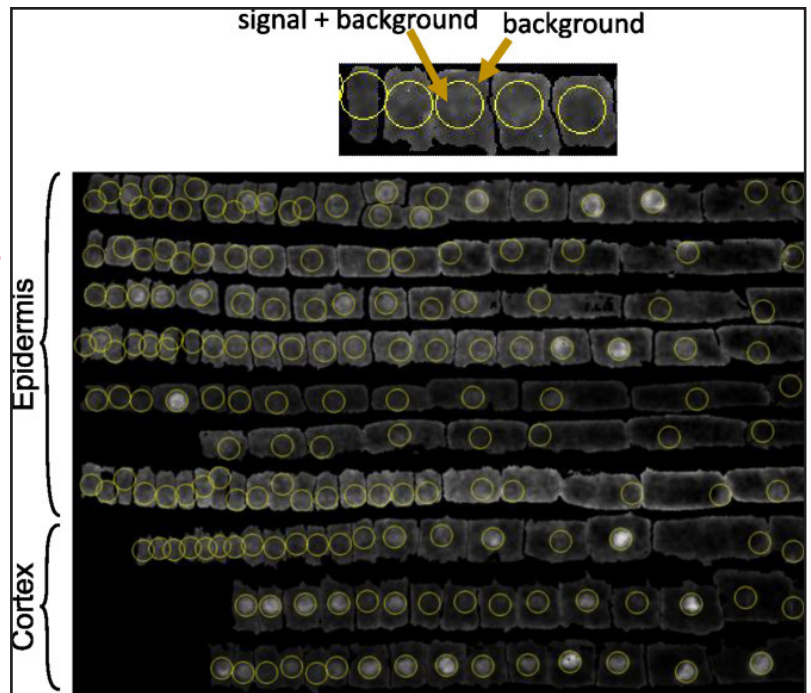
8-9 April 2025, Durham, UK

<https://genetics.org.uk/events/seed-plant/>

Selected Publications

Antoniou-Kourounioli RL, Meschichi A, Reeck S, Berry S, Menon G, Zhao Y, Fozard J, Holmes T, Zhao L, Wang H, Hartley M, Dean C, Rosa S, Howard M. Integrating analog and digital modes of gene expression at *Arabidopsis* FLC. *Elife*. 2023 Jul 19;12:e79743. doi: 10.7554/eLife.79743.

Using quantitative fluorescent imaging of FLC mRNA and protein, together with mathematical modeling, we find that FLC expression before cold is regulated by both analog and digital modes. We observe a temporal separation between the two modes, with analog preceding digital. The analog mode can maintain intermediate expression levels at individual FLC gene copies, before subsequent digital silencing, consistent with the copies switching OFF stochastically and heritably without cold. This switch leads to a slow reduction in FLC expression at the cell population level. These data present a new paradigm for gradual repression, elucidating how analog transcriptional and digital epigenetic memory pathways can be integrated.



Brazel AJ, Fattorini R, McCarthy J, Franzen R, Rümpler F, Coupland G, Ó'Maoiléidigh DS. AGAMOUS mediates timing of guard cell formation during gynoecium development. *PLoS Genet*. 2023 Oct 11;19(10):e1011000. doi: 10.1371/journal.pgen.1011000.

Here, we show that the MADS domain transcription factor AGAMOUS (AG) represses stomatal development on the gynoecial valves, so that maturation of stomatal complexes coincides with fertilization. We present evidence that this regulation by AG is mediated by direct transcriptional repression of a master regulator of the stomatal lineage, MUTE, and show data that suggests this interaction is conserved among several members of the Brassicaceae. This work extends our understanding of the mechanisms underlying floral organ formation and provides a framework to decipher the mechanisms that control floral organ photosynthesis.

Perrella G, Fasano C, Donald NA, Daddiego L, Fang W, Martignago D, Carr C, Conti L, Herzyk P, Amtmann A. Histone Deacetylase Complex 1 and histone 1 epigenetically moderate stress responsiveness of *Arabidopsis thaliana* seedlings. *New Phytol*. 2024 Jan;241(1):166-179. doi: 10.1111/nph.19165.

The combined findings of this study reveals a dual brake function of HDC1 via regulating both active and repressive epigenetic marks on stress-inducible genes. This natural 'anti-panic' device offers a molecular lever to tune stress responsiveness in plants.

Robson JK, Tidy AC, Thomas SG, Wilson ZA. Environmental regulation of male fertility is mediated through *Arabidopsis* transcription factors bHLH89, 91, and 10. *J Exp Bot*. 2024 doi: 10.1093/jxb/erad480.

bHLH89 and bHLH91 are shown to play a role in regulating fertility in response to light, suggesting that they function in mitigating environmental variation to ensure fertility is maintained under environmental stress.

Tavares H, Readshaw A, Kania U, de Jong M, Pasam RK, McCulloch H, Ward S, Shenhav L, Forsyth E, Leyser O. Artificial selection reveals complex genetic architecture of shoot branching and its response to nitrate supply in *Arabidopsis*. *PLoS Genet*. 2023 Aug 24;19(8):e1010863. doi: 10.1371/journal.pgen.1010863.

We use artificial selection under contrasting nitrate supplies to dissect the genetic architecture of this complex trait, where loci identified by association mapping failed to explain heritability estimates. We found a consistent response to selection for high branching, with correlated responses in other traits such as plasticity and flowering time. Genome-wide scans for selection and simulations suggest that at least tens of loci control this trait, with a distinct genetic architecture between low and high nitrate treatments. While signals of selection could be detected in the populations selected for high branching on low nitrate, there was very little overlap in the regions selected in three independent populations. Thus the regulatory network controlling shoot branching can be tuned in different ways to give similar phenotypes.

Major Funding Sources

Biotechnology and Biological Sciences Research Council (BBSRC) <http://www.bbsrc.ac.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 arabidopsisconference@gmail.com, NAASC

Additional NAASC members contributing to this report:

- Federica Brandizzi, Michigan State University, USA
- Anna Stepanova, NC State University, USA
- Keith Slotkin, Donald Danforth Plant Science Center & University of Missouri-Columbia, USA
- 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

NAASC Early Career Scholars (term: Oct. 2023-Oct 2024)

- Xiaohui Li, Purdue University, (Sept 2024- California Institute of Technology) , USA
- Mingyuan Zhu, Duke University, USA
- Adesola Tola, CANADA

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 2023 or early 2024.

Plant Membrane on a Chip: A new technique for creating supported lipid bilayers from plant protoplast membranes has been published. This technique allows for the assay of transmembrane proteins and other membrane constituents in a single lipid bilayer largely composed of the lipids from the plasma membrane of the plant cell, on a slide so it is accessible for microscopy and experimentation.

Stuebler, M. Manzer, Z.A., Liu, H.-Y., Miller, J., Richter, A., Krishnan, S., Selivanovitch, E., Banuna, B., Jander, G., Reimhult, E., Zipfel, W.R., Roeder, A.H.K., Piñeros, M.A., and Daniel, S. (2024). Plant membrane-on-a-chip: A platform for studying plant membrane proteins and lipids. *ACS Applied Materials & Interfaces* 16, 20092–20104. DOI: 10.1021/acsami.3c18562

PHYTOMap (plant hybridization-based targeted observation of gene expression map) is a multiplexed fluorescence in situ hybridization method that enables single-cell and spatial analysis of gene expression in whole-mount plant tissue.

Nobori T, Oliva M, Lister R, Ecker JR. (2023). Multiplexed single-cell 3D spatial gene expression analysis in plant tissue using PHYTOMap. *Nature Plants* 9, 1026-1033. doi: 10.1038/s41477-023-01439-4.

Single-cell proteomics on root cells.

Single-cell proteomics differentiates Arabidopsis root cell types

Montes C, Zhang J, Nolan TM, Walley JW (2024) Single-cell proteomics differentiates Arabidopsis root cell types. *New Phytologist* DOI: 10.1111/nph.19923 PMID: 38923440

EXPOSE: Expansion microscopy in plant Protoplast Systems (ExPOSE) increases the imaging resolution of protoplasts by physical expansion of the fixed cells.

ExPOSE: A comprehensive toolkit to perform expansion microscopy in plant protoplast systems.

Cox Jr. K.L., Pardi S.A., O'Connor L., Klebanovych A., Huss D., Nusinow D.A., Meyers B.C., Czymbek K.J. *bioRxiv*, DOI: 10.1101/2024.07.12.603300

Planned events for 2024 and 2025:

ICAR 2024

NAASC organized the 34th International Conference on Arabidopsis Research (ICAR2024) in San Diego, California July 15-19, 2024. Attendance was 538 in person and 45 virtual participants. 249 of the in-person participants were early career (18 undergraduate students, 127 graduate students, 104 postdocs) and 289 later career (83 pre-tenure or non-tenure track, 144 post-tenure faculty, and 62 others). NAASC awarded 128 full conference registration fee waivers and/or travel grants, including 86 registration waivers for students, postdoctoral scholars, and participants from non-US countries with severe financial barriers; 33 registration waivers and/or travel funds for invited plenary and keynote speaker, and 9 full-funding ISP (Inclusivity Scholar Program) awards for members of under-represented groups in US STEM.

The NAASC Early Career Scholars Subcommittee (ECSS) hosted an in-person workshop of “Career Opportunities in Academia and Industry”, with seven panelists from academia, industry, and non-profit sectors. There were more than 120 in-person attendees. The NAASC Inclusivity Scholars Subcommittee (ISS) led by Cris Argueso, Ment Ayalew and Joanna Friesner again organized the ISP Cohort Program to support members of under-represented groups in US STEM. These activities have been continuously supported by the US National Science Foundation (NSF) since 2004. The goal of the ISP program is to develop a cohort of awardees that may form lifelong supportive networks throughout their careers. ISP awardees met over Zoom prior to ICAR and engaged in informal and social activities during ICAR organized by ISS leaders including shared meals and career development and networking activities. New for ISP this year: NAASC invited 9 awardees funded by other groups to join several ISP activities, including two from Black in Plant Science UK and seven from ROOT and SHOOT LEAPs RCN. The program was successful, and we hope that the cross-program collaborations continue and expand in the future.

The conference kicked off with a touching Philip N. Benfey Memorial Symposium, which is available on YouTube (<https://www.youtube.com/watch?v=QCx1rPPg-Pw>). The conference had a total of 47 sessions including 10 plenary sessions with 37 talks: 4 keynote presentations (Dr. Keiko Sugimoto, Dr. Dolf Weijers, Dr. Seung Yon (Sue) Rhee and Dr. José Dinneny) and 33 additional talks including the inaugural NAASC Community Awards talks for “Excellence in Supporting Diversity, Equity, Inclusion & Belonging in the Arabidopsis Community” and “Dissemination of Arabidopsis Knowledge”. The final NAASC community award presentations were the “Philip N. Benfey Arabidopsis Community Lifetime Achievement Awards” (PACLA); awardee names are listed in the “Arabidopsis Community Awards” section below. Notably, ICAR 2024 featured ~300 additional talks in community organized sessions (9 workshops and 28 minisymposia) which highlighted cutting edge science, career development, and translation from Arabidopsis to crops and beyond. The community-organized minisymposia brought the most cutting-edge novel topics to the conference and highly diversified the speaker list. In addition, there were ~275 excellent posters presented in each of two poster sessions.

ICAR 2024 featured the 1st ICAR Science Art Show organized by NAASC member Cris Argueso with about 15 beautiful and creative entries. The conference dinner was hosted at the Salk Institute with iconic sunset views looking over the ocean. The Salk Institute provided sponsorship to lower ticket costs for the ~325 attendees. The 5th Weed Stampede 5K Fun Run/Walk had about 50 participants. NAASC organized the first Weed Stampede during ICAR 2011-Madison, USA.

In 2024, the top 2 finishers (pictured) were ->

#1 Isabella Burda, USA, time ~20:50

#2 Jim Fouracre UK, time ~21:30

Notably, Isabella and Jim took a slight wrong turn and completed ~5.3K vs the intended 5K!

The conference concluded with the Philip Benfey Arabidopsis Community Lifetime Achievement (PACLA) Awards panel. Three awardees joined in person (Dr. Joanne Chory, Dr. Joe Ecker, and Dr. Chris Somerville) and two by Zoom (Dr. Jeff Dangl and Dr. Elliot Meyerowitz). The awardees told stories of how they started working with Arabidopsis, some of their biggest achievements, and their ideas for the future. The video is available on YouTube (<https://www.youtube.com/watch?v=mJLtiHNI2M0>).



Additional North American Arabidopsis Steering Committee activities

- Professional development workshops & “My Plant Biology Story”
- Arabidopsis Community website and Reddit group
- Community awards
- ISP (Inclusivity Scholars Program) cohort mentoring & other DEIB initiatives
- Special issue of The Plant Cell focused on translational research from Arabidopsis to crops and other organisms
- ICAR-focused research topic in Frontiers in Plant Science
- Special Cell Biology Issue of Journal of Experimental Botany

Arabidopsis Community

The Arabidopsis Community has 444 members including 5 lifetime members and 35 members that were granted a membership waiver by request. Please join and become a member (<https://www.arabidopsiscommunity.org/join-ac>). Membership is open to all Arabidopsis aficionados from all geographic locations. The benefits of membership are:

- Early access to/discounts for NAASC-organized workshops and events
- Ability to nominate/be nominated for Arabidopsis community awards
- Access to the NAASC Arabidopsis Community (AC) Reddit board for sharing protocols, best practices, gear & reagent advice, resources, solutions to common problems, conversations, & discussions.
- Free job postings and listings
- 5% of member fees go to our Equity Fund to support of minoritized members & others with financial need
- Support of fundamental plant biology and DEIB initiatives in plant biology
- Opportunities to contribute to community initiatives
- (North American members only) Nomination, voting, and service eligibility for NAASC Board of Directors and Early Career Scholar members

Arabidopsis Community Awards

2024 marked the inaugural year of Arabidopsis 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. The inaugural PACLA awardees are:

Dr. Joanne Chory, Salk Institute for Biological Studies

Dr. Jeff Dangl, University of North Carolina, Chapel Hill

Dr. Joe Ecker, Salk Institute for Biological Studies

Dr. Elliot Meyerowitz, California Institute of Technology

Dr. Chris Somerville, University of California, Berkeley (emeritus) and Open Philanthropy LLC

NAASC Excellence in Supporting Diversity, Equity, Inclusion & Belonging in the Arabidopsis Community Awards for excellence in mentoring, supporting, training, and/or advocating for others that are members of under-represented communities. The inaugural awardees are:

Dr. Terri Long, North Carolina State University (NCSU)

Dr. Beronda Montgomery, Grinnell College

Dr. Román Ramos Báez, University of Chicago

Dr. Imani Madison, North Carolina State University (NCSU)

NAASC Dissemination of Arabidopsis Knowledge Awards for innovative teaching, outreach activities/initiatives, and/or communication for Arabidopsis & plant biology. The inaugural awardees are:

Dr. Alison Crowe, University of Washington

Dr. Molly Edwards, Science in Real Life

George Redei Seed Stock Award for the researcher that donates the most seeds to the Arabidopsis Biological Resource Center. The second annual awardee is:

Dr. Diana Wolf, University of Alaska, Fairbanks for donating 92 Arabidopsis kamchatica accessions in 2023.

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.

Selected Publications:

NAASC HIGHLIGHT: Yaschenko, A.E., Alonso, J.M., and Stepanova, A.N. (2024). Arabidopsis as a model for translational research. *Plant Cell*, koae065. <https://doi.org/10.1093/plcell/koae065>.

A comprehensive review summarizing the multitude of ways findings in Arabidopsis have been translated to crop plants and beyond.

Liu, P., Panda, K., Edwards, S.A., Swanson, R., Yi, H., Pandesha, P., Hung, Y.-H., Klaas, G., Ye, X., Collins, M.V., et al. (2024). Transposase-assisted target-site integration for efficient plant genome engineering. *Nature* 631, 593–600. <https://doi.org/10.1038/s41586-024-07613-8>.

The Slotkin lab has engineered a transposable element into a toolkit for sequence-specific insertion of DNA into plant genomes.

Olatunji D., Clark N.M., Kelley D.R. (2023) The class VIII myosin ATM1 is required for root apical meristem function. *Development* 150, dev201762. doi: 10.1242/dev.201762.PMID: 37306290

This paper demonstrates that plant-specific myosins can control cell division, which ultimately impacts organ size and stem cell proliferation.

Cao M., Platre M.P., Tsai H.H., Zhang L., Nobori T., Armengot L., Chen Y., He W., Brent L., Coll N.S., Ecker J.R., Geldner N., Busch W. (2024) Spatial IMA1 regulation restricts root iron acquisition on MAMP perception. *Nature*. 625, 750-759. doi: 10.1038/s41586-023-06891-y.

This paper reveals a mechanism through which the plant navigates the tradeoff between making iron bioavailable for itself and also for pathogenic bacteria.

Nolan, T.M., Vukašinović, N., Hsu, C.-W., Zhang, J., Vanhoutte, I., Shahan, R., Taylor, I.W., Greenstreet, L., Heitz, M., Afanassiev, A., et al. (2023). Brassinosteroid gene regulatory networks at cellular resolution in the *Arabidopsis* root. *Science* 379, eadf4721. <https://doi.org/10.1126/science.adf4721>.

Nolan used time-series single cell RNA-seq to show that the brassinosteroid signaling network regulates the transition from proliferation to elongation in the *Arabidopsis* root cortex.

Major Funding Sources

- US *Arabidopsis* Research is primarily supported by funding through the Federal Government via the National Science Foundation (NSF): <http://www.nsf.gov/>

- Additional support 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/>

International Conference on Arabidopsis Research ICAR2025

Ghent, Belgium

June 16th-20th 2025

<http://www.icar2025.com/>

Hosted at De Bijloke

6 Plenary Sessions

20+ Concurrents/Workshops

2x Poster Sessions

Social at Viernulvier Concertzall



Keynote Speakers

Paula Casati

Jiri Friml

Jane Parker



#ICAR2025

