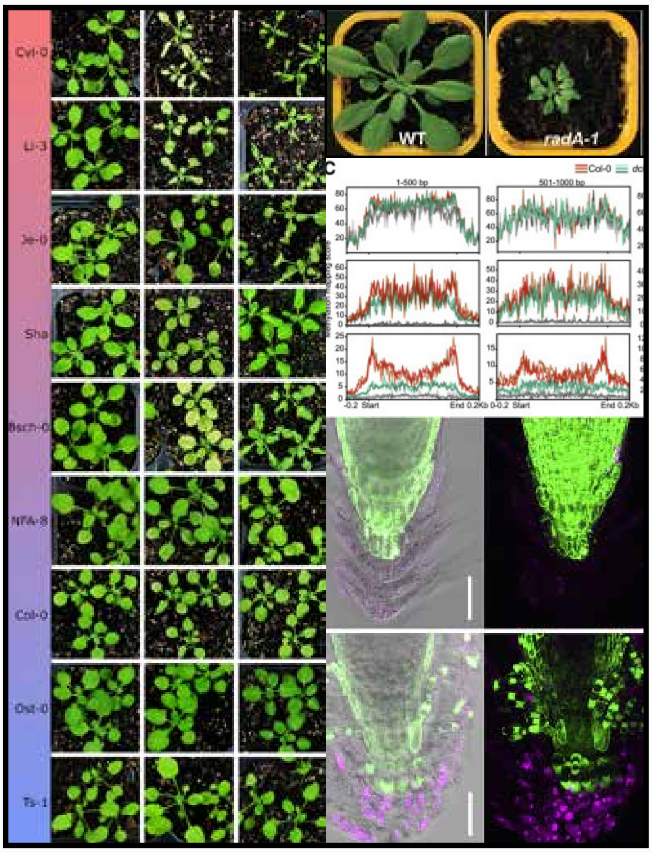
From Bench to Bountiful Harvests

Multinational Arabidopsis Steering Committee

Annual Report 2022-2023



MASC

Design and editing
Jamie Newbold
PhD student, Cranfield University, UK.
Arabidopsis Events UK Intern.

Geraint Parry
MASC Secretary, Arabidopsis Events UK
https://www.arabidopsisevents.uk/
arabidopsisventsuk@gmail.com

Cover images taken from Open Access publications

Left: Leppala *et al* (2022): Frontiers in Plant Science
https://www.frontiersin.org/articles/10.3389/fpls.2022.994779/full

Top Right: Chevigny *et al* (2022) PLOS Genetics
10.1371/journal.pgen.1010202

Middle Right: Acre *et al* 2023 Cell Reports
https://www.cell.com/cell-reports/fulltext/S2211-1247(23)00040-2?_

Lower Right: Feng *et al* (2022): Current Biology
https://www.cell.com/current-biology/fulltext/S0960-9822(22)00487-0?

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:
http://Arabidopsisresearch.org/index.php/publications/masc-reports

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

- TAIR, The Arabidopsis Information Resource:
http://www.Arabidopsis.org/portals/masc/masc_docs/masc_reports.jsp

Published by the Multinational Arabidopsis Steering Committee (MASC) August 2023

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 2022-23.

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 04

Activities of MASC 07

ICAR2023 Report 14

MASC Subcommittee Reports 16

MASC Project Reports 24

MASC Country Reports 39

The Multinational Arabidopsis Steering Committee

Annual Report 2022/2023

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

Rodrigo A. Gutiérrez
rgutierrez@bio.puc.cl
Yuling Jiao
yuling.jiao@pku.edu.cn
Masatomo Kobayashi
kobayasi@rtc.riken.jp
Shahid Mukhtar
smukhtar@uab.edu

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 Varation and Comparative Genomics
J. Chris Pires
chris.pires@colostate.edu
Ya-Long Guo
yalong.guo@ibcas.ac.cn

Plant Immunity
Shahid Mukhtar
smukhtar@uab.edu

Proteomics
Joshua Heazlewood
jheazlewood@unimelb.edu.au

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 Representatives

Argentina
Gabriela Auge
gauge@leloir.org.ar

Australia
Monika Murcha
monika.murcha@uwa.edu.au

Austria
Marie-Theres Hauser
marie-theres.hauser@boku.ac.at
J. Matthew Watson
james.watson@gmi.oeaw.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
Lynette Brownfield
lynette.brownfield@otago.ac.nz

Norway
Thorsten Hamann
thorsten.hamann@ntnu.no

Poland
Robert Malinowski
rmal@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 the 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 Nicholas Provart, Siobhan Brady and Geraint Parry respectively. These people have been in post since MASC Inc was incorporated in 2017 and so to move MASC forward we feel it is important that 'fresh-ideas' are brought into the team. Therefore over the coming year we are hoping to attract new people to take on the official positions. These are unpaid roles although there can be reimbursement for relevant expenses. In the meantime, Nicholas Provart will take on the role of Treasurer, while Siobhan Brady has agreed to be interim President.

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. To ensure that only two directors rotate off the board the initial term lengths will be less than 4 years. In 2021 and 2022 four directors have rotated off the list of directors but have not been replaced. In the upcoming MASC Annual meeting the membership of MASC (comprising the members of MASC subcommittees, MASC projects and Country representatives) hope to nominate up to six new members to become Directors. If you are interested in filling one of these positions, then 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 length of their terms. You will see that Rodrigo and Masatomo are also due to leave the group at the end of 2023 so we also look for their replacements.

- 2018-2023: Rodrigo Gutierrez (Chile), Masatomo Kobayashi (Japan)
- 2020-2024: Shahid Mukhtar (United States of America), Yuling Jiao (China)

In the upcoming election we aim to improve the gender balance on the board of directors as well as maintaining geographical diversity.

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 will directly pay 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 paid by MASC Inc to oversee its activities, which remain at the minimum level (anticipated to be a total 4 hours in 2023) to maintain the activity of the organisation. During the spring of 2023 Jamie Newbold, a PhD student at the Cranfield University in the UK, collated the MASC Annual Report as part of his Industrial Placement with Dr Parry's company, Arabidopsis Events UK..

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 ICAR2023 in Chiba, Japan the Bioinformatics subcommittee group organised an ‘Arabidopsis Informatics’ workshop and the MASC leadership organised a workshop on ‘MASC: Arabidopsis for SDGs/4th Decadal Vision’.

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 24 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 August 16th 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.

International Conference on Arabidopsis Research (ICAR)

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

ICAR2022 was the first in-person ICAR meeting since 2019 and was hosted as a hybrid event in Belfast, UK. The ongoing COVID19 pandemic meant that there was significant uncertainty ahead to the meeting but despite a lower-than-planned number of in-person attendees the meeting was able to break-even.

In 2023 the community came back together in full force with over 1200 attendees travelling to Chiba, Japan for ICAR2023. The organisers reported over 800 attendees were from outside of

Japan. There was a pleasingly high number of attendees from India, which highlights the growing importance of Arabidopsis research in that part of the world. In addition it might also nod toward recent challenges of Indian scientists receiving VISAs to the USA or Western Europe. Therefore, the meeting in Japan provided an excellent opportunity for researchers from India and the ‘East’ to attend an international plant science conference. We are delighted that Jessica Pritchard from the University of Liverpool in the UK has written a report from the meeting that can be read over on the next pages.

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:

- 34th ICAR, United States of America. July 15th-19th 2024. https://icar2024.weebly.com/

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

We are looking for a location for the ICAR scheduled to be held in 2026. The regular schedule would see this event organised somewhere away from Europe or 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.

It is important to note that NAASC has continued to be involved with the ROOTandSHOOT project which looks to improve accessibility within the plant sciences.

A PDF of the updated Code of Conduct for ICAR2024 can be downloaded here.

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.

These resources can be found here:¬

MASC subcommittees:
http://Arabidopsisresearch.org/index.php/en/subcommittees

MASC Projects and Resources:
http://Arabidopsisresearch.org/index.php/en/projects-resources

MASC Country reports:
http://Arabidopsisresearch.org/index.php/en/countries

If you would like to suggest any changes or content to be added to the MASC website then please contact Geraint Parry (arabidopsiseventuk@gmail.com).

Moving toward 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 preparation of the fourth decadal Roadmap has been in the works for the past few years, which will be a document looking toward 2030 and the future of the Arabidopsis research community. Arguably the greatest achievement of these years came with the sequencing of the Arabidopsis genome in 2020, which was reflected on in a recent publication (Provart NJ et al. [2020]: Anno genominis XX: 20 years of Arabidopsis genomics. Plant Cell. doi: 10.1093/plcell/koaa038).

The third decadal roadmap published in 2012 included the following broad recommendations:

1. Build a Predictive Model of an Arabidopsis Plant from its Molecular Parts
2. Build the International Arabidopsis Informatics Consortium, an International Informatics and Data Infrastructure
3. Exploit the Wealth of Natural Variation That Exists in Arabidopsis to Further Our Understanding of Adaptation and Evolution
4. Establish an Effective Knowledge Exchange Pipeline from the Laboratory to the Field and Vice Versa
5. Deepen International Cooperation and Coordination.

Progress has been made in each of these areas but work remains to be done. At the end of this decadal period, we now understand much more about the molecular and biochemical events that control how a plant grows and senses its environment. However there remain significant gaps in our knowledge, including a lack of understanding of the linkages between available 'omic datasets. Improvements in this area are needed to build a fully predictive model, which efforts like the Plant Cell Atlas project will help to address (https://www.plantcellatlas.org/). Fortunately, there is an acknowledgement that bioinformatics training and the development of digital infrastructures are key for the future in depth analysis of Arabidopsis-derived datasets.

At ICAR2023 MASC held a workshop entitled 'MASC: Arabidopsis for SDGs/4th Decadal Vision'. On the following pages Nick Provart has provided a short review of this event and its outcomes as we build together publication of this Vision.

MASC Workshop: 4th Decadal Vision for Arabidopsis / Arabidopsis for the UN's Sustainable Development Goals

June 8th 2023, 2-3.30 pm

Summarized by Nicholas Provart.

This workshop consisted of 5 panelists with broad geographic and demographic representation, with moderation by Nicholas Provart, the MASC president, and an introduction by Masatomo Kobayashi, the MASC Director from RIKEN BRC. The panelists were Dirk Inze from the VIB at the University of Gent Center for Plant Systems Biology in Belgium; Gabriela Auge from iB3, University of Buenos Aires, Argentina; Mentewab Ayalew, Department of Biology, Spelman College / NAASC representative; Kazuki Saito, RIKEN Center for Sustainable Resource Science in Japan; and Sureshkumar Balasubramanian, Biological Sciences at Monash University in Australia. There were about 25 people in the audience, who participated in the discussion in the 2nd half of the workshop.

The panelists were asked to summarize in a few slides where they thought the future of Arabidopsis research might lie, and to what extent Arabidopsis research could help achieve the UN's 17 Sustainable Development Goals (SDGs), most obviously "2: Zero Hunger", "13: Climate Action", and "15: Life on Land". In addition, participants will discuss how Arabidopsis research can help address important plant science questions, such as the one hundred questions posed in Armstrong et al. (2023; doi. 10.1111/nph.18771) and the kinds of projects that might be considered as part of a 4th decadal vision for Arabidopsis research.

After an introduction by Kobayashi, who highlighted the historical significance of MASC in promoting international collaboration and data sharing in Arabidopsis research, Provart stressed the importance of community input in shaping the fourth decadal vision for Arabidopsis research. He emphasized the ongoing opportunities for research in Arabidopsis, despite substantial progress since the Arabidopsis genome was sequenced in 2000. Provart also discussed MASC's role in coordinating projects and setting roadmap goals, drawing inspiration from the top 100 questions in plant biology identified by Armstrong et al. (2023).
Inze also emphasized the significant contributions of Arabidopsis to plant knowledge and its application in various plant processes and crop improvements. He encouraged further exploration of gene networks, proteome research, AI and machine learning, (pan-)genome-wide variation, and multiplex gene modifications. Inze advocated conducting research closer to real-world conditions to address global challenges effectively.

Auge presented Arabidopsis as a versatile tool for diverse research questions, ranging from ecological and evolutionary biology to molecular biology. She discussed her lab's translation of Arabidopsis findings to natural and agricultural ecosystems, aiming to address SDGs through sustainable agricultural practices and innovative tools for agriculture (targeting "2. Zero Hunger"). Auge also highlighted the importance of equitable access to resources to foster comprehensive research, which might fall under SDG 10: "Reduced Inequalities".

Ayalew discussed NAASC's efforts to foster diversity among researchers and promote workforce development (again, SDG 10). Ayalew highlighted the importance of computational and modeling approaches in pushing the boundaries of plant science. She also thought Arabidopsis could help solve issues related to crop transformation, multi-stress resistance, and herbicide resistance.

Kazuki Saito talked about RIKEN's efforts to address SDGs through six flagship projects involving plant biotechnology. He discussed the potential of plant science in conserving biodiversity, producing biodegradable materials, and improving agricultural efficiency by reducing runoff (thus help with SDG 14: "Life Below Water" and SDG 6: "Clean Water and Sanitation". Saito highlighted the need for interdisciplinary cooperation, risk-tolerant funding, and attracting bright minds to plant research careers.

Balasubramanian emphasized better communication regarding the potential impact of Arabidopsis research on human health (SDG 3: "Good Health and Well Being") and other sectors. He stressed the importance of accessibility and criticized reliance on metrics and university rankings as barriers to equality and opportunity (touching on SDG 1: "No Poverty", SDG 4: "Quality Education", and SDG: 5 "Gender Equality". Balasubramanian encouraged integrating AI and programming in Arabidopsis research to address future challenges effectively.

Part 2 - Discussion Summary:

The audience members and panelists engaged in a lively discussion covering various aspects of soliciting ideas and coordinating research in the Arabidopsis community.

1. Increasing Computational Approaches: Provart suggested a computational Arabidopsis competition to build a computational model of Arabidopsis growth and development, fostering interdisciplinary collaboration and innovation. Ayelew pointed out that there's been a shift and that Arabidopsis community has evolved to embrace quantitative and computational approaches, opening opportunities for such interdisciplinary competitions and hackathons. Can there be a ChatGPT for Arabidopsis data?

2. Supporting Research and Training: The importance of supporting Arabidopsis research and training for the 21st century was discussed as a means to bolster research efforts.

3. Studying Genes in Arabidopsis and Translating Results to Crops: The value of studying genes unique to Arabidopsis was debated, but it was agreed that Arabidopsis played an important role in understanding basic mechanisms and in helping these to be applied in other species. Suggestions from Galina Brychkova and Mary Williams about having agronomists and crop scientists (e.g., those part of DSSAT.net) participate in Arabidopsis publications and conferences might help address real-world applications and challenges more effectively.

4. Accessibility and Diversity in Conferences: Making conferences accessible and diverse by rotating them in different regions and encouraging top scientists to attend was emphasized to foster collaboration and exchange of ideas.

5. Soliciting Ideas for the 4th Decadal Vision: The panelists explored different approaches to gather ideas and visions for Arabidopsis research from the community, such as using platforms like Twitter blasts, SurveyMonkey links, open-ended questions, and ranking priorities. Auge proposed utilizing the country representatives of MASC to share and prioritize ideas regionally. Inze suggested involving Plant Cell and other journals to help with soliciting ideas from a diverse audience.

6. Coordinating Research Efforts and MASC's Role in Experiment Planning: The panelists highlighted the need for better coordination in Arabidopsis research, proposing a database or platform to connect researchers working on similar topics. Provart discussed the potential role of MASC in coordinating research efforts and planning experiments, drawing inspiration from successful initiatives like GreenNet. Ayelew stressed the importance of involving researchers from the Global South and fostering collaborations and training opportunities, while Tanya Berardini proposed transforming MASC reports into active opportunities for collaboration, facilitating connections among researchers seeking partners. It was suggested to use the MASC website or a similar platform to facilitate real-time connections among researchers seeking collaborations, making the process more dynamic and efficient.

For the next steps, it might be useful to poll MASC to see what its suggestions are for a 4th decadal vision. Do we need to collect more questions, or is the Armstrong et al. (2023) survey already enough and our job is to figure out how Arabidopsis can help answer those questions? Does MASC need to help coordinate projects if a single lab can already generate a seed-to-seed single cell RNA-seq atlas? Can NAASC and other organizations help with drafting a 4th decadal vision that includes a diversity of researchers? Stay tuned!

Report from ICAR2023 in Chiba, Japan

Jessica Pritchard, Jessica.Pritchard@liverpool.ac.uk

PhD student, James Hartwell lab, University of Liverpool, UK

My first (and hopefully not last) ICAR - ICAR23

As a ‘COVID-baby’ 4th year PhD candidate who started in October 2019, this year has been my first chance to travel long distances for conferences. I have always longed to visit Japan and as soon as I saw ICAR23 would be held just outside Tokyo in Chiba, I immediately jumped at the chance. It was also a good time to showcase some of the work I’ve done over the last few years, just before I settle into thesis writing madness. With my partner in tow, we arrived in Tokyo two days before the conference began. Exploring a couple of areas of Tokyo like Shibuya and Shinjuku was a great introduction. Then we headed to Chiba on a short train journey and checked into the conference held at Makuhari Messe, ready for ICAR23 to begin!

The first day started after lunch with a choice of workshops. I attended the “Integration of engineering, plant sciences, and agricultural research for translational research” as crop improvement is very high on my interest list and something I’ve tried to explore through a PIPs placement at CIAT in Colombia. It was also great to feel ICAR embracing research from other species, as my own PhD project uses the CAM model Kalanchoe as well as Arabidopsis. The workshop highlighted collaborative innovations between computer scientists, engineers, mathematicians and plant scientists. I especially loved the end to this session where the organisers Lucia Strader and Ross Sozzani outlined how they’ve built wider research communities and the need for us to work in a “trans-disciplinary” way, taking us through some step-by-step tips on building healthy research networks. There were then two brilliant keynotes by Kazuko Yamaguchi-Shinozaki and Dirk Inzé which demonstrated years of work, and then a welcome reception. Between Asahi’s, it was great to chat to fellow PhDs from all over the world, and compare notes on what had brought us here, the science we were doing and whether we’d tried out the ‘Onsen’ in our hotels yet.

Highlights of the next day, for me included a session “the environmentally responsive plant epigenome”, where I really enjoyed a talk by Doris Wagner on reprogramming cell identity and function in response to environmental and internal cues. Another important session for me was “Understanding circadian regulation in unpredictable environments” led by Anthony Dodd and Tokitaka Oyama, as it held some talks that were particularly pertinent to my own research. It felt great to be in a session where I could take away so much and think about it in the context of my own work, and I even worked up the courage to ask a question - terrifying! The evening of day two meant it was time to present my poster (also terrifying) along with a few hundred other people. I’m grateful for the opportunity to discuss my work in a group of experts and was really lucky so many people came and asked insightful questions, testing my own knowledge. It was also great to have a look round and speak to other people presenting, at every level. Attending a conference solo is quite intimidating but the poster session helped me appreciate we were all in it together and we all have something valuable to contribute.

The next day followed a similar format with sessions throughout the day and a poster session in the evening. My best bits from this day included a talk from Frank Johannes, introducing the idea of an epigenetic evolutionary molecular clock, Rebecca Roston who spoke wonderfully about cold tolerance of membranes and their circadian timing bringing together traditionally diverse topics in a nuanced way, and a poster about single cell regeneration presented as a monopoly board by Kelsey Reed - I'm passionate about posters that break the mould!

Day four, I attended a few sessions including talks on quantifying biochemical processes, discussing the innovations in plant genome engineering and one regarding visulaising the dynamics of the clock. Lots of the talks in the engineering session blew my mind with how far we've come since the first use of CRISPR technology and the possibilities today from tissue specific editing using RNA viruses to whole chromosome rearrangements. Also on this day there was the panel "Diversity and inclusion for excellence in science" which included wonderful speakers, representing and discussing different EDI issues from all over the world. It became clear that EDI is a highly location dependent issue and broadened my thinking, building from experience working overseas, that different communities face different challenges across the world and that as science is international, our solutions to these issues must reflect this. There was a lively conversation about addressing how to get everyone in the plant science community to engage in difficult conversations about power structures, sexism, racism, homophobia, transphobia, and other minority issues. Overall, it was lovely to feel a sense of community, and brainstorming ideas of how to increase diversity and inclusion, from the perspectives of PIs all the way down to us PhDs was inspiring. More panels and groups like this please!

Thursday night some of the attendees were off to the ICAR23 banquet. This was quite the experience, where at a dock near Tokyo bay we boarded traditional 'Yakatabune' wooden boats. There was an array of food including tempura, sashimi, a hotpot and free flowing Sake and plum wine. All in all it was a lovely last evening, and sadly for me was the end of the conference. I had an early train the next morning to start my travels through Japan, where we visited Kawaguchiko and caught a glimpse of Mount. Fuji, then got the bullet train to Osaka - which we mainly ate our way round - and finally had a day trip to historical Kyoto, before flying back to the UK. I'm really grateful to the organisers of the conference for hosting and welcoming us to a beautiful country that's long been on my bucket list and thanks to the BBSRC NLD DTP for my funding to attend.

Here's to the next ICAR!

MASC Subcommittee Reports

Bioinformatics 17

Epigenetics and Epigenomics 19

Natural Variation and Comparative Genomics 20

Plant Immunity 21

Systems and Synthetic Biology 23

Bioinformatics

Nicholas Provart, University of Toronto (nicholas.provart@utoronto.ca)
Leonore Reiser, TAIR
Tanya Berardini, TAIR

TAIR: New gene function data were added on a weekly basis to TAIR's databases, 1079 new/updated locus summaries, 1082 new/updated gene symbols, 4938 articles linked to 10539 genes, 15387 experimental Gene Ontology (GO) and Plant Ontology (PO) annotations, 876 new/updated alleles, and 1835 phenotypes linked to germplasms. Many GO associations were provided by individual researchers who submitted the updates via TAIR's Generic Ontology Annotation Tool. As usual, GO annotations were exported on a quarterly basis to the GO Consortium, and TAIR also provided quarterly public data releases with the updated data available after one year. Additional new data tracks provided by community members were added to the JBrowse instance TAIR rescued from Araport, including stress sORF encoded peptides and intergenic Transcriptionally Active Regions (TARs) that are induced by Oxidative Stress in Arabidopsis (Hazarika, De Coninck, Yamamoto, Martin, Cammue, and van Noort, 2017). Phylogenes (www.phylogenes.org) was updated to version 4.1 which includes trees from a new PANTHER 17.0 build and up to date GO annotations from the Gene Ontology Consortium (www.geneontology.org). Last, the Textpresso application has been updated to enable full text searching of over 50,000 Arabidopsis papers.

BAR: The BAR added an overarching search tool called Gaia to its homepage, which includes a Blast search option, whereby sequence matches to a given query are linked via their gene identifiers to their respective expression views in the BAR's eFP Browser and/or ePlant tools. Other nice features of Gaia include showing the top 10 expression hotspots for the gene, its interactors, linkouts to highly-cited publications and relevant tools. Gaia also indexes 67,291 Arabidopsis papers with 155,175 figures of which 11,205 are genetic models – these were identified using a triplet network (Hoffer and Ailon, 2018). We extracted 9,457 unique terms from the models by OCR using the Google Vision AI and these are highlighted in the figures if they match your search term. The BAR curators also enabled 26,782 Alphafold2 structures to be viewed in ePlant along with corresponding non-synonymous polymorphisms from the 1001 Genomes Project in the Molecule Viewer of ePlant. The BAR upgraded Thalemine to the current version based on the InterMine 5.10.0 release, with data updates from many sources from 2022-10-03. The BAR implemented a Nematode Infection view with much help as a beta-tester for our new Custom eFP Tool from Sebastian van den Akker (Siddique et al., 2022). We added 483 interactors for BIN2 to our Arabidopsis Interactions Viewer database (Kim et al., 2023).

An Arabidopsis genome update is coming! In October 2022, Tanya Berardini of TAIR and Nicholas Provart of BAR organized a conference call for members of the Arabidopsis genome sequencing and annotation community to hash out a plan for producing a new structural annotation of the A. thaliana Col-0 genome, to update the Araport11 version, released in June 2016. The community-driven process will encompass five steps: genome assembly, automated annotation, manual review, submission to GenBank/EBI/DDBJ, and dissemination. The Col-CC ("community consensus") assembly consisting of several groups telomere-to-telomere Col-0 sequences was submitted to GenBank at the end of 2022 by the Schneeberger group (Max Planck Institute for Plant Breeding Research/Maximilians-University Munich). In January 2023, GenBank curators approved this assembly for public release (https://www.ncbi.nlm.nih.gov/assembly/GCA_028009825.1), which the NCBI Eukaryotic Annotation team then ran through their automated annotation pipeline and completed in mid-April 2023. The review process has begun with an initial assessment of similarities and differences between V12 and Araport11. The TAIR team will coordinate the subsequent community-driven manual review process and will set up a WebApollo instance using the Col-CC assembly as the reference sequence, the predicted annotation from the NCBI team and the supporting evidence tracks that were used in the prediction pipeline. Follow progress at https://conf.phoenixbioinformatics.org/display/COM/A.+thaliana+Col-0+v12+reannotation+effort!

Large-scale Data Sets and Methods of Note: In a technical tour-de-force Travis Lee and colleagues in the Ecker Lab announced a seed-to-seed single cell RNA-seq expression atlas from more than 800,000 nuclei for Arabidopsis, available as a pre-print and explorable at http://arabidopsisdevatlas.salk.edu/ (Lee et al., 2023). Many of the same authors also published a “Time-resolved single-cell and spatial gene regulatory atlas of plants under pathogen attack“ using the Arabidopsis-Pseudomonas syringae pathosystem to explore how singe cells respond in leaves of DC3000, AvrRpt2 and AvrRpm1 infect plants (Nobori et al., 2023), see http://plantpathogenatlas.salk.edu. The Lewsey Lab’s scRNA-seq data set from germinating seeds showed that cells of the embryo pass through a common transcriptional state before establishing cell-type-specific profiles (Liew et al., 2023). Hainan Zhou and colleagues in Jiming Jiang’s group at Michigan State University and elsewhere generated a data set of 749 putative super enhancers in Arabidopsis. For PPIs, Ziding Zhang’s group at the China Agricultural University developed DeepAraPPI for predicting Arabidopsis PPIs using deep learning (Zheng et al., 2023), try it out at http://zzdlab.com/deeparappi. Sadly, Genevestigator announced at the end of December 2022 that it will no longer providing access to plant expression data. We recommend using the ~20,000 RNA-seq sample AthRDB (Yu et al., 2022) instead http://ipf.sustech.edu.cn/pub/athrdb/, from Jiaxin Zhai’s lab at the Southern University of Science and Technology (or the BAR ;-).

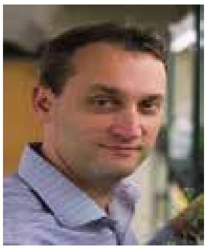
Pedagogy, Policy and Outreach: The Plant Cell Atlas continues to organize workshops on single-cell approaches in plant biology. Keep an eye on http://www.plantcellatlas.org/ for updates! TAIR continues its partnership with https://www.micropublication.org/, a platform for very short peer-reviewed reports. Nicholas Provart’s Plant Bioinformatics course on Cousera.org (https://www.coursera.org/learn/plant-bioinformatics/) was fully updated in June 2022.

References

Hazarika, R.R., De Coninck, B., Yamamoto, L.R., Martin, L.R., Cammue, B.P.A., and van Noort, V. (2017). ARA-PEPs: a repository of putative sORF-encoded peptides in Arabidopsis thaliana. BMC Bioinformatics 18: 37.
Hoffer, E. and Ailon, N. (2018). Deep metric learning using Triplet network.
Kim, T.-W., Park, C.H., Hsu, C.-C., Kim, Y.-W., Ko, Y.-W., Zhang, Z., Zhu, J.-Y., Hsiao, Y.-C., Branon, T., Kaasik, K., et al. (2023). Mapping the signaling network of BIN2 kinase using TurboID-mediated biotin labeling and phosphoproteomics. Plant Cell 35: 975–993.
Lee, T.A., Nobori, T., Illouz-Eliaz, N., Xu, J., Jow, B., Nery, J.R., and Ecker, J.R. (2023). A Single-Nucleus Atlas of Seed-to-Seed Development in Arabidopsis.: 2023.03.23.533992.
Liew, L.C., You, Y., Oliva, M., Peirats-Llobet, M., Ng, S., Tamiru-Oli, M., Berkowitz, O., Hong, U.V.T., Haslem, A., Stuart, T., et al. (2023). Establishment of cell transcriptional identity during seed germination.: 2023.01.21.523180.
Nobori, T., Monell, A., Lee, T.A., Zhou, J., Nery, J., and Ecker, J.R. (2023). Time-resolved single-cell and spatial gene regulatory atlas of plants under pathogen attack.: 2023.04.10.536170.
Siddique, S., Radakovic, Z.S., Hiltl, C., Pellegrin, C., Baum, T.J., Beasley, H., Bent, A.F., Chitambo, O., Chopra, D., Danchin, E.G.J., et al. (2022). The genome and lifestage-specific transcriptomes of a plant-parasitic nematode and its host reveal susceptibility genes involved in trans-kingdom synthesis of vitamin B5. Nat. Commun. 13: 6190.
Yu, Y., Zhang, H., Long, Y., Shu, Y., and Zhai, J. (2022). Plant Public RNA-seq Database: a comprehensive online database for expression analysis of ~45 000 plant public RNA-Seq libraries. Plant Biotechnol. J. 20: 806–808.
Zheng, J., Yang, X., Huang, Y., Yang, S., Wuchty, S., and Zhang, Z. Deep learning-assisted prediction of protein–protein interactions in Arabidopsis thaliana. Plant J. n/a.

Epigenetics and epigenomics

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

- International Conference on Arabidopsis Research, Chiba, Japan, June, 2023
  - Session on Plant Epigenetics and Chromatin Dynamics
  - The Environmentally Responsive Plant Epigenome
  - Transposable Elements, Epigenetics, and Environmental Adaptation
  - Arabidopsis Small RNA Biology

- Gordon Conference – Epigenetics, Holderness, NH, August, 2023

Selected Publications

Glucose-Driven TOR-FIE-PRC2 signalling controls plant development
Ruiqiang Ye, Meiyue Wang, Hao Du, Shweta Chhajed, Jin Koh, Kun-hsiang Liu, Jinwoo Shin, Yue Wu, Lin Shi, Lin Xu, Sixue Chen, Yijing Zhang, Jen Sheen
This study shows that the polycomb repressive pathway is sensitive to glucose-activated TOR signaling to control plant development.

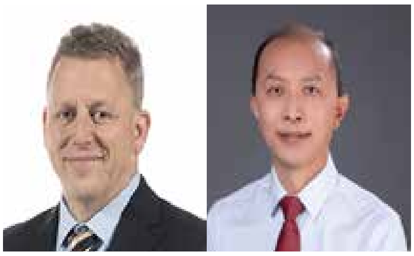
The histone H3.1 variant regulates TONSOKU-mediated DNA repair during replication.
Davarinejad H, Huang YC, Mermaz B, LeBlanc C, Poulet A, Thomson G, Joly V, Muñoz M, Arvanitis-Vigneault A, Valsakumar D, Villarino G, Ross A, Rotstein BH, Alarcon EI, Brunzelle JS, Voigt P, Dong J, Couture JF, Jacob Y.
This study presents the role of the H3.1 variant in recruiting TONSOKU to mediate DNA repair during post DNA-replication.

Local and global crosstalk among heterochromatin marks drives DNA methylome patterning in Arabidopsis.
To TK, Yamasaki C, Oda S, Tominaga S, Kobayashi A, Tarutani Y, Kakutani T.
This study shows how chromatin modification pathways are guided to targets by recognizing distinct modifications than the ones they enact.

Histone H2B.8 compacts flowering plant sperm through chromatin phase separation.
Buttress T, He S, Wang L, Zhou S, Saalbach G, Vickers M, Li G, Li P, Feng X.
This study shows that the histone H2B.8 can aggregate and compact chromatin in sperm cells and its absence leads to reduced male fertility.

Molecular basis of the plant ROS1-mediated active DNA demethylation.
Du X, Yang Z, Xie G, Wang C, Zhang L, Yan K, Yang M, Li S, Zhu JK, Du J.
This study presents the structure for ROS1, showing its substrate specificity and mode of action for demethylation of 5mC.

Natural Variation and Comparative Genomics



J. Chris Pires (jchrispires@gmail.com)
Colorado State University

Ya-Long Guo (yalong.guo@ibcas.ac.cn)
Institute of Botany, Chinese Academy of Sciences

Recent or Future activities of Subcommittee members

Beyond the model species Arabidopsis thaliana, many species of the family Brassicaceae have been sequenced and investigated deeply. In particular, studies of natural variation within model species continue to produce fascinating results. All these investigations may accelerate applied efforts ranging from crop improvement to the conservation of biodiversity. Subcommittee members jointly organized the XXIIIrd International Congress of Genetics will be held from 16-21 July 2023.

Selected Publications

Srikant T, Yuan W, Berendzen KW, Contreras-Garrido A, Drost HG, Schwab R, Weigel D. 2022. Canalization of genome-wide transcriptional activity in Arabidopsis thaliana accessions by MET1-dependent CG methylation. Genome Biol 23: 263. *This study reveals a dual role for CG methylation: for many genes, CG methylation appears to canalize expression levels, with methylation masking regulatory divergence. However, for a smaller subset of genes, CG methylation increases expression diversity beyond genetically encoded differences.*

Tergemina E, Elfarargi AF, Flis P, Fulgione A, Goktay M, Neto C, Scholle M, Flood PJ, Xerri SA, Zicola J et al. 2022. A two-step adaptive walk rewires nutrient transport in a challenging edaphic environment. Sci Adv 8: eabm9385. *This study provides a clear case of a multilocus adaptive walk and reveals how genetic variants reshaped a phenotype and spread over space and time.*

Gloss AD, Vergnol A, Morton TC, Laurin PJ, Roux F, Bergelson J. 2022. Genome-wide association mapping within a local Arabidopsis thaliana population more fully reveals the genetic architecture for defensive metabolite diversity. Philos Trans R Soc Lond B Biol Sci 377: 20200512. *This study used local populations complement geographically diverse mapping panels to reveal a more complete genetic architecture for metabolic traits.*

Reinar WB, Greulich A, Stø IM, Knutsen JB, Reitan T, Tørresen OK, Jentoft S, Butenko MA, Jakobsen KS. 2023. Adaptive protein evolution through length variation of short tandem repeats in Arabidopsis. Sci Adv 9: eadd6960. *This study showed that the length variations of short tandem repeats affect protein function and are likely adaptive, and the length variants modulating protein function at a global genomic scale has implications for understanding protein evolution and eco-evolutionary biology.*

Huang J, Yang L, Yang L, Wu X, Cui X, Zhang L, Hui J, Zhao Y, Yang H, Liu S et al. 2023. Stigma receptors control intraspecies and interspecies barriers in Brassicaceae. Nature 614: 303-308. *This study provides a breeding technology that breaks self-incompatibility and distant hybridization reproductive isolation, and makes it possible for Cruciferae to effectively use excellent gene resources in its relatives.*

Members of the subcommittee

Sureshkumar Balasubramanian sureshkumar.balasubramanian@monash.edu
Wolfgang Busch wbusch@salk.edu
Patrick Edger edgerpat@msu.edu

Plant Immunity

Dr. Shahid Mukhtar (smukhtar@uab.edu)
University of Alabama at Birmingham,Birmingham, AL, USA

Recently developed Open Tools and Resources for Arabidopsis Researchers

- EcoPLOT: dynamic analysis of biogeochemical data: Bioinformatics. 2022 Feb 7;38(5):1480-1482. doi: 10.1093/bioinformatics/btab842.
- EffectorO: motif-independent prediction of effectors in oomycete genomes using machine learning and lineage-specificity. (https://pubmed.ncbi.nlm.nih.gov/36853198/)
- PlantNLRatlas: a comprehensive dataset of full- and partial-length NLR resistance genes across 100 chromosome-level plant genomes (https://www.frontiersin.org/articles/10.3389/fpls.2023.1178069/full)
- WeCoNET: a host-pathogen interactome database for deciphering crucial molecular networks of wheat-common bunt cross-talk mechanisms (http://bioinfo.usu.edu/weconet/)
- TritiKBdb: A Functional Annotation Resource for Deciphering the Complete Interaction Networks in Wheat-Karnal Bunt Pathosystem. https://pubmed.ncbi.nlm.nih.gov/35806459/
- deepHPI: a comprehensive deep learning platform for accurate prediction and visualization of host-pathogen protein-protein interactions https://pubmed.ncbi.nlm.nih.gov/35511057/
- DWPPI: A Deep Learning Approach for Predicting Protein-Protein Interactions in Plants Based on Multi-Source Information With a Large-Scale Biological Network. https://pubmed.ncbi.nlm.nih.gov/35387292/
- PlantCV was updated: https://plantcv.danforthcenter.org/
- Large RNAseq co-expression dataset https://doi.org/10.1002/pld3.396
- NLRscape: an atlas of plant NLRs (https://nlrscape.biochim.ro/) – Martin et al., 2022 Nucleic Acid Research (https://doi.org/10.1093/nar/gkac1014)
- Single cell RNAseq datasets for plant immune responses - Single-cell profiling of complex plant responses to Pseudomonas syringae infection – Zhu et al., 2022, BioRxiv - https://doi.org/10.1101/2022.10.07.511353
- Time-resolved single-cell and spatial gene regulatory atlas of plants under pathogen attack – Nobori et al., 2023, BioRxiv - https://doi.org/10.1101/2023.04.10.536170

Recent or Future activities of Subcommittee members

- One of members of the plant immunity subcommittee organized workshop/conference sessions and presented talks and posters at various international conferences in 2022-2023, including the 14th IROAST International Symposium on plant development and Biotic Interaction held in Kumamoto University, and The annual meeting of plant pathology in Japan. One subcommittee member organized The International Helper- and Paired NLR Mini symposium – 20.-21. March 2023 – Tuebingen, Germany. The chair of the submitted organized and chaired the “Systems
- Biology and Machine Learning” workshop at the Plant and Animal Genome (PAG). The chair of the subcommittee organized and chaired a concurrent session on “systems biology of plant-microbe interactions”. ICAR2022, Belfast UK. June 2022.
- The subcommittee members will also organize an open lab in 2023. Several members of the subcommittee are planning to attend MPMI meeting. The chair of the submittee is organizing a concurrent session at MPMI meeting. The chair of the subcommittee is also organizing workshops at ICAR as well as PAG Australia and PAG 2024. Another member is planning to present their research at the VIII Brazilian Symposium on Plant Molecular Genetics, attending MPMI.

Selected Publications

- Jia A, Huang S, Song W, Wang J, Meng Y, Sun Y, Xu L, Laessle H, Jirschitzka J, Hou J, Zhang T, Yu W, Hessler G, Li E, Ma S, Yu D, Gebauer J, Baumann U, Liu X, Han Z, Chang J, Parker JE, Chai J. (2022) TIR-catalyzed ADP-ribosylation reactions produce signalling molecules for plant immunity. Science. 377(6605):eabq8180.
- Huang S, Jia A, Song W, Hessler G, Meng Y, Sun Y, Xu L, Laessle H, Jirschitzka J, Ma S, Xiao Y, Yu D, Hou J, Liu R, Sun H, Liu X, Han Z, Chang J, Parker JE, Chai J. (2022) Identification and receptor mechanism of TIR-catalyzed small molecules in plant immunity. Science. 2022 Jul 29;377(6605):eabq3297.
- *The above mentioned two articles show the molecular mechanisms of how TIR-containing proteins lead to the activation of signalling complexes of EDS1-SAG101-NRG1 and EDS1-PAD4-ADR1. These papers beautifully clarify the molecular basis connecting the missing link from the activation of TIR-containing proteins to the activation of signalling complexes of EDS1-SAG101-NRG1 and EDS1-PAD4-ADR1.*

- Liu L, Song W, Huang S, Jiang K, Moriwaki Y, Wang Y, Men Y, Zhang D, Wen X, Han Z, Chai J, Guo H. (2022) Extracellular pH sensing by plant cell-surface peptide-receptor complexes. Cell. 185(18):3341-3355.e13.
- *The article showed that plant cell-surface peptide-receptor complexes can function as extracellular pH sensors. The paper showed the molecular mechanisms of how extracellular pH affects the interaction between ligands and receptors and controls growth and immunity.*

- Ogawa-Ohnishi M, Yamashita T, Kakita M, Nakayama T, Ohkubo Y, Hayashi Y, Yamashita Y, Nomura T, Noda S, Shinohara H, Matsubayashi Y. (2022) Peptide ligand-mediated trade-off between plant growth and stress response. Science. 378(6616):175-180.
- *The article reported the identification of receptors for PLANT PEPTIDE CONTAINING SULFATED TYROSINE (PSY)-family peptides and showed how the recognition of PSY peptide controls the balancing growth and stress responses.*

- Kourelis J, Marchal C, Posbeyikian A, Harant A, Kamoun S. NLR immune receptor-nanobody fusions confer plant disease resistance. Science. 2023 Mar 3;379(6635):934-939. doi: 10.1126/science.abn4116. Epub 2023 Mar 2. PMID: 36862785
- *This article provides a plausible, generalizable strategy for engineering novel specificities for NLR immune receptors.*

Members of the subcommittee

- Dr. Yasuhiro Kadota, yasuhiro.kadota@riken.jp, RIKEN Center for Sustainable Resource Science (CSRS), Yokohama, Japan
- Dr. Karolina Mukhtar kmukhtar@uab.edu University of Alabama at Birmingham, AL, USA
- Dr. Farid El Kasmi, farid.el-kasmi@zmbp.uni-tuebingen.de, ZMBP – Center for Plant Molecular Biology, University of Tuebingen, Tuebingen, Germany
- Dr. Marc Nishimura, marc.nishimura@colostate.edu, Colorado State University, Fort Collins, CO, USA

Systems and Synthetic Biology

Siobhán Brady (sbrady@ucdavis.edu)
University of California, Davis

Recently developed Open Tools and Resources for Arabidopsis Researchers

- Functional annotation of proteins for signaling network inference: PF-Net and NetPhorce: (https://www.researchsquare.com/article/rs-2201240/v1)
- CentralityCosDist, an algorithm that ranks nodes based on a combination of centrality measures and seed nodes. Kumar N, Mukhtar MS. (2023) Ranking Plant Network Nodes Based on Their Centrality Measures. Entropy. 25(4):676.

Recent or Future activities of Subcommittee members

- International Conference on Arabidopsis Research 2022, Belfast, Northern Ireland. Session 1: Plant Logic; Session 2: Systems Biology of Plant-Pathogen Interactions
- Plant Systems Biology Conference at Cold Spring Harbor, December 2023
- New Gordon Conference on Single-Cell Approaches in Plant Biology, Ventura, California; July 30-August 4, 2023

Selected Publications

- Development of a collection of synthetic "parts" to create genetic circuits that can be used to predictably alter root structure. Brophy JAN, Magallon KJ, Duan L, Zhong V, Ramachandran P, Kniazev K, Dinneny JR. (2022) Synthetic genetic circuits as a means of reprogramming plant roots. Science. 377(6607):747-751
- An endodermis-specific nitrate regulatory network coordinated by the major hubs ABF2 and ABF3. Contreras-López O, Vidal EA, Riveras E, Alvarez JM, Moyano TC, Sparks EE, Medina J, Pasquino A, Benfey PN, Coruzzi GM, Gutiérrez RA. (2022) Spatiotemporal analysis identifies ABF2 and ABF3 as key hubs of endodermal response to nitrate. PNAS. 119(4):e2107879119.
- Single cell RNA sequencing is used to reveal a brassinosteroid regulatory network that coordinates the shift from root proliferation to elongation. Nolan TM, Vukašinković N, Hsu C-W, Zhang J, Vanhoutte I, Shahan R, Taylor IW, Greenstreet L, Heitz M, Afanassiev A, Wang P, Szekely P, Brosnan A, Yin Y, Schiebinger G, Ohler U, Russinova E, Benfey PN. (2023) Brassinosteroid gene regulatory networks at cellular resolution in the Arabidopsis root. Science. 379(6639):ead4721.
- A special issue of Plant Physiology focused on the application of single cell technologies to plant cell biology. https://academic.oup.com/plphys/pages/plant-cell-atlas-focus-collection

Members of the subcommittee
- Rosangela Sozzani, North Carolina State University
- Seung Rhee, Carnegie Institute of Plant Science
- Miriam Gifford, University of Warwick
- Lisa Van den Broeck, North Carolina State University
- Nicola Patron, Earlham Institute
- Siobhán Brady, University of California, Davis
- Gloria Coruzzi, New York University
- Gabriel Krouk, CNRS Montpellier
- Rodrigo Gutierrez, Universidad Católica de Chile

MASC Project Reports

Arabidopsis Biological Resource Center 25

BioAnalytic Resource (BAR) 26

EMPHASIS 28

Global Plant Council 29

Grameme 31

International Plant Phenotyping Network 34

Nottingham Arabidopsis Stock Centre (NASC) 35

RIKEN Bioresource Research Center 37

The Arabidopsis Information Resource (TAIR) 38

Arabidopsis Biological Resource Center

Emma Knee (knee.2@osu.edu)
David Somers (somers.24@osu.edu)
The Ohio State University

Recent activities of project

In 2022 ABRC distributed 98,564 samples to 1,579 individuals located in 43 countries. While the number of customers has remained approximately the same, this represents a significant increase in the number of samples shipped in comparison to 2020 and 2021. 60% of orders were shipped to researchers in the US, 11% to Japan, 6% to Korea, and 5% to Canada. Other countries each accounted for less than 5% of total orders. We also provided bulk seed to NASC for 1,953 lines, and smaller aliquots of seed to be grown at NASC for 2,153 lines. In addition, 2,281 individual samples were requested by NASC to be distributed to NASC users. ABRC received donations of 590 seed stocks in 2022. These included characterized mutant and transgenic lines as well as natural variants. 52 non-seed resources were also added to the collection including 40 ORF clones of transcription factors from Camelina sativa. 76% of donors were from the US, donations were also received from Canada, Mexico, China, Hong Kong, Germany and the UK.

The current collection is composed of almost 1 million stocks. Over 500,000 of these are Arabidopsis seed stocks including large mutant populations, individual characterized mutants, natural variants, and transgenic reporter lines. The collection also includes 1,733 seed stocks from 43 other members of the Brassicaceae. The non-seed portion of the collection numbers close to 450,000 stocks. These lines include individual clones and libraries from Arabidopsis thaliana, and other members of the Brassicaceae, as well as constructs, host strains, antibodies, cell lines and education resources. ABRC performed quality control testing for 2,807 new and existing stocks in 2022, involving either germination testing or verifying stock identity.

ABRC's outreach program served over 500 individuals in 2022 through participation in community events and distribution of education kits. ABRC was awarded funding for 5 years through the National Science Foundation (NSF) SIBR Sustaining program to partially support the ongoing activities of the Center.

Planned future activities of project

ABRC will continue to solicit donations of new resources with a particular focus on characterized Arabidopsis mutants including multiple (stacked) mutants. The ABRC is also in coordination with NAASC to initiate an annual George Redei award for the most seed donations within a calendar year from a single lab.

In 2023 ABRC plans to retire some non-seed resources that are infrequently ordered or have never been ordered. These include EST and BAC clones from other members of the Brassicaceae and Maize resources. Researchers interested in archiving or maintaining these resources should contact ABRC. Distribution of overall resources is expected to equal that of 2022 but will likely not show a complete recovery to pre-pandemic levels. Quality control testing of new donations and stocks reproduced at ABRC will be carried out at similar levels to 2022. ABRC and NASC collaboration via exchange of seed stock resources and related data will also continue. ABRC outreach will focus on in-person programming in collaboration with The Ohio State University and local community partners. The ABRC Director will attend ICAR 2023 and information about ABRC stocks and activities will be available at the NASC booth.

Bio-Analytic Resource for Plant Biology

Nicholas Provart (director) (nicholas.provart@utoronto.ca)
Asher Pasha (BAR bioinformatics technician)
University of Toronto (http://bar.utoronto.ca)

Open Tools and Resources for Arabidopsis Researchers

The Bio-Analytic Resource is a collection of user-friendly web-based tools for working with functional genomics and other data for hypothesis generation and confirmation. Most are designed with plant (mainly Arabidopsis) researchers in mind. Data sets include:

- 175 million gene expression measurements (100 million from Arabidopsis), plus “expressologs” (homologs showing similar patterns of expression in equivalent tissues) for many genes across 12 species. View expression patterns with our popular eFP Browsers or newer ePlant tools.
- More than 80k predicted protein-protein interactions, more than 100k experimentally determined PPIs and ~2.8 million protein-DNA interactions, which can be explored with our Arabidopsis Interactions Viewer 2 tool. The experimentally-determined interactions now include 21,910 interactions from the Marcotte Lab’s plant protein complex co-fractionation study (McWhite et al., 2020).
- ~55k predicted protein tertiary structures and experimentally determined structures for 402 Arabidopsis proteins (~26k AlphaFold2 models are now available in ePlant).
- Millions of non-synonymous SNPs from the 1001 Arabidopsis Genomes project, now delivered via the 1001 Genomes API.
- Documented subcellular localizations for 11.7k proteins, predicted localization for most of Arabidopsis proteome, from the SUBA database at the University of Western Australia.
- Thalemine (Pasha et al., 2020).

Recent activities of project

The BAR added an overarching search tool called Gaia to its homepage at bar.utoronto.ca, which includes a Blast search option, whereby sequence matches to a given query are linked via their gene identifiers to their respective expression views in the BAR’s eFP Browser and/or ePlant tools. Other nice features of Gaia include showing the top 10 expression hotspots for the gene, its interactors, linkouts to highly-cited publications and relevant tools. Gaia also indexes 67,291 Arabidopsis papers with 155,175 figures of which 11,205 are genetic models – these were identified using a triplet network (Hoffer and Ailon, 2018). We extracted 9,457 unique terms from the models by OCR using the Google Vision AI and these are highlighted in the figures if they match your search term. The BAR curators also enabled 26,782 Alphafold2 structures to be viewed in ePlant along with corresponding non-synonymous polymorphisms from the 1001 Genomes Project in the Molecule Viewer of ePlant. The BAR upgraded Thalemine to the current version based on the InterMine 5.10.0 release, with data updates from many sources from 2022-10-03. The BAR implemented a Nematode Infection view with much help as a beta-tester for our new Custom eFP Tool from Sebastian van den Akker(Siddique et al., 2022). We added 483 interactors for BIN2 to our Arabidopsis Interactions Viewer database (Kim et al., 2023).

Planned future activities of project

A custom eFP view in ePlant for a researcher’s own RNA-seq data is in beta-testing, check it out at https://bar.utoronto.ca/~dev/svg_editor_lite.

References

- Hoffer, E. and Ailon, N. (2018). Deep metric learning using Triplet network.
- Kim, T.-W., Park, C.H., Hsu, C.-C., Kim, Y.-W., Ko, Y.-W., Zhang, Z., Zhu, J.-Y., Hsiao, Y.-C., Branon, T., Kaasik, K., et al. (2023). Mapping the signaling network of BIN2 kinase using TurboID-mediated biotin labeling and phosphoproteomics. Plant Cell 35: 975–993.

- McWhite, C.D., Papoulas, O., Drew, K., Cox, R.M., June, V., Dong, O.X., Kwon, T., Wan, C., Salmi, M.L., Roux, S.J., et al. (2020). A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. Cell 181: 460-474.e14.
- Pasha, A., Subramaniam, S., Cleary, A., Chen, X., Berardini, T.Z., Farmer, A., Town, C., and Provart, N.J. (2020). Araport Lives: An Updated Framework for Arabidopsis Bioinformatics. Plant Cell.
- Siddique, S., Radakovic, Z.S., Hiltl, C., Pellegrin, C., Baum, T.J., Beasley, H., Bent, A.F., Chitambo, O., Chopra, D., Danchin, E.G.J., et al. (2022). The genome and lifestage-specific transcriptomes of a plant-parasitic nematode and its host reveal susceptibility genes involved in trans-kingdom synthesis of vitamin B5. Nat. Commun. 13: 6190.

EMPHASIS

Dr. Roland Pieruschka (r.pieruschka@fz-juelich.de) Forschungszentrum Jülich, IBG-2

Project aims

The Research Infrastructure for plant phenotyping, EMPHASIS, was integrated into the ESFRI Roadmap in 2016 because of its strategic importance in enhancing European research area excellence and attractiveness by addressing the plant phenotyping as the essential step towards advancement in plant sciences, agriculture, food systems, and bioeconomy. EMPHASIS fills an important gap within the RI ecosystem in Europe addressing primary plant production as the key step in agro-food-systems or bioeconomy. The overarching goal is to connect the national infrastructure and ensure their long-term sustainable operation. Currently EMPHASIS entered the implementation phase working with the Interim General Assembly (IGA), a board with ministry and scientific representatives from twelve countries (status June 2023) that have formally declared their intention of moving EMPHASIS towards operation that will include a sustainable provision of plant phenotyping services to the community.

Recent activities of project

EMPHASIS is involved in research infrastructure projects that aim at providing or developing new services towards thecommunity. Specifically:

- AI4Life (https://ai4life.eurobioimaging.eu/): Building digital space for the life sciences and providing access to AI method development, and biological imaging as urgently needed services through the European trans-national and virtual access scheme.
- AgroServ: Integrated SERVices supporting a sustainable AGROecological transition (https://agroserv.eu/). The project connects twelve different Research Infrastructures with the to support research and innovation by providing customized and integrated Research Infrastructure services in view of achieving a sustainable and resilient agriculture and supporting agroecological transitions. More specifically, this project will aim at advancing knowledge on agronomic and husbandry practices and supporting the development of new agroecological practices by providing access to the services of the twelve research infrastructures
- PHENET: Tools and methods for extended plant PHENotyping and EnviroTyping services of European Research Infrastructures (https://www.phenet.eu/) The project aims at developing next generation tools, methods and approaches towards sustainable agriculture and agroecological transition by addressing two mayor bottlenecks. (i) phenotyping and enveloping data generated by the involved research infrastructures are based on a limited number of sites with top-level instruments, which cannot cover the diversity of agroecosystems and environments (ii) data produced are still under-utilized, insufficiently connected and poorly interfaced with predictive models.

Planned future activities of project

Further research infrastructure project that will enable access to the EMPHASIS services are under evaluation and under development.

The Global Plant Council

Isabel Mendoza Poudereux, isabel@globalplantcouncil.org, The Global Plant Council

Introduction

This report provides an overview of the activities carried out by the Global Plant Council (GPC) between May 2022 and May 2023. The GPC is an international organization dedicated to promoting plant science research, knowledge exchange, and global collaboration. During this period, the GPC made significant strides in advancing plant science and addressing global challenges related to food security, climate change, and sustainable agriculture.

Recent activities of project

International Conferences, Webinars, and Workshops: The GPC actively participated in key international conferences and organized webinars and workshops to facilitate knowledge exchange and collaboration. In December 2022, the GPC attended the COP15 Convention on Biological Diversity in Montreal, Canada. Dr. Deena Errampalli presented a case study on “How DSI can revolutionize food security: understanding the Sterility Mosaic Disease of Pigeonpea” at a side event organized by the DSI Scientific Network. This event provided an opportunity to showcase the impact of digital sequence information (DSI) on agriculture.
Moreover, the GPC organized a series of webinars throughout the reporting period, bringing together over 1,000 researchers, scientists, policymakers, industry experts, students, and plant enthusiasts. These webinars covered various topics such as crop improvement, plant genetics, sustainable farming practices, and novel technologies for plant research. The webinars served as valuable platforms for sharing cutting-edge research and fostering global collaboration.

Advocacy for Plant Science: The GPC intensified its advocacy efforts to raise awareness about the importance of plant science and secure increased investment in research, innovation, and education. To enhance its influence, the GPC is part various coalitions and organizations, including the SPG Coalition, AIM for Climate, and the Convention for Biological Diversity (with observer status). Additionally, the GPC applied for observer or consultative status at the COP28 Climate Summit and the ECOSOC (United Nations Economic and Social Council).

Science Communication and Education: Recognizing the significance of science communication, the GPC actively supported initiatives to promote public understanding of plant science. The GPC encouraged scientists to engage with the public through online outreach activities. The organization organized online webinars and workshops, including an upcoming workshop at SEB2023, aimed at inspiring the next generation of plant scientists.

Additionally, throughout the period, we have diligently maintained and updated the over 250 resources hosted in our resources section (https://globalplantcouncil.org/resources/). This comprehensive collection encompasses various sections, including Useful (4), Awards (28), Policy (1), Education (18), Organizations (75), Reports (+40), potential funders (76), scicomm (4), and DSI (4). Furthermore, we have dedicated a specific section to DSI, providing valuable resources to navigate the scientific ecosystem and effectively manage DSI data (https://globalplantcouncil.org/activities/challenges/dsi-wg/).

Planned future activities of project

Looking ahead, the Global Plant Council has an exciting array of activities planned to promote plant science, collaboration, and science communication. In June 2023, the council will collaborate with Frontiers in Plant Science to organize a webinar on “AI, Sensors, and Robotics in Plant Phenotyping and Precision Agriculture.” This webinar will explore the latest advancements in technology and their applications in plant research and agriculture.

In July 2023, the council will conduct two online workshops on science communication, one in Spanish and the other in English, in partnership with Women in Crops Science. These workshops will focus on enhancing science communication skills and strategies, empowering researchers to effectively engage with diverse online audiences.

The council will also participate in the SEB2023 conference in Edinburgh, Scotland, in early July. This in-person event will feature a workshop on social media and science communication, facilitating discussions on leveraging digital platforms to disseminate scientific knowledge and engage with the public effectively.

Another important event on the council's agenda is attending the Climate Summit in Dubai in December 2023 as an observer. This engagement will enable the council to contribute to discussions on climate change and emphasize the role of plant science in mitigating its impacts.

Furthermore, the GPC's executive team will continue seeking new topics for webinars and exploring potential collaborations with other entities, ensuring that the council remains at the forefront of emerging trends and developments in plant science.

Conclusion

The Global Plant Council's activities between May 2022 and May 2023 showcased its commitment to advancing plant science, advocating for increased investment, and fostering science communication. Through international conferences, webinars, workshops, and advocacy efforts, the GPC played a pivotal role in promoting innovation, collaboration, and addressing global challenges related to agriculture, food security, and climate change. The future activities further reinforce the council's dedication to these goals, ensuring the continued advancement of plant science for a sustainable future.

Gramene

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

Marcela Karey Tello-Ruiz (telloruiz@cshl.edu)
Doreen Ware (ware@cshl.edu, doreen.ware@usda.gov)
Cold Spring Harbor Laboratory

Resources

The Gramene project (www.gramene.org) is a knowledgebase founded on comparative functional analyses of genomic and pathway data for model plants and major crops aiming to support agricultural researchers.

Gramene PanGenome resources:
https://maize-pangenome.gramene.org/
https://oryza.gramene.org/
https://vitis.gramene.org/
http://www.sorghumbase.org/

Recent activities of project

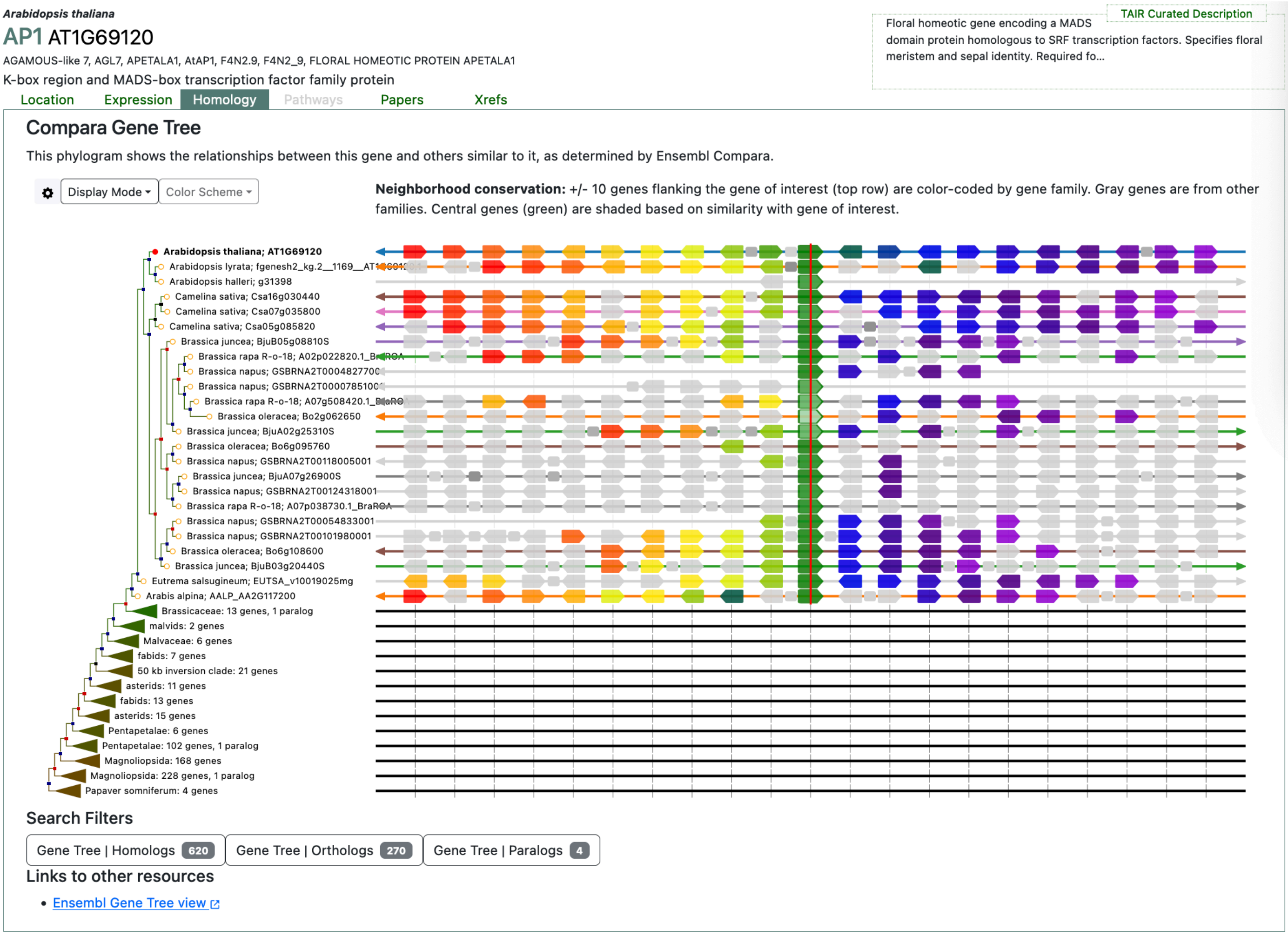
Arabidopsis is a central model organism for the comparative Gramene and Gramene Pan Genome Crop Species databases. In the past year, we had two data releases on Gramene (R65, May 2022; R66, Dec. 2022) and seven on its PanGenome resources (Oryza: R4 - May 2022; R5 - Oct. 2022, and R6 - Jan. 2023; Sorghum: R4 - July 2022, and R5 - Dec. 2022; Grape: R3 - May 2022; and Maize: R3 - March 2023). There were a total of 51 new genomes new genomes added across the sites (14 in Gramene, 11 in SorghumBase, 11 in Gramene Oryza, 8 in Gramene Maize, and 7 in Gramene Vitis), with orthologs/homeologs assigned to Arabidopsis. Pairwise whole-genome alignments with Arabidopsis were also added for Brassica juncea (brown mustard), Corymbia citriodora (lemon-scented gum), and Brassica rapa R-o-18 (which replaced cultivar Chiifu-401-42) in Gramene (see Figure 1), and for Sorghum bicolor ssp. bicolor cultivars BTx623, RTx430, RTx436, Tx2783, and Rio (PI 651496) in SorghumBase. Putative gene annotation artifacts (also known as contiguous gene split models) were calculated for every data release based on the corresponding Compara Gene Tree database. An example of a putative split gene model can be visualized for the AT5G17140 gene, part of the super family of Cysteine proteinases, suggesting that even in a well curated model like Arabidopsis, there still may exist gene structural annotation artifacts that can be improved (see Figure 2).

Also new this year was the integration of gene functional annotations from the literature for 7 184 Arabidopsis (see Figure 3), 4 006 rice, and 354 maize genes, sourced from NCBI's GeneRIF and RAP-DB. The access to these curated annotations were deployed in a new Publications tab as part of the results of our integrated search interface. This Publications tab renders a table of PubMed linked papers associated with a given gene, and its associated annotations, utilizing Trait Ontology (TO) or Plant Ontology (PO) terms, which are indexed and now searchable.

Planned future activities of project

We will continue to maintain and build the Gramene and Crop Pan-genome resources for maize, rice, sorghum and grapevine resources aiming to have a minimum of one release per year: 1) update and expand our reference data collection of plant genomes and standardized comparative gene annotations and metadata; 2) biocurate metadata for germplasm and genetic variation; 3) biocurate single-cell expression data; 4) biocurate gene functional annotations from the literature; and 5) transform the community through communication and training opportunities.

The Gramene portal is supported by the USDA-ARS (8062-21000-041-00D).



Arabidopsis thaliana

AP1 AT1G69120

AGAMOUS-like 7, AGL7, APETALA1, AtAP1, F4N2.9, F4N2_9, FLORAL HOMEOTIC PROTEIN APETALA1

K-box region and MADS-box transcription factor family protein

TAIR Curated Description

Floral homeotic gene encoding a MADS domain protein homologous to SRF transcription factors. Specifies floral meristem and sepal identity. Required fo...

Compara Gene Tree

This phylogram shows the relationships between this gene and others similar to it, as determined by Ensembl Compara.

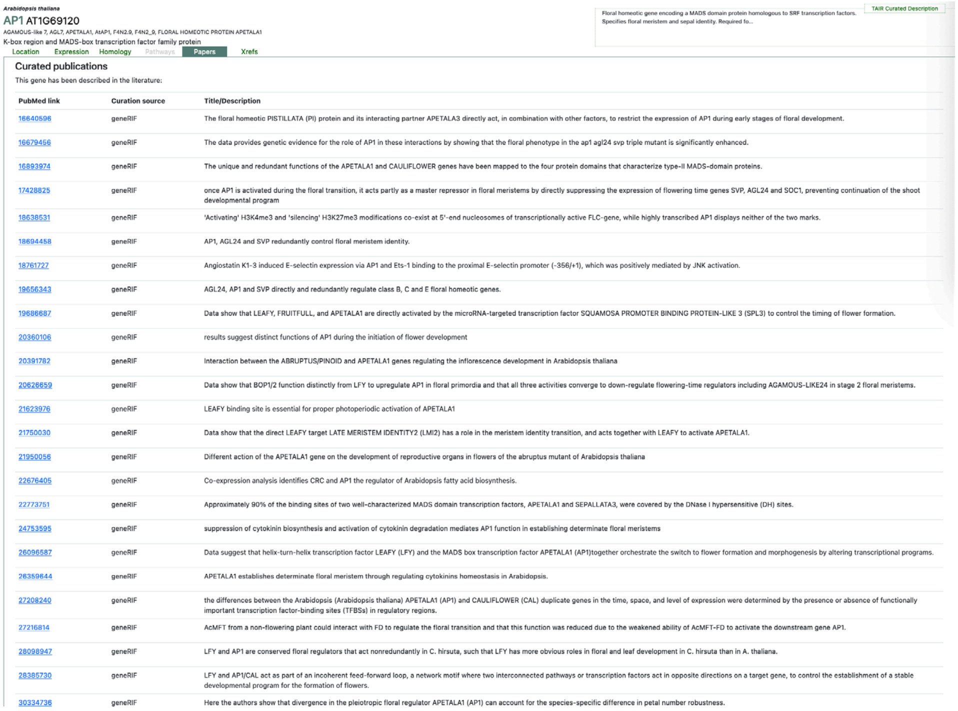
Neighborhood conservation: +/- 10 genes flanking the gene of interest (top row) are color-coded by gene family. Gray genes are from other families. Central genes (green) are shaded based on similarity with gene of interest.

Search Filters

Links to other resources

- Ensembl Gene Tree view

Figure 1. The gene neighborhood view of the Arabidopsis AP1 gene is complemented/improved with the addition of two additional Brassica genomes to Gramene in the past year: brown mustard (*Brassica juncea*, added in R66) and *B. rapa* R-o-18 (added in R65). The gene neighborhood for BjuB05g08810S, the closest *B. junacea* ortholog of AP1, appears to have higher conservation with the neighborhoods of the Arabidopsis spp AP1 genes than any of other Brassica species (*B. rapa, B. napus, and B. oleracea*).



Arabidopsis thaliana

AP1 AT1G69120

AGAMOUS-like 7, AGL7, APETALA1, AtAP1, F4N2.9, F4N2_9, FLORAL HOMEOTIC PROTEIN APETALA1

K-box region and MADS-box transcription factor family protein

TAIR Curated Description

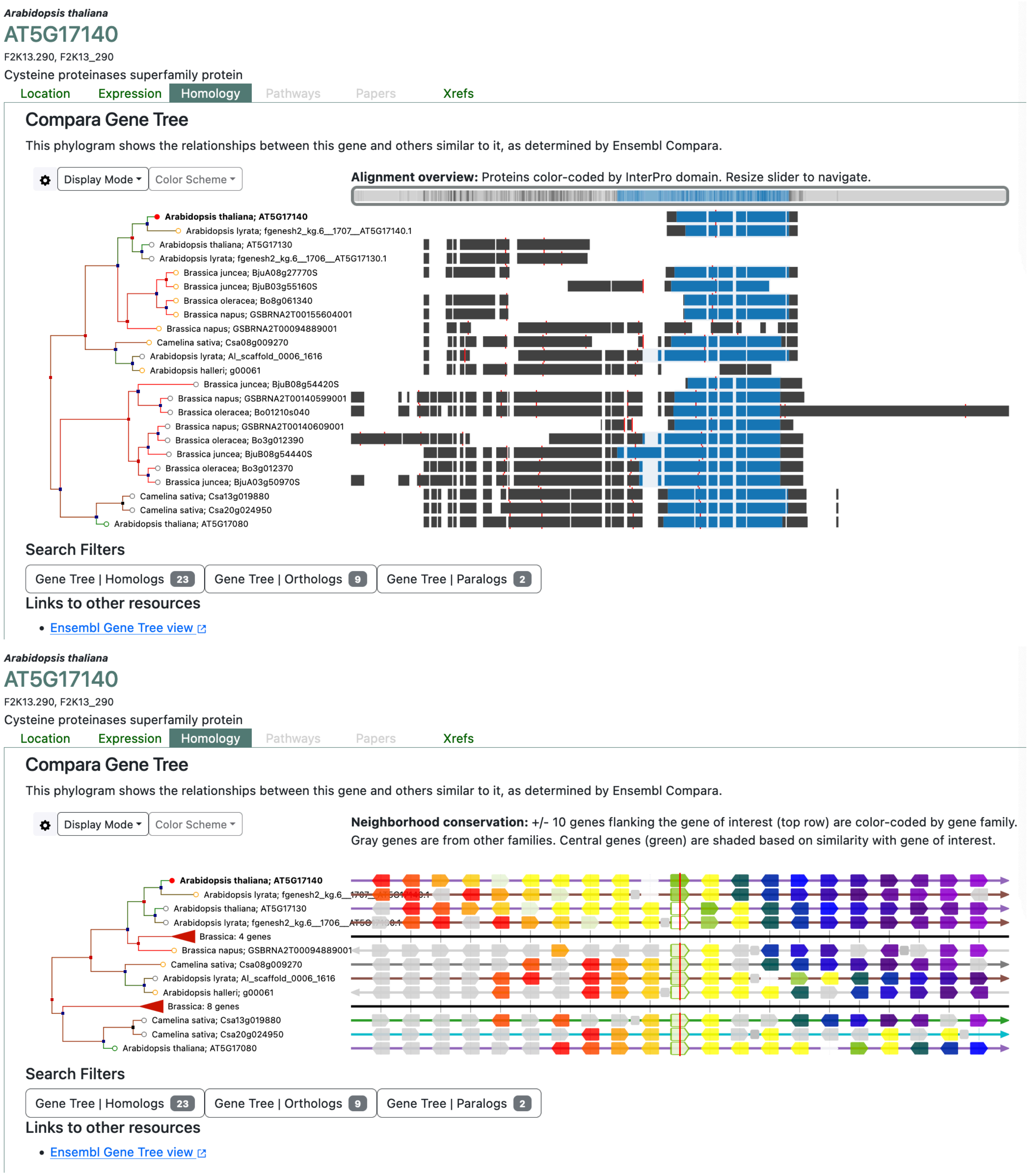
Floral homeotic gene encoding a MADS domain protein homologous to SRF transcription factors. Specifies floral meristem and sepal identity. Required fo...

Curated publications

This gene has been described in the literature:

PubMed link	Curation source	Title/Description
16640596	geneRIF	The floral homeotic PISTILLATA (PI) protein and its interacting partner APETALA3 directly act, in combination with other factors, to restrict the expression of AP1 during early stages of floral development.
16679456	geneRIF	The data provides genetic evidence for the role of AP1 in these interactions by showing that the floral phenotype in the ap1 agl24 svp triple mutant is significantly enhanced.
16893974	geneRIF	The unique and redundant functions of the APETALA1 and CAULIFLOWER genes have been mapped to the four protein domains that characterize type-II MADS-domain proteins.
17428825	geneRIF	once AP1 is activated during the floral transition, it acts partly as a master repressor in floral meristems by directly suppressing the expression of flowering time genes SVP, AGL24 and SOC1, preventing continuation of the shoot developmental program
18638531	geneRIF	'Activating' H3K4me3 and 'silencing' H3K27me3 modifications co-exist at 5'-end nucleosomes of transcriptionally active FLC-gene, while highly transcribed AP1 displays neither of the two marks.
18694458	geneRIF	AP1, AGL24 and SVP redundantly control floral meristem identity.
18761727	geneRIF	Angiostatin K1-3 induced E-selectin expression via AP1 and Ets-1 binding to the proximal E-selectin promoter (-356/+1), which was positively mediated by JNK activation.
19656343	geneRIF	AGL24, AP1 and SVP directly and redundantly regulate class B, C and E floral homeotic genes.
19686687	geneRIF	Data show that LEAFY, FRUITFULL, and APETALA1 are directly activated by the microRNA-targeted transcription factor SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 3 (SPL3) to control the timing of flower formation.
20360106	geneRIF	results suggest distinct functions of AP1 during the initiation of flower development
20391782	geneRIF	Interaction between the ABRUPTUS/PINOID and APETALA1 genes regulating the inflorescence development in Arabidopsis thaliana
20626659	geneRIF	Data show that BOP1/2 function distinctly from LFY to upregulate AP1 in floral primordia and that all three activities converge to down-regulate flowering-time regulators including AGAMOUS-LIKE24 in stage 2 floral meristems.
21623976	geneRIF	LEAFY binding site is essential for proper photoperiodic activation of APETALA1
21750030	geneRIF	Data show that the direct LEAFY target LATE MERISTEM IDENTITY2 (LMI2) has a role in the meristem identity transition, and acts together with LEAFY to activate APETALA1.
21950056	geneRIF	Different action of the APETALA1 gene on the development of reproductive organs in flowers of the abruptus mutant of Arabidopsis thaliana
22676405	geneRIF	Co-expression analysis identifies CRC and AP1 the regulator of Arabidopsis fatty acid biosynthesis.
22773751	geneRIF	Approximately 90% of the binding sites of two well-characterized MADS domain transcription factors, APETALA1 and SEPALLATA3, were covered by the DNase I hypersensitive (DH) sites.
24753595	geneRIF	suppression of cytokinin biosynthesis and activation of cytokinin degradation mediates AP1 function in establishing determinate floral meristems
26096587	geneRIF	Data suggest that helix-turn-helix transcription factor LEAFY (LFY) and the MADS box transcription factor APETALA1 (AP1)together orchestrate the switch to flower formation and morphogenesis by altering transcriptional programs.
26359644	geneRIF	APETALA1 establishes determinate floral meristem through regulating cytokinins homeostasis in Arabidopsis.
27208240	geneRIF	the differences between the Arabidopsis (Arabidopsis thaliana) APETALA1 (AP1) and CAULIFLOWER (CAL) duplicate genes in the time, space, and level of expression were determined by the presence or absence of functionally important transcription factor-binding sites (TFBSs) in regulatory regions.
27216814	geneRIF	AcMFT from a non-flowering plant could interact with FD to regulate the floral transition and that this function was reduced due to the weakened ability of AcMFT-FD to activate the downstream gene AP1.
28098947	geneRIF	LFY and AP1 are conserved floral regulators that act nonredundantly in C. hirsuta, such that LFY has more obvious roles in floral and leaf development in C. hirsuta than in A. thaliana.
28385730	geneRIF	LFY and AP1/CAL act as part of an incoherent feed-forward loop, a network motif where two interconnected pathways or transcription factors act in opposite directions on a target gene, to control the establishment of a stable developmental program for the formation of flowers.
30334736	geneRIF	Here the authors show that divergence in the pleiotropic floral regulator APETALA1 (AP1) can account for the species-specific difference in petal number robustness.

Figure 2. The Papers tab of the search results in Gramene now shows publications associated with a gene from NCBI's GeneRIF. Plant and Trait Ontology terms derived from the GenRIF and RAP-DB gene annotations have been indexed and are now searchable.



Arabidopsis thaliana

AT5G17140

F2K13.290, F2K13_290

Cysteine proteinases superfamily protein

Compara Gene Tree

This phylogram shows the relationships between this gene and others similar to it, as determined by Ensembl Compara.

Alignment overview: Proteins color-coded by InterPro domain. Resize slider to navigate.

Search Filters

Links to other resources

- Ensembl Gene Tree view

Arabidopsis thaliana

AT5G17140

F2K13.290, F2K13_290

Cysteine proteinases superfamily protein

Compara Gene Tree

This phylogram shows the relationships between this gene and others similar to it, as determined by Ensembl Compara.

Neighborhood conservation: +/- 10 genes flanking the gene of interest (top row) are color-coded by gene family. Gray genes are from other families. Central genes (green) are shaded based on similarity with gene of interest.

Search Filters

Links to other resources

- Ensembl Gene Tree view

Figure 3. Putative split gene pair in A. thaliana and A. lyrata: AT5G17130 (fgenesh2_kg.6__1706__AT5G17130.1) and AT5G17140 (fgenesh2_kg.6__1707__AT5G17140.1). A) Protein alignment overview showing that the Peptidase C1A, papain C-terminal protein domain (colored in blue) is shared among the vast majority (83%) of genes in the tree, while AT5G17130 and fgenesh2_kg.6__1706__AT5G17130.1 line up with only the 5'-end of the tree and lack this highly conserved domain, yet the contiguous gene models AT5G17140 and fgenesh2_kg.6__1707__AT5G17140.1, respectively, include it.
B) Neighborhood conservation view shows 10 genes flanking the gene of interest (top row) and are color-coded by gene family. Central genes (green) are shaded based on similarity with the gene of interest, and gray genes are from unrelated families.

International Plant Phenotyping Network

Dr. Philipp von Gillhaussen (p.von.gillhaussen@fz-juelich.de, IPPN)

Project aims

The International Plant Phenotping Network e.V. (IPPN) aims to provide all relevant information about plant phenotyping, to increase the development, visibility and impact of plant phenotyping and enable cooperation by fostering communication between stakeholders in academia, industry, government, and the general public.

Recent activities of project

The Controlled Environment Plant Phenotyping working Group (CEPPG) of the International Plant Phenotyping Network held a workshop on 24/25th of May 2022 as a hybrid meeting at IPK Gatersleben, Germany

IPPN provides a quarterly newsletter circulating news, articles, videos, publications from in- & outside the plant phenotyping community, which are in many cases dealing with A. Thaliana (as it is still one of the most used model organisms).

IPPN has organized international symposia across the globe for over a decade addressing an increasing number of participants at each symposium, with over 450 attendees from over 40 different countries, attending the most recent 7th International Plant Phenotyping Symposium, that was held in October 2022 in Wageningen (NL).
regular special issues & Research topics.

Planned future activities of project

Expert- & Technology Databases which list experts in a field relevant to plant phenotyping and/or technologies which reflect the current sate-of-art ,or which are used in plant phenotyping.

Working Group Workshops

IPPS 8 -presumably end of 2024 in the Americas.

Nottingham Arabidopsis Stock Centre

Sean May, Director (sbzstm@exmail.nottingham.ac.uk)
Marcos Castellanos-Uribe, Operations Manager (Marcos.Castellanos@nottingham.ac.uk)

Recent activities of project

Orders sent from NASC increased again to 60,347 stocks total for the 2022 calendar year. At the time of writing (early April 2023) greater numbers again (>26.5K) have already been sent for 2023 compared to the same period in the last three years. So far, the top users in 2023 are China, Germany, Netherlands, Spain, and the UK. The other major recent NASC news has been a successful conversion of large sections of our growing space to speed-breeding lights, which are already showing dividends in both time and energy use.

Also, happily in contrast to the immediate post-Brexit/covid difficulties with phytosanitary certification and customs delays reported last year, we have seen a return to normal delivery rates, with fewer than 4% of orders remaining in transit two weeks after dispatch (2023 data). We have, however, noticed a small number of regional pockets showing unusual difficulties in receiving seeds. We urge users (strongly) to get in touch with us immediately (and directly) if there are any problems, delays, or queries about your package.

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 (and do 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.

Thank you to all those generous groups continuing to donate new stocks and populations of seed. 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.

We are looking forward to the ICAR in beautiful Japan, 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 and ABRC) 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 us an email, we can help.

http://arabidopsis.info/

In July 2023, the council will conduct two online workshops on science communication, one in Spanish and the other in English, in partnership with Women in Crops Science. These workshops will focus on enhancing science communication skills and strategies, empowering researchers to effectively engage with diverse online audiences.

The council will also participate in the SEB2023 conference in Edinburgh, Scotland, in early July. This in-person event will feature a workshop on social media and science communication, facilitating discussions on leveraging digital platforms to disseminate scientific knowledge and engage with the public effectively.

Another important event on the council's agenda is attending the Climate Summit in Dubai in December 2023 as an observer. This engagement will enable the council to contribute to discussions on climate change and emphasize the role of plant science in mitigating its impacts.

Furthermore, the GPC's executive team will continue seeking new topics for webinars and exploring potential collaborations with other entities, ensuring that the council remains at the forefront of emerging trends and developments in plant science.

Conclusion

The Global Plant Council's activities between May 2022 and May 2023 showcased its commitment to advancing plant science, advocating for increased investment, and fostering science communication. Through international conferences, webinars, workshops, and advocacy efforts, the GPC played a pivotal role in promoting innovation, collaboration, and addressing global challenges related to agriculture, food security, and climate change. The future activities further reinforce the council's dedication to these goals, ensuring the continued advancement of plant science for a sustainable future.

Riken BioResource Research Center

Masatomo Kobayashi (masatomo.kobayashi@riken.jp)

Recent activities of project

- Together with RIKEN CSRS, RIKEN BRC sponsors 3 Keynotes and MASC Workshop in ICAR2023. We intend to support face-to-face discussion among the attendees on “Arabidopsis for SDGs/4th Decadal Vision”.
- We have added 96 mutant and transgenic lines to the web catalog “Exp-Plant“. This resource category now includes 439 strains.
- Arabidopsis Transcription Factor-Glucocorticoid Receptor (TF-GR) lines were developed by Synthetic Genomics Research Group (Group Director, Dr. Minami Matsui), RIKEN Center for Sustainable Resource Science (CSRS) and deposited to RIKEN BRC. Information of the resource is in the following manuscript. Shimada S et al. Plant J. doi: 10.1111/tpj.15796. PMID: 35510416
- We have released 7 lines of plant cultured cells including 3 lines of transgenic tobacco BY-2 cells (TBY2-31/ST, TBY2-41/ST and TBY2-R31) and 2 lines of Arabidopsis cells (MM2d and MM2d-LS). Visit following page to find more information. https://epd.brc.riken.jp/en/archives/5496 https://epd.brc.riken.jp/en/archives/5572

Planned future activities of project

- We have started collecting genotype and phenotype information of natural accessions collected in Japan. The obtained data will be uploaded to the Exp-Plant Catalog for promoting the research on SDGs.
- Recent studies have disclosed that symbiotic microorganisms may affect growth of host plants. We are going to characterize the microbiome in our cultivation room to improve the reliability and reproducibility of the phenotype data of our resources.

The Arabidopsis Information Resource

Leonore Reiser (lreiser@arabidopsis.org)
Tanya Berardini (tberardi@arabidopsis.org)
Phoenix Bioinformatics

Recent activities of project

Data:

- We continue to add new gene function data on a weekly basis including: 1079 new/updated locus summaries, 1082 new/updated gene symbols, 4938 articles linked to 10539 genes, 15387 experimental Gene Ontology (GO) and Plant Ontology (PO) annotations, 876 new/updated alleles, and 1835 phenotypes linked to germplasms. 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).Quarterly releases now include the GFF annotation tracks that underlie the JBrowse Araport11 tracks.
- The plant homolog data on TAIR locus pages was updated to reflect PANTHER 17.0 trees (doi: 10.1002/pro.4218). The protein domain data has been updated to InterPro release 90.0 (doi: 10.1093/nar/gkac993).
- The data underlying Phylogenes (www.phylogenes.org) was updated to version 4.1 which includes trees from the new PANTHER 17.0 build and up to date GO annotations from the Gene Ontology Consortium (www.geneontology.org).
- New data tracks in JBrowse include data for stress sORF encoded peptides and intergenic Transcriptionally Active Regions (TARs) that are induced by Oxidative Stress in Arabidopsis thaliana (doi:10.1186/s12859-016-1458-y). For more information see the JBrowse release notes (https://www.arabidopsis.org/download_files/Help_Documents/JBrowse_updates.pdf). Please contact TAIR curators (curator@arabidopsis.org) if you have data you wish to display in JBrowse. Private browsing is available for peer review.

Tools

- In collaboration with the Sternberg Lab at Caltech, the Textpresso application (https://arabidopsis.textpresso.org/tpc/) has been updated to enable full text searching of over 50,000 ‘Arabidopsis’ papers.

Conferences

- TAIR was present at PAG30 in San Diego and will be presented at ICAR (June 2023) and ASPB (August 2023) in the AgBioData Plant Bioinformatics Workshop Session.

Planned future activities of project

Data

- In the coming year a major effort will be to generate and release a new genome annotation sourced by the research community (described elsewhere in this report.) This will be the first new genome release since Araport 11 in 2016. For data curation, we will continue to emphasize capturing information about new gene functions and in 2023, we will be placing a special emphasis on capturing allele and phenotype information from the literature.

Tools

- We will continue to accept and display user contributed data on TAIR gene pages, and in JBrowse. We anticipate transitioning to a new TAIR locus page layout by the end of 2023. This new layout will speed loading times, increase visibility of the data, and facilitate interoperability. We also plan to release a TAIR instance of JBrowse2 that will include all of the datasets from the current JBrowse instance as well as some new visualization tracks such as a synteny view.

MASC Country Reports

Argentina	40
Australia	41
Austria	42
Belgium	43
Brazil	44
Canada	46
Chile	48
China	49
Czech Republic	50
Finland	51
France	52
Greece	54
India	55
Ireland	56
Italy	57
Japan	59
New Zealand	61
Norway	62
Poland	63
Portugal	64
Sweden	65
Switzerland	68
Turkey	70
United Kingdom	71
United States	73

Argentina

Gabriela Auge (gabyauge@gmail.com)
Consejo Nacional de Investigaciones Científicas y Tecnológicas (CONICET)

New experimental resources and/or software tools available to Arabidopsis researchers

Mayta M, Dotto M, Orellano E, Krapp A. An experimental protocol for teaching CRISPR/Cas9 in a post-graduate plant laboratory course: An analysis of mutant-edited plants without sequencing. Biochemistry and Molecular Biology Education, 50: 537-546. *A clever protocol to teach plant transformation by CRISPR/Cas9 to undergrads.*

Planned events for 2023 and 2024

- 51° Congreso Argentino de Genética, October, 2023.
- 59° Reunión de la Sociedad Argentina de Investigación Bioquímica y Biología Molecular, November 2023.
- 34° Reunión Argentina de Fisiología Vegetal, September, 2023.
- 39° Jornadas Argentinas de Botánica, September, 2023.
- 3° Reunión Argentina de Biología de Semillas, November, 2023.
- 30° Reunión Argentina de Ecología, October, 2023 .

Major Funding Sources

- Agencia Nacional de Promoción de la Investigación, el Desarrollo Tecnológico y la Innovación.
- Consejo Nacional de Investigaciones Científicas y Tecnológicas (CONICET).
- Instituto Nacional de Tecnología Agropecuaria (INTA).
- National Universities such us Universidad de Buenos Aires, Universidad
- Nacional de Córdoba, Universidad Nacional del Litoral, etc.
- Ministerio de Ciencia, Tecnología e Innovación.
- International Center for Genetic Engineering and Biotechnology (ICGEB).

Selected publications

- Camoirano A, Alem A, Gonzalez D, Viola I. The N-terminal region located upstream of the TCP domain is responsible for the antagonistic action of the Arabidopsis thaliana TCP8 and TCP23 transcription factors on flowering time. Plant Science, 328: 111571. *A description at molecular level of the regulation of TCP proteins on a critical developmental process, flowering.*
- Arce A, Mencia R, Cambiagno D, Lang P, Liu C, Burbano H, Weigel D, Manavella P. Polymorphic inverted repeats near coding genes impact chromatin topology and phenotypic traits in Arabidopsis thaliana. Cell Reports, 42: 112029. *An outstanding study that shows transposon-derived inverted repeats can modify the genomic environment when inserted close to coding genes, in this way setting the stage for the expression of potentially relevant adaptive traits.*
- Petrillo E. Do not panic: An intron-centric guide to alternative splicing. The Plant Cell, koad009. *A critical review intended as a guide on alternative splicing focused on intron-retention as a mechanism to provide post-transcriptional variation. Led by a leading early-career researcher.*
- Pereyra C, Parola R, Lando A, Rodriguez M, Martínez-Noël G. High Sugar Concentration Inhibits TOR Signaling Pathway in Arabidopsis thaliana. Journal of Plant Growth Regulation, DOI: 10.1007/s00344-022-10894-w. *This study sheds light on the multiple layers of TOR-signaling and its regulation of developmental processes focusing on the role of different sugar molecules to activate the signal pathway, its interaction with hormones and the effect on root growth.*
- Martínez Pacheco J, et al. Cell surface receptor kinase FERONIA linked to nutrient sensor TORC signaling controls root hair growth at low temperature linked to low nitrate in Arabidopsis thaliana. New Phytologist, 238: 169-185. *Yet another paper from a highly prolific and highly collaborative group on the molecular regulation of root hair initiation and development, which can impact the the adaptation of plants to changing environments.*

Australia

Monika Murcha (monika.murcha@uwa.edu.au)
The University of Western Australia

New experimental resources and/or software tools available to Arabidopsis researchers

scCloudMine: A cloud-based app for visualization, comparison, and exploration of single-cell transcriptomic data. http://Single-Cell-Visualisation.loomesoftware.com

StomaAI: an efficient and user-friendly tool for measurement of stomatal pores and density using deep computer vision. https://github.com/xdynames/sai-app

Planned events for 2023 and 2024

- 7th International Plant Dormancy Symposium 12th-15th September 2023, Perth, Western Australia.
- Nitrogen 2023, fifth international symposium on nitrogen nutrition of plants 6th-9th Nov 2023 in Sydney, New South Wales, Australia.
- Australian Society of Plant Scientists meeting 28th Nov-1st Dec 2023 in Hobart, Tasmania, Australia.
- The International Plant Molecular Biology (IPMB) Congress 24th -28th June 2024, in Cairns, Queensland, Australia.

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)

Selected publications

- Lloyd JPB, Ly F, Gong P, Pflueger J, Swain T, Pflueger C, Fourie E, Khan MA, Kidd BN, Lister R. Synthetic memory circuits for stable cell reprogramming in plants. Nat Biotechnol. 2022 Dec;40(12):1862-1872. doi: 10.1038/s41587-022-01383-2. *Using Arabidopsis protoplasts, this study has developed and optimized recombinase-based synthetic gene circuits for sophisticated stable transcriptional reprograming.*
- Taleski M, Chapman K, Novák O, Schmülling T, Frank M, Djordjevic MA. CEP peptide and cytokinin pathways converge on CEPD glutaredoxins to inhibit root growth. Nat Commun. 2023 Mar 27;14(1):1683. *C-TERMINALLY ENCODED PEPTIDE (CEP) and cytokinin signalling converges to inhibit primary root growth requiring CEPD glutaredoxins.*
- Li L, Duncan O, Ganguly DR, Lee CP, Crisp PA, Wijerathna-Yapa A, Salih K, Trösch J, Pogson BJ, Millar AH. Enzymes degraded under high light maintain proteostasis by transcriptional regulation in Arabidopsis. Proc Natl Acad Sci U S A. 2022 May 17;119(20):e2121362119. *Protein turnover, mRNA and protein abundance analysis reveals a light-induced transcriptional regulation of key targets to maintain proteostasis under high light stress.*
- Haywood J, Breese KJ, Zhang J, Waters MT, Bond CS, Stubbs KA, Mylne JS. A fungal tolerance trait and selective inhibitors proffer HMG-CoA reductase as a herbicide mode-of-action. Nat Commun. 2022 Sep 22;13(1):5563. *The crystal structure of a HMGR from Arabidopsis thaliana (AtHMG1) was determined revealing a promising new herbicide target site.*
- Li X, Deng D, Cataltepe G, Román Á, Buckley CR, Cassano Monte-Bello C, Skirycz A, Caldana C, Haydon MJ. A reactive oxygen species Ca2+ signalling pathway identified from a chemical screen for modifiers of sugar-activated circadian gene expression. New Phytol. 2022 Nov;236(3):1027-1041. doi: 10.1111/nph.18380. *A chemical screen on luciferase reporter lines identified compounds that affect sugar dependent signalling pathways.*

Austria

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

New experimental resources and/or software tools available to Arabidopsis researchers

- **PHENOPlant** – Multi-sensor and multi-approach high-throughput plant phenotyping platform
- **A lineage tracing system for living plants**: A versatile CRISPR-based system for lineage tracing in living plants
- **Revisiting the chromatin landscape in Arabidopsis:** Transcriptional activity is shaped by the chromatin landscapes in Arabidopsis
- **The 1001 Genomes Consortium** plans to release several hundred nearly complete genomes of Arabidopsis accessions in 2023. https://1001genomes.org/index.html

Planned events for 2023 and 2024

Mendel Early Career Symposium May 25-26, 2023 (oeaw.ac.at)

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

Selected publications

- Qi et al.(2022) Adenylate cyclase activity of TIR1/AFB auxin receptors in plants Nature 611:133-138. *An adenylate cyclase activity was identified as additional function of the TIR1/AFB receptors across land plants. It is stimulated by auxin, together with Aux/IAAs, to produce cAMP. It is essential to mediate gravitropism and auxin-induced root growth inhibition.*
- Friml et al. (2022) ABP1-TMK auxin perception for global phosphorylation and auxin canalization. Nature 609:575-581. *This paper describes the ABP together with its plasma-membrane-localized partner, transmembrane kinase 1 (TMK1) is the auxin receptor for cell-surface signaling essential for the global phospho-response and auxin canalization.*
- Konstantinova et al.(2022) WAVY GROWTH Arabidopsis E3 ubiquitin ligases affect apical PIN sorting decisions. Nat Commun. 13:5147. *This paper describes WAVY GROWTH E3 ligases as essential determinants for PIN polarity by selective targeting apically localized PINs.*
- Picchianti et al. (2023) Shuffled ATG8 interacting motifs form an ancestral bridge between UFMylation and autophagy. EMBO J e112053. *This paper describes a conserved regulatory switch that regulates ER-phagy*
- Zhao et al. (2022) Plant autophagosomes mature into amphisomes prior to their delivery to the central vacuole. J Cell Biol 221(12):e202203139. *This paper describes the trafficking pathways that sort autophagosomes during autophagy.*
- Jaegle et al. (2023) Extensive sequence duplication in Arabidopsis revealed by pseudo-heterozygosity. Genome Biol 24(1):44. *This paper suggests that much of the SNP diversity in Arabidopsis may be artifacts caused by copy-number variation.*
- Clauw et al. (2022) Locally adaptive temperature response of vegetative growth in Arabidopsis thaliana. Elife 11:e77913. *By growing different Arabidopsis accessions at temperatures similar to those in Northern latitudes, this paper shows that accessions from northern latitudes have responses indicative of local adaptation.*
- Sasaki et al. (2022) Conditional GWAS of non-CG transposon methylation in Arabidopsis thaliana reveals major polymorphisms in five genes. PLoS Genet 18(9):e1010345. *Using a conditional GWAS approach, this paper shows identifies 5 key trans-regulators that modulate CHG methylation.*

Belgium

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

New experimental resources and/or software tools available to Arabidopsis researchers

- 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 2023 and 2024

- 10th International Symposium on Root Development
  15-18 May 2023, Ghent, Belgium
  https://www.vibconferences.be/events/10th-international-symposium-on-root-development

- Translational Research in Crops
  22-23 June 2023, Ghent, Belgium
  https://www.vibconferences.be/events/translational-research-in-crops

- 4th International Brassinosteroid Conference
  16-18 August 2023, Ghent, Belgium
  https://www.vibconferences.be/events/4th-international-brassinosteroid-conference

- 74th International Symposium on Crop Protection
  23 May 2023
  https://www.ugent.be/bw/plants-and-crops/iscp/en

- 2023 Summer Institute in Plant Breeding
  3 July 2023
  https://www.eventbrite.com/e/2023-summer-institute-in-plant-breeding-tickets-486947191157

- 2023 EU AgriResearch Conference
  31 May - 1 June 2023
  https://agriculture.ec.europa.eu/events/2023-eu-agriresearch-conference-2023-05-31_en

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/)

Selected Publications

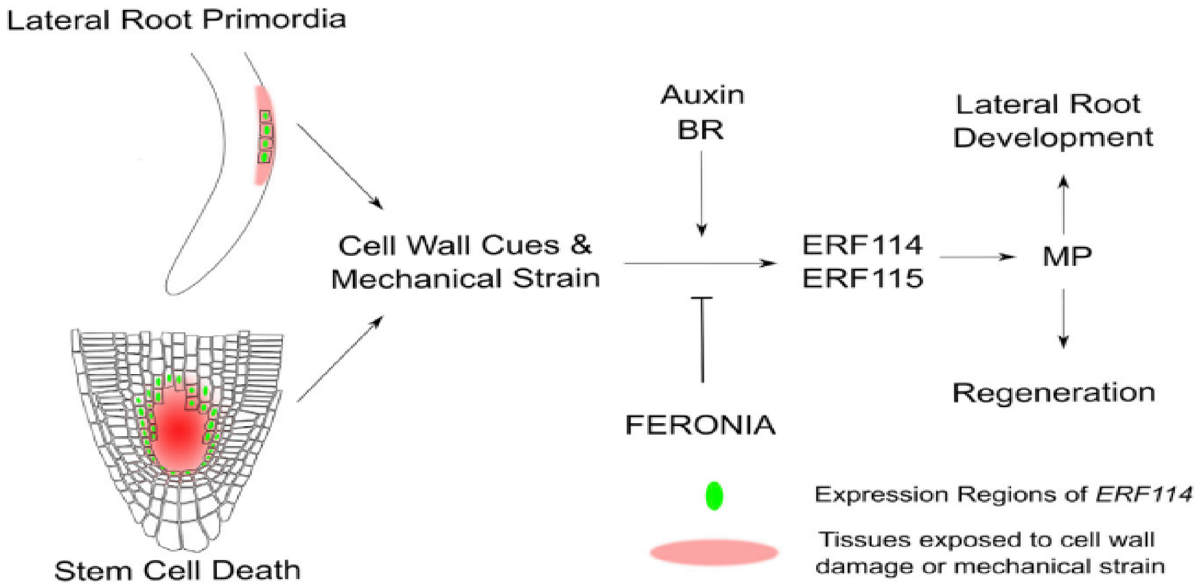
Nolan TM, Vukašinović N, Hsu CW, et al. Brassinosteroid gene regulatory networks at cellular resolution in the Arabidopsis root. Science. 2023;379(6639):eadf4721. doi:10.1126/science.adf4721 Time series single-cell RNA sequencing revealed brassinosteroid-responsive transcription factors specific to different cell types and developmental stages of the Arabidopsis root, identifying the elongating cortex as a site where brassinosteroids trigger a shift from cell proliferation to cell elongation.

Van Leene J, Eeckhout D, Gadeyne A, et al. Mapping of the plant SnRK1 kinase signalling network reveals a key regulatory role for the class II T6P synthase-like proteins. Nat Plants. 2022;8(11):1245-1261. doi:10.1038/s41477-022-01269-w
A phosphoproteomics approach inferred the sucrose-dependent processes targeted upon starvation by kinases as the central metabolic regulator SnRK1, and the interaction landscape of the SnRK1 heterotrimer revealed class II T6P synthase (TPS)-like proteins as negative regulators of SnRK1.

Canher B, Lanssens F, Zhang A, et al. The regeneration factors ERF114 and ERF115 regulate auxin-mediated lateral root development in response to mechanical cues. Mol Plant. 2022;15(10):1543-1557. doi:10.1016/j.molp.2022.08.008
The activators of regeneration ETHYLENE RESPONSE FACTOR 114 (ERF114) and ERF115 govern developmental growth in the absence of wounding, promoting xylem and lateral root formation in response to cell-wall derived mechanical signals.

Develtere W, Waegneer E, Debray K, et al. SMAP design: a multiplex PCR amplicon and gRNA design tool to screen for natural and CRISPR-induced genetic variation [published online ahead of print, 2023 Jan 31]. Nucleic Acids Res. 2023;gkad036. doi:10.1093/nar/gkad036
SMAP design is a bioinformatics command-line tool to enable reliable and specific primer designs and simultaneous gRNA designs for eco-tilling or multiplex CRISPR screens, as benchmarked in Arabidopsis, soybean, maize, and chicory.

Feng Q, De Rycke R, Dagdas Y, Nowack MK. Autophagy promotes programmed cell death and corpse clearance in specific cell types of the Arabidopsis root cap. Curr Biol. 2022;32(9):2110-2119.e3. doi:10.1016/j.cub.2022.03.053
Autophagic flux is strongly increased prior to programmed cell death execution the entire Arabidopsis root cap, but only plays a death-promoting role in the columella root cap, while cell death execution in the lateral root cap occurs independent of autophagy



Brazil

Wagner L. Araújo (wlaraujo@ufv.br)
Adriano Nunes Nesi (nunesnesi@ufv.br)
Departamento de Biologia Vegetal Universidade Federal de Viçosa 36570-900 Viçosa, MG, Brazil

Planned events for 2023 and 2024

- VIII Simpósio Brasileiro de Genética Molecular de Plantas, Florianópolis, Santa Catarina, Brazil, May 30 - June 02, 2023.
- XIX Brazilian Congress of Plant Physiology, Viçosa, Minas Gerais, Brazil, October 7 - 12, 2024.

Major Funding Sources

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

Selected publications

- Rodrigues WFC, Lisboa ABP, Lima JE, Ricachenevsky FK, Del-Bem LE. (2023) Ferrous iron uptake via IRT1/ZIP evolved at least twice in green plants. New Phytol. 237(6):1951-1961. doi: 10.1111/nph.18661. Epub 2023 Jan 10. PMID: 36626937.*This study revealed the phylogenetic origin of Iron (Fe) uptake and that evolutionary diversity remains to be found in Fe uptake in land plants.*
- Thiers KLL, da Silva JHM, Vasconcelos DCA, Aziz S, Noceda C, Arnholdt-Schmitt B, Costa JH. (2023) Polymorphisms in alternative oxidase genes from ecotypes of Arabidopsis and rice revealed an environment-induced linkage to altitude and rainfall. Physiol Plant. 175(1):e13847. doi: 10.1111/ppl.13847. PMID: 36562612. *This work demonstrated that polymorphism in amino acid in the available Arabidopsis ecotypes confer better enzyme-subtract interactions ultimately indicating environment-related, more efficient AOX activity.*
- Pereira LB, Thomazella DPT, Teixeira PJPL. (2023) Plant-microbiome crosstalk and disease development. Curr Opin Plant Biol. 72:102351. doi: 10.1016/j.pbi.2023.102351. Epub 2023 Feb 26. PMID: 36848753. *This review highlights the involvement of the plant microbiome in disease development, with an special focus on the biochemical crosstalk between plants and their associated microbiota before, during and after infection.*
- Tran S, Ison M, Ferreira Dias NC, Ortega MA, Chen YS, Peper A, Hu L, Xu D, Mozaffari K, Severns PM, Yao Y, Tsai CJ, Teixeira PJPL, Yang L. (2023) Endogenous salicylic acid suppresses de novo root regeneration from leaf explants. PLoS Genet. 1;19(3):e1010636. doi: 10.1371/journal.pgen.1010636. PMID: 36857386; PMCID: PMC10010561. *This study revealed that Salicylic acid (SA), a key hormone for plant defense, suppresses root regeneration. More importantly, this work provides new knowledge for overcoming challenges in vegetative propagation by manipulating the SA response.*
- Barros JAS, Cavalcanti JHF, Pimentel KG, Medeiros DB, Silva JCF, Condori-Apfata JA, Lapidot-Cohen T, Brotman Y, Nunes-Nesi A, Fernie AR, Avin-Wittenberg T, Araújo WL. (2022) The significance of WRKY45 transcription factor in metabolic adjustments during dark-induced leaf senescence. Plant Cell Environ. 45(9):2682-2695. doi: 10.1111/pce.14393. Epub 2022 Jul 25. PMID: 35818668. *By using a combination of genetic and biochemical approaches, this study revealed that the transcription factor WRKY45 in involved on the modulation of mitochondrial signalling pathways.*

Canada

Dario Bonetta, dario.bonetta@ontariotechu.ca, Ontario Tech University, with input from Nicholas Provart, nicholas.provart@utoronto.ca

Planned events for 2023 and 2024

- The Canadian Society of Plant Biologists (CSPB) Annual General Meeting 2023 was held on June 18-21 at Université Laval, Quebec City, Canada. .

Major Funding Sources

National Science and Engineering Research Council (NSERC) (http://www.nserc-crsng.gc.ca)

Genome Canada (http://www.genomecanada.ca/en/)

New Frontiers in Research Fund (https://www.sshrc-crsh.gc.ca/funding-financement/nfrf-fnfr/index-eng.aspx)

Selected publications

Pacey EK, Maherali H, Husband BC. Polyploidy increases storage but decreases structural stability in Arabidopsis thaliana. Curr Biol. 2022; 32(18):4057-4063.e3. doi: 10.1016/j.cub.2022.07.019.

This study explores how whole-genome duplication results in increased cell size, which leads to greater storage capacity and resource limitation tolerance, albeit with biomechanical costs due to reduced cell wall per tissue volume, revealing potential for adaptation but also variation in effects based on accession identity.

Breit-McNally C, Desveaux D, Guttman DS. The Arabidopsis effector-triggered immunity landscape is conserved in oilseed crops. Sci Rep. 2022 12(1):6534. doi: 10.1038/s41598-022-10410-w.

This research examines how immune responses to Pseudomonas syringae in Arabidopsis are conserved in oilseed crops Brassica napus and Camelina sativa, finding that the degree of immune conservation is inversely related to evolutionary divergence, with quantitative aspects of immunity diverging more than qualitative ones.

Le Gloanec C, Collet L, Silveira SR, Wang B, Routier-Kierzkowska AL, Kierzkowski D. Cell type-specific dynamics underlie cellular growth variability in plants. Development. 2022; 149(14):dev200783. doi: 10.1242/dev.200783.

This study uses time-lapse imaging to reveal that the local growth variability in developing organs, particularly the leaf blade, is primarily driven by the differentiation of stomata, specialized cells which follow a unique growth program, with this variability being balanced by neighboring cells to maintain consistent organ shapes.

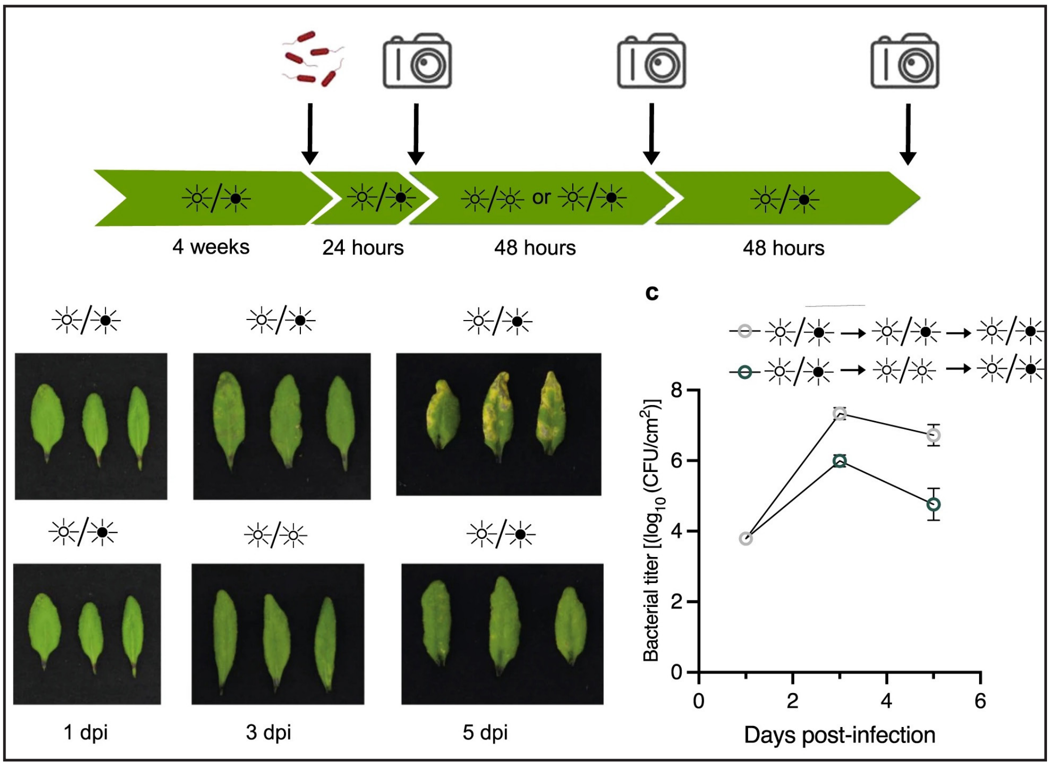
Zhang L, Ambrose C. CLASP balances two competing cell division plane cues during leaf development. Nat Plants. 2022; 8(6):682-693. doi: 10.1038/s41477-022-01163-5.

This research shows that the organization of cells and air spaces is shaped by two competing cell division patterns, orchestrated by the microtubule-associated protein CLASP, which balance the distribution of cells and intercellular spaces; influencing the internal surface area of the leaf.

Linh NM, Scarpella E. Leaf vein patterning is regulated by the aperture of plasmodesmata intercellular channels. PLoS Biol. 2022; 20(9):e3001781. doi: 10.1371/journal.pbio.3001781.

The study reveals that the formation of vein networks involves the coordinated action of three pathways dependent on the GNOM regulator: auxin signaling, polar auxin transport, and the movement of auxin or an auxin-dependent signal through plasmodesmata, intercellular channels which regulate their aperture under the control of GNOM.

Lajeunesse G, Roussin-Léveillée C, Boutin S, Fortin É, Laforest-Lapointe I, Moffett P. Light prevents pathogen-induced aqueous microenvironments via potentiation of salicylic acid signaling. Nat Commun. 2023; 14(1):713. doi: 10.1038/s41467-023-36382-7.



The research uncovers that constant light exposure reduces the virulence of the plant pathogen Pseudomonas syringae by preventing stomatal closure and water-soaking via increased salicylic acid production, suggesting a potential strategy for disrupting common pathogenic mechanisms and providing insight into how salicylic acid functions in plant defense.

Chile

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

Planned events for 2023 and 2024

XV Annual Meeting of Chilean Society of Plant Biologists (CSPB) December 5, 6 & 7, 2023; Talcahuano, Chile. A meeting hosted by the Chilean Society of Plant Biologists. It includes talks, symposiums, and poster presentations. Examples of covered topics are Natural Variation & Plant Breeding, Plant Cell and Molecular Biology, Plant Physiology and Hormones, Cell Wall of Trees, Fruit and Vegetables, Physiological and Molecular Biology of Grains, Biosensors and Fruit Response to Stress. Organizer: Chilean Society of Plant Biologists (https://www.biologiavegetal.cl/)

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/)

Selected publications

- Ugalde JM, Aller I, Kudrjasova L, Schmidt RR, Schlößer M, Homagk M, Fuchs P, Lichtenauer S, Schwarzländer M, Müller-Schüssele SJ, Meyer AJ. Endoplasmic reticulum oxidoreductin provides resilience against reductive stress and hypoxic conditions by mediating luminal redox dynamics. Plant Cell. 2022 Sep 27;34(10):4007-4027. doi: 10.1093/plcell/koac202. PMID: 35818121; PMCID: PMC9516139. (https://academic.oup.com/plcell/article/34/10/4007/6633943). *The redox potential of the endoplasmic reticulum (ER) was determined using a genetically-encoded fluorescent sensor, along with the importance of ER Oxidoreductins (EROs) on ER redox potential, plant tolerance to reductive stress and plant resistance to hypoxia.*
- Zavala D, Fuenzalida I, Gangas MV, Peppino Margutti M, Bartoli C, Roux F, Meneses C, Herrera-Vásquez A, Blanco-Herrera F. Molecular and Genomic Characterization of the Pseudomonas syringae Phylogroup 4: An Emerging Pathogen of Arabidopsis thaliana and Nicotiana benthamiana. Microorganisms. 2022 Mar 25;10(4):707. doi: 10.3390/microorganisms10040707. PMID: 35456758; PMCID: PMC9030749. (https://www.mdpi.com/2076-2607/10/4/707). *This research describes the characterization of a newly discovered plant pathogen strain and possible virulence mechanisms underlying the infection process shaped by natural and changing environmental conditions.*
- Quiroz-Iturra LF, Simpson K, Arias D, Silva C, González-Calquin C, Amaza L, Handford M, Stange C. Carrot DcALFIN4 and DcALFIN7 Transcription Factors Boost Carotenoid Levels and Participate Differentially in Salt Stress Tolerance When Expressed in Arabidopsis thaliana and Actinidia deliciosa. Int J Mol Sci. 2022 Oct 12;23(20):12157. doi: 10.3390/ijms232012157. PMID: 36293018; PMCID: PMC9603649. (https://www.mdpi.com/1422-0067/23/20/12157). *Arabidopsis thaliana was used to assess the role of two Daucus carota transcription factors that can confer salt stress tolerance to plants. These genes are relevant to address the current climate change issues that we are facing.*

China

Yuling Jiao, yuling.jiao@pku.edu.cn, School of Life Sciences, Peking University

New experimental resources and/or software tools available to Arabidopsis researchers

TBtools: 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
EXPLICIT: An Arabidopsis expression predictor https://github.com/mashisonglab/explicit
AtMAD: Arabidopsis multi-omics association database http://www.megabionet.org/atmad

Planned events for 2023 and 2024

- 2023 National Congress of Plant Biology, August 2-6, 2023, Lanzhou, Gansu (http://ncpb.net/)
- The 8th International Symposium on Plant Reproductive Development, July 31-August 2, 2023, Shanghai
- International Symposium of Plant Ecological Evolutionary Developmental Biology, October 29-31, 2023, Wuhan, Hubei
- 2024 National Congress of Plant Biology, October 8-12, 2024, Guangzhou, Guangdong (http://ncpb.net/)

Major Funding Sources

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

Selected publications

- Zhong S, Li L, Wang Z, Ge Z, Li Q, Bleckmann A, Wang J, Song Z, Shi Y, Liu T, Li L, Zhou H, Wang Y, Zhang L, Wu HM, Lai L, Gu H, Dong J, Cheung AY, Dresselhaus T, Qu LJ. 2022. RALF peptide signaling controls the polytubey block in Arabidopsis. Science 375(6578):290-296. doi: 10.1126/science.abl4683*. This study details signaling between pollen tube and female gametophyte ensures that only one pollen tube gets through but can re-establish access in case of failure.*
- Jia A, Huang S, Song W, Wang J, Meng Y, Sun Y, Xu L, Laessle H, Jirschitzka J, Hou J, Zhang T, Yu W, Hessler G, Li E, Ma S, Yu D, Gebauer J, Baumann U, Liu X, Han Z, Chang J, Parker JE, Chai J. 2022. TIR-catalyzed ADP-ribosylation reactions produce signaling molecules for plant immunity. Science 377(6605): eabq8180. doi: 10.1126/science.abq8180*. This paper reports second messengers link diverging pathways in plant pathogen detection to immune response.*
- Hou X, Wang D, Cheng Z, Wang Y, Jiao Y. 2022. A near-complete assembly of an Arabidopsis thaliana genome. Mol. Plant 15(8):1247-1250. doi: 10.1016/j.molp.2022.05.014*. This paper presents a near-complete assembly Col-PEK that fills all centromeres.*
- Liu L, Song W, Huang S, Jiang K, Moriwaki Y, Wang Y, Men Y, Zhang D, Wen X, Han Z, Chai J, Guo H. 2022. Extracellular pH sensing by plant cell-surface peptide-receptor complexes. Cell 185(18):3341-3355.e13. doi: 10.1016/j.cell.2022.07.012. *Cell-surface peptide-receptor complexes RGF1-RGFR and Pep1-PEPR function as pH sensors to regulate extracellular pH mediated growth and immunity in root apical meristem region in Arabidopsis.*
- Yang Z, Xia J, Hong J, Zhang C, Wei H, Ying W, Sun C, Sun L, Mao Y, Gao Y, Tan S, Friml J, Li D, Liu X, Sun L. 2022. Structural insights into auxin recognition and efflux by Arabidopsis PIN1. Nature 609(7927):611-615. doi: 10.1038/s41586-022-05143-9*. This paper reports the structure of the long-waited Arabidopsis auxin efflux carrier PIN-FORMED1.*

Czech Republic

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

Planned events for 2023 and 2024

- Methods in Plant Science conference 24.-27.9.2023 in Srní, Czech Republic and also the student conference: Student days in Plant Sciences 22.-24.9.2023 also in Srní, Czech Republic. https://csebr.cz/plantmethods2023/
- Czech Plant Nucleus Workshop 2023 (CPNW2023) 20 - 21 June, 2023, Mendel Refectory, Augustinian Abbey, Brno, Czech Republic. https://olomouc.ueb.cas.cz/en/cpnw
- Auxins and Cytokinins in Plant Development Symposium (ACPD 2023), Prague from 25–29 June 2023, Prague, Czech Republic. https://www.acpd2023.org/

Major Funding Sources

- Czech Science Foundation/GAČR, Prague (http://www.gacr.cz)
- Ministry of Education, Youth and Sports of Czech Republic, Prague (http://www.msmt.cz/research-and-development-1)
- Technology Agency of the Czech Republic (http://www.tacr.cz/english/)
- Ministry of Agriculture, National Agency for Agricultural Research (NAZV) (http://eagri.cz/public/web/mze/poradenstvi-a-vyzkum/vyzkum-a-vyvoj/narodni-agentura-pro-zemedelsky-vyzkum/)

Selected publications

- Cairo, A., Vargova, A., Shukla, N., Capitao, C., Mikulkova, P., Valuchova, S., Pecinkova, J., Bulankova, P., & Riha, K. (2022). Meiotic exit in Arabidopsis is driven by P-body-mediated inhibition of translation. Science (New York, N.Y.), 377(6606), 629–634. https://doi.org/10.1126/science.abo0904. *New regulatory principle of plant cells exit from meiosis is described based on the formation of processing bodies - eIF4F, the main translation initiation complex, temporarily sequestering it in P-bodies.*
- Kusová, A., Steinbachová, L., Přerovská, T., Drábková, L. Z., Paleček, J., Khan, A., Rigóová, G., Gadiou, Z., Jourdain, C., Stricker, T., Schubert, D., Honys, D., & Schrumpfová, P. P. (2023). Completing the TRB family: newly characterized members show ancient evolutionary origins and distinct localization, yet similar interactions. Plant molecular biology, 112(1-2), 61–83. https://doi.org/10.1007/s11103-023-01348-2. *All TRB proteins participate in telomerase complex binding.¨*
- Dvořák Tomaštíková, E., Prochazkova, K., Yang, F., Jemelkova, J., Finke, A., Dorn, A., Said, M., Puchta, H., & Pecinka, A. (2023). SMC5/6 complex-mediated SUMOylation stimulates DNA-protein cross-link repair in Arabidopsis. The Plant cell, 35(5), 1532–1547. https://doi.org/10.1093/plcell/koad020. *SMC5/6 complex as crucial regulator of DNA repair.*
- Brunoni, F., Pěnčík, A., Žukauskaitė, A., Ament, A., Kopečná, M., Collani, S., Kopečný, D., & Novák, O. (2023). Amino acid conjugation of oxIAA is a secondary metabolic regulation involved in auxin homeostasis. The New phytologist, 10.1111/nph.18887. Advance online publication. https://doi.org/10.1111/nph.18887. *AA conjugation of oxIAA as a new level of overall auxin metabolism regulation.*
- Bellinvia, E., García-González, J., Cifrová, P., Martinek, J., Sikorová, L., Havelková, L., & Schwarzerová, K. (2022). CRISPR-Cas9 Arabidopsis mutants of genes for ARPC1 and ARPC3 subunits of ARP2/3 complex reveal differential roles of complex subunits. Scientific reports, 12(1), 18205. https://doi.org/10.1038/s41598-022-22982-8. *Specific functions for the subunits of ARP2/3 complex are uncovered.*

Finland

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

Major Funding Sources

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

Selected publications

- Rantala, M., Ivanauskaite, A., Laihonen, L., Kanna, S.D., Ughy, B. and Mulo, P. (2022) Chloroplast acetyltransferase GNAT2 is involved in the organization and dynamics of thylakoid structure. Plant and Cell Physiology 63,1205-1214. *Loss of chloroplast acetyltransferase GNAT2 results in defective dynamics of thylakoid structure in response to dark-light shift.*
- 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, in press. *The chloroplast acetyltransferase family enzymes (GNATs) affect the metabolic profile of the plant and have an impact on the recruitment of Rubisco and Rubisco activase to the thylakoid membrane.*
- Cui, F., Li, X., Wu, W., Luo, W., Wu, Y., Brosché, M., Overmyer, K. (2022) Ectopic expression of BOTRYTIS SUSCEPTIBLE1 reveals its function as a positive regulator of wound-induced cell death and plant susceptibility to Botrytis, Plant Cell 34: 4105–4116. *Using new crispr mutants, the transcription factor BOS1 is shown to be a positive regulator of plant cell death*
- Leppälä, J., Gaupels, F., Xu, E., Morales, L.O., Durner J., Brosché, M. (2022). Ozone and nitrogen dioxide regulate similar gene expression responses in Arabidopsis but natural variation in the extent of cell death is likely controlled by different genetic loci. Frontiers in Plant Science. DOI=10.3389/fpls.2022.994779. *A GWAS screen was performed with two air pollutants, ozone and nitrogen dioxide, which revealed new candidate genes that regulate plants responses to stress from air pollutants.*
- Mäkilä, R., Wybouw, B., Smetana, O., Vainio, L., Solé-Gil, A., Lyu, M., Ye, L., Wang, X., Siligato, R., Jenness, M.K., Murphy, A.S., Mähönen, A.P. (2023) Gibberellins promote polar auxin transport to regulate stem cell fate decisions in cambium. Nat Plants. 9: 631-644. *This study shows that gibberellins promote polar auxin transport along the root, which leads to broadening of high auxin signalling domain in cambium, and thus, to increased xylem formation.*

France

Cécile BOUSQUET-ANTONELLI (insb.das5f@cnrs.fr)
CNRS, Université de Perpignan, LGDP & CNRS-INSB, 3 rue Michel Ange, Paris

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

New experimental resources and/or software tools available to Arabidopsis researchers

Arabidopsis stock center (http://publiclines.versailles.inra.fr)
PHENOSCOPE (http:// www.ijpb.versailles.inra.fr/en/plateformes/ppa/index. html) and **PHENOPSIS** (www1.montpellier.inra.fr/ibip/lepse/english/ressources/ phenopsis.htm) are high-throughput automated phenotyping platforms at Versailles and Montpellier.
SPS tools for Functional Genomics (https://www6.inra.fr/saclay-plant-sciences_eng/Infrastructures).
Plant Genomic center (https://cnrgv.toulouse.inra.fr/Library/Arabidopsis)
PHENOPSIS DB is an information system (http://bioweb.supagro.inra.fr/phenopsis/ Accueil. php?lang=En)
ATOMEdb: Arabidopsis thaliana ORFeome database, http://tools.ips2.u-psud.fr/ATOMEdb
ChloroKb decoding the chloroplast, LPCV, Grenoble, http://chlorokb.fr/

Planned events for 2023 and 2024

- https://www.icpp2023.org, 12th International Congress of Plant Pathology, 20 - 25 August 2023, Lyon, France
- https://europlantbiology2023.org, The Plant Biology Europe meeting which will be held at Marseille (France) from July 3 to 6.
- https://pprmeeting.sciencesconf.org, The Plant Peptides and Receptors Meeting, Lyon from the 2nd to the 4th of October, 2023,
- https://icp2023.symposium.inrae.fr, International Conference on Polyphenols - ICP2023 - July 3rd to 6th 2023
- https://isss2023.sciencesconf.org, The 14th ISSS biennal conference will be held at Sorbonne Université (Paris) from 3 to 7 july 2023.
- https://www.labex-tulip.fr/labex-tulip_eng/Home/Focus-on/Summer-School-2023, The TULIP 11th International Summer School “Biological interactions from genes to ecosystems” from July 1st to 7, 2023 in the French Pyrénées.
- https://www6.inrae.fr/saclay-plant-sciences_eng/Teaching-and-training/Summer-schools/Summer-School-2023, Summer School 2023 – SUCSEED, Seeds as a keystone for the transition to agroecology June 25 - July 1st, 2023 – Versailles (France)

Major Funding Sources

- Research organizations such as CNRS, INRAE, CEA or Universities provide recurrent funding to their laboratories in addition to payment of salaries of permanent researchers and technicians. Thematic calls can also be opened by these research organizations for their research laboratories to support emerging or risky projects or to facilitate the development of interdisciplinary projects.
- The French national research agency, ANR (http:// www. agence-nationale-recherche.fr/en/ about-anr/about- the- french-national-research-agency/), provides funding for project-based research
- PPR “Growing and Protecting crops Differently” The French Priority Research Programme “Cultiver et Protéger Autrement” (Growing and Protecting crops Differently) (PPR-CPA) was created to meet the French government’s objectives of reducing the use of pesticides while developing effective alternatives. To achieve these objectives, financial support is provided through the third investment programme for the future (PIA3). Thus, the PPR-CPA is a 30 millions euro programme which is part of the national investment plan with French National Research Agency as operator.

Selected Publications

- Zhang et al. 2022, Science, 10.1126/science.add4250, The control of carpel determinacy pathway leads to sex determination in cucurbits. *This work suggests that sex genes evolved interfering with flower meristematic function, leading to unisexual flower development.*
- P. Rieu et al. 2022, Nature plant, 10.1038/s41477-022-01336-2, The F-box protein UFO controls flower development by redirecting the master transcription factor LEAFY to new cis-elements. *This work reveals a unique mechanism of an F-box protein directly modulating the DNA binding specificity of a master transcription factor.*
- Y. Du et al. 2022, Nature plants, 10.1038/s41477-022-01172-4, Spatially expressed WIP genes control Arabidopsis embryonic root development. *This works reveal cross-communication between the embryonic and maternal WIPs in controlling root development.*
- Chevigny et al, 2022; Plos genetics, 10.1371/journal.pgen.1010202, RADA-dependent branch migration has a predominant role in plant mitochondria and its defect leads to mtDNA instability and cell cycle arrest. *This work reveals that the deficient maintenance of the mtDNA in radA triggers a retrograde signal that activates nuclear genes repressing cell cycle progression.*
- Da Ines et al., 2022, Plos genetics, 10.1371/journal.pgen.1010322, DMC1 attenuates RAD51-mediated recombination in Arabidopsis. *This work reveals that DMC1 prevents RAD51-mediated recombination in Arabidopsis and that this down-regulation requires local assembly of DMC1 nucleofilaments.*

Greece

Stamatis Rigas (srigas@aua.gr) Agricultural University of Athens

Planned events for 2023 and 2024

5th Conference of the International Plant Proteomics Organization (ThessInPPO2023) May 22-25, 2023; Thessaloniki, Greece https://thessinppo2023.com/

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
- Marie Curie – Research and Innovation Staff Exchange (RISE)
- Rural Development Program of Greece, Sub-Measure 16.1 ‘Cooperation’

Selected publications

- Michalopoulou VA, Mermigka G, Kotsaridis K, Mentzelopoulou A, Celie PHN, Moschou PN, Jones JDG, Sarris PF. The host exocyst complex is targeted by a conserved bacterial type-III effector that promotes virulence. Plant Cell (2022) 34: 3400-3424. doi: 10.1093/plcell/koac162. *Inhibition of exocyst function without activating the related defenses represents an effective virulence strategy, indicating the ability of pathogens to adapt to host defenses by avoiding host immunity responses.*
- Dervisi I, Petropoulos O, Agalou A, Podia V, Papandreou N, Iconomidou VA, Haralampidis K, Roussis A. The SAH7 Homologue of the Allergen Ole e 1 Interacts with the Putative Stress Sensor SBP1 (Selenium-Binding Protein 1) in Arabidopsis thaliana. Int. J. Mol. Sci. (2023) 24: 3580. doi: 10.3390/ijms24043580. *The allergen AtSAH7 interacts with Selenium-binding protein 1 (AtSBP1) possibly forming a complex for antioxidant production and the activation of defense responses triggered by ER stress.*
- Samakovli D, Roka L, Plitsi PK, Drakakaki G, Haralampidis K, Stravopodis DJ, Hatzopoulos P, Milioni D. BRI1 and BAK1 Canonical Distribution in Plasma Membrane Is HSP90 Dependent. Cells (2022) 11: 3341. doi: 10.3390/cells11213341. *HSP90 is crucial in the activation of hormonal receptors. This study shows that the BRI1 that associates with BAK1 to mediate hypocotyl elongation, requires the function of HSP90. HSP90 physically interacts with both BRI1 and BAK1 receptors and modulates their abundance and spatial organization at the plasma membrane.*
- Poulios S, Tsilimigka F, Mallioura A, Pappas D, Seira E, Vlachonasios K. Histone Acetyltransferase GCN5 Affects Auxin Transport during Root Growth by Modulating Histone Acetylation and Gene Expression of PINs. Plants (Basel) (2022) 11: 3572. doi: 10.3390/plants11243572. *GCN5 histone acetyltransferase and ADA2b transcriptional adaptor protein promote the expression of PIN1, PIN3 and PIN4 auxin transporters by modulating histone acetylation to maintain a proper auxin distribution for normal root growth.*
- Tsilimigka F, Poulios S, Mallioura A, Vlachonasios K. ADA2b and GCN5 Affect Cytokinin Signaling by Modulating Histone Acetylation and Gene Expression during Root Growth of Arabidopsis thaliana. Plants (Basel) (2022) 11: 1335. doi: 10.3390/plants11101335. *GCN5 and ADA2b are positive regulators of cytokinin signaling during root growth by modulating histone acetylation and the expression of genes involved in cytokinin synthesis and catabolism. Furthermore, GCN5 and ADA2b are required for the auxin-induced cytokinin signaling in early root growth.*

India

Sourav Datta (sdatta@iiserb.ac.in) Indian Institute of Science Education and Research
Jyothilakshmi Vadassery (jyothi.v@nipgr.ac.in) National Institute of Plant Genome Research

New experimental resources and/or software tools available to Arabidopsis researchers

MedProDB: Mediator Protein Database (http://www.nipgr.ac.in/MedProDB/)
AlnC: An extensive database of long non-coding RNAs (lncRNAs) in Angiosperms (http://www.nipgr.ac.in/AlnC)

Planned events for 2023 and 2024

- Plant Physiology Conference and Chemical Ecology Meetings are planned for 2022-23
- International Symposium On Plant Photobiology, 9-12 January 2024, NISER, Bhubaneswar

Major Funding Sources

- Department of Biotechnology (DBT), Government of India http://dbtindia.nic.in/index.asp
- Science and Engineering Research Board (SERB), India
- Council of Scientific and Industrial Research (CSIR), New Delhi http://www.csirhrdg.res.in/
- Department of Science &Technology (DST), Government of India http://www.dst.gov.in/scientific-programme/serindex.html
- University Grants Commission, New Delhi https://www.ugc.ac.in/
- Ministry of Human Resource and Development, India (MHRD-STARS)

Selected publications

- Agrawal R, Sharma M, Dwivedi N, Maji S, Thakur P, Junaid A, Fajkus J, Laxmi A*, Thakur JK (2022) MEDIATOR SUBUNIT17 integrates jasmonate and auxin signaling pathways to regulate thermomorphogenesis. Plant Physiol. 189(4):2259-2280. *The study reveals the role of the mediator complex as an integrator of JA and auxin signaling pathways during thermomorphogenesis*
- Ojha, M., Verma, D., Chakraborty, N., Pal, A., Bhagat, P.K., Singh, A., Verma, N., Sinha, A.K. and Chattopadhyay, S. (2023). MKKK20 works as an upstream triple-kinase of MKK3-MPK6-MYC2 module in Arabidopsis seedling development. iScience 26, 106049. doi.org/10.1016/j.isci. 2023.106049 *The study functionally characterized MKKK20 as the triple kinase working upstream to MKK3-MPK6-MYC2 module in the regulation of photomorphogenic growth.*
- Sharma M, Sharma Mohan, Jamsheer KM, Laxmi A (2022a) Jasmonic acid coordinates with light, glucose and auxin signalling in regulating branching angle of Arabidopsis lateral roots. Plant Cell Environ. 45:1554–1572 *The work shows how glucose signaling interacts with Jasmonic acid and light signaling in controlling lateral root angle in model plant Arabidopsis thaliana.*
- Gargi Prasad Saradadevi, Dalen Fultz, Murali Krishna Ramgopal, Abirami T. Subramanian, Gerin Prince, Vivek Thakur, and Gireesha Mohannath. Structural variation among assembled genomes facilitates development of rapid and low-cost NOR-linked markers and NOR-telomere junction mapping in Arabidopsis. Plant Cell Rep (2023). https://doi.org/10.1007/s00299-023-03012-x *The genome-wide structural variants we identified and new NOR-linked markers we developed would be useful for future genome-wide association studies (GWAS) and for new gene/trait mapping purposes.*
- Singh D, Datta S. BBX30/miP1b and BBX31/miP1a form a positive feedback loop with ABI5 to regulate ABA-mediated post-germination seedling growth arrest. New Phytologist, 2023 Jun;238(5):1908-1923. doi: 10.1111/nph.18866 *This study shows that two B-box containing microproteins BBX30 and BBX31 together with ABI5 arrest seedling development after germination in an interdependent manner.*

Ireland

Prof. Charles Spillane, Genetics & Biotechnology Lab, Agriculture, Food Systems & Bioeconomy Research Centre, Ryan Institute, University of Galway

New experimental resources and/or software tools available to Arabidopsis researchers

Sherwood OL, Carroll R, Burke S, McCabe PF, Kacprzyk J. A simple and cost-effective method for studying anoxia tolerance in plants. Appl Plant Sci. 2023 11(1):e11509. doi: 10.1002/aps3.11509.

Díez AR, Duque P, Henriques R. Assessing Abscisic Acid-Mediated Changes in Stomatal Aperture Through High-Quality Leaf Impressions. Methods Mol Biol. 2022;2494:217-227. doi: 10.1007/978-1-0716-2297-1_15.

Major Funding Sources

- Science Foundation Ireland www.sfi.ie
- Irish Research Council https://research.ie/

Selected publications

- Badmus UO, Crestani G, Cunningham N, Havaux M, Urban O, Jansen MAK. UV Radiation Induces Specific Changes in the Carotenoid Profile of Arabidopsis thaliana. Biomolecules. 2022 12(12):1879. doi: 10.3390/biom12121879.

- Quiroz-Iturra LF, Simpson K, Arias D, Silva C, González-Calquin C, Amaza L, Handford M, Stange C. Carrot DcALFIN4 and DcALFIN7 Transcription Factors Boost Carotenoid Levels and Participate Differentially in Salt Stress Tolerance When Expressed in Arabidopsis thaliana and Actinidia deliciosa. Int J Mol Sci. 2022 23(20):12157. doi: 10.3390/ijms232012157.

- Bhagat PK, Verma D, Singh K, Badmi R, Sharma D, Sinha AK. Dynamic Phosphorylation of miRNA Biogenesis Factor HYL1 by MPK3 Involving Nuclear-Cytoplasmic Shuttling and Protein Stability in Arabidopsis. Int J Mol Sci. 2022 23(7):3787. doi: 10.3390/ijms23073787.

- Castillo-Bravo R, Fort A, Cashell R, Brychkova G, McKeown PC, Spillane C. Parent-of-Origin Effects on Seed Size Modify Heterosis Responses in Arabidopsis thaliana. Front Plant Sci. 2022 13:835219. doi: 10.3389/fpls.2022.835219.

- Dupouy G, McDermott E, Cashell R, Scian A, McHale M, Ryder P, de Groot J, Lucca N, Brychkova G, McKeown PC, Spillane C. Plastid ribosome protein L5 is essential for post-globular embryo development in Arabidopsis thaliana. Plant Reprod. 2022 Sep;35(3):189-204. doi: 10.1007/s00497-022-00440-9.

Italy

Alice Pajoro (Alice.pajoro@cnr.it)
Institute of Molecular Biology and Pathology, National Research Council

Planned events for 2023 and 2024

- Plant Biotechnology for Agriculture of the XXI Century 23-24 February 2023, Milan
- Workshop on Plant Biology SIBV 2023 22-24 February 2023, Forli
- Inauguration of the Nikon Center of Excellence for Plant Biology and Other Life Sciences at University of Milan. 12th May 2023, Milan
- Congress of the Italian Society of Agricultural Genetics SIGA 5-9 September 2023, Bari
- Congress of the Italian Society of Plant Biology SIBC 11-14 September 2023, Bari
- Congress of the Italian Society of Botany 13-16 September 2023, Pisa

Major Funding Sources

- Ministero dell’Università e della Ricerca (MIUR) https://www.mur.gov.it/
- Program PRIN2017
- Program PRIN2020
- National Research Centre for Agricultural Technologies (Agritech) - European Union Next-Generation EU PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR) – Missione 4 Componente 2, Investimento 1.4 – Project CN00000022. https://www.mur.gov.it/sites/default/files/2022-06/22_06_28%20Scheda_centro%20nazionale%20agritech_PNRR_MUR.pdf
- 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.
- Grant of Excellence Departments MIUR-ARTICOLO 1, COMMI 314-337 LEGGE 232/2016; Italy)
- Regione Lazio http://www.lazioinnova.it/
- Regione Lombardia https://www.regione.lombardia.it
- Sapienza University of Rome https://www.uniroma1.it
- Università degli Studi di Milano www.unimi.it
- University of Padova (Italy), Dotazione Ordinaria della Ricerca (DOR) 2020-2022
- Fondazione Cariplo
- Max Planck Society, Partner Group https://www.mpg.de/272644/partner-groups
- European Union Grants
- HORIZON-MSCA-2021-PF-01 (MSCA Postdoctoral Fellowships 2021) https://cordis.europa.eu/project/id/101059695 DEMEtRA “DEcoding Metabolic Effectors in plant sTress Response and Acclimation” 2022-10 to 2024-09 | Grant
- ERANET COFUND FOSC - C4C; CropsForChange: Tacking climate change in crops.
- H2020 RISE The Polyploidy Paradigm And Its Role In Plant Breeding (2021-2025)
- H2020 RISE Evolution of genetic network required for fruit and fruit-like structures development of land plants (2021-2025)
- Joint Bilateral Agreement CNR/Royal Society of London (UK). Biennial Programme 2023-2024. 2023-01 to 2025-01 | Grant Royal Society of London (UK). Biennial Programme 2023-2024 (London, GB)
- PRIMA_2020. Partnership for Research and Innovation in the Mediterranean Area (Barcelona, ES) Plant micRObiome in Sustainable vITiculture. 2021-06 to 2025-06 https://mel.cgiar.org/projects/prosit

Selected publications

- Ghelli R, Brunetti P, Marzi D, Costantino P, Cardarelli M. “The full-length Auxin Response Factor 8 isoform ARF8.1 controls pollen cell wall formation and directly regulates TDF1, AMS and MS188 expression” Plant Journal, 2023, 113(4), pp. 851–865. https://doi.org/10.1111/tpj.16089 *In Arabidopsis, pollen maturation takes place during late stages of flower development and, to ensure male fertility, it is coordinated with two other developmental processes occurring in stamens, anther dehiscence and stamen elongation. Here, we characterized the role of ARF8 isoforms in pollen fertility.*

- Grenzi M, Buratti S, Parmagnani AS, Abdel Aziz I, Bernacka-Wojcik I, Resentini F, Šimura J, Doccula FG, Alfieri A, Luoni L, Ljung K, Bonza MC, Stavrinidou E, Costa A. “Long-distance turgor pressure changes induce local activation of plant glutamate receptor-like channels.” Current Biology 2023 Feb 10:S0960-9822(23)00076-3. doi: 10.1016/j.cub.2023.01.042. *Wound, burn and osmotic-induced changes of turgor pressure trigger an increase of apoplastic L-Glutamate that activates the AtGLR3.3 through its ligand-binding domain.*

- Korwin Krukowski P, Visentin I, Russo G, Minerdi D, Bendahmane A, Schubert A, Cardinale F. “Transcriptome Analysis Points to BES1 as a Transducer of Strigolactone Effects on Drought Memory in Arabidopsis thaliana.” Plant and Cell Physiology, Volume 63, Issue 12, December 2022, Pages 1873–889, https://doi.org/10.1093/pcp/pcac058 *Our findings reveal that strigolactones are master regulators of Arabidopsis transcriptional memory upon drought and that this role is partially mediated by the BES1 transcription factor.*

- Kunkowska AB, Fontana F, Betti F, Soeur R, Beckers GJM, Meyer C, Jaeger GD, Weits DA, Loreti E, and Perata P. “Target of rapamycin signaling couples energy to oxygen sensing to modulate hypoxic gene expression in Arabidopsis.” Proceedings of the National Academy of Sciences of the United States of America. 2023 Jan 17; 120(3):e2212474120 https://doi.org/10.1073/pnas.2212474120 *Flooding events limiting oxygen availability are more frequent due to climate change and impact negatively on plant growth and productivity. We demonstrate that oxygen sensing by ERF-VIIs is fine-tuned by target of rapamycin (TOR) kinase, a master energy sensor widely conserved in all eukaryotes.*

- Scortica A, Giovannoni M, Scafati V, Angelucci F, Cervone F, De Lorenzo G, Benedetti M, Mattei B. “Berberine bridge enzyme-like oligosaccharide oxidases act as enzymatic transducers between microbial glycoside hydrolases and plant peroxidases. Mol Plant Microbe Interact. (2022) Oct;35(10):881-886. doi: 10.1094/MPMI-05-22-0113-TA. *Research article studying H2O2 generation downstream of a fungal polygalacturonase and OGOX1 or an endoglucanase and CELLOX directed by plant peroxidases involved in plant defense or development*

Japan

Motoaki Seki (motoaki.seki@riken.jp)
Masatomo Kobayashi (masatomo.kobayashi@riken.jp) RIKEN BRC

New experimental resources and/or software tools available to Arabidopsis researchers

RIKEN Center for Sustainable Resource Science (CSRS) (http://www.csrs.riken.jp/en/).

- Platform for RIKEN Metabolomics (http://prime.psc.riken.jp/)
- Plant-Protein Annotation Suite (http://plant-pras.riken.jp/)
- RIKEN Arabidopsis Genome Encyclopedia (http://rarge-v2.psc.riken.jp/)

RIKEN BioResource Research Center (BRC) (https://epd.brc.riken.jp/en/)

- Entire seed stocks of TF-GR (transcription factor-glucocorticoid receptor) lines have been deposited to RIKEN BRC. The seeds will be available after propagation. If you have interests in this resource, send your inquiry to plant.brc@riken.jp.
- We have added the information of 96 mutant and transgenic lines of Arabidopsis to the Exp-Plant Catalog (https://plant.rtc.riken.jp/resource/fox/fox_list.htmlt). Now 443 mutant and transgenic lines deposited from Japanese scientists are on the Catalog.

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://pgdbjsnp.kazusa.or.jp/app/kusakidb) (https://hub.docker.com/r/ghelfi/kusakidb)

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

- ChaetoBase: Chaetoceros gracilis gene annotation database (https://chaetoceros.nibb.ac.jp/)

Planned events for 2023 and 2024

- Mar. 15-17, 2023: 64th Annual Meeting of Japanese Society of Plant Physiologists. Tohoku Univ., Sendai, Japan.
- Jun. 5-9, 2023: The 33rd International Conference on Arabidopsis Research (ICAR2023), Makuhari Messe, Chiba, Japan (https://icar2023.org/).

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)

Selected publications

- Kinoshita, A., Naito, M., Wang, Z., Inoue, Y., Mochizuki, A., Tsukaya, H. (2022) Position of meristems and the angles of the cell division plane regulate the uniqueness of lateral organ shape. Development 149: dev199773. https://doi.org/10.1242/dev.199773 *This study revealed the mechanism determining different organ morphologies between leaves and floral organs through intimate collaboration of molecular genetics, image-processing, and a mathematical simulation.*

- Kozgunova, E., Yoshida, M.W., Reski, R., Goshima, G. (2022) Spindle motility skews division site determination during asymmetric cell division in Physcomitrella. Nature Commun. 13: 2488. doi: 10.1038/s41467-022-30239-1. *The study identified what determines the site of cell division in moss, revealing unexpected similarity between moss and animals.*

- Sakamoto, Y., Kawamura, A., Suzuki, T., Segami, S., Maeshima, M., Polyn, S., Veylder, L.D., Sugimoto, K. (2022) Transcriptional activation of auxin biosynthesis drives developmental reprogramming of differentiated cells. Plant Cell 34: 4348–4365. doi: 10.1093/plcell/koac218. *This study revealed that auxin biosynthesis is an important step for resumption of cell division in cell reprogramming from leaf mesophyll protoplasts, and identified important transcription factors involved in the process.*

- Bashir, K., Todaka, D., Rasheed, S., Matsui, A., Ahmad, Z., Sako, K., Utsumi, Y., Vu, A.T., Tanaka, M., Takahashi, S., Ishida, J., Tsuboi, Y., Watanabe, S., Kanno, Y., Ando, E., Shin, K.C., Seito, M., Motegi, H., Sato, M., Li, R., Kikuchi, S., Fujita, M., Kusano, M., Kobayashi, M., Habu, Y., Nagano, A.J., Kawaura, K., Kikuchi, J., Saito, K., Hirai, M.Y., Seo, M., Shinozaki, K., Kinoshita, T. and Seki, M. (2022) Ethanol-mediated novel survival strategy against drought stress in plants. Plant Cell Physiol. 63:1181-1192. doi: 10.1093/pcp/pcac114. *This study revealed that ethanol treatment enhances drought stress tolerance in plants, such as Arabidopsis, rice and wheat by the induction of stomatal closure, highlighting a new survival strategy for increasing crop production under water-limited conditions.*

New Zealand

Lynette Brownfield (lynette.brownfield@otago.ac.nz)
University of Otago, Department of Biochemistry, Dunedin

Planned events for 2023 and 2024

- Plant Science Central July 4-6, 2023, Massey University, Palmerston North, New Zealand
- Australian Society of Plant Scientists and New Zealand Society of Plant Biologist joint hybrid meeting, September 2024

Major Funding Sources

- The Marsden Fund administered by the Royal Society of New Zealand (http://www.royalsociety.org.nz/programmes/funds/marsden/)
- Ministry for Business, Innovation and Employment (MBIE; http://www.mbie.govt.nz/) through:
- Core funding to Crown Research Institutes
- The Endeavour fund (http://www.mbie.govt.nz/info-services/science-innovation/investment-funding/current-funding/2018-endeavour-round)
- The Catalyst Fund (http://www.mbie.govt.nz/info-services/science-innovation/investment-funding/current-funding/catalyst-fund)

Selected publications

- Collins, P.P., Broad, R.C., Yogeeswaran, K., Varsani A, Poole A.M. and Collings, D.A. (2023) Characterisation of the trans-membrane nucleoporins GP210 and NDC1 in Arabidopsis thaliana. Plant Science 332; 111719 *This research, with authors affiliated to two New Zealand universities, used Arabidopsis mutants to show two proteins are likely components of plant nucleopore anchors highlighting the use of Arabidopsis to investigate gene function.*

- Herath, D., Voogd, C., Mayo-Smith, M., Yang B., Allan, A.C., Putterill, J., Varkonyi-Gasic, E. (2022) CRISPR-Cas-mediated mutagenesis of kiwifruit BFT genes results in an evergrowing but not early flowering phenotype. Plant Biotechnology Journal 20:2064-2076 *This article from researchers at the New Zealand Institute for Plant and Food Research Limited and University of Auckland highlights how Arabidopsis can be used as an experimental plant to help determine the role of genes in plants of commercial interest.*

- Le Lievre, L.L., Chakkatu, S.P., Varghese, S, Day, R.C., Pilkington, S.M., Brownfield, L.R. (2023) RNA-Seq analysis of synchronised pollen isolated from a single anther. Frontiers in Plant Science 14: 1121570 *This article from researchers at the University of Otago and New Zealand Institute for Plant and Food Research used Arabidopsis as a model to establish as system for low-input transcriptomic analysis on pollen that can applied to other plant species.*

- Daniel A Careno, D.A., Perez-Santangelo S., Macknight, R.C., Yanovsky, M.J. (2022) The 5'-3' mRNA Decay Pathway Modulates the Plant Circadian Network in Arabidopsis. Plant and Cell Physiology 63, 1709–1719. *This article from researchers at the University of Otago working with collaborators from Argentina revealed an important role for the 5'-3' mRNA decay pathway in the fine-tuning of circadian oscillations in Arabidopsis.*

Norway

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

New experimental resources and/or software tools available to Arabidopsis researchers
Establishment of the first national graduate school in Plant Biology (Photosyntech https://photosyntech.no/).

Planned events for 2023 and 2024

- Norwegian Plant Biology conference organized in association with the National Norwegian PhD school in Plant Biology (Photosyntech), 2/3. November 2023 Oslo
- Fascination of Plants day 2023 and 2024 https://plantday18may.org organized by the Norwegian University of Life Sciences.

Major Funding Sources
Norwegian Research Council, forskningsradet.no

Selected publications

- Kornstad et al., 2022 Ecology and Evolution https://doi.org/10.1002/ece3.8915 *The authors used the allopolyploid Arabidopsis suecica in combination with its´ parent species A. arenosa and A. thaliana as model system to investigate relationships between phenotypic plasticity, fitness, and genetic variation. Their intriguing findings include the observation of a positive relationship between genetic diversity and phenotypic plasticity.*

- Reinar et al., 2023 Science Advances DOI: 10.1126/sciadv.add6960 *This publication investigates how natural selection shapes length variation in tracts of identical amino acids in intrinsically disordered proteins, which play important roles in responses to biotic and abiotic stress.*

- Van Ekelenburg et al., 2023 Plant Physiology https://doi.org/10.1093/plphys/kiac520 *The authors used luorescence-activated nuclear sorting (FANS) to investigate genomic imprinting in the endosperm of Arabidopsis with high degrees of spatial and temporal resolution, enabling them to suggest that regulation of dynamic imprinting is dynamic and to challenge the canonical concepts for genomic imprinting.*

Poland

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

Planned events for 2023 and 2024

- 19-22 September 2023 Poznań 11th Conference of the Polish Society of Experimental Plant Biology https://ptber.org.pl/default/en/conferences/11th-conference/
- 28-30 September 2023 Warsaw Polish RNA biology meeting https://pl-rna.iimcb.gov.pl/

Major Funding Sources

Due to the fact that Arabidopsis thaliana is a model plant the major funding source that supports work on it is the National Science Centre Poland (NCN) – government agency supervised by the Ministry of Science and Higher Education. The NCN mission is to support basic research in Poland. https://www.ncn.gov.pl/en

Selected publications

- Arasimowicz-Jelonek, M., Floryszak-Wieczorek, J., Suarez, S., Doctorovich, F., Sobieszczuk-Nowicka, E., Bruce King, S., Milczarek, G., Rębiś, T., Gajewska, J., Jagodzik, P., et al. (2023). Discovery of endogenous nitroxyl as a new redox player in Arabidopsis thaliana. Nature Plants 9, 36-44. *In this work generation of the Nitroxyl (HNO) molecules in Arabidopsis upon abiotic stress and its signalling potential is described.*

- Montez, M., Majchrowska, M., Krzyszton, M., Bokota, G., Sacharowski, S., Wrona, M., Yatusevich, R., Massana, F., Plewczynski, D., and Swiezewski, S. (2023). Promoter-pervasive transcription causes RNA polymerase II pausing to boost DOG1 expression in response to salt. The EMBO Journal 42, e112443. *The work describes seed germination delay mechanism that is mediated by IncRNAs transcribed from the 5' upstream region of the Delay Of Germination (DOG1) gene upon salt stress.*

- Szymanska-Lejman, M., Dziegielewski, W., Dluzewska, J., Kbiri, N., Bieluszewska, A., Poethig, R.S., and Ziolkowski, P.A. (2023). The effect of DNA polymorphisms and natural variation on crossover hotspot activity in Arabidopsis hybrids. Nature Communications 14, 33. *The authors showed that in Arabidopsis thaliana meiotic crossovers occur preferentially within polymorphic hotspots and depends on the mismatch repair gene MSH2.*

Portugal

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

Planned events for 2023 and 2024

- XVIII Spanish-Portuguese Congress on Plant Biology 2023 (PB2023). Braga, Portugal, 9-12 July.
- SUMOylation: From discovery to translation. EMBO WORKSHOP, Póvoa De Varzim, Portugal 25-28 September 2023.

Major Funding Sources

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

Selected publications

- 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. Plant Journal. 114: 371-389.doi: 10.1111/tpj.16141. *The present work reveals how AGPs involved in plant reproduction are controlled by Hyp-GALTs through glycosylation, using a quintuple galt mutant previously generated, namely galt25789. So, the functional importance of the carbohydrate moieties of AGPs in ovule development and pollen–pistil interactions in Arabidopsis is demonstrate in this work.*
- D Moreira, AL Lopes, J Silva, MJ Ferreira, S Pinto, S Mendes, LG Pereira, S Coimbra, Pereira AM. 2022. New insights on the expression patterns of specific arabinogalactan proteins in reproductive tissues of Arabidopsis thaliana. Frontiers in Plant Science, 13:1083098. doi: 10.3389/fpls.2022.1083098. *This work describes the expression pattern of a specific group of Arabinogalactan Proteins, a large family of cell wall glycoproteins with important functions in plant reproduction. This adds on to recent literature on this family of glycoproetins contributing to the AGPs atlas of expression in the reproductive tissues, allowing further detailed characterization of its functional roles in this process.*
- 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. mcad046, https://doi.org/10.1093/aob/mcad046. *The findings described in this work reveal distinct Arabinogalactan Proteins' 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 remodeling nature of the cell wall in developmental processes.*
- Misra, C. S., Sousa, A. G. G., Barros, P. M., Kermanov, A., & Becker, J. D. (2023). Cell-type-specific alternative splicing in the Arabidopsis germline. Plant Physiology, 192(1), 85–101. doi:10.1093/plphys/kiac574 *Misra et al. reveal the complex alternative splicing landscape of isolated male and female Arabidopsis gametes*
- Klodová, B., Potěšil, D., Steinbachová, L., Michailidis, C., Lindner, A.-C., Hackenberg, D., … Honys, D. (2022). Regulatory dynamics of gene expression in the developing male gametophyte of Arabidopsis. Plant Reproduction. doi:10.1007/s00497-022-00452-5 *Klodová et al. provide a comprehensive transcriptome analysis of male gametogenesis in two Arabidopsis ecotypes.*

Sweden

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

New experimental resources and/or software tools available to Arabidopsis researchers

- This year I want to highlight the network of protein production facilities hosted by Swedish universities: https://ppns.ki.se/

As listed on previous occasions other important sites are:

- Max Lab hosted by Lund University; https://www.maxiv.lu.se/ Dedictated to high-throughput, nanovolume characterization and crystallization of biological macromolecules
- Science for Life Laboratory (SciLifeLab) is a national resource center dedicated to large scale research in molecular biosciences and medicine with two sites; in Stockholm and Uppsala. The major funding for SciLifeLab comes from strategic grants from the Swedish government, http://www.scilifelab.se
- Umeå Plant Science Centre has developed and maintains platforms of genomics, proteomics, metabolomics, quantification of plant growth regulators and wood analysis http://www.upsc.se, found under “resources”
- The Swedish Metabolomics Centre in Umeå is a national resource, http://www.swedishmetabolomicscentre.se/

Important resources may also be listed on these plant centers’ sites:

- Plant Research and Higher Education in Southern Sweden https://www.plantlink.se/
- The Linnean Centre for Plant Biology in Uppsala https://lcpu.se/

Planned events for 2023 and 2024

- The 16th Nordic Photosynthesis Congress and the 5th Nordic Algae Symposium, ‘From Photosynthesis to Industrial Applications’, Umeå, Sweden, 19 – 21 June, 2023 https://tinyurl.com/Photosynthesis-conference-site
- 12th Scandinavian Plant Physiology Society (SPPS) PhD Student Conference – PhD 101: Everything is hard before it gets easy, Lund, Sweden, 27-29 September, 2023. Open to all PhD students studying plant science. http://sppsphd2023.org/
- Final NordPlant Annual meeting: The future of plant phenotyping, Båstad Sweden, 22-23 November 2023 https://www.nordplant.org/2023/02/23/final-nordplant-annual-meeting-the-future-of-plant-phenotyping-22-23-november/
- Sites to query to find information on ongoing research and activities for Plant Research and Higher Education in Southern Sweden (PlantLink) have activities regularly, they also list meetings and courses https://www.plantlink.se/

Additional information can be found at centers with Plant research such as:

- The Linnean Centre for Plant Biology in Uppsala (both Uppsala University and the University of Agricultural Sciences), https://lcpu.se/
- Uppsala University Departments of Ecology and Genetics https://www.ieg.uu.se/research/ and Department of Organism Biology https://www.iob.uu.se/research/ - may be accessed patly through the The Linnean Centre for Plant Biology (above)
- Umeå Plant Science Centre, Umeå www.upsc.se
- Stockholm University, https://www.su.se/deep/english/
- Örebro University, https://www.oru.se/english/research/research-environments/ent/lsc/
- Linköping University, https://liu.se/en/research/electronic-plants
- The Fascination of Plants Day site contain information on Plant Day and other, https://plantday18may.org/category/europe/sweden/
- European Plant Science Organisation (EPSO), https://epsoweb.org/

Major funding sources

- The Royal Swedish Academy of Sciences research funding https://www.kva.se/en/research-funding/
- 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 support postdoctoral stays outside the EU/EFTA (incl. the United Kingdom).
- The Wallenberg Foundations; http://www.wallenberg.org/en Private foundations supporting researcher initiated basic research as well as larger centers of excellence devoted to functional genomics and other strategic areas
- SciLifeLab & Wallenberg National Program for Data-Driven Life Science
- Carl Trygger's Foundation for Scientific Research; http://www.carltryggersstiftelse.se/ A private foundation supporting research within the areas of agriculture, forestry, biology, chemistry and physics
- The Kempe Foundations; http://www.kempe.com Private foundations devoted to support scientific research in Northern Sweden
- The Magnus Bergvall Foundation https://www.magnbergvallsstiftelse.nu/ A private foundation supporting basic science
- Stiftelsen Olle Engkvist Byggmästare; http://engkviststiftelserna.se/ A private foundation supporting basic science
- Sven and Lily Lawski's foundation for research in Natural Sciences (Biochemistry and Genetics); http://www.lawskistiftelsen.se/ A private foundation supporting basic science
- The Wenner-Gren Foundations https://www.swgc.org/the-foundations.aspx Private foundations that support international scientific exchange
- Governmental agencies as well as private foundations support basic research devoted to plant sciences and many of the grantees use Arabidopsis as their main model system. Most funders have one call per year and award project grants to support research and salary or stipend over a few years, with occasional calls for larger grants with a focus area. Typically, larger research grants are awarded to groups of and are used to support basic core facilities in major research facilities (as listed above), enabling access also to smaller research groups to carry out most type of research. Larger, individual competitive grants are regularly awarded to Scientists using Arabidopsis as a model system. Several grants also employ alternative model species and/or crops.
- In addition, most major international grant agencies have calls applicable for Swedish arabidopsis research. Those would be for instance Nordic sources like Novo Nordisk Foundation https://novonordiskfonden.dk/en/grants/, Nordforsk https://www.nordforsk.org/
- More general such as EMBO https://www.embo.org/funding/,
- Human Frontiers https://www.hfsp.org/funding/hfsp-funding/research-grants,
- ERC https://erc.europa.eu/,
- https://www.mariecuriealumni.eu/news/european-funding-opportunities-10-web-sites-you-need-know

Selected publications

- Darwish, E. et al. (2022) Touch signaling and thigmomorphogenesis are regulated by complementary CAMTA3- and JA-dependent pathways. Sci Adv 8, eabm2091, doi:10.1126/sciadv.abm2091 *This work identified key regulators of two independent touch-signaling pathways.*

- Meschichi, A. et al. (2022) The plant-specific DDR factor SOG1 increases chromatin mobility in response to DNA damage. EMBO reports 23 (12) DOI10.15252/embr.202254736 *Help characterise the role of SUPPRESSOR OF GAMMA RESPONSE 1 (SOG1) a plant-specific transcription factor that plays a central role in the DDR and counterpart of animal p53.*

- Augstein, F and Carlsbecker, A (2022) Salinity induces discontinuous protoxylem via a DELLA-dependent mechanism promoting salt tolerance in Arabidopsis seedlings New Phytologist 236 (1) 195-209 *Important work for understanding plants response to salt and acid and gibberellin signalling with importance for xylem differentiation.*

- Serivichyaswat, P.T. et al. (2022) High temperature perception in leaves promotes vascular regeneration and graft formation in distant tissues. Development 149 (5): dev200079. *Shed lights on interplay between temperature perception and auxin signaling with importance for development and healing of grafts.*

- Menard, D., Blaschek, L. Pesquet, E (2022) Plant biomechanics and resilience to environmental changes are controlled by specific lignin chemistries in each vascular cell type and morphotype. Plant Cell 34 (12) 4877-4896 I*t shows that plants adjust their biomechanics and hydraulic properties better adapt to variable environmental conditions.*

Switzerland

Misako Yamazaki (misako.yamazaki@uzh.ch)
Kentaro K. Shimizu (kentaro.shimizu@uzh.ch)
University of Zurich
Swiss Plant Science Web coordination-spsw@unibas.ch

New experimental resources and/or software tools available to Arabidopsis researchers

Detecting frequency-dependent selection through the effects of genotype similarity on fitness components. Evolution, 2023 Apr 1;77(4):1145-1157. PMID: 36801936 https://github.com/yassato/RegressionFDS

Planned events for 2023 and 2024

Conferences, symposiums

- International Conference on Evolution in Action, 11 - 15 June 2023, Monte Verità. https://evolution.uzh.ch/en/conference.html
- Two-days symposium, “Genome duplication at the intersection of biodiversity and crop sciences” 10th-11th of July 2023, UNIFR Seminar room Per21 https://events.unifr.ch/summerschool_polyploidy/en/program/workshop-1.html
- 25th Anniversary Symposium of the Zurich-Basel Plant Science Center Impact of plant sciences on our lives – food, environment, health and knowledge. 8th of December 2023, University of Zurich https://www.plantsciences.uzh.ch/en/outreach/conferences/Anniversary-Symposium.html
- SwissPLANT symposium 2024, 17 - 19 January 2024, Les Diablerets https://swissplantscienceweb.unibas.ch/en/swissplant/
- Lausanne Genomics Days 2024, (second week of February) 2024, Lausanne https://wp.unil.ch/gtf/lgd-2023/
- LS2 Annual Meeting 2024, February 2024 https://www.ls2.ch/about-us/ls2
- Biology 24, 15 - 16 February 2024, Zurich https://swiss-systematics.ch/en/events/biologyxx

Outreach activities

- Polyploid evolutionary genomics: challenges and opportunities. Summer school, 10 to 20 July, University of Fribourg, Switzerland. https://events.unifr.ch/summerschool_polyploidy/en/
- Outreach in general: https://www.plantsciences.uzh.ch/en/outreach.html
- Plant Science at School: https://www.plantsciences.uzh.ch/en/outreach/atschool.html
- Biotinkering: Biotinkering for children, young people and school classes (in German) https://www.plantsciences.uzh.ch/de/experimente/Biotinkering.html

Major funding sources

- Swiss National Science Foundation (SNSF) http://www.snf.ch/en/Pages/default.aspx
- European Research Council (ERC), https://erc.europa.eu/
- Syngenta (Plant Science Center - Syngenta Fellowship), https://www.plantsciences.uzh.ch/en/research/fellowships/syngenta.html
- State Secretariat for Education, Research, and Innovation (SERI), https://www.sbfi.admin.ch/sbfi/en/home.html
- 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
- The Human Frontier Science Program (HFSP), https://www.hfsp.org/

Selected publications

- Ricca’s factors as mobile proteinaceous effectors of electrical signaling. Yong-Qiang Gao, Pedro Jimenez-Sandoval, Satyam Tiwari, Stéphanie Stolz, Jing Wang, Gaëtan Glauser, Julia Santiago, Edward E Farmer, Cell. 2023 Mar 30;186(7):1337-1351, PMID: 36870332 *‘This study demonstrates long-distance protein transport activates electrical signalling in wounded plants’*

- Recent speciation associated with range expansion and a shift to self-fertilization in North American Arabidopsis. Yvonne Willi, Kay Lucek, Olivier Bachmann, Nora Walden, Nat Commun. 2022 Dec 8;13(1):7564, PMID: 36481740 *‘Range limits can be viewed as places where adaptive evolution fails, and this study describes conditions under which populations can break this constraint, with the result of peripheral parapatric speciation.’*

- A phosphoinositide hub connects CLE peptide signaling and polar auxin efflux regulation. Qian Wang, A Cecilia Aliaga Fandino, Moritz Graeff, Thomas A DeFalco, Cyril Zipfel, Christian S Hardtke, Nat Commun. 2023 Jan 26;14(1):423, PMID: 36702874 *‘This study demonstrates that a CLE peptide signaling pathway interferes directly with an auxin efflux control machinery in an essential root development process.’*

- A combination of plasma membrane sterol biosynthesis and autophagy is required for shade-induced hypocotyl elongation. Yetkin Çaka Ince, Johanna Krahmer, Anne-Sophie Fiorucci, Martine Trevisan, Vinicius Costa Galvão, Leonore Wigger, Sylvain Pradervand, Laetitia Fouillen, Pierre Van Delft, Manon Genva, Sebastien Mongrand, Hector Gallart-Ayala, Julijana Ivanisevic, Christian Fankhauser
- Nat Commun. 2022 Oct 10;13(1):5659, PMID: 36216814 *‘The authors show that depending on resource availability Arabidopsis seedlings use different metabolic strategies to fuel growth: particularly under conditions of limited photosynthetic capacity, Arabidopsis uses autophagy (recycling) to enable hypocotyl growth.’*

- Mapping phyllosphere microbiota interactions in planta to establish genotype-phenotype relationships. Martin Schäfer, Christine M Vogel, Miriam Bortfeld-Miller, Maximilian Mittelviefhaus, Julia A Vorholt, Nat Microbiol. 2022 Jun;7(6):856-867. *As spotlighted by the editor, “Bacteria-bacteria interactions and resultant microbiota changes were characterized using a synthetic phyllosphere community in planta.”, in this paper*

Highly cited researchers 2022 (members of the Swiss Plant Science Web)
https://swissplantscienceweb.unibas.ch/en/news/news-details/highly-cited-researchers-2022

Turkey

Baris Uzilday (baris.uzilday@ege.edu.tr) Ege University

Planned events for 2023 and 2024

- National Plant Physiology Symposium (UBFS) – webpage: TBA
- 10th National Botany Congress - https://www.botanik.web.tr/congre/default.asp?id=2
- Fascination of Plants Day 2024 – Symposium held at Ege University (18 May).

Major funding sources

The Scientific and Technological Research Council of Turkey (TUBITAK)
https://www.tubitak.gov.tr/en

Selected publications

- Aslam, N., Sameeullah, M., Yildirim, M., Baloglu, M. C., Yucesan, B., Lössl, A. G., ... & Gurel, E. (2022). Isolation of the 3β-HSD promoter from Digitalis ferruginea subsp. ferruginea and its functional characterization in Arabidopsis thaliana. Molecular Biology Reports, 49(7), 7173-7183.

- Kahraman, N., & Pehlivan, N. (2022). Harboured cation/proton antiporters modulate stress response to integrated heat and salt via up-regulating KIN1 and GOLS1 in double transgenic Arabidopsis. Functional Plant Biology, 49(12), 1070-1084.

- Ozfidan-Konakci, C., Yildiztugay, E., Arikan, B., Elbasan, F., Alp, F. N., & Kucukoduk, M. (2023). Hydrogen Sulfide Protects Damage From Methyl Viologen-Mediated Oxidative Stress by Improving Gas Exchange, Fluorescence Kinetics of Photosystem II, and Antioxidant System in Arabidopsis thaliana. Journal of Plant Growth Regulation, 42(2), 1031-1050.

- Ozgur, R. (2022). Involvement of poly (ADP-ribose) ylation (PARylation) in the regulation of antioxidant defense system in Arabidopsis thaliana under salt stress. Turkish Journal of Botany, 46(4), 333-345.

United Kingdom

Geraint Parry (arabidopsiseventsuk@gmail.com) Arabidopsis Events UK

New experimental resources and/or software tools available to Arabidopsis researchers

- **Low-Cost Nematode Imaging** Kranse OP, Ko I, Healey R, Sonawala U, Wei S, Senatori B, De Batté F, Zhou J, Eves-van den Akker S (2022) A low-cost and open-source solution to automate imaging and analysis of cyst nematode infection assays for Arabidopsis thaliana. Plant Methods. doi: 10.1186/s13007-022-00963-2.
- **Pikobodies for plant disease resistance** Kourelis J, Marchal C, Posbeyikian A, Harant A, Kamoun S (2023) NLR immune receptor-nanobody fusions confer plant disease resistance. Science. doi: 10.1126/science.abn4116
- **Novel transformation system for Oomycete pathogens** Wang L, Zhao F, Liu H, Chen H, Zhang F, Li S, Sun T, Nekrasov V, Huang S, Dong S. (2023) A modified Agrobacterium-mediated transformation for two oomycete pathogens. PLoS Pathog. doi: 10.1371/journal.ppat.1011346
- **Reference genes for smRNA FISH** Duncan S, Johansson HE, Ding Y (2023) Reference genes for quantitative Arabidopsis single molecule RNA fluorescence in situ hybridization. J Exp Bot. doi: 10.1093/jxb/erac521
- **Identification of a Plasmodesmal proteome** Johnston MG, Breakspear A, Samwald S, Zhang D, Papp D, Faulkner C, de Keijzer J (2023) Comparative phyloproteomics identifies conserved plasmodesmal proteins. J Exp Bot. doi: 10.1093/jxb/erad022

Planned events for 2023 and 2024

- SEB Annual Conference 2023, 4 – 7 July 2023, Edinburgh, UK https://www.sebiology.org/events/seb-annual-conference-2023.html
- BSPP Plant Pathology Meeting, 5-8 September 2023, Birmingham, UK https://www.bspp.org.uk/conferences/plant-pathology-2023/
- Advances in Nematology, 7th December 2023, London UK https://www.aab.org.uk/events/
- AAB Early Career Professional Science and Training event, 18th-19th December 2023, Leicester, UK https://www.aab.org.uk/events/

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/

Selected publications

Rhodes J, Roman AO, Bjornson M, Brandt B, Derbyshire P, Wyler M, Schmid MW, Menke FLH, Santiago J, Zipfel C. Perception of a conserved family of plant signalling peptides by the receptor kinase HSL3. Elife. doi: 10.7554/eLife.74687

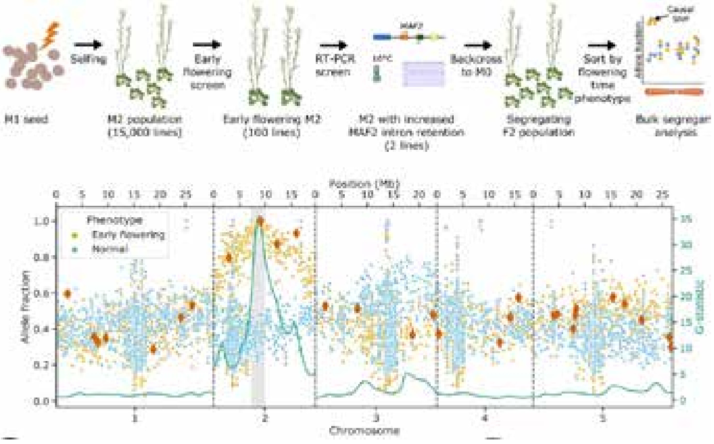
Plant genomes encode hundreds of secreted peptides; however, relatively few have been characterised. We report here an uncharacterised, stress-induced family of plant signalling peptides, which we call CTNIPs. Based on the role of the common co-receptor BRASSINOSTEROID INSENSITIVE 1-ASSOCIATED KINASE 1 (BAK1) in CTNIP-induced responses, we identified in Arabidopsis thaliana the orphan receptor kinase HAESA-LIKE 3 (HSL3) as the CTNIP receptor via a proteomics approach. The identification of this novel signalling module will further shed light on the diverse functions played by plant signalling peptides.

Abbas M, Sharma G, Dambire C, Marquez J, Alonso-Blanco C, Proaño K, Holdsworth MJ. An oxygen-sensing mechanism for angiosperm adaptation to altitude. Nature. doi: 10.1038/s41586-022-04740-y. *Angiosperms can grow at extreme altitudes, and have been observed growing as high as 6,400 metres above sea level but the molecular mechanisms that enable plant adaptation specifically to altitude are unknown. This study investigates the relationship between altitude and oxygen sensing in relation to chlorophyll biosynthesis-which requires molecular oxygen-and hypoxia-related gene expression. They show that in etiolated seedlings, steady-state levels of the phototoxic chlorophyll precursor protochlorophyllide are influenced by sensing of atmospheric oxygen concentration. In natural populations representing diverse angiosperm clades, we find oxygen-dependent altitudinal clines for steady-state levels of protochlorophyllide and hypoxia-related genes. Arabidopsis accessions from contrasting altitudes display altitude-dependent gene expression and protein accumulation.*

Parker MT, Soanes BK, Kusakina J, Larrieu A, Knop K, Joy N, Breidenbach F, Sherwood AV, Barton GJ, Fica SM, Davies BH, Simpson GG (2022) m6A modification of U6 snRNA modulates usage of two major classes of pre-mRNA 5’ splice site. Elife. doi: 10.7554/eLife.78808. *Splicing is mediated by the spliceosome, and docking of the pre-mRNA 5’ splice site into the spliceosome active site depends upon pairing with the conserved ACAGA sequence of U6 snRNA. This research shows that m6A modified U6 snRNA determines the accuracy and efficiency of splicing since the conserved methyltransferase, FIONA1, is required for Arabidopsis U6 snRNA m6A modification. These findings are generalized to reveal two major classes of 5’ splice site in diverse eukaryotes, which display anti-correlated interaction potential with U5 snRNA loop 1 and the U6 snRNA ACAGA box. They conclude that U6 snRNA m6A modification contributes to the selection of degenerate 5’ splice sites crucial to alternative splicing.*

Waterworth WM, Latham R, Wang D, Alsharif M, West CE (2022) Seed DNA damage responses promote germination and growth in Arabidopsis thaliana. Proc Natl Acad Sci U S A. doi: 10.1073/pnas.2202172119. *The desiccated, quiescent state of seeds confers extended survival of the embryonic plant. However, accumulation of striking levels of genome damage in quiescence impairs germination and threatens plant survival. The mechanisms by which seeds mitigate this damage remain unclear. Here, we reveal that imbibed Arabidopsis seeds display high resistance to DNA damage, which is lost as seeds advance to germination, coincident with increasing cell cycle activity. In contrast to seedlings, we show that seeds minimize the impact of DNA damage by reducing meristem disruption and delaying SOG1-dependent programmed cell death.*

Parkinson SJ, Tungsirisurp S, Joshi C, Richmond BL, Gifford ML, Sikder A, Lynch I, O’Reilly RK, Napier RM (2022) Polymer nanoparticles pass the plant interface. Nat Commun. doi: 10.1038/s41467-022-35066-y *To learn about the accumulation of nanoplastics by plants, we prepared well-defined block copolymer nanoparticles by aqueous dispersion polymerisation. A fluorophore was incorporated via hydrazone formation and uptake into roots and protoplasts of Arabidopsis thaliana was investigated using confocal microscopy. Here we show that uptake is inversely proportional to nanoparticle size. Positively charged particles accumulate around root surfaces and are not taken up by roots or protoplasts, whereas negatively charged nanoparticles accumulate slowly and become prominent over time in the xylem of intact roots.*



Loss of FIO1 causes early flowering and reduced splicing of pre-mRNA encoding the floral repressor MAF2. (A) Schematic showing the format of the two-step mutant screen. (B) Scatter plot showing allele fractions of ethyl methanesulfonate (EMS)-induced G to A transitions in pooled phenotypically normal plants (blue) and early flowering sisters (orange). Dark orange diamonds show SNPs predicted to have a significant impact on the functional expression of a protein-coding gene (nonsense mutations and splice site mutations). The green line shows the test statistic for the G-test between the allele fractions found in early flowering and normal plants, which has been smoothed using a tri-cube kernel with a window size of two megabases (Mb). The 2.6 Mb mapping interval containing FIO1 is highlighted in grey.

United States and North American Arabidopsis Steering Committee

Joanna Friesner (arabidopsisconference@gmail.com) NAASC

New experimental resources and/or software tools available to Arabidopsis researchers

Single-nucleus RNA sequencing **(sNucRNA-seq)** and single-nucleus assay for transposase accessible chromatin sequencing **(sNucATAC-seq)** technologies on Arabidopsis roots. https://pubmed.ncbi.nlm.nih.gov/33422696/

CRISPR-Combo platform: This publication used CRISPR base editors and gene activation at the same time. They used Arabidopsis to create and refine the system that was then used for gene editing in poplar and rice. https://pubmed.ncbi.nlm.nih.gov/35596077/

This publication integrates publicly available databases with advanced genomics to dissect the signaling pathway of proteotoxic stress. The work could have not been conducted without the resources available in Arabidopsis. https://pubmed.ncbi.nlm.nih.gov/35577961/

"An optimized pipeline for live imaging whole Arabidopsis leaves at cellular resolution"
This publication integrates both the protocol for live imaging Arabidopsis leaves with the MorphoGraphX cellular growth analysis pipeline for quantifying growth and cell division characteristics." https://plantmethods.biomedcentral.com/articles/10.1186/s13007-023-00987-2

"Using positional information to provide context for biological image analysis with MorphoGraphX 2.0." This paper updates the poplar MorphoGraphX image analysis software with new features including a framework for giving organs a local coordinate system, allowing gene expression and growth to be quantified in the context of position. https://elifesciences.org/articles/72601

Planned events for 2023 and 2024

In January, 2023, we initiated a membership drive for our new Arabidopsis Community group as supported by NAASC, and launched a new webpage and new community activities. Membership for 2023 is free and open to all people interested in Arabidopsis around the world. Membership will incur a fee in 2024 (tiered rates by career stage) and members will enjoy benefits including discounted registration for ICAR 2024 https://www.arabidopsiscommunity.org/

Career Development & Community Seminars/Panels. Recordings posted for public access at www.arabidopsiscommunity.org/upcoming-recorded
My Plant Biology Story. José Dinneny. March 2023
Pathways to New Positions: April 2023
Getting Started as a Group Leader: May 2023
Diversity & Inclusion for Excellence in Science: June 2023 (at ICAR 2023, will not be publicly-posted by choice of the ICAR organizers)

NAASC will organize the 34th International Conference on Arabidopsis Research (ICAR) July 15-19, 2024, in San Diego, California, USA https://icar2024.weebly.com/. Confirmed Keynote Speakers are José Dinneny (Stanford University, USA), Seung Yon (Sue) Rhee (Michigan State University, USA), Keiko Sugimoto (RIKEN, Japan) and Dolf Weijers (Wageningen University, Netherlands). The conference will be held at University of California, San Diego (UCSD) and will include planning and participation from local plant biologists at UCSD and the Salk Institute. To increase community interactions, we are planning pre-ICAR community workshops (July 15, 2024) with sessions for early career scholars, members of underrepresented groups in science, and more, including opportunities for informal networking. We are planning social events including a community art show and the 5K Weed Stampede Fun Run/Walk. We are also scheduling a free half day for attendees to enjoy tourist activities and optional conference-organized field trips. NAASC will continue the novel approaches we developed in 2020 including an emphasis on diversifying speakers and science and providing opportunities for attendees to present their work. The platform program will include (in addition to four keynote speakers): 17 invited plenary speakers and 1 invited special talk by the recipient of the new NAASC Arabidopsis Community Lifetime Achievement Award. The majority of the program will follow the approach we established for ICAR 2020/2021: community-proposed and led mini-symposia and workshops selected during a community submission process scheduled for late summer-fall, 2023. Please reference the ICAR 2024 website for updates on proposal submission and join the Arabidopsis Community group to receive ICAR updates by email (www.arabidopsiscommunity.org/)

New Community Award: in collaboration with the Arabidopsis Biological Resource Center (ABRC, USA), NAASC will establish an annual award to the scientist that has made the most Arabidopsis seed donations to the ABRC within a calendar year. We expect to announce the first recipient during ICAR 2023.

Upcoming Community Awards: In late 2023 we will seek nominations from the community for three new awards. The NAASC Arabidopsis Community Lifetime Achievement Award (awarded on a triennial basis) will include an invitation to give a special talk at ICAR 2024-San Diego. Annual recognition awards will include the Excellence in Supporting Diversity, Equity, Inclusion, and Belonging in the Arabidopsis Community Award and the Dissemination of Arabidopsis Knowledge Award through Outreach and Teaching. We ask the community to nominate scientists for each award. Nominees and nominators must be members of the new NAASC Arabidopsis Community group (free for 2023).

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/
- American Association of University Women (AAUW): https://www.aauw.org/

Selected publications

“Climate change challenges, plant science solutions”. *This is a vignette style review presents examples of research being conducted to engineer crops with enhanced resilience to the harsh conditions generated by climate change and to engineer carbon capturing and sequestering plants.* https://academic.oup.com/plcell/article/35/1/24/6759373

“Arabidopsis apoplastic fluid contains sRNA- and circular RNA-protein complexes that are located outside extracellular vesicles” *The authors describe extracellular RNAs in Arabidopsis leaves and propose that exRNAs located outside of extracellular vesicles mediate host-induced gene silencing.* https://pubmed.ncbi.nlm.nih.gov/35171271/

Joanna Friesner (NAASC) answers questions about supporting activities for the Arabidopsis community, challenges she has faced as a woman promoting Diversity, Equity, Inclusion and Belonging in STEM, and provides advice to early career scholars, among other topics. https://onlinelibrary.wiley.com/do/10.1111/tpj.0090030/full/

“Synthetic genetic circuits as a means of reprogramming plant roots” *The authors designed and built synthetic transcriptional regulators and used these to alter root structure.* https://www.science.org/doi/10.1126/science.abo4326

”The N-terminally truncated helper NLR NRG1C antagonizes immunity mediated by its full-length neighbors NRG1A and NRG1B “ *The authors find a surprising negative regulatory effect by NRG1C, a truncated version of a nucleotide-binding (NB) leucine-rich repeat (LRR) immune receptor (NLR.) They found that NRG1C plays an opposite role from its full-length paralogs NRG1A/1B suggesting that the N-terminally truncated hNLRs evolved to balance the activities of their corresponding full-length hNLRs.* https://doi.org/10.1093/plcell/koab285

NAASC members contributing to report

- Federica Brandizzi, Michigan State University
- Anna Stepanova, NC State University
- Keith Slotkin, Donald Danforth Plant Science Center & University of Missouri-Columbia
- Cris Argueso, Colorado State University
- Adrienne Roeder, Cornell University
- Dior Kelley, Iowa State University
- Gloria Muday, Wake Forest University
- Mentewab Ayalew, Spelman College
- Liang Song, University of British Columbia

34TH International Conference on Arabidopsis Research

José DINNENY
Sue RHEE
Keiko SUGIMOTO
Dolf WEIJERS

SAN DIEGO, USA
July 15 - 19

ICAR2024

Arabidopsis as a Nexus for Discovery, Innovation, Application, and Impact

Hailing Jin ✻ Ryan Lister ✻ Jenny Mortimer
Roger Innes ✻ Xiaoqi Feng ✻ Pablo Manavella
Rebecca Mosher ✻ Dave Jackson ✻ Sophia Stone
Lily Cheung ✻ Cristobal Uauy ✻ Jiawei Wang
Cara Haney ✻ Li-Jia Qu ✻ Rashmi Sasidharan
Kris Niyogi ✻ Patricia León ✻ Holger Puchta

www.arabidopsiscommunity.org/icar

Organized by the North American Arabidopsis Steering Committee