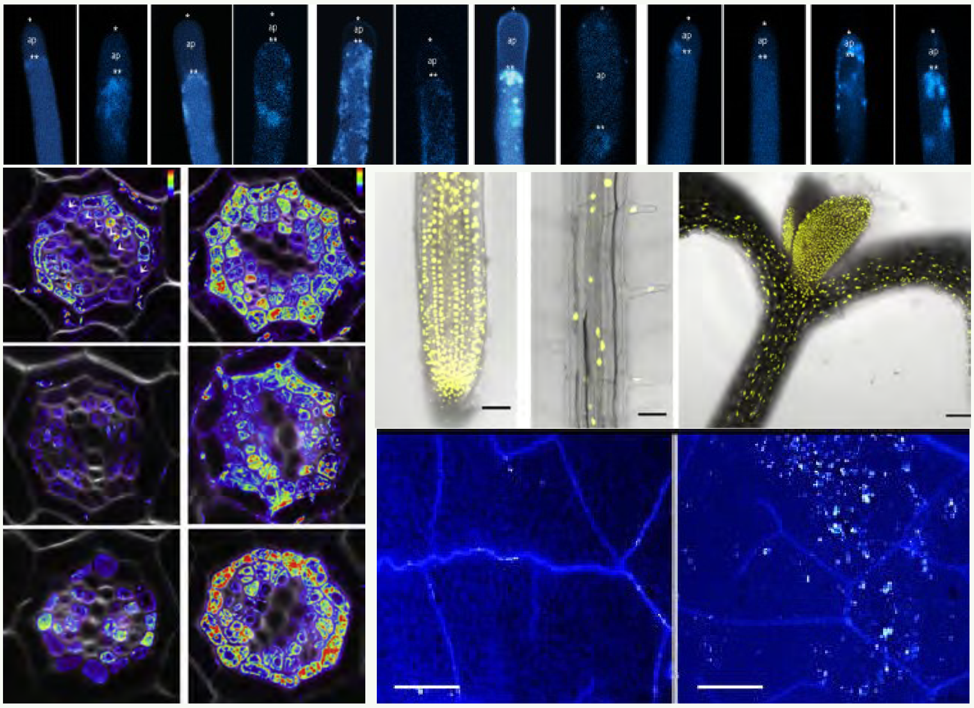
From Bench to Bountiful Harvests

Multinational Arabidopsis Steering Committee (MASC)

Annual Report 2021/2022



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Cover images taken from Open Access publications

Top: Martinez-Pacheco et al (2022): *Nature Communications* https://doi.org/10.1038/s41467-022-28833-4
Middle Right: McKay et al (2022): *Elife* https://doi.org/10.7554/eLife.70701
Lower Right: Giovannoni, Lironi et al 2021: *Plant, Cell and Environment*. https://doi.org/10.1111/pce.14192
Left: Ye et al (2021): *Current Biology* https://doi.org/10.1016/j.cub.2021.05.036

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

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The Multinational Arabidopsis Steering Committee

Annual Report 2021/2022

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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, the current incumbents are Nicholas Provart, Siobhan Brady and Geraint Parry respectively.

In 2017 eight MASC Inc 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 Xuelu Wang and Elizabeth Haswell rotated off the list of directors but were not replaced. At the end of 2022 Blake Meyers and Sean May will end their terms as directors. In the upcoming MASC Annual meeting the membership of MASC (comprising members of MASC subcommittees, MASC projects and country / region representatives) will nominate up to four new members to become a director. If you are interested in filling one of these positions then please contact Geraint Parry. These roles are VERY light-touch and require very little additional work.

This is a current list of the MASC board of directors and the length of their terms:

- 2018-2022: Blake Meyers (United States of America), Sean May (United Kingdom)
- 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.

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 ~10 hours in 2022) to maintain the activity of the organisation. During the summer of 2022 Cara Wheeldon, a PhD student at the University of Leeds, collated the MASC Annual Report as part of her Industrial Placement working with Dr Parry's company, Arabidopsis Events UK. We are very grateful for Cara's help which significantly reduces MASC costs.

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

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 / region 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 5 subcommittees: Bioinformatics, Epigenetics and Epigenomes, Natural Variation and Comparative Genomics, Proteomics, Plant Immunity.

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

Over the next few years the MASC directors will encourage subcommittee members to take an increased role in the organisations of workshops at ICAR meetings. At ICAR2022 in Belfast the Bioinformatics subcommittee group organised an 'Arabidopsis Informatics' workshop session and the Epigenetics and Epigenomes subcommittee organised a workshop on 'Plant Epigenetics and Chromatin Dynamics'.

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, a major international phenotyping projects and Gramene database. Finally the report includes submissions from TAIR and the BAR projects.

Country / Region 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 27 country / region representatives that submitted for this report. We are delighted to have received an inaugural report from Portugal submitted by Silvia Coimbra.

We are extremely grateful to all representatives of subcommittees, projects or countries / regions as they voluntarily give their time toward MASC activities. All MASC contributors were invited to attend the remote MASC annual meeting that will take place on August 25th 2pm GMT.

Overall we very much encourage Arabidopsis researchers to become involved in MASC activities, e.g. subcommittees, projects and resources or as country / region 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.

In 2021 ICAR was a virtual event organised by the North American Arabidopsis Steering Committee, led by Joanna Friesner. This event attracted 1000 attendees and hosted a remarkable 300+ virtual talks within 7 plenary and an amazing 36 community-selected minisymposia. This meeting was characterised by the level of community involvement as well as a major focus on equality, diversity and inclusivity. The success of this event has resolved the MASC community to embrace these ideas for the future.

Held on June 20-24 2022, ICAR2022 was the first in-person ICAR meeting since 2019 and was hosted as a hybrid event in Belfast, UK. ~450 delegates attended the meeting in-person with over 200 joining online. The global Arabidpopsis community proposed ~30 ideas for concurrent sessions, all of which were incorporated into the event. Each Concurrent session organiser was awarded 2 free registrations, which were used to support the attendance of invited speakers or session organisers.

The ongoing COVID19 pandemic meant that there was significant uncertainty ahead to the meeting but despite a lower-than-hoped-for number of in-person attendees the meeting was financially sound. In total the organisers provided 60 free registrations for invited speakers, concurrent session organisers and helpers. The hybrid aspects of the meeting was very competantly managed by the technical staff at the ICC conference venue. The online platform included a poster room in which all delegates could view poster PDFs. This gave online delegates the opportunity to present their research. The post-meeting survey showed that ~75% of online delegates viewed the posters at least once or twice. Overall 88% of online delegates were at least partially satisfied with the online platform. **Hybrid is here to stay and must be a feature of all future ICAR meetings.**

However only 28% of in-person delegates looked at any part of the online poster platform indicating that there isn't great cross-over between the two types of delegates. ICAR2022 innovated with an all-vegetarian menu of which 55% thought it was 'great' and only 13% would have preferred a meat-option at every meal. The meeting was organised as a collaboration between Arabidopsis Events UK (https://www.arabidopsisevents.uk/) and the Association of Applied Biologists (https://www.aab.org.uk/).

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:
- 33rd ICAR, Chiba, Japan: June 5th-9th 2023. The concept for ICAR2023 will be 'Arabidopsis for Sustainable Development Goals'. https://icar2023.org/

- 34th ICAR, United States of America. 2024

- 35th ICAR, Ghent, Belgium. 2025

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.

- A PDF of the updated Code of Conduct for ICAR2022 can be downloaded here -> http://arabidopsisresearch.org/images/ICAR/MASC_code-of-conduct_ICAR2022.pdf

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 / Region 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 / Region 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 do. 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.

As part of the 2020-21 MASC Annual Report the MASC subcommittee chairs provided suggestions for the research areas that they would like included within the 4th roadmap:

- Identification of all both cis and trans epigenetic regulatory elements across all cell types and genotypes under both normal and various stress conditions.
- Production of full-length cDNAs and open reading frame (ORFS) clones for all annotated Arabidopsis protein-coding genes
- How can plants and people adapt to the changing climate in a sustainable manner, which will be reflected in the theme of ICAR2023 in Japan. https://icar2023.org/
- How do we integrate studies across disciplines, evolutionary depth (population biology to cross-clade comparisons), and various ecological challenges to answer these fundamental questions?
- How can we improve on the collection and standardisation of imaging data and the images’ metadata and provide this information to the wider community?
- Understanding the eco-evolutionary dynamics of pathogens in natural plant communities from a mechanistic and molecular point of view
- Improvement of single cell techniques, particularly in proteomics and metabolomics
- Understanding of uORFs in plant immunity and their roles in crop improvement.
- Improved techniques for whole proteome quantification (to make it as simple as RNAseq) and improved targeted analysis (to make it as simple as qPCR).
- Integration across technologies to provide predictive modelling of plant development and response
- Ensure that the research recovery from COVID19 is managed in an equitable manner in order to mitigate effects that have disproportionally affected particular groups. The recently funded

ROOT and SHOOT project is beginning to work in this area. https://rootandshoot.org/

MASC calls on all Arabidopsis researchers to consider other topics for inclusion in the next decadal Roadmap. We expect strong participation from long-time community leaders, such as the North American Arabidopsis Steering Committee (NAASC), and collaborators from the UK, Germany, and Japan. We strongly hope that there will be contributions toward decadal priorities from a broader group of MASC members, especially those representing countries with significant Arabidopsis research.

The leadership of ICAR2023 will host a workshop that will bring together researchers to discuss the next dedacal roadmap. The conclusions from this workshop alongside wider discussions will be integrated into an article mooted for publication in The Plant Cell.

MASC Subcommittee Reports

Bioinformatics

Nicholas Provart

With input from MASC Bioinformatics Subcommittee members and the wider Arabidopsis community.

Recently developed Open Tools and Resources for Arabidopsis Researchers

- TAIR

  New gene function data were added on a weekly basis to TAIR's databases, including 1264 new/updated locus summaries, 812 new/updated gene symbols, 5096 articles linked to 10489 genes, 16395 experimental Gene Ontology (GO) and Plant Ontology (PO) annotations, 1039 new/updated alleles, and 2021 phenotypes linked to germplasms.

  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.

  Excitingly, TAIR has incorporated the Col-0 telomere to telomere sequence as a new genome option (Naish et al., 2021) and is actually looking for collaborators to use this as a basis for developing a new genome release – contact curator@arabidopsis.org if you're interested in participating in this project.

- BAR

  The BAR added a Blast search option at http://bar.utoronto.ca/blast/. 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.

  The BAR upgraded Thalemine to the current version based on the InterMine 5.0.8 release in August 2022, with data updates from many sources from 2022-01-04.

  The BAR implemented a Guard Cell Drought view (van Weringh et al., 2021) for ePlant and a DNA Damage view (Bourbousse et al., 2018) for our eFP Browser/ePlant.

  We also developed a new API for faster provision of eFP images to partner websites like TAIR.

- Large-scale Data Sets and Methods of Note

  In a structure-prediction breakthrough, AlphaFold released more than 360k protein structures for 21 model organisms, including Arabidopsis. Structures are released with quality prediction scores for each residue of the sequence (https://alphafold.ebi.ac.uk/; Varadi et al., 2022). The BAR will be incorporating these structures into its ePlant tool in the near future.

Klaas van Wijk, Eric Deutsch and colleagues published the Arabidopsis Peptide Atlas (www.peptideatlas.org/builds/arabidopsis/; van Wijk et al., 2021), which incorporates published mass spectrometry data sets analyzed via a "uniform processing and metadata annotation pipeline". TAIR has incorporated this useful "metadata set" as a track in its JBrowse instance – check out the atlas to see if your favourite protein of interest has post-translational modifications!

In terms of transcription factor binding specificity, Carol Huang's group described a method called "double DAP-seq" for identifying the genome-wide transcription factor binding for twenty Group S1 and C heterodimer bZIP pairs (Li et al., 2022). Binding data may be explored at http://hlab.bio.nyu.edu/?data=projects/bzip_code.

- Pedagogy, Policy and Outreach

The Plant Cell Atlas published a white paper about its vision for a plant cell atlas (Plant Cell Atlas Consortium et al., 2021). Keep an eye on http://www.plantcellatlas.org/ for updates! Alex Cantó-Pastor and colleagues published a review of "Arabidopsis Bioinformatics: Tools and Strategies", covering several useful Arabidopsis tools and websites (Cantó-Pastor et al., 2021). TAIR continued its partnership with https://www.micropublication.org/, a platform for very short peer-reviewed reports, and this year curated/shepherded 6 Arabidopsis into the Micropublication framework. Nicholas Provart's Plant Bioinformatics course on Cousera.org (https://www.coursera.org/learn/plant-bioinformatics/) was fully updated in June 2022.

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- Cantó-Pastor, A., Mason, G.A., Brady, S.M., and Provart, N.J. (2021). Arabidopsis bioinformatics: tools and strategies. Plant J. Cell Mol. Biol. 108: 1585–1596. https://doi.org/10.1111/tpj.15547

- Li, M., Lin, W., Hinckley, W., Yao, T., Muchero, W., Chen, J.-G., and Huang, S.C. (2022). Uncovering the "ZIP code" for bZIP dimers reveals novel motifs, regulatory rules and one billion years of cis-element evolution.: 2022.04.17.488518.

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- Varadi, M. et al. (2022). AlphaFold Protein Structure Database: massively expanding the structural coverage of protein-sequence space with high-accuracy models. Nucleic Acids Res. 50: D439–D444. https://doi.org/10.1093/nar/gkab1061

- van Weringh, A., Pasha, A., Esteban, E., Gamueda, P.J., and Provart, N.J. (2021). Generation of guard cell RNA-seq transcriptomes during progressive drought and recovery using an adapted INTACT protocol for Arabidopsis thaliana shoot tissue. bioRxiv: 2021.04.15.439991.

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(2021). The Arabidopsis PeptideAtlas: Harnessing worldwide proteomics data to create a comprehensive community proteomics resource. Plant Cell 33: 3421–3453. [DOI: 10.1093/plcell/koab211](https://doi.org/10.1093/plcell/koab211)

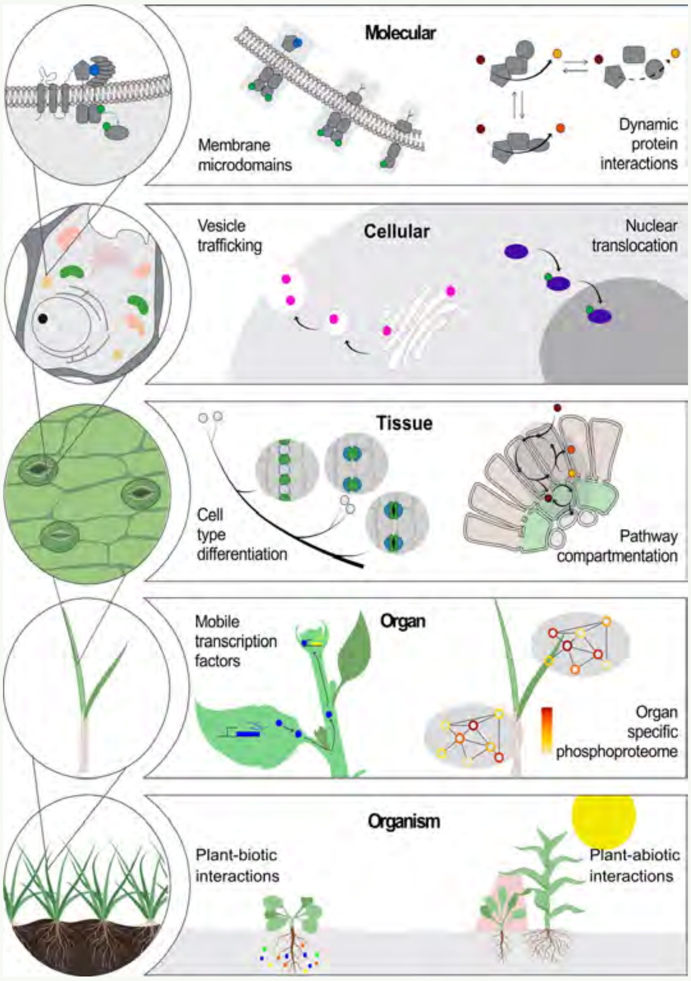

Figure 1: ''Location-to-function paradigm.'' Plant Cell Atlas Consortium et al. 2021. *Elife.* https://doi.org/10.7554/eLife.66877

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Recently developed Open Tools and Resources for Arabidopsis Researchers

- Greenscreen – this analysis pipeline is aimed at increasing the detection of true positives DNA:protein interactions from a variety of sequencing methods include ChIP-seq and CUT & RUN.
  https://www.biorxiv.org/content/10.1101/2022.02.27.482177v1.abstract

Recent or Future activities of Subcommittee members

- International Conference on Arabidopsis Research – Plant Epigenetics and Chromatin Dynamics Workshop, Belfast, Northern Ireland, June, 2022

- Epiplant 2022, Banyuls-sur-mer, France, 2022

- Cold Spring Harbor-Asia Conference: Integrative Epigenetics in Plants, Awaji, Japan December, 2022

Selected Publications

- Long J, Walker J, She W, Aldridge B, Gao H, Deans S, Vickers M, Feng X: Nurse cell--derived small RNAs define paternal epigenetic inheritance in Arabidopsis. Science 2021, 373. DOI: 10.1126/science.abh0556

  Tapetum specific small RNAs assist in reprogramming DNA methylation of a susbet of genes in the male gamete.

- Marimuthu MPA, Maruthachalam R, Bondada R, Kuppu S, Tan EH, Britt A, Chan SWL, Comai L: Epigenetically mismatched parental centromeres trigger genome elimination in hybrids. Sci Adv 2021, 7:eabk1151. https://doi.org/10.1126/sciadv.abk1151

  The centromeric histone, CENH3, is unstable in epigenetically mistmacthed parents leading to loss of chromosomes.

- Naish M, Alonge M, Wlodzimierz P, Tock AJ, Abramson BW, Schmucker A, Mandakova T, Jamge B, Lambing C, Kuo P, Yelina N, Hartwick N, Colt K, Smith LM, Ton J, Kakutani T, Martienssen RA, Schneeberger K, Lysak MA, Berger F, Bousios A, Michael TP, Schatz MC, Henderson IR: The genetic and epigenetic landscape of the Arabidopsis centromeres. Science 2021, 374:eabi7489. https://doi.org/10.1126/science.abi7489

Long-read DNA sequencing resolved the complete sequence of the Arabidopsis centromeres along with their DNA methylation states.

- Sigman MJ, Panda K, Kirchner R, McLain LL, Payne H, Peasari JR, Husbands AY, Slotkin RK, McCue AD: An siRNA-guided ARGONAUTE protein directs RNA polymerase V to initiate DNA methylation. Nat Plants 2021, 7:1461-1474. DOI: 10.1038/s41477-021-01008-7

  This study shows that siRNA-guided ARGONAUTE proteins are able to initiate DNA methylation and previously unmethylated loci.

- Willige BC, Zander M, Yoo CY, Phan A, Garza RM, Trigg SA, He Y, Nery JR, Chen H, Chen M, Ecker JR, Chory J: PHYTOCHROME-INTERACTING FACTORs trigger environmentally responsive chromatin dynamics in plants. Nat Genet 2021, 53:955-961. DOI: 10.1038/s41588-021-00882-3

  PIFs achieve light-activated changes in gene expression by recruiting a chromaitn remodeller.

Members of the subcommittee

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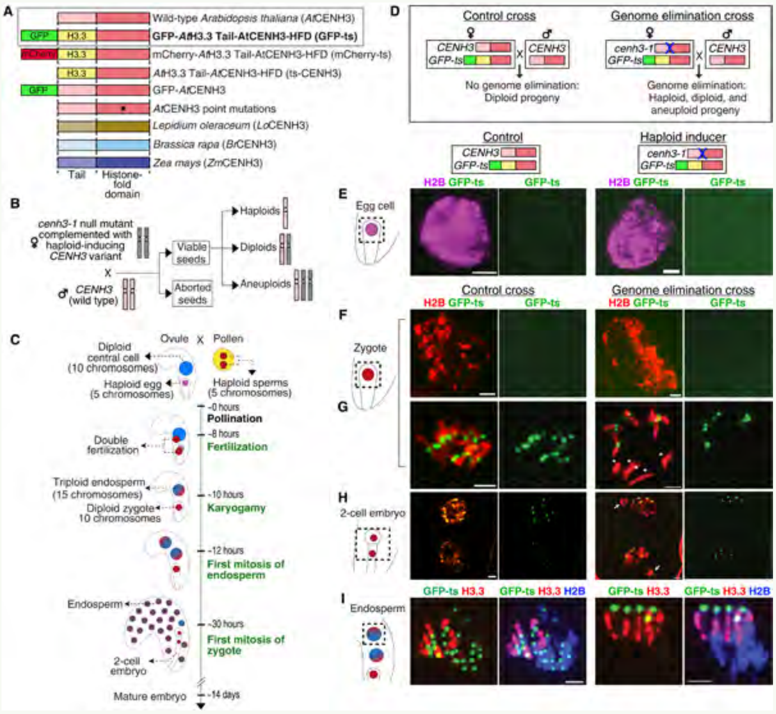

Figure 1: ‘‘Biased localization of GFP-ts in zygotes, early embryos, and endosperm from GE crosses in Arabidopsis.’’ Marimuthu et al, 2021. *Science Advances.* https://doi.org/10.1126/sciadv.abk1151

Natural Variation and Comparative Genomics

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Recently developed Open Tools and Resources for Arabidopsis Researchers

- Many new genomic resources have been created across species in the Brassicaceae (too many to list); see selected publications below for examples.

Recent or Future activities of Subcommittee members

- Beyond the model species Arabidopsis thaliana, many species of the family Brassicaceae have been investigated deeply. In particular, studies of natural variation within model species continues to produce fascinating results. All these investigations may accelerate applied efforts ranging from crop improvement to the conservation of biodiversity. Subcommittee members organized a concurrent Session in ICAR 2022 meeting.

Selected Publications

- Monroe, J. G., T. Srikant, P. Carbonell-Bejerano, C. Becker, M. Lensink, M. Exposito-Alonso, M. Klein, J. Hildebrandt, M. Neumann, D. Kliebenstein, M. L. Weng, E. Imbert, J. Agren, M. T. Rutter, C. B. Fenster and D. Weigel. 2022. Mutation bias reflects natural selection in Arabidopsis thaliana. Nature 602(7895): 101-105. doi: 10.1038/s41586-021-04269-6

  This study challenges the paradigm that mutation is a directionless force in evolution because mutations occur less often in functionally constrained regions, and epigenomic and physical features explain over 90% of variance in the genome-wide pattern of mutation bias surrounding genes.

- Burns, R., T. Mandakova, J. Gunis, L. M. Soto-Jimenez, C. Liu, M. A. Lysak, P. Y. Novikova and M. Nordborg. 2021. Gradual evolution of allopolyploidy in Arabidopsis suecica. Nat Ecol Evol 5(10): 1367-1381. DOI: 10.1038/s41559-021-01525-w

  This study found gradual evolution after polyploidy, including upregulation of meiosis-related genes and cyto-nuclear processes, which are not seen in synthetic hybrids, and thus are likely to represent subsequent evolution.

- Naish, M., M. Alonge, P. Wlodzimierz, A. J. Tock, B. W. Abramson, A. Schmucker, T. Mandakova, B. Jamge, C. Lambing, P. Kuo, N. Yelina, N. Hartwick, K. Colt, L. M. Smith, J. Ton, T. Kakutani, R. A. Martienssen, K. Schneeberger, M. A. Lysak, F. Berger, A. Bousios, T. P. Michael, M. C. Schatz and I. R. Henderson. 2021. The genetic and epigenetic landscape of the Arabidopsis centromeres. Science 374(6569): eabi7489. https://doi.org/10.1126/science.abi7489

  This study demonstrated that Arabidopsis centromeres are evolving through cycles of satellite homogenization and retrotransposon-driven diversification, and clarified one of the evolutionary mystery of centromeres.

- Zhu, P., C. Lister and C. Dean. 2021. Cold-induced Arabidopsis FRIGIDA nuclear condensates for FLC repression. Nature 599(7886): 657-661. DOI: 10.1038/s41586-021-04062-5

  This paper showed a temperature-controlled condensation mechanism that modulates FRI activation of FLC transcription, could facilitate FLC shutdown in natural fluctuating temperatures, this type of mechanism may have widespread roles in the plasticity of plant responses to varying environments.

- Baduel, P., B. Leduque, A. Ignace, I. Gy, J. Gil, Jr., O. Loudet, V. Colot and L. Quadrana. 2021. Genetic and environmental modulation of transposition shapes the evolutionary potential of Arabidopsis thaliana. Genome Biol 22(1): 138. https://doi.org/10.1186/s13059-021-02348-5

  This study reveals that TE mobilization is a major generator of genetic variation in A. thaliana that is finely modulated by genetic and environmental factors, indicating that TEs may be essential genomic players in the demise or rescue of native populations in times of climate crises.

Members of the subcommittee

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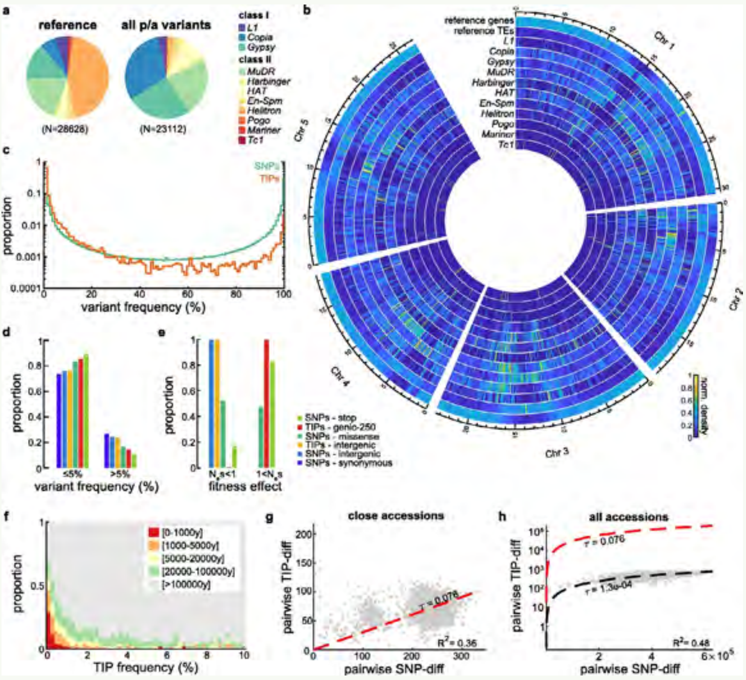

Figure 1: ''Recent TE mobilization at the species level''. Baduel et al, 2021. *Genome Biology.* https://doi.org/10.1186/s13059-021-02348-5

Plant Immunity

Chair: Shahid Mukhtar

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Recently developed Open Tools and Resources for Arabidopsis Researchers

- RFPDR: a random forest approach for plant disease resistance protein prediction (Simon et al. PeerJ . 2022 Apr 22;10:e11683. doi: 10.7717/peerj.11683. eCollection 2022.
- iRegNet: an integrative Regulatory Network analysis tool for Arabidopsis thaliana (Shim et al., 2021 Plant Physiol. 187, 1292-1309) provides the possible upstream regulatory network for genes of interest and genomic regions of interest in the Arabidopsis genome.
- Virulent agrobacterium expressing a type III secretion system from pathogenic bacteria (Raman et al., 2022 Nature communications 13, 2581) for higher efficiency of Agrobacterium-mediated plant transformation.
- AlphaFold server for de novo structural predictions: https://colab.research.google.com/github/sokrypton/ColabFold/blob/main/AlphaFold2.ipynb
- Arabidopsis proteins added to AlphaFold database: https://alphafold.ebi.ac.uk/
- ePlant/TorontoBAR updated; https://bar.utoronto.ca/eplant/
  Waese-Perlman, B. et al. (2021) ePlant in 2021: New Species, Viewers, Data Sets, and Widgets. bioRxiv, 2021.04.28.441805.
- PastDB, database of alternative splicing, includes biotic and abiotic stresses
  http://pastdb.crg.eu/wiki/Main_Page Martín, G., et al. Alternative splicing landscapes in Arabidopsis thaliana across tissues and stress conditions highlight major functional differences with animals. Genome Biol 22, 35 (2021). https://doi.org/10.1186/s13059-020-02258-y
- OpenLeaf; open-source, high-throughput phenotyping of Arabidopsis rosettes.
  https://www.biorxiv.org/content/10.1101/2021.12.17.472861v1
- Plant Resistance Genes database updated: http://prgdb.org/prgdb4/ Joan Calle García, et al. PRGdb 4.0: an updated database dedicated to genes involved in plant disease resistance process, Nucleic Acids Research, Volume 50, Issue D1, 7 January 2022, Pages D1483–D1490, https://doi.org/10.1093/nar/gkab1087
- RefPlantNLR dataset published (Kourelis et. Al. 2022 https://doi.org/10.1371/journal.pbio.3001124
- An atlas of Arabidopsis protein S-acylation (Kumar et al., 2022 Nature Plants)
- A transcriptional landscape of Arabidopsis thaliana pattern-triggered immunity (Bjornson et al., 2021 Nature Plants)

Recent or Future activities of Subcommittee members

The members of the plant immunity subcommittee organized workshop/conference sessions and presented talks and posters at various international conferences in 2021-2022, including an online international meeting of the plants-nematodes interaction organized by RIKEN in Japan and INRA in France, the 7th international congress of Nematology (ICN 2022) and 2021 IS-MPMI (International Society of Molecular Plant-Microbe Interactions) congress. Some of the subcommittee members virtually attended IS-MPMI 2022 Early Career Showcase meeting. The committee members also attended the Fall international conference of the Korean Society of Plant Pathology (KSPP), the 10th International meeting on plant peptides and receptors 2022, and the 10th International Workshop on Plant Peptides and Receptors. Another subcommittee member attended ZMBP Summer Academy 2022. Moreover, the subcommittee members co-organized a virtual southern section of the American Society of Plant Biologists (ss-ASPB) in 2021. The subcommittee chair organized the ss-ASPB 2022 meeting in Birmingham. The chair of the subcommittee organized a systems biology and machine learning workshop at PAG, but it got canceled due to COVID19. Finally, a subcommittee member is organizing an open lab and science café for ordinary people and high school students in 2022.

Selected Publications

- Pruitt RN, Locci F, Wanke F, Zhang L, Saile SC, Joe A, Karelina D, Hua C, Fröhlich K, Wan WL, Hu M, Rao S, Stolze SC, Harzen A, Gust AA, Harter K, Joosten MHAJ, Thomma BPHJ, Zhou JM, Dangl JL, Weigel D, Nakagami H, Oecking C, Kasmi FE, Parker JE, Nürnberger T. The EDS1-PAD4-ADR1 node mediates Arabidopsis pattern-triggered immunity. Nature. 2021 Oct;598(7881):495-499. doi: 10.1038/s41586-021-03829-0. Epub 2021 Sep 8. PMID: 34497423.

  This publication provides evidence that immunity mediated by cell-surface receptors also require the presence of an signbal hub essential for intracellular immune receptor signaling.

- Ngou BPM, Ahn HK, Ding P, Jones JDG. Mutual potentiation of plant immunity by cell-surface and intracellular receptors. Nature. 2021 Apr;592(7852):110-115. doi: 10.1038/s41586-021-03315-7. Epub 2021 Mar 10. PMID: 33692545.

  This article showed for the first time that two types of immune receptors, cell-surface receptors and intracellular receptors, are working cooperatively during pathogen infection by mutual potentiation of both signaling axes.

- Jacob P, Kim NH, Wu F, El-Kasmi F, Chi Y, Walton WG, Furzer OJ, Lietzan AD, Sunil S, Kempthorn K, Redinbo MR, Pei ZM, Wan L, Dangl JL. Plant “helper” immune receptors are Ca2+-permeable nonselective cation channels. Science. 2021 Jul 23;373(6553):420-425. doi: 10.1126/science.abg7917. Epub 2021 Jun 17. PMID: 34140391; PMCID: PMC8939002.

  This ground-breaking article demonstrates that both CC-NLR and RNL “helper” NLR immune receptors generate calcium channels upon activation, providing a common mechanism for NLR function and potential convergence point for CC-NLR and TIR-NLR immune pathways

- Tzipilevich E, Russ D, Dangl JL, Benfey PN. Plant immune system activation is necessary for efficient root colonization by auxin-secreting beneficial bacteria. Cell Host Microbe. 2021 Oct 13;29(10):1507-1520.e4. doi: 10.1016/j.chom.2021.09.005. Epub 2021 Oct 4. PMID: 34610294.

This article dissects how the plant immune system helps shape interactions with beneficial microbes, and vice-versa, in the rhizosphere

- Kato, H., Nemoto, K., Shimizu, M., Abe, A., Asai, S., Ishihama, N., Matsuoka, S., Daimon, T., Ojika, M., Kawakita, K., Onai, K., Shirasu, K., Yoshida, M., Ishiura, M., Takemoto, D., Takano, Y. and Terauchi, R. (2022) Recognition of pathogen-derived sphingolipids in Arabidopsis. Science 376, 857-860. DOI: 10.1126/science.abn0650

  This article reported that plants recognize pathogen-derived 9-methyl sphingoid base by a plasma membrane lectin receptor-like kinase, RDA2 to induce immune responses.

Members of the subcommittee

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Members:

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

Proteomics

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Recently developed Open Tools and Resources for Arabidopsis Researchers

- A new Arabidopsis portal at PeptideAtlas containing peptide matches derived from mass spectral data residing in public proteomics databases (e.g. PRIDE) is now online and available for browsing. See http://www.peptideatlas.org/builds/arabidopsis/

Recent or Future activities of Subcommittee members

- Updating a searchable registry of peptide matches for Arabidopsis at PeptideAtlas has been a major goal for members of this subcommittee. This program was led by Klaas van Wijk (Cornell University).

Selected Publications

- Clark NM, Nolan TM, Wang P, Song G, Montes C, Valentine CT, Guo H, Sozzani R, Yin Y, Walley JW (2021) Integrated omics networks reveal the temporal signaling events of brassinosteroid response in Arabidopsis. Nat Commun 12: 5858. https://doi.org/10.1038/s41467-021-26165-3

  Integrated ‘omic approach, including proteomics and phosphoproteomics, to assess temporal signaling events of brassinosteroid response in Arabidopsis

- van Wijk KJ, Leppert T, Sun Q, Boguraev SS, Sun Z, Mendoza L, Deutsch EW (2021) The Arabidopsis PeptideAtlas: Harnessing worldwide proteomics data to create a comprehensive community proteomics resource. Plant Cell 33: 3421-3453. DOI: 10.1093/plcell/koab211

  Release of the Arabidopsis PeptideAtlas to the community. Contains searchable proteomics data matched against the Arabidopsis proteome.

- Synek L, Pleskot R, Sekeres J, Serrano N, Vukasinovic N, Ortmannova J, Klejchova M, Pejchar P, Batystova K, Gutkowska M, Jankova-Drdova E, Markovic V, Pecenkova T, Santrucek J, Zarsky V, Potocky M (2021) Plasma membrane phospholipid signature recruits the plant exocyst complex via the EXO70A1 subunit. Proc Natl Acad Sci U S A 118. DOI: 10.1073/pnas.2105287118

  Demonstrates the power of co-immunoprecipitation to identify components of protein complexes, in this example, the ability to tease out two distinct modules within the exocyst complex.

- Kumar M, Carr P, Turner SR (2022) An atlas of Arabidopsis protein S-acylation reveals its widespread role in plant cell organization and function. Nat Plants 8: 670-681. DOI: 10.1038/s41477-022-01164-4

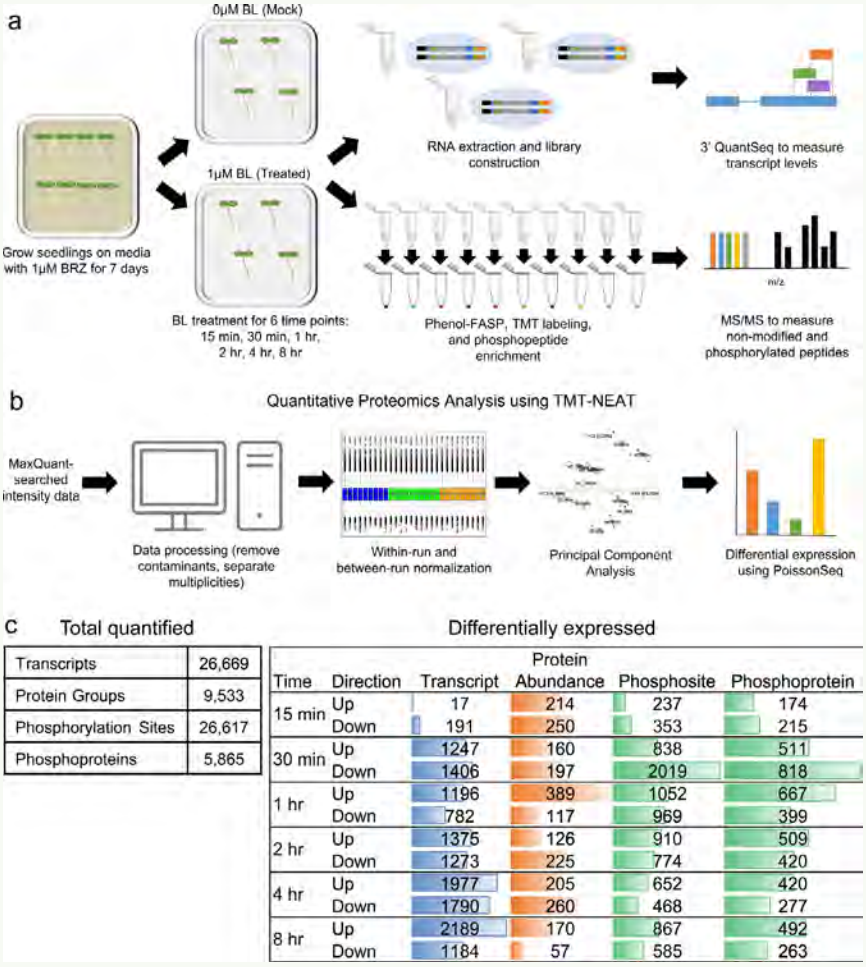
Mapping S-acylation in the Arabidopsis proteome with a focus on its role in cellulose synthase structure demonstrating the importance of this post translational modification.

- Dahhan DA, Reynolds GD, Cardenas JJ, Eeckhout D, Johnson A, Yperman K, Kaufmann WA, Vang N, Yan X, Hwang I, Heese A, De Jaeger G, Friml J, Van Damme D, Pan J, Bednarek SY (2022) Proteomic characterization of isolated Arabidopsis clathrin-coated vesicles reveals evolutionarily conserved and plant-specific components. Plant Cell 34: 2150-2173. DOI: 10.1093/plcell/koac071

  Enrichment and proteomic characterization of clathrin-coated vesicles from Arabidopsis. The dataset reveals evolutionary conserved proteins and plant specific components.

Members of the subcommittee

- Joshua Heazlewood (chair) University of Melbourne, Australia
- Hans-Peter Braun - Leibniz Universität Hannover, Hannover, Germany
- Steve Briggs - University of California, San Diego, California, USA
- Alexandra Jones - University of Warwick, Coventry, UK
- Harvey Millar - University of Western Australia, Perth, Australia
- Hirofumi Nakagami - Max Planck Institute for Plant Breeding Research, Köln, Germany
- Loïc Rajjou - AgroParisTech, Paris, France
- Klaas van Wijk - Cornell University, Ithaca, New York, USA



Total quantified

Transcripts	26,669
Protein Groups	9,533
Phosphorylation Sites	26,617
Phosphoproteins	5,865

Differentially expressed

Time	Direction	Transcript	Protein Abundance	Phosphosite	Phosphoprotein
15 min	Up	17	214	237	174
	Down	191	250	353	215
30 min	Up	1247	160	838	511
	Down	1406	197	2019	818
1 hr	Up	1196	389	1052	667
	Down	782	117	969	399
2 hr	Up	1375	126	910	509
	Down	1273	225	774	420
4 hr	Up	1977	205	652	420
	Down	1790	260	468	277
8 hr	Up	2189	170	867	492
	Down	1184	57	585	263

Figure 1: “An integrated omics time course of BR response’’. Clark et al, 2021. *Nature Communications.* https://doi.org/10.1038/s41467-021-26165-3

Systems and Synthetic Biology

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Recently developed Open Tools and Resources for Arabidopsis Researchers

- Plants & Python: VanBuren R, Rougon-Cardoso A, Amézquita EJ, Coss-Navarrete EL, Espinosa-Jaime A, Gonzalez-Iturbe OA, Luckie-Duque AC, Mendoza-Galindo E, Pardo J, Rodríguez-Guerrero G, Rosiles-Loeza PY, Vásquez-Crus M, Fernandez-Valverte SL, Hernández-Hernández T, Palande S, Chitwood DH. (2022) Plants & Python: A series of lessons in coding, plant biology, computation and bioinformatics. Plant Cell. 34(7):e1. https://doi.org/10.1093/plcell/koac187

  A series of English and Spanish lessons that serve as a common starting point for interdisciplinary and intercultural collaboration in the plant and computational sciences.

- González-Grandío E, Demirer GS, Ma W, Brady S, Landry MP. A Ratiometric Dual Color Luciferase Reporter for Fast Characterization of Transcriptional Regulatory Elements in Plants. ACS Synth Biol. 2021 Oct 15;10(10):2763-2766. doi: 10.1021/acssynbio.1c00248.

  Luminescent transcriptional reporters to use in both protoplasts and leaf discs. This further enables high-throughput measurements of gene regulatory activity in planta.

- Spurney, R., Schwartz, M., Gobble, M., Sozzani, R., & Van den Broeck, L. (2021). Spatiotemporal Gene Expression Profiling and Network Inference: A Roadmap for Analysis, Visualization, and Key Gene Identification. Methods in molecular biology (Clifton, N.J.), 2328, 47–65. https://doi.org/10.1007/978-1-0716-1534-8_4

A methodology paper that describes a clear roadmap for network inference from spatiotemporal expression data and which can be used to prioritize candidate genes for future studies.

- MD Brooks, CL Juang, MS Katari, JM Alvarez, A Pasquino, H-J Shih, J. Huang, C. Shanks, J. Cirrone, GM Coruzzi (2021). ConnecTF: A platform to integrate transcription factor–gene interactions and validate regulatory networks. Plant Physiology, Volume 185, Issue 1, January 2021, Pages 49–66, https://doi.org/10.1093/plphys/kiaa012

  A web-based, species-independent platform that integrates genome-wide studies of TF-target binding, TF-target regulation and other TF-centric omic datasets and uses these to build and refine validated or inferred gene regulatory networks.

Recent or Future activities of Subcommittee members

- Plant Cell Atlas Symposium, December 1, 2021.
- Plant Cell Atlas Symposium, December 12-13, 2022
- 5th International Conference on Plant Synthetic Biology, Bioengineering and Biotechnology, November 15-17th, 2021
- 6th International Conference on Plant Synthetic Biology, Bioengineering and Biotechnology, December 9-11, Fort Lauderdale, USA
- The Plant Synthetic Biology Conference, CRAG, Barcelona, Spain, September 19-21, 2022

Selected Publications

- JM Alvarez, MD Brooks, J. Swift & G. Coruzzi (2021). Time-based systems biology approaches to capture and model dynamic gene regulatory networks. Annual Review of Plant Biology. Vol. 72:105-131. https://doi.org/10.1146/annurev-arplant-081320-090914

  A review describing recent progress in capturing dynamic interactions of transcription factors with their targets, both locally and genome wide, and how they are used to determine how gene regulatory networks operate as a function of time.

- Van den Broeck, L., Spurney, R., Fisher, A., Schwartz, M., Clark, N., Nguyen, T., . . . Sozzani, R. (2021). A hybrid model connecting regulatory interactions with stem cell divisions in the root. Quantitative Plant Biology, 2, E2. doi:10.1017/qpb.2021.1

  A multiscale hybrid model that integrates ordinary differential equations and agent-based modeling of dynamics within a single cell population.

- Lee M, Dominguez-Ferreras A, Kaliyadasa E, Huang WJ, Antony E, Stevenson T, Lehmann S, Schäfer P, Knight MR, Ntoukakis V, Knight H. (2021) Mediator Subunits MED16, MED14, and MED2 Are Required for Activation of ABRE-Dependent Transcription in Arabidopsis. Front Plant Sci. 12:649720. https://doi.org/10.3389/fpls.2021.649720

  The MEDIATOR complex is required for transcription of most eukaryotic genes, and in this study the authors use synthetic biology to determine how specificity of this complex is determined for responses to ABA.

- Dorrity MW, Alexandre CM, Hamm MO, Vigil AL, Fields S, Queitsch C, Cuperus JT. The regulatory landscape of Arabidopsis thaliana roots at single-cell resolution. Nat Commun. 2021 Jun 7;12(1):3334. doi: 10.1038/s41467-021-23675-y

The first publication in Arabidopsis to demonstrate open-chromatin accessibility at cellular resolution.

- Brophy JAN, Magallon KJ, Duan L, Zhong V, Ramachandran P, Kniazev K, Dinneny JR. (2022) Synthetic gene circuits as a means of reprogramming roots. (2022) Science. 377(6607):747-751. doi: 10.1126/science.abo4326

A collection of synthetic regulatory elements that can be used to control gene expression.

Planning for Fourth Decadal Roadmap

- Translation of Arabidopsis research to crop plants – including close relatives like other Brassicas, and other relatives like tomato and more distantly related dicots
- Model-guided predictable engineering of complex traits.
- Spatial and temporal dynamics in plant biology.
- Single cell and intercellular gene regulatory network models.

Members of the subcommittee

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- Katherine Denby
- Miriam Gifford
- Rodrigo Gutierrez
- Gabriel Krouk
- Nicola Patron
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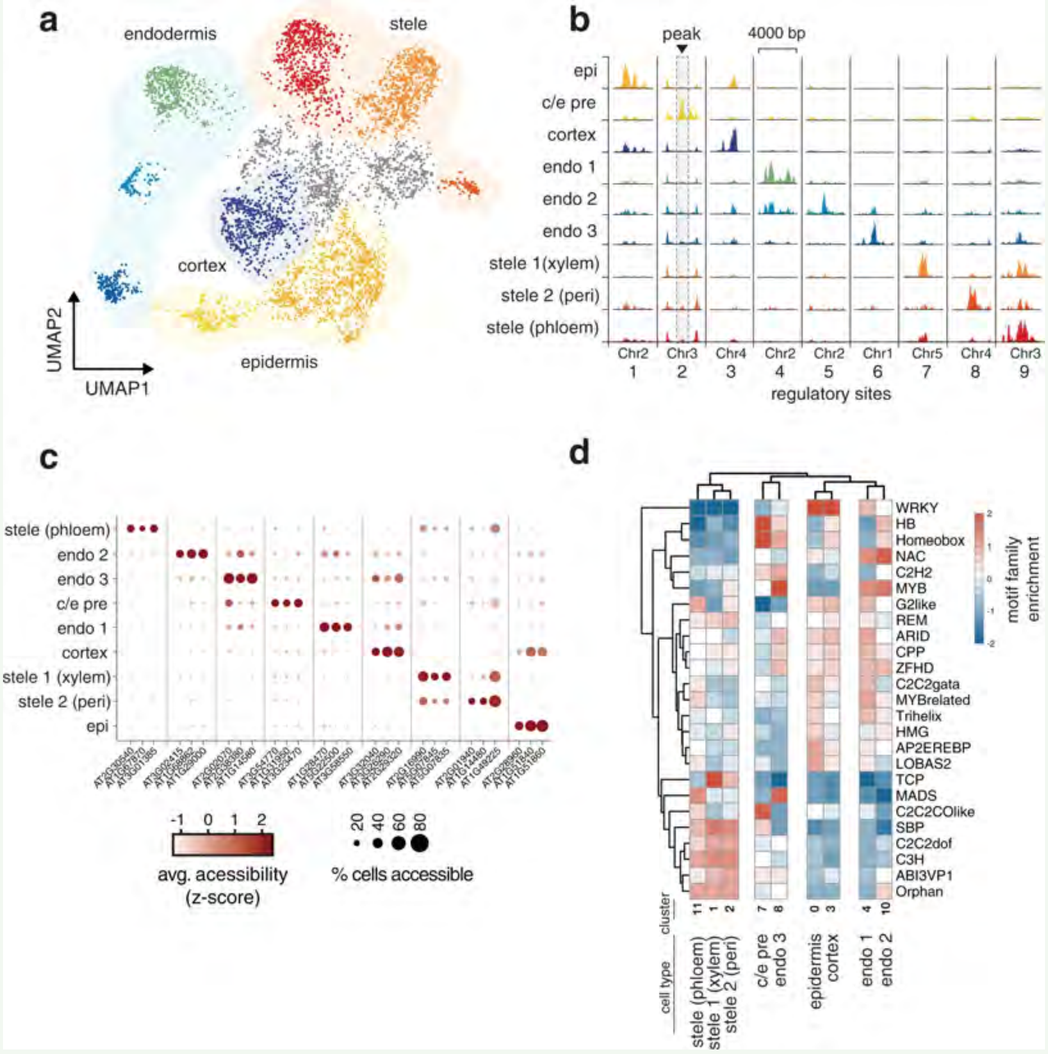

Figure 1: ''scATAC-seq identifies known root cell types''. Dorrity et al, 2021, *Nature Communications*. doi: 10.1038/s41467-021-23675-y

MASC Project Reports

ABRC: The Arabidopsis Biological Resource Center


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

In 2021 ABRC distributed 65,950 samples to 1,578 individuals located in 41 countries. We also provided bulk seed to NASC for 5,010 lines and an additional 2,682 individual samples of seed requested by NASC users. ABRC received donations of 734 seed stocks in 2021 including characterized mutants from multiple donors and wild-collected pennycress accessions from J. Sedbrook and collaborators. Bulk seed for a further 5,460 seed stocks was received from NASC. 348 non-seed resources were also added to the collection in 2021, mostly vectors. A new education kit consisting of plasmids and positive control seed lines for small-scale genome editing experiments in minimal lab settings was received from W. Lukowitz.

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, recombinant inbred and mapping populations, transgenic reporter lines, and RNAi lines and pools. The collection also includes 1,741 seed stocks from 33 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 1,628 new and existing stocks in 2021, involving either germination testing or verifying stock identity.

Two ABRC publications in 2021 include:
- Calhoun C., Crist D., Knee E., Miller J., Nagy E., Somers D.E. (2021) Handling Arabidopsis and Other Brassicaceae: Growth, Preservation of Seeds, Transformation, and Genetic Crosses. In: Sanchez-Serrano J.J., Salinas J. (eds) Arabidopsis Protocols. Methods in Molecular Biology, vol 2200. Humana, New York, NY. (https://doi.org/10.1007/978-1-0716-0880-7_1)

- Brkljacic J., Wittler B., Lindsey B. E., Devi Ganeshan V., Sovic M. G., Niehaus J., Ajibola W., Bachle S. M., Fehér T., Somers D. E. (2021) Frequency, composition and mobility of Escherichia coli-derived transposable elements in holdings of plasmid repositories. Microbial Biotechnology 15:455-468 (https://doi.org/10.1111/1751-7915.13962). This latter work is a collaboration with Addgene and Dr. Tamas Feher (Hungarian Academy of Sciences) that characterized the presence of unintended integrations of bacterial mobile genetic elements in the plasmid stock collections of the ABRC and Addgene.

ABRC outreach served more than 3,000 individuals in 2021 through participation in virtual community events and through an online citizen science project. ABRC was awarded funding for 2 years through the National Science Foundation (NSF) SIBR Capacity program and early this year we submitted a 5-year NSF SIBR Sustaining proposal to partially support the ongoing activities of the Center.

Planned future activities of your project/resource

ABRC will continue to solicit donations of new resources with a particular focus on characterized Arabidopsis mutants including multiple (stacked) mutants. A number of Pennycress researchers have also expressed interest in donating resources from potential DOE funded projects. Distribution of resources is expected to exceed 2021 levels by approximately 10% but will still fall short of pre-pandemic levels of distribution. Quality control testing of new donations and stocks reproduced at ABRC will be carried out at similar levels to 2021. ABRC and NASC collaboration via exchange of seed stock resources and related data will also continue with ABRC transitioning to providing seed for bulking at NASC rather than individual aliquots for distribution to NASC customers. ABRC outreach will focus on a return to in-person programming in collaboration with local community partners. The ABRC Director will attend ICAR and information about ABRC stocks and activities will be available at the NASC booth.

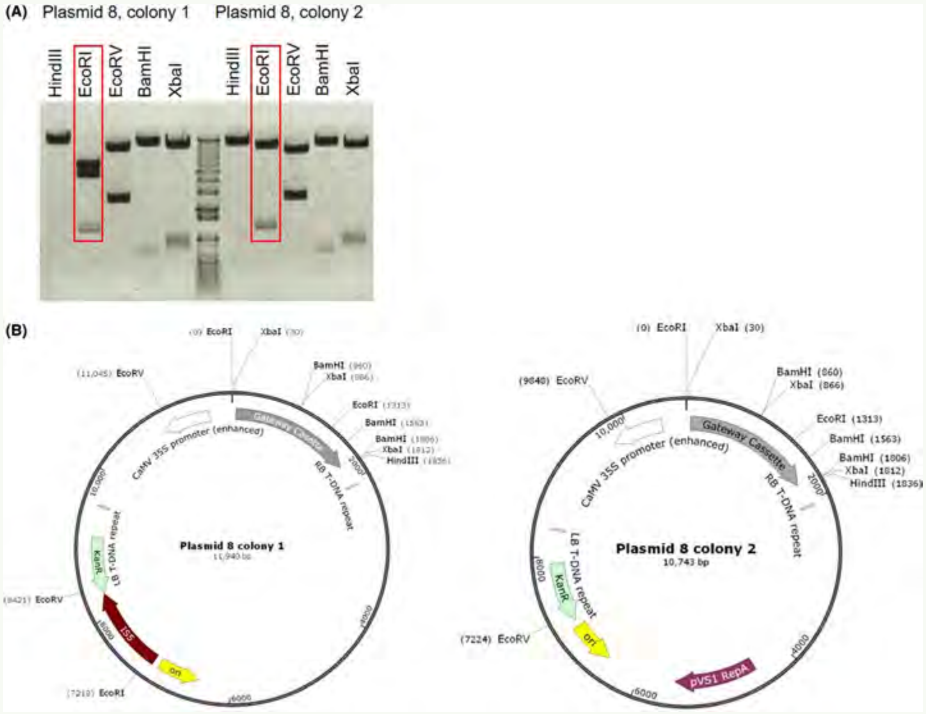

Figure 1: ‘‘Identification of IS5 in a plant binary vector by restriction digest’’. Brkljacic et al, 2021. *Microbial Biotechnology.* https://doi.org/10.1111/1751-7915.13962

Bio-Analytic Resource for Plant Biology (BAR)

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

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 the plant (mainly Arabidopsis) researcher 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).

- 29,180 predicted protein tertiary structures and experimentally determined structures for 402 Arabidopsis proteins (Alphafold models will be incorporated soon).

- 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 your project or resource

The BAR introduced a Blast search option at http://bar.utoronto.ca/blast/. 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. The BAR upgrades Thalemine on a regular basis, and the current version as of August 2022 is based on the InterMine 5.0.8 release, with data updates from 2022-01-04. We implemented a Guard Cell Drought view (van Weringh et al., 2021) for ePlant and a DNA Damage view (Bourbousse et al., 2018) for our eFP Browser/ePlant. We also developed a new API for faster provision of eFP images to partner websites like TAIR and MaizeGDB.
For non-Arabidopsis researchers, new expression views were added for several other species including tomato, soybean and rice.

BAR Publications

The BAR's Nicholas Provart published a review and a how-to book chapter of mostly web-based informatics tools with colleagues from UC Davis (Cantó-Pastor et al., 2021; Alex Mason et al., 2021). Note: the Bourbousse et al. (2018) and McWhite et al. (2020) publications are not BAR publications.

- Mason, G.A., Cantó-Pastor, A., Brady, S.M., and Provart, N.J. (2021). Bioinformatic Tools in Arabidopsis Research. In Arabidopsis Protocols, J.J. Sanchez-Serrano and J. Salinas, eds, Methods in Molecular Biology. (Springer US: New York, NY), pp. 25–89. DOI: 10.1007/978-1-0716-0880-7_2
- Bourbousse, C., Vegesna, N., and Law, J.A. (2018). SOG1 activator and MYB3R repressors regulate a complex DNA damage network in Arabidopsis. Proc. Natl. Acad. Sci. U. S. A. 115: E12453–E12462. https://doi.org/10.1073/pnas.1810582115
- Cantó-Pastor, A., Mason, G.A., Brady, S.M., and Provart, N.J. (2021). Arabidopsis bioinformatics: tools and strategies. Plant J. Cell Mol. Biol. 108: 1585–1596. https://doi.org/10.1111/tpj.15547
- McWhite, C.D. et al. (2020). A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. Cell 181: 460-474.e14. DOI: 10.1016/j.cell.2020.02.049
- 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. doi: 10.1105/tpc.20.00358
- Van Weringh, A., Pasha, A., Esteban, E., Gamueda, P.J., and Provart, N.J. (2021). Generation of guard cell RNA-seq transcriptomes during progressive drought and recovery using an adapted INTACT protocol for Arabidopsis thaliana shoot tissue. bioRxiv: 2021.04.15.439991.

Planned future activities of your project or resource

A custom eFP view in ePlant for a researcher's own RNA-seq data is in beta-testing, along with "Gaia" (kind of like Siri or Alexa, but for Arabidopsis information) as part of an award from Genome Canada: check out a beta version at http://bar.utoronto.ca/gaia. In addition to bringing together search results from many different tools, Gaia indexes 67,291 Arabidopsis papers with 155,175 figures of which 11,205 are genetic models – these were identified using a triplet network. We extracted 9,457 unique terms from the models by OCR using the Google Vision AI. Thus, Gaia is able to identify if your favourite gene is present in a genetic model figure – you can also search to see if it co-occurs with another search term in a figure.

Conferences, Workshops and Training events

The BAR participated in the 2021 and 2022 American Society of Plant Biology (ASPB) virtual Plant Biology conference, as part of the Plant AgData Outreach booth and in the Plant Bioinformatics workshop, which it helped co-organize with TAIR. The BAR additionally took part in the virtualized PAGXXIX in January 2022. The BAR also participated in the Community Tools and Arabidopsis Informatics sessions at ICAR2022 in Belfast.

EMPHASIS

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

The European Infrastructure for Multi-scale Plant Phenomics and Simulation (EMPHASIS) is a distributed ESFRI listed Research Infrastructure to develop and provide access to facilities and services addressing multi-scale plant phenotyping in different agro-climatic scenarios. EMPHASIS will establish an integrated European phenotyping infrastructure to analyse genotype performance under diverse environmental conditions and quantify the diversity of traits contributing to performance in diverse environmental conditions − plant architecture, major physiological functions and output, yield components and quality. EMPHASIS aims to address the technological and organizational limits of European Phenotyping, for a full exploitation of genetic and genomic resources available for crop improvement in changing climate. Listed on the ESFRI Roadmap in 2016, EMPHASIS is in the transition from the Preparatory Phase (2017-2021) supported by the EU project EMPHASIS Prep (Grant Agreement: 739514) to the Implementation Phase (2022-2025) supported by the EU project EMPHASIS GO (Grant Agreement: 101079772) and is supposed to become operational in 2024 and provide a full set of services to plant scientists. EMPHASIS related project EPPN2020 (2017-2021, Grant Agreement: 731013) has been successful finalized enabling 144 Transnational Access experiments within plant phenotyping facilities including 21 experiments with Arabidopsis. The results developed in EPPN2020 such as standards in experimental and data management approaches that were developed in parallel to the provision of Access will be further developed and made available within EMPHASIS.

Planned future activities of your project/resource

EMPHASIS was involved in infrastructure proposals that will provide services to the community:

- AgroServ will start on 1st of September (2022-2027, Grant Agreement: 101058020), the project integrates 12 different research infrastructures that will develops and provide services towards a sustainable and resilient agriculture and agroecological transitions.

- Ai4Life will start on 1st of September (2022-2025) and enable the life science community to benefit from Artificial Intelligence and Machine Learning powered image analysis by providing sustainable research services to exploit AI/ML to improve the utility and interpretability of image data.

Gramene: A comparative genomics and pathways resource for plants

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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 Pan Genome resources:
https://maize-pangenome.gramene.org/
https://oryza.gramene.org/
https://vitis.gramene.org/
http://www.sorghumbase.org/

Recently developed Open Tools and Resources for Arabidopsis Researchers

New this year was the addition of a mirror of an Arabidopsis thaliana CLIMtools portal (Ferrero-Serrano et al, 2022) where users can explore Genome x Environment (G x E) associations for 473 climate variables and 2,999 Arabidopsis accessions, which hosts four R Shiny apps that provide distinct views of the data. Since the last report, we added 25 new plant genomes summing a total of 118 plant reference genomes, from which new ortholog and paralog assignments were drawn for the nearly 100,000 Arabidopsis genes in A. thaliana, A. lyrata, and A. halleri. Gramene's codebase was rewritten and deployed across four crop-specific pangenome sites targeting each of sorghum, rice, maize and grapevine, which are searchable and interconnected to support the genetic basis of agronomically important traits. Each of these sites includes six plant outgroup species, one of them being A. thaliana. EBI Atlas has been a leader in FAIR access for gene expression data, including single-cell expression (SCE). We contributed to the biocuration efforts of bulk plant RNA-seq data hosted at the EBI Atlas with three new Arabidopsis studies, including 24 assays of a circadian time series (Yang et al, 2020), 18 assays of a transcriptome profile of wild-type vs mea mutant ovary and seed at different developmental time points (Simonini et al, 2021), and 24 assays for acclimation of photosynthesis to changes in the environment resulting in decreased oxidative stress (Karim and Johnson, 2021). This was done in addition to eight new SCE Arabidopsis data sets (Tenorio Berrío et al, 2022; Shahan et al, 2022; Zhang et al, 2020; Wendrich et al, 2020; Song et al, 2020; Liu et al, 2020; Gala et al, 2020; Kim et al, 2021) comprising 567,590 cells, an increase of 491,764 cells from the previous year.

Here are the current contents of the Gramene database (build 65, May 2022) and their relevance to Arabidopsis research:

- Structural and functional annotations for 2.9 million gene models in 118 plant reference genomes including three Arabidopsis model species: A. thaliana, A. lyrata, and A. halleri, cereals, vegetables, and fruit crops (e.g., Brassicas, Fabaceas, Solanaceas), basal plants and algae.

- 124,010 phylogenetic tree families (built with 89 plant and 5 non-plant species), 320 whole-genome alignments (81 with Arabidopsis species), and 80 synteny maps (4 with Arabidopsis spp).

- Over 237 million genetic and structural variants for 17 plant species, including 12.9 million Arabidopsis SNPs from the 1001 Arabidopsis Genomes Project. The Arabidopsis SNP set includes genotypes for over 1,000 accessions, and was combined with phenotypic data (107 phenotypes associated with 95 inbred lines) from the GWAS study by Atwell et al (2010). Variant effect predictor (VEP) analysis in Arabidopsis indicates that most SNPs occur in introns (29.4%), and missense variants are the most frequent deleterious category (15.3%), followed by synonymous (10.9%), upstream of gene (10.3%), 3’-UTR (10.1%), downstream of gene (9.7%), and 5’-UTR (7.7%) variants.

- Genome x Environment associations for 473 climate variables and 2,999 Arabidopsis accessions via the CLIMtools portal (Ferrero-Serrano et al, 2022). AraCLIM, CLIMGeno, GenoCLIM, PhenoCLIM, TCLIM (v2 only), and FDRCLIM (v1 only) are utilities to visualize and analyze this data. For example, users can search for climate-gene associations for an Arabidopsis gene of interest (GenoCLIM) or a climate parameter of interest (CLIMGeno). CLIMGeno is a GWAS browser with tabular and graphical views of variants –- climate association analysis results, while AraCLIM lets users explore the distribution of the climate variables for each geo-referenced Arabidopsis accession in an interactive map view and on scatter plots comparing a pair of climate variables. Variants within spliced transcripts include a SNPfold correlation coefficient that compares the predicted RNA secondary structures of transcripts with the reference and alternate alleles (Halvorsen et al, 2010) to assess the presence of structure-altering polymorphisms or riboSNitches. T-CLIM displays transcript abundance variation among the 558 Arabidopsis accessions associated with climate data.

- Experimental baseline and differential expression data for 982 experiments in 28 plant species, including A. thaliana (531 baseline assays; 604 differential experiments) and A. lyrata (3 baseline assays; 1 differential experiment).

- The SCE Atlas currently includes 20 single-cell RNA-seq data sets from four plant species, 13 of them are in Arabidopsis (Moreno et al, 2022). Organ anatomograms are now accompanied by interactive cell type heatmaps, which react to selections in the anatomogram to display average cell type expression for marker genes. tSNE plot and expression heatmaps can now be exported as images, and tSNE plots are colored by inferred cell type, if available. All SCE datasets now include links to GEO/ENA, and a standardized downloadable AnnData object. UMAP plotting was added as an alternative to existing tSNE plots for dimensionality reduction.

- 320 reference metabolic and regulatory pathways curated in rice and inferred in a total of 120 plant species, including the three Arabidopsis species in Gramene.

- Integrated search capabilities and interactive views to query and visualize gene features, gene neighborhoods, phylogenetic trees, gene expression profiles, pathways, and cross-references to other bioinformatics resources (e.g., TAIR, AraPort, Thalemine, and NASC).

- Analysis tools to support comparative analyses of our data as well as user-provided data (e.g., BLAST/BLAT sequence aligner, sequence assembly converter for TAIR9/TAIR10 genomic co-ordinates, genetic VEP, BioMart, Reactome pathways analysis/visualization of OMICS data and multi-species pathway comparisons).

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

Cited literature

- Ferrero-Serrano, Á. et al. (2022) Experimental demonstration and pan-structurome prediction of climate-associated riboSNitches in Arabidopsis. Genome Biol. 23, 101. https://doi.org/10.1186/s13059-022-02656-4

- Gala, H. P. et al. (2021) A single-cell view of the transcriptome during lateral root initiation in Arabidopsis thaliana. Plant Cell 33, 2197–2220. DOI: 10.1093/plcell/koab101

- Halvorsen, M., Martin, J. S., Broadaway, S. & Laederach, A. (2010) Disease-associated mutations that alter the RNA structural ensemble. PLoS Genet. 6, e1001074. https://doi.org/10.1371/journal.pgen.1001074

- Karim, M. F. & Johnson, G. N. (2021) Acclimation of photosynthesis to changes in the environment results in decreases of oxidative stress in Arabidopsis thaliana. Front. Plant Sci. 12, 683986. https://doi.org/10.3389/fpls.2021.683986

- Kim, J.-Y. et al. (2021) Distinct identities of leaf phloem cells revealed by single cell transcriptomics. Plant Cell 33, 511–530. https://doi.org/10.1093/plcell/koaa060

- Liu, Z. et al. (2020) Global dynamic molecular profiling of stomatal lineage cell development by single-cell RNA sequencing. Mol. Plant 13, 1178–1193. DOI: 10.1016/j.molp.2020.06.010

- Moreno, P. et al. (2022) Expression Atlas update: gene and protein expression in multiple species. Nucleic Acids Res. 50, D129–D140. https://doi.org/10.1093/nar/gkab1030

- Shahan, R. et al. (2022) A single-cell Arabidopsis root atlas reveals developmental trajectories in wild-type and cell identity mutants. Dev. Cell 57, 543–560.e9. https://doi.org/10.1016/j.devcel.2022.01.008

- Simonini, S. et al. (2021) The Polycomb group protein MEDEA controls cell proliferation and embryonic patterning in Arabidopsis. Dev. Cell 56, 1945–1960.e7. https://doi.org/10.1016/j.devcel.2021.06.004

- Song, Q., Ando, A., Jiang, N., Ikeda, Y. & Jeffrey Chen, Z. (2020) Single-cell RNA-seq analysis reveals ploidy-dependent and cell-specific transcriptome changes in Arabidopsis female gametophytes. Genome Biology vol. 21. https://doi.org/10.1186/s13059-020-02094-0

- Tenorio Berrío, R. et al. (20202) Single-cell transcriptomics sheds light on the identity and metabolism of developing leaf cells. Plant Physiol. 188, 898–918. doi: 10.1093/plphys/kiab489.

- Wendrich, J. R. et al. (2020) Vascular transcription factors guide plant epidermal responses to limiting phosphate conditions. Science 370. doi: 10.1126/science.aay4970

- Yang, Y., Li, Y., Sancar, A. & Oztas, O. (2020) The circadian clock shapes the Arabidopsis transcriptome by regulating alternative splicing and alternative polyadenylation. J. Biol. Chem. 295, 7608–7619. doi: 10.1074/jbc.RA120.013513

- Zhang, T.-Q., Chen, Y. & Wang, J.-W. (2021) A single-cell analysis of the Arabidopsis vegetative shoot apex. Dev. Cell 56, 1056–1074.e8. https://doi.org/10.1016/j.devcel.2021.02.021

Planned future activities of your project/resource

We will continue to maintain and build the Gramene resource 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 genetic variation and germplasm metadata; 3) biocurate additional baseline and differential expression data sets, as well as single-cell expression data; 4) biocurate new metabolic pathways; 5) continue to expand pan-genome resources for maize, rice, sorghum and grapevine; and 6) transform the community through communication and training opportunities.

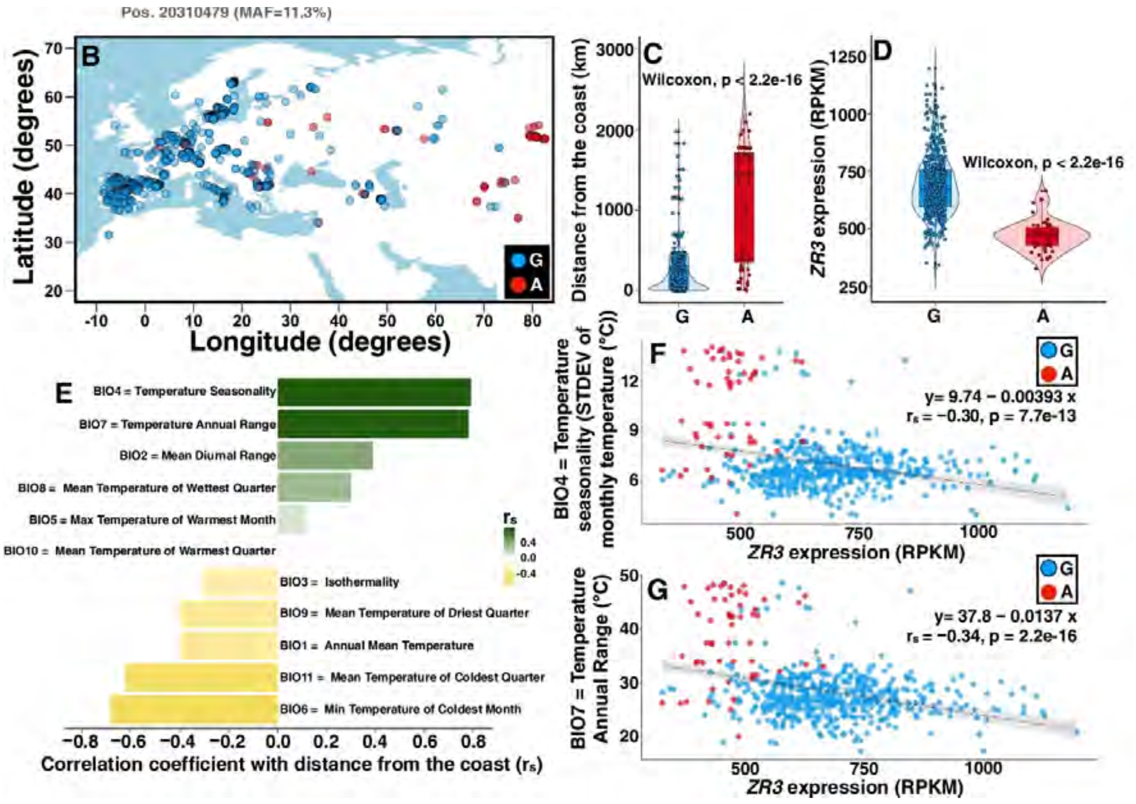

Figure 1: ‘‘Allele distribution in a synonymous SNP in ZR3 and its cis-regulated transcript abundance are correlated with the distance from the coast and temperature variability.’’ Ferrero-Serrano et al 2022. *Genome Biology*. https://doi.org/10.1186/s13059-022-02656-4

The Nottingham Arabidopsis Stock Centre (NASC)

Sean May, Director

Marcos Castellanos-Uribe, Operations Manager.

http://arabidopsis.info/

During 2021, ongoing issues with covid have resulted in slightly unpredictable numbers of orders compared to a ‘normal’ year and totalled 48,800 stocks sent to more than 40 countries, from China to Ukraine. In common with previous years our top 5 users (China/Germany/UK/France/Belgium) accounted for more than half of the seed sent.

Initial numbers for the first half of 2022 suggest a similar ongoing forecast. Currently the order numbers for 2022 stands at top 5 users: Germany/UK/China/France/Singapore. We have noticed ongoing local covid restrictions leading to a patchy reduction in orders from China which we trust will be temporary.

Thousands of seed have been donated in 2021/2 from 15 countries. We really appreciate every stock donated both as single lines and as collections. The largest numbers over this reporting period have come from USA/Germany/UK and China.

In funding news, our 5-year renewal grant was successfully awarded from the BBSRC Bioinformatics and Biological Resources Fund. This funding started in February 2022.

We had a great ICAR, distributing a lot of ‘thank you’ goodies to you, the community from our booth. If you missed out on picking up any of these, please have a look at the photos in our tweets: https://twitter.com/NascArabidopsis and just ask for what you want (we can include it in your seed order if we still have some).

Marcos gave a talk at ICAR and explained our current priorities in catching up on seed bulking after the covid hiatus (our glasshouses are now back to full productivity and capacity). He also detailed the changes resultant from BREXIT and the need for new phytocertificates for our EU users. If you have questions on these issues, please do ask us.

For up-to-date details on stock donations or anything else that you wish to know, please visit the NASC site, or contact curators@arabidopsis.info 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 contact us - don’t wait for us to come to you.

See you in Japan.

RIKEN

Masatomo Kobayashi

RIKEN BRC
masatomo.kobayashi@riken.jp

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

- The RIKEN Arabidopsis Full-length cDNA Over-eXpressing gene hunting (FOX) lines are gain-of-function mutants that were created by introducing the Arabidopsis full-length cDNA driven by the CMV 35S promoter into Col-0. The lines were deposited from RIKEN Plant Science Center and deposited to RIKEN BRC. We have distributed this resource as seed pools for phenotype screening. Now the Exp-Plant Catalog of RIKEN BRC provides the information of genes inserted in each individual line to make them available for reverse genetics approach. (https://epd.brc.riken.jp/en/archives/5403)

- Since November 2021, the Exp-Plant Catalog provides the records of 379 binary vectors deposited from Dr. Nakagawa, Shimane University, Japan. (https://epd.brc.riken.jp/en/archives/4813)

- The 5th term of National BioResource Project was launched in April 2022. RIKEN BRC continuously preserves and distributes Arabidopsis seeds, cultured plant cells and genes deposited from Japanese research community. (https://nbrp.jp/en/)

Planned future activities of your project/resource

- We plan to collect genotype and phenotype information of natural accessions collected in Japan. The obtained data will be uploaded to the Exp-Plant Catalog.

- Studies on biotic and abiotic stress responses as well as plant-microbe interactions are indispensable for sustainable development of human society. RIKEN BRC will collect and distribute plant resources useful for these research fields to support SDGs.

The Arabidopsis Information Resource (TAIR)

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

New and updated data:

- We continue to add new gene function data on a weekly basis including 1264 new/updated locus summaries, 812 new/updated gene symbols, 5096 articles linked to 10489 genes, 16395 experimental Gene Ontology (GO) and Plant Ontology (PO) annotations, 1039 new/updated alleles, and 2021 phenotypes linked to germplasms. These data are included in the quarterly data releases that are made publicly available after one year. Current GO annotations are exported on a quarterly basis to the GO Consortium.

- Since January 2021 we have collaborated with several community members to add new data tracks to JBrowse including updated CAGE datasets (Thieffry et al. 2020), AtPeptide Atlas tracks (van Wijk, et al., 2021), and stress induced sORFs and transcriptionally active regions (Hazarika et al., 2017). We also incorporated the Col-0 telomere to telomere sequence as a new genome option (Naish et al., 2021) For more information see the JBrowse release notes (https://www.arabidopsis.org/download_files/Help_Documents/JBrowse_updates.pdf). Members of the community who have datasets that can be visualized in JBrowse or have suggestions for datasets to incorporate are encouraged to contact us at curator@arabidopsis.org.

- Gene family data from PANTHER was updated to release16 and the corresponding data display on the locus page was updated to include new functions like downloading lists of paralogs and orthologs and downloading paralog sequences. Loci that are part of PANTHER families include links to the corresponding gene families in PhyloGenes (www.phylogenes.org).

- Protein domain data was updated to the latest InterPro release (v. 87.0). Future updates will be timed to quickly follow new InterPro releases.

New and updated tools:

- In late 2021 we began the process of overhauling the TAIR website and backend, essentially rewriting the entire TAIR application. The changes will eventually improve usability, stability, extensibility and accessibility compliance. The overhaul is being done in stages with the initial rollout of a new locus page planned for late 2022. Work in progress will be released incrementally to beta.arabidopsis.org. User feedback on design and function is encouraged.

- GFF annotation tracks that underlie the JBrowse Araport11 tracks are now being updated from TAIR on a quarterly basis. This largely affects the display of gene names and summaries.

Conferences and workshops:

- TAIR co-organized and presented at virtual conferences for ICAR2021, ASPB 2021 and in an unexpected pivot, PAG2022. TAIR was pleased to participate in person at ICAR2022 in Belfast and presented at two sessions (Community Resources and Arabidopsis Informatics).

Other:

- TAIR continues to collaborate with microPublication Biology helping to shepherd 6 Arabidopsis microPublications through the review and publication process and incorporating the data into TAIR.

- The AgBioData Consortium of which TAIR is a member, received funding through a NSF for Research Coordination Network Grant “Reimagining a Sustainable Data Network to Accelerate Agricultural Research and Discovery“. Please visit the AgBioData website (www.agbiodata.org) or contact Dr. Annarita Marrano, the Program Coordinator, at agbiodata@gmail.com to learn more.

Gratitude:

- In December 2021, Dr. Eva Huala retired and Dr. Tanya Berardini took over as TAIR director. We thank Eva for her many years of service to the research community and we welcome Tanya.

Planned future activities of your project/resource

Data:

- We are currently looking for interested collaborators/partners who wish to work with us to make use of available high quality genome sequences to update the reference genome annotation. Please contact us at curator@arabidopsis.org if you are interested in participating in this effort.

- As always we will continue our weekly updates of gene function information and quarterly data releases.

Tools:

- We plan to update JBrowse to JBrowse2. Along with replicating the current datasets, this will enable new functionalities including viewing and comparing syntenic regions within Arabidopsis or between Arabidopsis and other species.

- We are working with the Textpresso developer team to update the Arabidopsis Textpresso instance. This includes the addition of over 14k open access papers to the corpus as well as improved search and retrieval functionality.

- We will continue with the TAIR application overhaul throughout the next year.

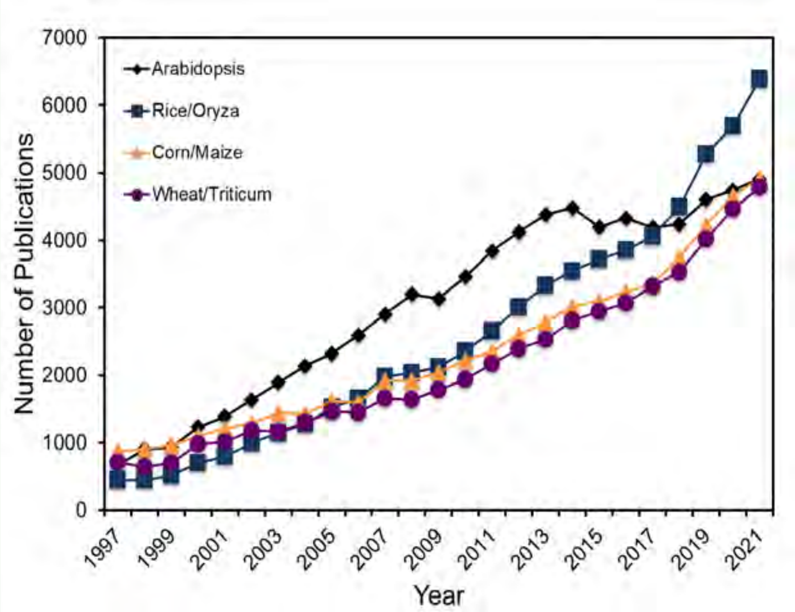
- We will update the tree data in PhyloGenes and homologs TAIR after the next PANTHER update is released.

Conferences and Presentations:

- TAIR/Phoenix will be present at ASPB2022 in Portland OR and PAG2023 in San Diego.

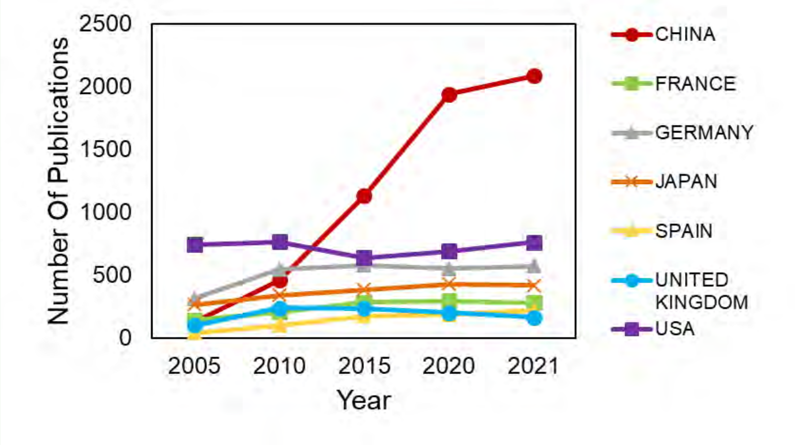
Update on Arabidopsis Publications

Global Outlook in 2022



The number of ‘Arabidopsis Publications’ is now all but tied with those that include ‘Maize’ or ‘Wheat’ as the second most ‘popular’ plant from a PubMed search; falling further behind the number of ‘Rice publications’.

This is driven by the continued increase in the outputs from scientists in countries in which rice is an important crop. For example ‘Pubmed Rice publications’ from China have doubled over the past five years to an annual total of over 3000 papers.



Looking at Arabidopsis only, China remains far and away the country with most publicatiions although this rate of increase has slowed, surely an impact of the global pandemic.

Other countries with the most annual publications remain stable with only a small reduction in the number of ‘Arabidopsis publications’ from British, French and Japanese scientists. This continues to reflect that in in the ‘Western World’ Arabidopsis has found its level and will continue to be the most important non-crop model organism.

Historic Lookback

In this report we have taken a look-back on the number of Arabidopsis publications over the past two decades. Over that time the most prominent country has changed from the USA to China with a relative peak from Western European countries and Japan in 2011.

It will be of no surprise to regular readers of the MASC report to see the rise in Chinese publications from next to nothing in 2001 to over 2000 articles in 2021. The maps on the following page obviously only feature ‘MASC-participating countries’.

We hope to see a rise in Arabidopsis research across developing nations as the barriers to entry fall for the uptake of routine molecular techniques and there is an increased understanding of the utility of Arabidopsis research to explore region-specific questions that might impact local crops.


Publications by Country
2001
2001
467
1
Powered by Bing
© Australian Bureau of Statistics, GeoNames, Microsoft, Navinfo, OpenStreetMap, TomTom


Publications by Country
2011
2011
740
9
Powered by Bing
© Australian Bureau of Statistics, GeoNames, Microsoft, Navinfo, OpenStreetMap, TomTom


Publications by Country
2021
2021
2085
2
Powered by Bing
© Australian Bureau of Statistics, GeoNames, Microsoft, Navinfo, OpenStreetMap, TomTom

MASC Country / Region Reports

Argentina

Gabriela Auge

CONICET / Instituto de Biociencias, Biotecnología y Biología Traslacional (iB3), University of Buenos Aires
gauge@fbmc.fcen.uba.ar

Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- ASpli, a computational suite implemented in R statistical language, that allows the identification of changes in both, annotated and novel alternative-splicing events and can deal with simple, multi-factor or paired experimental designs.
  Reference: “ASpli: integrative analysis of splicing landscapes through RNA-Seq assays” 2021. Mancini et al. Bioinformatics, 37: 2609. DOI: 10.1093/bioinformatics/btab141

Planned events for 2022 and 2023

- 50° Congreso Argentino de Genética, October 2-5, 2022.

- Reunión de la Sociedad Argentina de Investigación Bioquímica y Biología Molecular, November 2022.

- Reunión de la Sociedad Argentina de Investigación Bioquímica y Biología Molecular, 2023.

- Reunión Argentina de Fisiología Vegetal, 2023.

- Jornadas Argentinas de Botánica, 2023.

- 3° Reunión Argentina de Biología de Semillas, 2023.

Selected Publications

These papers were selected according to one or more of the following criteria: led by and ECR (graduate student or postdoc), list of authors composed by a multi-disciplinary team, PI is a woman, or overall relevance of the work.

- Bellido et al. A mitochondrial ADXR–ADX–P450 electron transport chain is essential for maternal gametophytic control of embryogenesis in Arabidopsis. 2022. PNAS, 119 (4) e2000482119. https://doi.org/10.1073/pnas.2000482119

  A well-described steroid synthesis pathway in animals is conserved and described in Arabidopsis showing it is required for reproduction.

- Martinez-Pacheco et al. Apoplastic class III peroxidases PRX62 and PRX69 promote Arabidopsis root hair growth at low temperature. 2022. Nature Communications, 13: 1310. DOI: 10.1038/s41467-022-28833-4

A multi-disciplinary group of authors shows ROS homeostasis and cell wall extensibility mediated regulated by apoplastic peroxidases affect root hair development plasticity in response to environmental changes.

- Fernández Nevyl and Battaglia. Developmental plasticity in Arabidopsis thaliana under combined cold and water deficit stresses during flowering stage. 2021. Planta, 253: 50. DOI: 10.1007/s00425-021-03575-7

  Acclimation to simultaneous long-term stresses such as drought and cold affect the range of developmental plasticity in Arabidopsis, showing this study model could be used to infer developmental responses that are relevant for other species of agricultural relevance.

- Cecchini et al. Alternative splicing of an exitron determines the subnuclear localization of the Arabidopsis DNA glycosylase MBD4L under heat stress. The Plant Journal, 110: 377. https://doi.org/10.1111/tpj.15675

  Heat stress directs the alternative splicing of an exitron-carrying DNA glycosylase leading to isoforms with differential subnuclear localization, first exitron mediated mechanism of subnuclear localization described in eukaryotes.

- Giustozzi et al. Arabidopsis mediator subunit 17 connects transcription with DNA repair after UV-B exposure. 2022. The Plant Journal, 110: 1047. https://doi.org/10.1111/tpj.15722

  A member of the highly conserved MEDIATOR complex, MED17, regulates the DNA damage response to high UV-B irradiance.

Major Funding Sources

- Agencia Nacional de Promoción de la Investigación, el Desarrollo Tecnológico y la Innovación.
- Consejo Nacional de Investigaciones Científicas y Tecnológicas (CONICET).
- National Universities such us Universidad de Buenos Aires, Universidad Nacional de Córdoba, Universidad Nacional del Litoral, etc.
- Ministerio de Ciencia, Tecnología e Innovación.

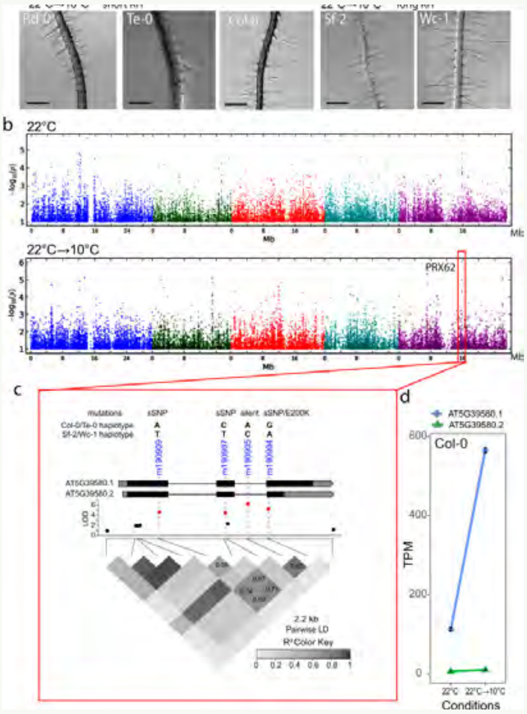


Figure 1: "PRX62 associates with enhanced RH growth under low temperature condition". Martinez-Pacheco et al 2022. *Nature Communications*. doi: 10.1038/s41467-022-28833-4

Australia

Monika Murcha

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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- TRUEE; a bioinformatic pipeline to define the functional microRNA targetome of Arabidopsis https://osf.io/k7rcs/

Planned events for 2022 and 2023

- ComBio2022, International Convention Centre, Melbourne 27-30th September 2022. Annual national conference that includes several symposia dedicated to plant research. https://www.combio.org.au/combio2022/

Selected Publications

- He, C., Liew, L.C., Yin, L., Lewsey, M.G., Whelan, J., and Berkowitz, O. (2022). The retrograde signalling regulator ANAC017 recruits the MKK9-MPK3/6, ethylene, and auxin signalling pathways to balance mitochondrial dysfunction with growth. Plant Cell. Jun 16;koac177. doi: 10.1093/plcell/koac177.

  ANAC017, a master regulator of mitochondrial stress recruits the ethylene and auxin pathways in Arabidopsis.

- Le, X.H., Lee, C.P., Monachello, D., and Millar, A.H. (2022). Metabolic evidence for distinct pyruvate pools inside plant mitochondria. Nature Plants 8, 694-705. DOI: 10.1038/s41477-022-01165-3

  Respiratory substrate supply in plants involves distinct pyruvate pools inside the mitochondrial matrix suggesting metabolic compartmentalisation for the regulation of cellular resources.

- McKay, D.W., McFarlane, H.E., Qu, Y., Situmorang, A., Gilliham, M., and Wege, S. (2022). Plant Trans-Golgi Network/Early Endosome pH regulation requires Cation Chloride Cotransporter (CCC1). Elife 11. https://doi.org/10.7554/eLife.70701

  A single cation chloride cotransporter (CCC1) in Arabidopsis thaliana provides a mechanism to regulate pH in the trans-Golgi/Early Endosome Network.

- Royan, S., Gutmann, B., Colas des Francs-Small, C., Honkanen, S., Schmidberger, J., Soet, A., Sun, Y.K., Vincis Pereira Sanglard, L., Bond, C.S., and Small, I. (2021). A synthetic RNA editing factor edits its target site in chloroplasts and bacteria. Commun Biol 4, 545. DOI: 10.1038/s42003-021-02062-9

A functional editing factor was created from synthetic PPR motifs able to target the Arabidopsis chloroplast transcriptome.

- Soares da Costa, T.P., Hall, C.J., Panjikar, S., Wyllie, J.A., Christoff, R.M., Bayat, S., Hulett, M.D., Abbott, B.M., Gendall, A.R., and Perugini, M.A. (2021). Towards novel herbicide modes of action by inhibiting lysine biosynthesis in plants. Elife 10. doi: 10.7554/eLife.69444

  A high-throughput screen of compounds identified inhibitors of a novel herbicide target enzyme involved in lysine biosynthesis.

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)

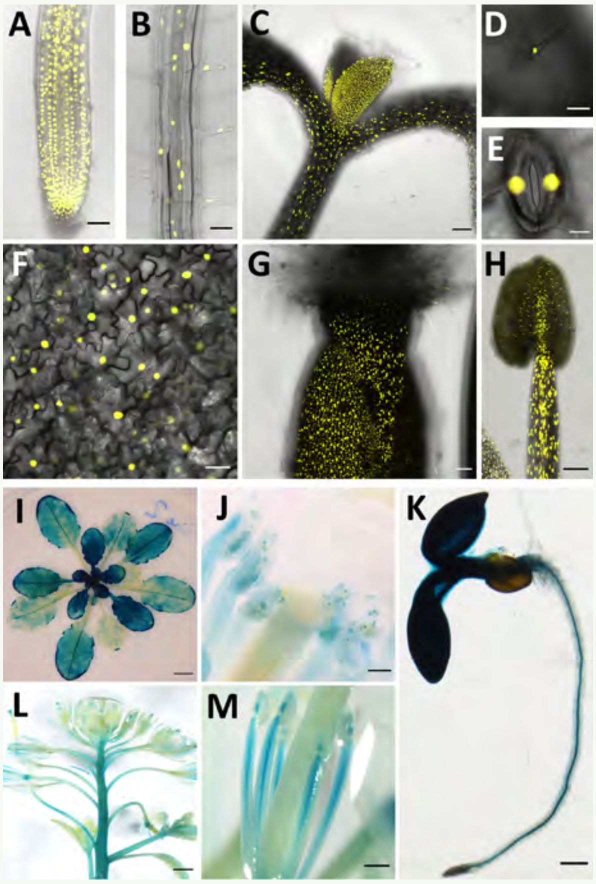

Figure 1: "CCC1 is expressed ubiquitously". McKay et al, 2022, *Elife.* https://doi.org/10.7554/eLife.70701

Austria

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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- Phenoplant, a multi-sensor and multi-approach high-throughput plant phenotyping platform at the VBCF.
- Methylscore for analyzing DNA methylation from WGBS in plants.
- Bookend a software package for transcript assembly.

Planned events for 2022 and 2023

- Mendel Early Career Symposium, 12.-13. May 2022, at the Gregor Mendel Institute in Vienna, Austria https://www.oeaw.ac.at/gmi/symposium
- Two plant sessions at the ÖGMBT, 19.-22. Sept. 2022 https://oegmbt.at/events/annual-meeting

Selected Publications

- Waidmann S, Petutschnig E, Rozhon W, Molnár G, Popova O, Mechtler K, Jonak C. (2022). GSK3-mediated phosphorylation of DEK3 regulates chromatin accessibility and stress tolerance in Arabidopsis. FEBS J, 289, 473-493. doi.org/10.1111/febs.16186
- Stephani M, Picchianti L, Dagdas Y. (2021) C53 is a cross-kingdom conserved reticulophagy receptor that bridges the gap betweenselective autophagy and ribosome stalling at the endoplasmic reticulum. Autophagy. 17, 586-587. doi: 10.1080/15548627.2020.1846304.
- Schmücker A, Lei B, Lorković ZJ, Capella M, Braun S, Bourguet P, Mathieu O, Mechtler K, Berger F. (2021) Crosstalk between H2A variant-specific modifications impacts vital cell functions. PLoS Genet. 17, e1009601. doi: 10.1371/journal.pgen.1009601.
- Osakabe A, Jamge B, Axelsson E, Montgomery SA, Akimcheva S, Kuehn AL, Pisupati R, Lorković ZJ, Yelagandula R, Kakutani T, Berger F. (2021) The chromatin remodeler DDM1 prevents transposon mobility through deposition of histone variant H2A.W. Nat Cell Biol. 23, 391-400. doi: 10.1038/s41556-021-00658-1.

- Borg M, Papareddy RK, Dombey R, Axelsson E, Nodine MD, Twell D, Berger F. (2021) Epigenetic reprogramming rewires transcription during the alternation of generations in Arabidopsis. Elife.,10:e61894. doi: 10.7554/eLife.61894.

- Bente H, Foerster AM, Lettner N, Mittelsten Scheid O. (2021) Polyploidy-associated paramutation in Arabidopsis is determined by small RNAs, temperature, and allele structure.PLoS Genet. 17, e1009444. doi: 10.1371/journal.pgen.1009444.

- Burns R, Mandáková T, Gunis J, Soto-Jiménez LM, Liu C, Lysak MA, Novikova PY, Nordborg M. (2021) Gradual evolution of allopolyploidy in Arabidopsis suecica. Nat Ecol Evol. 5, 1367-1381. doi: 10.1038/s41559-021-01525-w.

- Mutanwad KV, Lucyshyn D. (2022) Balancing O-GlcNAc and O-fucose in plants.FEBS J. 289, 3086-3092. doi: 10.1111/febs.16038.

- Guo T, Weber H, Niemann MCE, Theisl L, Leonte G, Novák O, Werner T. (2021) Arabidopsis HIPP proteins regulate endoplasmic reticulum-associated degradation of CKX proteins and cytokinin responses. Mol Plant. 14, 1918-1934. doi: 10.1016/j.molp.2021.07.015.

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

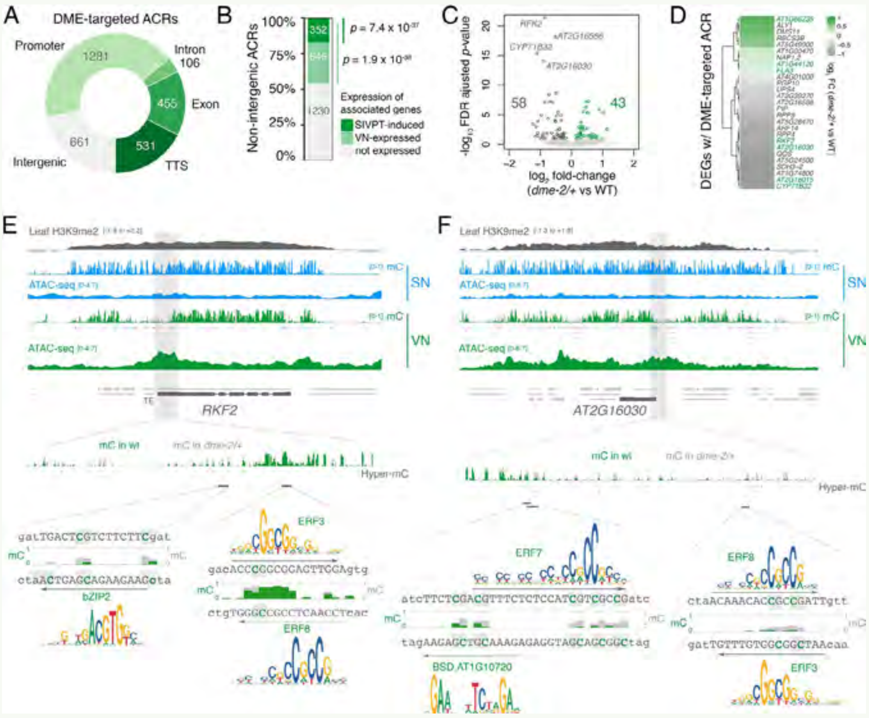

Figure 3: “DEMETER (DME) activity regulates the expression of pollen tube-related genes”. Borg et al, 2021. *Elife* https://doi.org/10.7554/eLife.61894

Brazil

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Planned Events for 2022 and 2023

- VIII Simpósio Brasileiro de Genética Molecular de Plantas
  Florianópolis, Santa Catarina, Brazil, from May 30 to June 02, 2023.

- XVIII Brazilian Congress of Plant Physiology, and I Ibero-latinamerican Congress of Plant Biology
  Porto Alegre, Rio Grande do Sul, Brazil, from September 6 to 9, 2022.

Selected Publications

- Barreto P, Dambire C, Sharma G, Vicente J, Osborne R, Yassitepe J, Gibbs DJ, Maia IG, Holdsworth MJ, Arruda P. (2022) Mitochondrial retrograde signaling through UCP1-mediated inhibition of the plant oxygen-sensing pathway. Curr Biol. 32(6):1403-1411.e4. doi: 10.1016/j.cub.2022.01.037.

  By using a combination of genetic and biochemical approaches, this study revealed that mitochondrial retrograde signaling relies on highly compartmentalized individual pathways previously not taken into account. This involves a link between mitochondrial oxygen consumption and cytosolic oxygen sensing via the N-degron pathway.

- Siqueira JA, Wakin T, Batista-Silva W, Silva JCF, Vicente MH, Silva JC, Clarindo WR, Zsögön A, Peres LEP, De Veylder L, Fernie AR, Nunes-Nesi A, Araújo WL. (2022) A long and stressful day: Photoperiod shapes aluminium tolerance in plants. J Hazard Mater. 15;432:128704. doi: 10.1016/j.jhazmat.2022.128704.

  Aluminium (Al) is a major constraint for crop yield worldwide. This study demonstrated that photoperiod acts as a barrier for Aluminum tolerance in plants. This could ultimately contribute to improving crop growth and productivity, particularly in many developing countries where the majority of acid soils reside and Al toxicity limits crop production

- Arcuri MLC, Nunes-Laitz AV, Lima RPM, Barreto P, Marinho AN, Arruda P, Maia IG. Knockdown of Mitochondrial Uncoupling Proteins 1 and 2 (AtUCP1 and 2) in Arabidopsis thaliana Impacts Vegetative Development and Fertility. Plant Cell Physiol. 2021;62(10):1630-1644. doi: 10.1093/pcp/pcab117. PMID: 34314506.

  This study demonstrate that the activity of mitochondrial uncoupling proteins (UCP1 and UCP2) and adjustments of mitochondrial metabolism are required for plant fertility and early growth development.

- Feitosa-Araujo E, da Fonseca-Pereira P, Pena MM, Lana-Costa J, Coelho DG, de Oliveira Silva FM, Medeiros DB, Linka N, Araújo WL, Weber APM, Fernie AR, Nunes-Nesi A. (2022) Mitochondrial and peroxisomal NAD+uptake are important for improved photosynthesis and seed yield under elevated CO2 concentrations. Plant J. 111(3):713-730. doi: 10.1111/tpj.15846.

  This work demonstrated that an impaired NAD+ uptake into mitochondria and peroxisomes reduced seed production under ambient CO2 concentration and did not allow for reproductive improvements under high CO2.

- Moreira VJV, Lourenço-Tessutti IT, Basso MF, Lisei-de-Sa ME, Morgante CV, Paes-de-Melo B, Arraes FBM, Martins-de-Sa D, Silva MCM, de Almeida Engler J, Grossi-de-Sa MF. (2022) Minc03328 effector gene downregulation severely affects Meloidogyne incognita parasitism in transgenic Arabidopsis thaliana. Planta. 255(2):44. doi: 10.1007/s00425-022-03823-4. PMID: 35050413.

  This study demonstrated that Minc03328, an effector protein, is of crucial importance for successful Meloidogyne incognita parasitism in plants.

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)

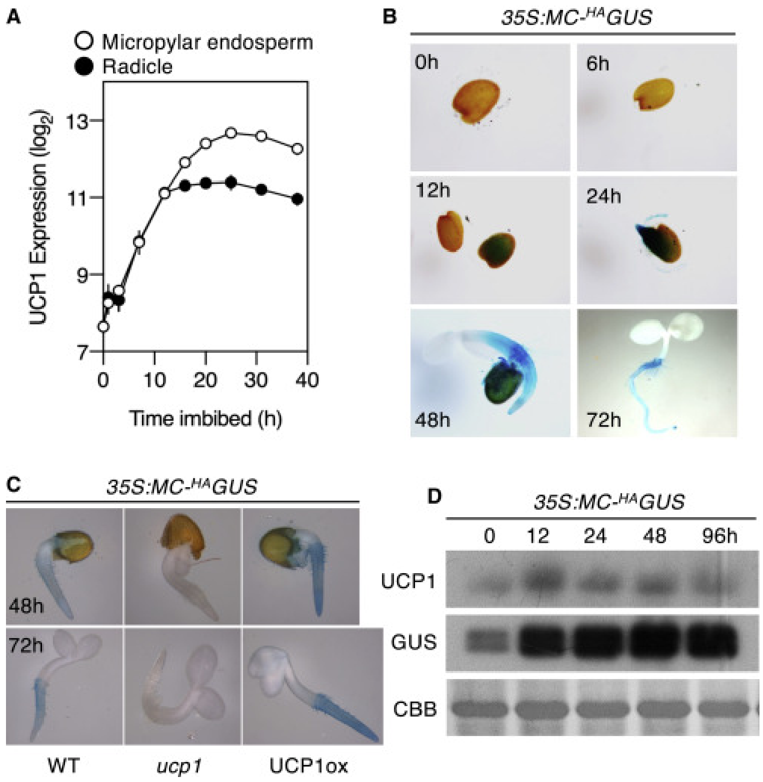
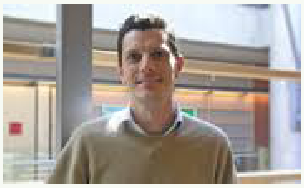


Figure 3. ‘‘Expression of UCP1 during germination influences GUS accumulation’’. Barreto et al, 2022. *Current Biology.* https://doi.org/10.1016/j.cub.2022.01.037

Canada



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With input from:

Nicholas Provart

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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- The Bio-Analytic Resource for Plant Biology at BAR.utoronto.ca introduced a Blast search option at http://bar.utoronto.ca/blast/. 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. The BAR maintains and regularly upgrades Thalemine, and the current version as of August 2022 is based on the InterMine 5.0.8 release, with data updates from 2022-01-04. The BAR also developed a new API for faster provision of eFP images to partner websites like TAIR and MaizeGDB.

Planned events for 2022 and 2023

- The Canadian Society of Plant Biologists' (CSPB) Eastern Regional Meeting is tentatively scheduled to occur on December 3rd, 2022 at the University of Toronto Scarborough campus. The 2023 CSPB annual general meeting will be held at Dalhousie University in Halifax, Nova Scotia in the summer of 2023. Check out https://cspb-scbv.ca/events closer to the dates for more details.

Selected Publications

- Tian H, Wu Z, Chen S, Ao K, Huang W, Yaghmaiean H, Sun T, Xu F, Zhang Y, Wang S, Li X, Zhang Y. Activation of TIR signalling boosts pattern-triggered immunity. Nature. 2021 Oct;598(7881):500-503. doi: 10.1038/s41586-021-03987-1. Epub 2021 Sep 20. PMID: 34544113

  This is an interesting paper outlining the role of TIR signalling in pattern-triggered immunity (PTI) mediated by pattern recognition receptors.

- Seto D, Khan M, Bastedo DP, Martel A, Vo T, Guttman D, Subramaniam R, Desveaux D. The small molecule Zaractin activates ZAR1-mediated immunity in Arabidopsis. Proc Natl Acad Sci U S A. 2021 Nov 23;118(47):e2116570118. doi: 10.1073/pnas.2116570118. PMID: 34799454

  The paper describes the identification of a small molecule (Zaractin) that mimics the immune eliciting activity of the Pseudomonas syringae type III secreted effector (T3SE) HopF1r.

- Arellano-Saab A, Bunsick M, Al Galib H, Zhao W, Schuetz S, Bradley JM, Xu Z, Adityani C, Subha A, McKay H, de Saint Germain A, Boyer FD, McErlean CSP, Toh S, McCourt P, Stogios PJ, Lumba S. Three mutations repurpose a plant karrikin receptor to a strigolactone receptor. Proc Natl Acad Sci U S A. 2021 Jul 27;118(30):e2103175118. doi: 10.1073/pnas.2103175118. PMID: 34301902

  This paper is an interesting example of how a small number of mutations can convert receptor specificity of a non-strigolactone receptor, KAI2, into a receptor that recognizes the plant hormone strigolactone.

- Qin L, Liu L, Tu J, Yang G, Wang S, Quilichini TD, Gao P, Wang H, Peng G, Blancaflor EB, Datla R, Xiang D, Wilson KE, Wei Y. The ARP2/3 complex, acting cooperatively with Class I formins, modulates penetration resistance in Arabidopsis against powdery mildew invasion. Plant Cell. 2021 Sep 24;33(9):3151-3175. doi: 10.1093/plcell/koab170. PMID: 34181022

  The paper outlines how the ARP2/3 complex and formins have a cooperative role in contributing to Arabidopsis penetration resistance to fungal invasion.

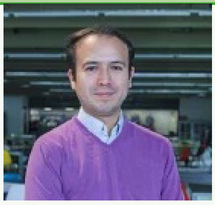
- Song Y, Wilson AJ, Zhang XC, Thoms D, Sohrabi R, Song S, Geissmann Q, Liu Y, Walgren L, He SY, Haney CH. FERONIA restricts Pseudomonas in the rhizosphere microbiome via regulation of reactive oxygen species. Nat Plants. 2021 May;7(5):644-654. doi: 10.1038/s41477-021-00914-0. Epub 2021 May 10.PMID: 33972713

  This paper shows that FER-mediated ROS production influences the levels of beneficial pseudomonads in the rhizosphere microbiome.

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)

Chile



Adrian A. Moreno

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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- Dussarrat T, Prigent S, Latorre C, Bernillon S, Flandin A, Díaz FP, Cassan C, Van Delft P, Jacob D, Varala K, Joubes J, Gibon Y, Rolin D, Gutiérrez RA, Pétriacq P. Predictive metabolomics of multiple Atacama plant species unveils a core set of generic metabolites for extreme climate resilience. New Phytol. 2022 Jun;234(5):1614-1628. doi: 10.1111/nph.18095.

  A dataset and protocol for metabolomic analysis from plant adapted to the driest desert of the world. (https://nph.onlinelibrary.wiley.com/doi/10.1111/nph.18095)

- Eshel G, Araus V, Undurraga S, Soto DC, Moraga C, Montecinos A, Moyano T, Maldonado J, Díaz FP, Varala K, Nelson CW, Contreras-López O, Pal-Gabor H, Kraiser T, Carrasco-Puga G, Nilo-Poyanco R, Zegar CM, Orellana A, Montecino M, Maass A, Allende ML, DeSalle R, Stevenson DW, González M, Latorre C, Coruzzi GM, Gutiérrez RA. Plant ecological genomics at the limits of life in the Atacama Desert. Proc Natl Acad Sci U S A. 2021 Nov 16;118(46):e2101177118. doi: 10.1073/pnas.2101177118.

  Transcriptomic and microbiome datasets from plants and its microbiome adapted to the driest desert of the world. (https://www.pnas.org/doi/full/10.1073/pnas.2101177118)

Planned events for 2022 and 2023

- XIV Annual Meeting of Chilean Society of Plant Biologists (CSPB), December 5, 6 & 7, 2022; Hotel Enjoy, La Serena, Chile

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

Selected Publications

- Eshel G, Araus V, Undurraga S, Soto DC, Moraga C, Montecinos A, Moyano T, Maldonado J, Díaz FP, Varala K, Nelson CW, Contreras-López O, Pal-Gabor H, Kraiser T, Carrasco-Puga G, Nilo-Poyanco R, Zegar CM, Orellana A, Montecino M, Maass A, Allende ML, DeSalle R, Stevenson DW, González M, Latorre C, Coruzzi GM, Gutiérrez RA. Plant ecological genomics at the limits of life in the Atacama Desert. Proc Natl Acad Sci U S A. 2021 Nov 16;118(46):e2101177118. doi: 10.1073/pnas.2101177118. (https://www.pnas.org/doi/full/10.1073/pnas.2101177118)

- 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. (https://www.mdpi.com/2076-2607/10/4/707)

  This research describes the characterization of a newly discovered plant pathogen strain and its possible virulence mechanisms.

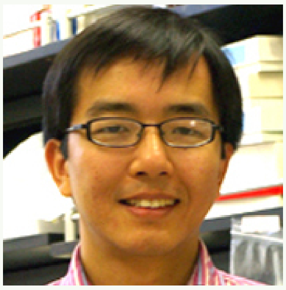
Major Funding Sources

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

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

- CORFO - Corporación de Fomento de la Producción
  (https://www.corfo.cl/)

China



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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022

- PmiREN2.0: Plant microRNA database
  https://pmiren.com/

- EXPLICIT: An Arabidopsis expression predictor
  https://github.com/mashisonglab/explicit

- Col-PEK: A near-complete assembly of Col-0
  http://col-pek.arashare.cn/

- GreenCircRNA: plant circRNA database
  http://greencirc.cn

- AtMAD: Arabidopsis multi-omics association database
  http://www.megabionet.org/atmad

- PlantPhoneDB: a pan-plant database comprising high-confidence ligand-receptor pairs
  https://jasonxu.shinyapps.io/PlantPhoneDB/

Planned events for 2022 and 2023

- 2021 National Congress of Plant Biology, October 11-14, 2021, Xi'an, Shaanxi (http://ncpb.net/)

- The First National Conference on Frontiers in Plant Science, July 18-21, 2022, Nanjing, Jiangsu (https://sps1.casconf.cn)

- 2022 National Congress of Plant Biology, September 16-20, 2022, Lanzhou, Gansu (http://ncpb.net/)

- CSPB 2022 Meeting, September 27-30, 2022, Xiamen, Fujian (https://www.cspb.org.cn/2022/)

Selected Publications

- Fu L, Liu Y, Qin G, Wu P, Zi H, Xu Z, Zhao X, Wang Y, Li Y, Yang S, Peng C, Wong CCL, Yoo SD, Zuo Z, Liu R, Cho YH, Xiong Y. (2021) The TOR-EIN2 axis mediates nuclear signalling to modulate plant growth. Nature 591(7849):288-292. https://doi.org/10.1038/s41586-021-03310-y

  This study shows that TOR, a master regulator of cell proliferation and growth, directly phosphorylates EIN2 to prevent its nuclear localization and subsequent ethylene siganlling.

- Yu X, Zhang X, Zhao P, Peng X, Chen H, Bleckmann A, Bazhenova A, Shi C, Dresselhaus T, Sun MX. (2021) Fertilized egg cells secrete endopeptidases to avoid polytubey. Nature 592(7854):433-437. DOI: 10.1038/s41586-021-03387-5

By identifying two aspartic endopeptidases, this study explains how plant egg cells regulate the rejection of extra tubes after successful fertilization.

- Bi G, Su M, Li N, Liang Y, Dang S, Xu J, Hu M, Wang J, Zou M, Deng Y, Li Q, Huang S, Li J, Chai J, He K, Chen YH, Zhou JM. (2021) The ZAR1 resistosome is a calcium-permeable channel triggering plant immune signaling. Cell 184(13):3528-3541.e12. DOI: 10.1016/j.cell.2021.05.003

  This study shows that ZAR1 resistosome is a calciumpermeable channel that triggers immune signaling and cell death in plants.

- Wang Q, Xue Y, Zhang L, Zhong Z, Feng S, Wang C, Xiao L, Yang Z, Harris CJ, Wu Z, Zhai J, Yang M, Li S, Jacobsen SE, Du J. (2021) Mechanism of siRNA production by a plant Dicer-RNA complex in dicing-competent conformation. Science 374(6571):1152-1157. DOI: 10.1126/science.abl4546

  By solving the structure of DCL3, this study explicitly shows how DCL3 recognizes a pre-small siRNA.

- Huang K, Wu XX, Fang CL, Xu ZG, Zhang HW, Gao J, Zhou CM, You LL, Gu ZX, Mu WH, Feng Y, Wang JW, Zhang Y. (2021) Pol IV and RDR2: A two-RNA-polymerase machine that produces double-stranded RNA. Science 374(6575):1579-1586. https://doi.org/10.1126/science.abj9184

  This study determined the cryo-electron microscopy structure of the Pol IV-RDR2 complex, which is responsible for the production of double-stranded precursors of siRNA.

Major Funding Sources

- National Natural Science Foundation (NSFC) (http://www.nsfc.gov.cn/publish/portal1/)

Czech Republic

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Planned events for 2022 and 2023

- 26th ICSPR Plant Reproduction conference June 20-24, 2022, at Prague (Czech Republic)
- 7th European Workshop on Plant Chromatin 2022 (EWPC 2022), Průhonice, Prague, Date: 18.05.2022 - 20.05.2022

Selected Publications

- Kolářová, K., Nešpor Dadejová, M., Loja, T., Lochmanová, G., Sýkorová, E., & Dvořáčková, M. (2021). Disruption of NAP1 genes in Arabidopsis thaliana suppresses the fas1 mutant phenotype, enhances genome stability and changes chromatin compaction. The Plant Journal 106(1), 56–73. https://doi.org/10.1111/tpj.15145

  NAP1 proteins play an essential role in DNA repair in fas1 mutant, which is coupled to nucleosome assembly through modulation of H3 levels in the nucleus.

- Samakovli, D., Tichá, T., Vavrdová, T., Závorková, N., Pecinka, A., Ovečka, M., & Šamaj, J. (2021). HEAT SHOCK PROTEIN 90 proteins and YODA regulate main body axis formation during early embryogenesis. Plant Physiology, 186(3), 1526–1544. https://doi.org/10.1093/plphys/kiab171

  HSP90s together with YDA signaling cascade affect transcriptional networks shaping the early embryo development.

- Serre, N., Kralík, D., Yun, P., Slouka, Z., Shabala, S., & Fendrych, M. (2021). AFB1 controls rapid auxin signalling through membrane depolarization in Arabidopsis thaliana root. Nature Plants, 7(9), 1229–1238. https://doi.org/10.1038/s41477-021-00969-z

  Rapid auxin-induced membrane depolarization tightly correlates with rapid root growth inhibition and both require the AFB1 auxin co-receptor which is essential for the rapid formation of the membrane depolarization gradient across the gravistimulated root.

- Synek, L., Pleskot, R., Sekereš, J., Serrano, N., Vukašinović, N., Ortmannová, J., Klejchová, M., Pejchar, P., Batystová, K., Gutkowska, M., Janková-Drdová, E., Marković, V., Pečenková, T., Šantrůček, J., Žárský, V., & Potocký, M. (2021). Plasma membrane phospholipid signature recruits the plant exocyst complex via the EXO70A1 subunit. Proceedings of the National Academy of Sciences of the United States of America, 118(36), e2105287118. https://doi.org/10.1073/pnas.2105287118

  Plant-specific features of the exocyst complex are described and the importance of the specific protein-lipid code for the recruitment of peripheral membrane proteins demonstrated.

- Yang, F., Fernández-Jiménez, N., Tučková, M., Vrána, J., Cápal, P., Díaz, M., Pradillo, M., & Pecinka, A. (2021). Defects in meiotic chromosome segregation lead to unreduced male gametes in Arabidopsis SMC5/6 complex mutants. The Plant cell, 33(9), 3104–3119. https://doi.org/10.1093/plcell/koab178

  Mutants for several Arabidopsis (Arabidopsis thaliana) SMC5/6 complex subunits produce triploid offspring due to a meiotic defect leading to the production of unreduced male gametes linked with an absence of chromosome segregation during the first and/or the second meiotic division, as well as a partially disorganized microtubule network.

Major Funding Sources

Both major funding agencies for basic research - Czech Science Foundation (GACR) and Ministry of Education of CR (MSMT CR) - support regularly projects based on the use of Arabidopsis as a model plant.

- Czech Science Foundation/GAČR, Prague (http://www.gacr.cz)

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

  Both institutions support also bilateral projects with selected countries.

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

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

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

Denmark

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Selected Publications

- Hunziker P, Lambertz SK, Weber K, Crocoll C, Halkier BA, Schulz A. Herbivore feeding preference corroborates optimal defense theory for specialized metabolites within plants. Proc Natl Acad Sci U S A. 2021 118:e2111977118. doi: 10.1073/pnas.2111977118.

  This study tests the optimal defense theory according to which plant defenses are concentrated at the highest level in tissues and in organs that are the most valuable for survival and fitness.

- Arribas-Hernández L, Rennie S, Köster T, Porcelli C, Lewinski M, Staiger D, Andersson R, Brodersen P. Principles of mRNA targeting via the Arabidopsis m6A-binding protein ECT2. Elife. 2021 10:e72375. doi: 10.7554/eLife.72375.

  This work helps explaining how proteins recognize, bind and regulate methylated RNA in plants.

- Bavnhøj L, Paulsen PA, Flores-Canales JC, Schiøtt B, Pedersen BP. Molecular mechanism of sugar transport in plants unveiled by structures of glucose/H+ symporter STP10. Nat Plants. 2021 7: 1409-1419. doi: 10.1038/s41477-021-00992-0.

  This work solves structures of a monosaccharide transporter that represent glucose- and proton-bound states and address the molecular mechanism of glucose import by sugar transport proteins.

- Lilay GH, Persson DP, Castro PH, Liao F, Alexander RD, Aarts MGM, Assunção AGL. Arabidopsis bZIP19 and bZIP23 act as zinc sensors to control plant zinc status. Nat Plants. 2021 7:137-143. doi: 10.1038/s41477-021-00856-7.

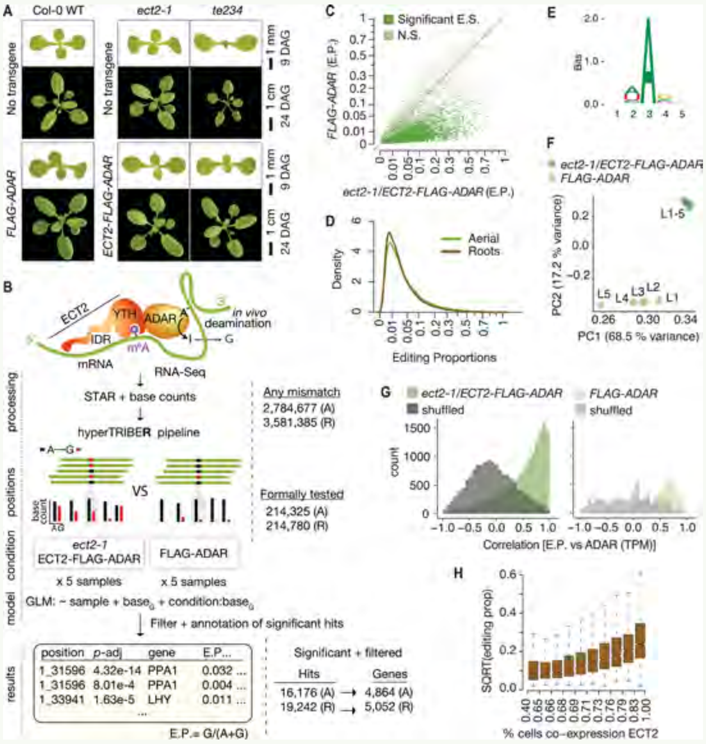
  This study identifies F-group bZIP transcription factors bZIP19 and bZIP23, which are the central regulators of the Zn deficiency response, as Zn sensors.

- Schneider R, Klooster KV, Picard KL, van der Gucht J, Demura T, Janson M, Sampathkumar A, Deinum EE, Ketelaar T, Persson S. Long-term single-cell imaging and simulations of microtubules reveal principles behind wall patterning during proto-xylem development. Nat Commun. 2021 12:669. doi: 10.1038/s41467-021-20894-1.

  This study provides new insight into how microtubules are re-arranged to sustain cell wall patterning.

Major Funding Sources

- Villum Foundation
- Novo Nordisk Foundation
- Carlsberg Foundation



position	p-adj	gene	E.P...
1_31596	4.32e-14	PPA1	0.032 ...
1_31596	8.01e-4	PPA1	0.004 ...
1_33941	1.63e-5	LHY	0.011 ...
...			

Figure 1: ‘‘Drosophila ADARcd fused to ECT2 can edit target mRNAs in vivo in plants’’. Arribas-Hernández et al, 2021. *Elife*. doi.org/10.7554/eLife.72375

Finland

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Selected Publications

- Ye L, Wang X, Lyu M, Siligato R, Eswaran G, Vainio L, Blomster T, Zhang J, Mähönen AP. (2021) Cytokinins initiate secondary growth in the Arabidopsis root through a set of LBD genes Current Biology 31, 3365-3373.e7. https://doi.org/10.1016/j.cub.2021.05.036

  Cytokinin induces the expression of four LBD transcription factors to initiate and maintain secondary growth in Arabidopsis thaliana root.

- Roszak P, Heo JO, Blob B, Toyokura K, Sugiyama Y, de Luis Balaguer MA, Lau WWY, Hamey F, Cirrone J, Madej E, Bouatta AM, Wang X, Guichard M, Ursache R, Tavares H, Verstaen K, Wendrich J, Melnyk CW, Oda Y, Shasha D, Ahnert SE, Saeys Y, De Rybel B, Heidstra R, Scheres B, Grossmann G, Mähönen AP, Denninger P, Göttgens B, Sozzani R, Birnbaum KD, Helariutta Y. (2021) Cell-by-cell dissection of phloem development links a maturation gradient to cell specialization. Science. 2021 374(6575). https://doi.org/10.1126/science.aba5531

  Combining single cell transcriptome analysis and molecular genetics with live cell imaging, phloem differentiation from stem cell to mature sieve element was dissected in detail.

- Gollan PJ, Trotta A, Bajwa AA, Mancini I, Aro E-M. (2021) Characterization of the Free and Membrane-Associated Fractions of the Thylakoid Lumen Proteome in Arabidopsis thaliana. Int. J. Mol. Sci. 2021, 22(8126). doi: 10.3390/ijms22158126

  Novel chloroplast lumenal proteins, including a new PsbP domain-containing isoform, as well as several novel post-translational modifications and N-termini, are reported.

- Grabsztunowicz M, Rantala M, Ivanauskaite I, Blomster T, Koskela MM, Vuorinen K, Tyystjärvi E, Burow M, Overmyer K, Mähönen AP, Mulo P. (2021) Root-type ferredoxin-NADP+ oxidoreductase isoforms in Arabidopsis thaliana: Expression patterns, location and stress responses. Plant Cell Environ. 44(2):548-558. https://doi.org/10.1111/pce.13932

  Spatial and temporal analysis of RFNR1 and RFNR2 gene expression revealed differential accumulation of the isoforms under various stresses implying that the RFNRs have redundant, but essential roles in Arabidopsis metabolism.

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

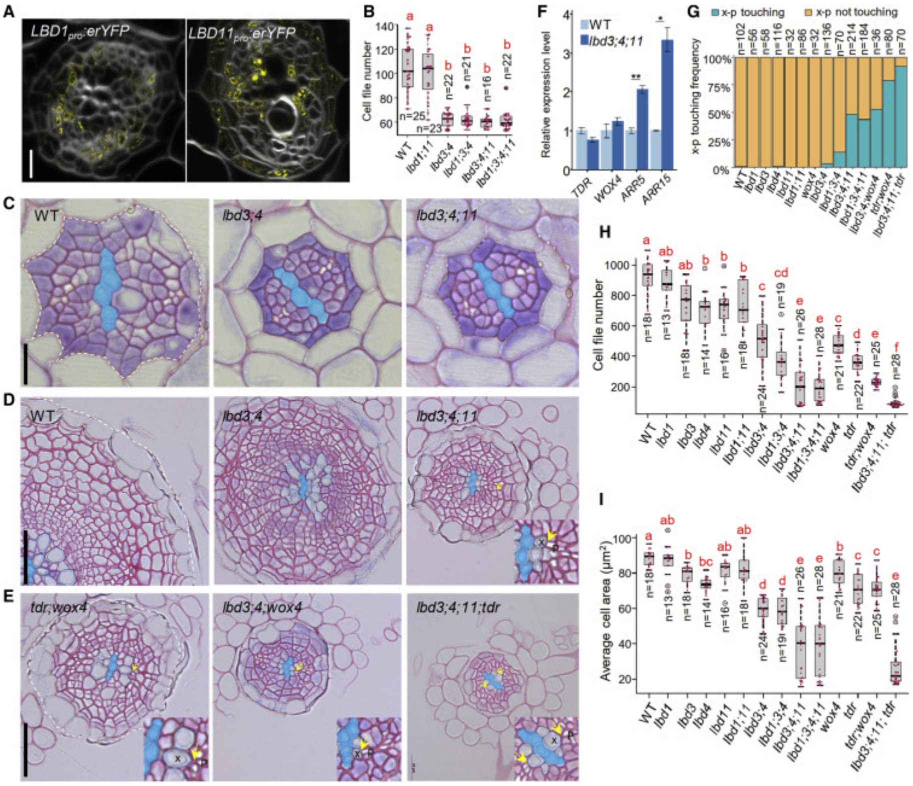
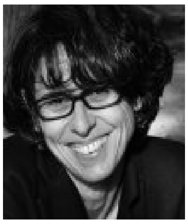


Figure 3: ‘‘LBDs redundantly promote cambium stem cell maintenance together with TDR and WOX4’’. Ye et al, 2021. *Current Biology*. https://doi.org/10.1016/j.cub.2021.05.036

France



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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- 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 2022 and 2023

- 13th International Conference of the French Society of Plant Biology - August 29-31 2022
- Summer School on Plant cell walls in development, plant-microbe interactions and for the bio-economy June 19-25, 2022 – Versailles (France)
- Summer School on Plant sugar metabolism, transport and signaling in a challenging environment, July 3-8, 2022 – Saint-Lambert-des-Bois (France)
- Summer School on Biological interactions from genes to ecosystems" will take place from July 2 to 8, 2022, the TULIP 10th International summer schoom
- 10th International Plant Biomechanics Conference – 21-26 Août 2022, Lyon – France
- From genes to plant architecture: the shoot apical meristem in all its states – 28-30 november, Poitiers (France)
- Symposium on redox regulation and carbon-nitrogen interactions in plants. A tribute to Pierre Gadal, June 20, 2022

Selected Publications

- Azpeitia E, Tichtinsky G, Le Masson M, Serrano-Mislata A, Lucas J, Gregis V, Gimenez C, Prunet N, Farcot E, Kater MM, Bradley D, Madueño F, Godin C, Parcy F. Cauliflower fractal forms arise from perturbations of floral gene networks, Science. 2021 Jul 9;373(6551):192-197. doi: 10.1126/science.abg5999.

- Truskina J, Han J, Chrysanthou E, Galvan-Ampudia CS, Lainé S, Brunoud G, Macé J, Bellows S, Legrand J, Bågman AM, Smit ME, Smetana O, Stigliani A, Porco S, Bennett MJ, Mähönen AP, Parcy F, Farcot E, Roudier F, Brady SM, Bishopp A, Vernoux T. A network of transcriptional repressors modulates auxin responses, Nature. 2021 Jan;589(7840):116-119. doi: 10.1038/s41586-020-2940-2

- Hani S, Cuyas L, David P, Secco D, Whelan J, Thibaud MC, Merret R, Mueller F, Pochon N, Javot H, Faklaris O, Maréchal E, Bertrand E, Nussaume L. Live single-cell transcriptional dynamics via RNA labelling during the phosphate response in plants, Nat Plants, 2021 Aug;7(8):1050-1064., doi: 10.1038/s41477-021-00981-3.

- Doumane M, Lebecq A, Colin L, Fangain A, Stevens FD, Bareille J, Hamant O, Belkhadir Y, Munnik T, Jaillais Y, Caillaud MC. Inducible depletion of PI(4,5)P-2 by the synthetic iDePP system in Arabidopsis, Nat Plants, 2021 May;7(5):587-597, doi: 10.1038/s41477-021-00907-z

- Hacquard T, Clavel M, Baldrich P, Lechner E, Pérez-Salamó I, Schepetilnikov M, Derrien B, Dubois M, Hammann P, Kuhn L, Brun D, Bouteiller N, Baumberger N, Vaucheret H, Meyers BC, Genschik P. The Arabidopsis F-box protein FBW2 targets AGO1 for degradation to prevent spurious loading of illegitimate small RNA, Cell Reports, 2022 Apr 12;39(2):110671, doi: 10.1016/j.celrep.2022.110671

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. In 2020, the overall score of funding was around 17% of the submitted ANR projects

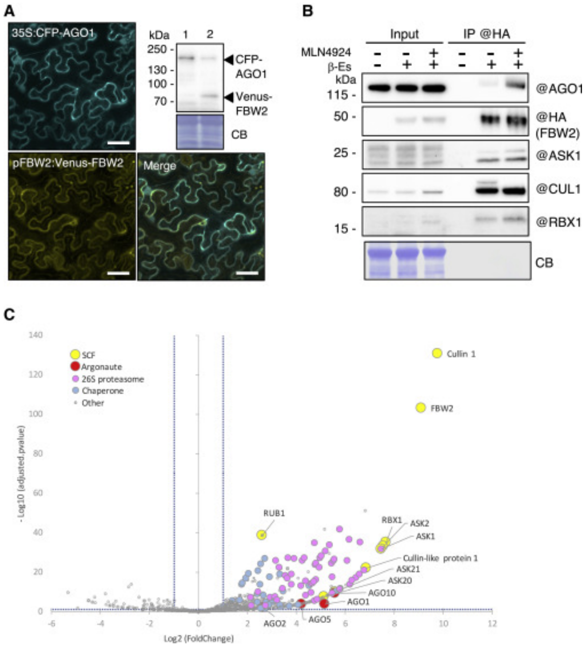

Figure 2: ‘‘FBW2 assembles an SCF complex and interacts with AGO1 in planta’’. Hacquard et al 2022, *Cell Reports*. doi: 10.1016/j.celrep.2022.110671

Greece

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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- 2 Aralab cabinets equipped with SPIRO automated imaging platform
- Arabidopsis Co-expression Tool (ACT): A gene co-expression analysis web tool for Arabidopsis thaliana, identifies genes which are correlated to a driver gene. ACT is freely available at www.michalopoulos.net/act

Planned events for 2022 and 2023

- EMBO Workshop: Dying in self-defense: Cell death signaling in animals and plants
  May 01–05, 2022 | Crete, Greece
  https://meetings.embo.org/event/21-cell-death
- PLANT CELL BIOLOGY INTERNATIONAL
  August 01-05, 2022| Crete, Greece
  http://plantcellbiologyinternational.org/
- EMBO Workshop: Membrane transporters as essential elements of cellular function and homeostasis
  August 23-27, 2022| Chania, Greece
  https://meetings.embo.org/event/21-membrane-transporters
- The XVII International Conference on the Plant Family of Solanaceae (SOL2022)
  November 01-05, 2022| Thessaloniki, Greece
  https://sol2022.web.auth.gr/
- 20th National conference on plant pathology
  October 03-06, 2022| Thessaloniki, Greece
  https://20.phytopath.gr/

Selected Publications

- Zogopoulos VL, Saxami G, Malatras A, Angelopoulou A, Jen CH, Duddy WJ, Daras G, Hatzopoulos P, Westhead DR, Michalopoulos I. Arabidopsis Coexpression Tool: a tool for gene coexpression analysis in Arabidopsis thaliana. iScience (2021) 24:102848. doi: 10.1016/j.isci.2021.102848.

An Arabidopsis Co-expression Tool (ACT) was developed to present subclades of co-expressed genes, as well as to perform gene set enrichment analysis, being unique in revealing enriched transcription factors targeting co-expressed genes.

- Poulios S, Dadarou D, Gavriilidis M, Mougiou N, Kargios N, Maliori V, Hark AT, Doonan JH, Vlachonasios KE. The Transcriptional Adaptor Protein ADA3a Modulates Flowering of Arabidopsis thaliana. Cells (2021) 10:904. doi: 10.3390/cells10040904.

  This research article presents the biological role of a component of the SAGA complex, ADA3a, in the flowering mechanisms of Arabidopsis thaliana.

- Beris D, Podia V, Dervisi I, Kapolas G, Isaioglou I, Tsamadou V, Pikoula L, Rovoli M, Vallianou A, Roussis A, Milioni D, Giannoutsou H, Haralampidis K. RNAi silencing of the Arabidopsis thaliana ULCS1 gene results in pleiotropic phenotypes during plant growth and development. Int J Dev Biol. (2021) Aug 9. doi: 10.1387/ijdb.210114kh.

  RNAi-mediated downregulation of ULCS1, encoding a WD40-repeat-containing protein, results in a fast-growing phenotype during vegetative development, increased number of mitotic cell divisions and significant differences at the cell walls and the mucilage of the seeds. ULCS1 interacts with the UBA-like protein.

- Konkina A, Klepadlo M, Lakehal A, Zein ZE, Krokida A, Botros M, Iakovidis M, Chernobavskiy P, Elfatih Zerroumda M, Tsanakas G, Petrakis N, Dourou A-M and Kalaitzis P. An Arabidopsis Prolyl 4 Hydroxylase Is Involved in the Low Oxygen Response. Front. Plant Sci. (2021) 12:637352. doi: 10.3389/fpls.2021.637352

  A T-DNA knock out mutant of AtP4H3 prolyl 4 hydroxylase gene supports the involvement of proline hydroxylation, a post-translational modification, to low oxygen response in Arabidopsis.

- Templalexis D, Tsitsekian D, Liu C, Daras G, Šimura J, Moschou P, Ljung K, Hatzopoulos P, Rigas S. Potassium transporter TRH1/KUP4 contributes to distinct auxin-mediated root system architecture responses. Plant Physiol. (2022) 188:1043-1060. doi: 10.1093/plphys/kiab472.

  TINY ROOT HAIR 1 (TRH1), a member of plant high-affinity potassium (K+) transporters (HAK/KUP/KT), controls root gravitropism in the central cylinder and root hair development in root peripheral cell layers, including epidermis and cortex.

Major Funding Sources

- The Hellenic Foundation for Research and Innovation (H.F.R.I.)
- Greece and the European Union (European Social Fund) through the Operational Program «Human Resources Development, Education and Lifelong Learning 2014–2020» and the Program encoded EDBM103
- 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)

India

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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

Arabidopsis labs have generated mutants and genetic resources related to plant development, metabolism, biotic and abiotic stress tolerance. Various databases have been developed

- tncRNAdb: Plant transfer RNA-derived non-coding RNAs (tncRNAs) database (https://nipgr.ac.in/PtncRNAdb)
- 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)
- tncRNA: A pipeline for the identification of tRNA-derived small ncRNAs (tncRNAs) from high throughput sequencing data (http://www.nipgr.ac.in/tncRNA)
- PlantPepDB: A database of plant peptides having different functions and therapeutic activities (http://www.nipgr.ac.in/PlantPepDB/)
- PtRNAdb: A database containing information of tRNA genes (http://www.nipgr.ac.in/PtRNAdb/)
- AtFusionDB: A Database of Fusion Transcripts in Arabidopsis thaliana (http://www.nipgr.ac.in/AtFusionDB/)
- PtRFdb: Plant transfer RNA-derived fragments database (http://www.nipgr.ac.in/PtRFdb/)
- A simple, low-cost, high-throughput strategy for the rapid and easy bacterial infection of large numbers of Arabidopsis plants was demonstrated. Choudhary A, Senthil-Kumar M. An efficient, high-throughput method for the simultaneous exposure of drought stress and bacterial infection in plants. Appl Plant Sci. 2020 Dec 1;8(11): e11399. doi: 10.1002/aps3.11399.

Planned events for 2022 and 2023

- Plant Physiology Conference and Chemical Ecology Meetings are planned for 2022-23

Selected Publications

- Challa KR, Rath M, Sharma AN, Bajpai AK, Davuluri S, Acharya KK, Nath U. (2021) Active suppression of leaflet emergence as a mechanism of simple leaf development. Nature Plants. Sep;7(9):1264-1275. doi: 10.1038/s41477-021-00965-3.

  The study reports that CIN-TCP-KNOXII proteins downregulate KNOX-I and CUC genes to suppress leaflet initiation in simple leaves.

- Jamsheer KM, Jindal S, Sharma M, Sharma M, Sivaj S, Mannully CT, Laxmi A (2022) A negative feedback loop of the TOR signaling moderates growth and enables rapid sensing of stress signals in plants. Cell Reports. 5; 39 (1):110631. DOI: 10.1016/j.celrep.2022.110631

  Plant specific negative feedback regulator of TOR kinase has been deciphered. This negative feedback loop moderates the TOR-growth signaling axis in the favorable condition and helps in the activation of stress signaling in unfavorable conditions, establishing its importance in the adaptability of plants.

- Job N, Datta S. (2021) PIF3-HY5 module regulates BBX11 to suppress protochlorophyllide levels in dark and promote photomorphogenesis in light. New Phytologist. 230(1):190-204. https://doi.org/10.1111/nph.17149

  PIF3 directly binds to the promoter of BBX11 and represses its expression to regulate protochlorophyllide levels in the dark, whereas in light HY5 activates BBX11 expression to promote photomorphogenesis.

- Devi, L.L., Pandey, A., Gupta, S., Singh, A.P. (2022) The interplay of auxin and brassinosteroid signaling tunes root growth under low and different nitrogen forms. Plant Physiology. https://doi.org/10.1093/PLPHYS/KIAC157

  In this article, authors describe that auxin and brassinosteroid signaling underlie adaptive root growth under low nitrogen (N) and different N forms (nitrate and ammonium)

- Kanwar P, Sanyal SK, Mahiwal S, Ravi B, Kaur K, Fernandes JL, Yadav AK, Tokas I, Srivastava AK, Suprasanna P, Pandey GK (2021) CIPK9 targets VDAC3 and modulates oxidative stress responses in Arabidopsis. Plant Journal. 109(1):241-260 doi: 10.1111/tpj.15572

  CIPK9 is involved with the outer membrane mitochondrial channel VDAC3 in mediating the oxidative stress responses in the plant and CIPK9-VDAC3 module is identified as a probable signalling mediator of ROS and Ca2+ signalling pathway in plants.

Major Funding Sources

- Department of Biotechnology (DBT), Government of India http://dbtindia.nic.in/index.asp
- Science and Engineering Research Board (SERB), India http://www.serbonline.in/
- 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) http://www.serbonline.in/

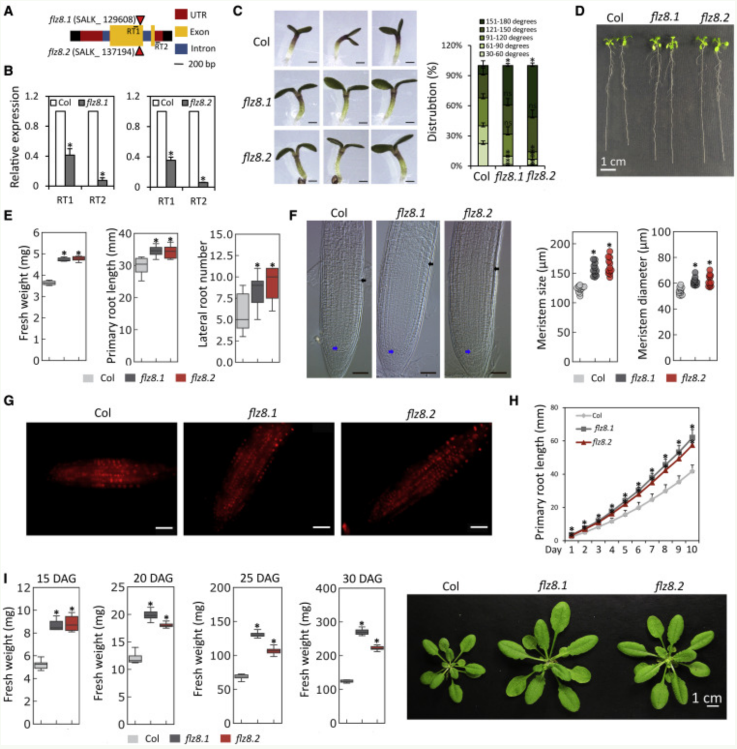

Figure 3. ‘‘Meristem activity and growth are enhanced in *flz8* mutants’’. Jamsheer et al, 2022. *Cell Reports*. https://doi.org/10.1016/j.celrep.2022.110631

Ireland

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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- Barros, K.A., Inaba, M., Martins, A.O. and Sulpice, R., 2022. High-Throughput Extraction and Enzymatic Determination of Sugars and Fructans in Fructan-Accumulating Plants. In Plant Circadian Networks (pp. 107-119). Humana, New York, NY. DOI: 10.1007/978-1-0716-1912-4_10

Selected Publications

- 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 Reproduction. 2022 Mar 5:1-6. DOI: 10.1007/s00497-022-00440-9

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

- Lopez, F.B., Fort, A., Tadini, L., Probst, A.V., Mchale, M., Friel, J., Ryder, P., Pontvianne, F., Pesaresi, P., Sulpice, R. Mckeown, P., Brychkova, G and Spillane C. 2021. Gene dosage compensation of rRNA transcript levels in Arabidopsis thaliana lines with reduced ribosomal gene copy number. The Plant Cell, 33(4), pp.1135-1150. https://doi.org/10.1093/plcell/koab020

- Belton S, McCabe PF, Ng CK. The cyanobacterium, Nostoc punctiforme can protect against programmed cell death and induce defence genes in Arabidopsis thaliana. Journal of Plant Interactions. 2021 Jan 1;16(1):64-74. https://doi.org/10.1080/17429145.2021.1891306

- Kwaśniewska, K., Breathnach, C., Fitzsimons, C., Goslin, K., Thomson, B., Beegan, J., Finocchio, A., Prunet, N., Ó'Maoiléidigh, D.S. and Wellmer, F., 2021. Expression of KNUCKLES in the stem cell domain is required for its function in the control of floral meristem activity in arabidopsis. Frontiers in Plant Science, p.1479. DOI: 10.3389/fpls.2021.704351

Major Funding Sources

- Science Foundation Ireland

- Irish Research Council

Italy

Alice Pajoro

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Planned events for 2022 and 2023

Congress:

- Riunione annuale dei Gruppi di Lavoro SBI. Biologia Cellulare e Molecolare. Biotecnologie e Differenziamento. Rome June 2022.
- Plant-based approaches to clean up contaminated environments. Summer School. Bicocca University. Milano July 2022.
- 14th International Conference on Plant Pathogenic Bacteria. Assisi (Italy) 3-8 July, 2022
- Plant Calcium Signaling Conference, Milano, July 11th – 13th, 2022
- XVII FISV Congress – Portici (Naples), September 14-16, 2022
- LXIV SIGA Annual Congress From genes to fork – On Mendel's footsteps, Piacenza, 6 – 9 September 2022.
- Botanical Society conference 2022 (Bologna, Settembre 2022).

Outreach event:

- Fascination of Plants Day 2022 18th May 2022 info.2022@plantday.it

Webinar:

- Virtual Club SIBV - Webinar series http://www.sibv.eu/congressi-ed-eventi/virtual-club-sibv

Selected Publications

- Coordination of biradial-to-radial symmetry and tissue polarity by HD-ZIP II proteins. Carabelli M, Turchi L, Morelli G, Ostergaard L, Ruberti I, Moubayidin L. Nature Communications 12, 4321 (2021). https://doi.org/10.1038/s41467-021-24550-6

  The research article shows that the transcription factors of the HD-ZIP II class control the radialization of the style through auxin and cytokinin hormone balance

- Cucinotta M, Cavalleri A, Guazzotti A, Astori C, Manrique S, Bombarely A, Oliveto S, Biffo S, Weijers D, Kater MM, Colombo L. Alternative Splicing Generates a MONOPTEROS Isoform Required for Ovule Development. Curr Biol. 2021 Feb 22;31(4):892-899.e3. doi: 10.1016/j.cub.2020.11.026. Epub 2020 Dec 3. PMID: 33275890.

  In this work was identified a splice variant of Monopteros (MP) that encodes a biologically functional isoform that lacks the Aux/IAA interaction domain, describing a novel scenario in which MP post-transcriptional modification leads to the production of an isoform that can function as a transcriptional activator in regions of subthreshold auxin concentration.

- Lorenzo Brocca, Melania Zuccaro, Giovanna Frugis, Davide Mainieri, Claudia Marrano, Laura Ragni, Eva Maria Klein, Alessandro Vitale and Emanuela Pedrazzini. Two γ-zeins induce the unfolded protein response. Plant Physiology (2021) 187:1428–1444. doi: 10.1093/plphys/kiab367

  The evolution of seed storage proteins in grasses can be related to their increasing stress-inducing properties in the endoplasmic reticulum.

- Giovannoni, M., Lironi, D., Marti, L., Paparella, C., Vecchi, V., Gust, A. A., De Lorenzo, G., Nürnberger, T., Ferrari, S. (2021). The Arabidopsis thaliana LysM containing Receptor Like Kinase 2 is required for elicitor induced resistance to pathogens. Plant, Cell & Environment, 44(12), 3775-3792. https://doi.org/10.1111/pce.14192

  The research article shows that the LysM-containing Receptor-Like Kinases (LYKs) CERK1, LYK2 and LYK5 are dispensable for basal susceptibility to B. cinerea but are necessary for chitin-induced resistance to this pathogen

- Wang R, Himschoot E, Grenzi M, Chen J, Safi A, Krebs M, Schumacher K, Nowack MK, Van Damme D, De Smet I, Geelen D, Beeckman T, Friml J, Costa A*, Vanneste S*. (2021) 1-Naphtalene acetic acid-induced Ca2+ signaling is independent from its inhibition of endosomal aggregation. J Exp Bot. erac019, https://doi.org/10.1093/jxb/erac019.

  This work investigates the possible role of cytosolic Ca2+ in the inhibition of PINs endosomal recycling.

- Mattioli R, Pascarella G, D'Incà R, Cona A, Angelini R, Morea V, Tavladoraki P. (2022) Arabidopsis N-acetyltransferase activity 2 preferentially acetylates 1,3-diaminopropane and thialysine. Plant Physiol Biochem. 170, 123-132. https://doi.org/10.1016/j.plaphy.2021.11.034

  The research article shows substrate specificity, structural determinants and expression pattern of an Arabidopsis N-acetyltransferase.

Major Funding Sources

- Ministry of University and Research (MIUR) https://www.miur.gov.it/
  Program PRIN2017
  Program PRIN2020
- Ministry of Foreign Affairs
  Apomixis, a reproductive mechanism for genetic improvement (2020-2023)
- Regione Lazio http://www.lazioinnova.it/
  POR FERS 2014-2020 Lazio: SMART- BREED
  POR FERS 2014-2020 Lazio: Top of the crops
- Regione Lombardia
  POR FESR 2014-2020 Lombardia: sPATIALS3
- 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
- Ente Nazionale per l'Aviazione Civile https://www.enac.gov.it/
- Fondazione Cariplo (WAKE-APT)
- European Union Grants
  HORIZON-MSCA-2021-PF-01 (MSCA Postdoctoral Fellowships 2021)
  ERANET COFUND FOSC - C4C; CropsForChange: Tacking climate change in crops.

H2020-MSCA-RISE-2020. Mechanisms of Apomictic Developments.
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)

- National Companies
  Green HAS group https://www.greenhasgroup.com/

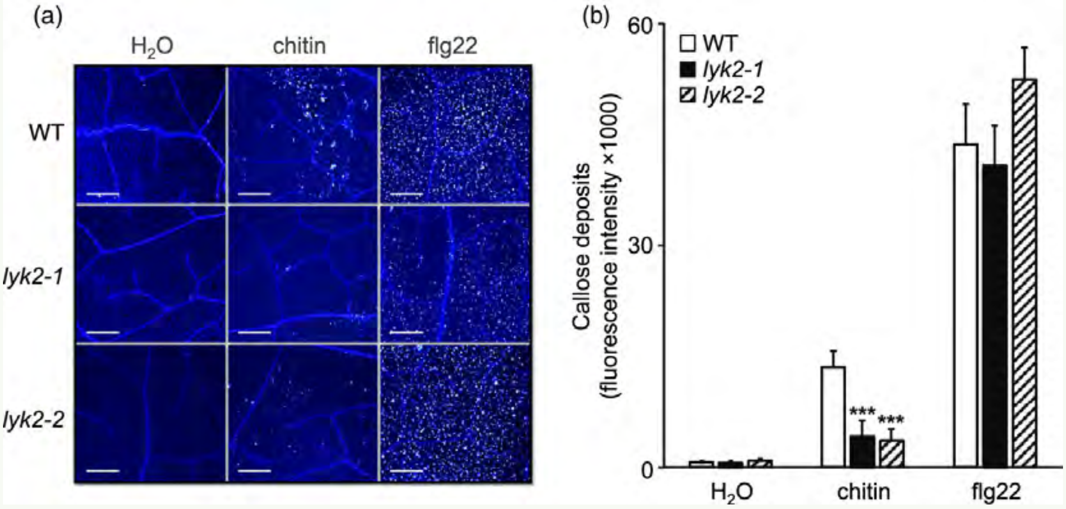

Figure 3: ‘‘Chitin-induced callose deposition is reduced in *lyk2* mutants’’. Giovannoni, Lironi et al 2021, *Plant, Cell and Environment*. https://doi.org/10.1111/pce.14192

Japan

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Masatomo Kobayashi

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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- 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/)
  Arabidopsis TF-GR (transcription factor-glucocorticoid receptor) line seeds are now available from RIKEN BRC (send your inquiry to plant.brc@riken.jp).
  We have added the information of 7,031 individual lines of Arabidopsis FOX (Full-length cDNA Over-eXpressing) to the Exp-Plant Catalog (https://plant.rtc.riken.jp/resource/fox/fox_list.htmlt).

- 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 (Gene annotation database for Chaetoceros gracilis) (https://chaetoceros.nibb.ac.jp/)

Planned events for 2022 and 2023

- Mar. 22-24, 2022: 63rd Annual Meeting of Japanese Society of Plant Physiologists (on line meeting). Tsukuba, Japan. (http://jspp.org/annualmeeting/63/e_greeting.php)
- Dec. 12-15, 2022: Cold Spring Harbor Asia Conference “Integrative Epigenetics in Plants”, Awaji Yumebutai Conference Center, Japan. (https://www.csh-asia.org/?content/1210)
- 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/).

Selected Publications

- Zhang Y, Mitsuda N, Yoshizumi T, Horii Y, Oshima Y, Ohme-Takagi M, Matsui M, Kakimoto T (2021) Two types of bHLH transcription factor determine the competence of the pericycle for lateral root initiation. Nature Plants 7: 633–643. https://doi.org/10.1038/s41477-021-00919-9

  Zhang et al. identified master transcriptional regulators that determine the competence of the pericycle for auxin-induced cell division and lateral root formation.

- Yamaguchi N, Matsubara S, Yoshimizu K, Seki M, Hamada K, Kamitani M, Kurita Y, Nomura Y, Nagashima K, Inagaki S, Suzuki T, Gan ES, To T, Kakutani T, Nagano AJ, Satake A, Ito T (2021) H3K27me3 demethylases alter HSP22 and HSP17.6C expression in response to recurring heat in Arabidopsis. Nature Commun. 12: 3480. https://doi.org/10.1038/s41467-021-23766-w

  Yamaguchi et al. show that plants adapt to repeated heat stress via an epigenetic memory mechanism, where JUMONJI proteins control small heat shock genes.

- Takahashi N, Inagaki S, Nishimura K, Sakakibara H, Antoniadi I, Karady M, Ljung K, Umeda M (2021) Alterations in hormonal signals spatially coordinate distinct responses to DNA double-strand breaks in Arabidopsis roots. Science Advances 7: eabg0993. https://doi.org/10.1126/sciadv.abg0993

  This paper shows that combinatorial control of two hormones auxin and cytokinin coordinates distinct DNA damage responses, representing an elegant strategy to maintain genome stability and ensure persistent organ growth under changing environments.

- Bao L, Inoue N, Ishikawa M, Gotoh E, The OK, Higa T, Morimoto T, Ginanjar EF, Harashima H, Noda N, Watahiki M, Hiwatashi Y, Sekine M, Hasebe M, Wada M, Fujita T (2021) A PSTAIRE-type cyclin-dependent kinase controls light responses in land plants. Science Advances 8: eabk2116. https://doi.org/10.1126/sciadv.abk2116

  Bao et al. demonstrated for the first time that PSTAIRE-type CDK kinase is dispensable in multicellular eukaryotes and regulates light responses, such as chloroplast movement, and phototropic and polarotropic responses, which is independent of the cell-cycle progression and likely conserved in land plants.

- Kim JS, Sakamoto Y, Takahashi F, Shibata M, Urano K, Matsunaga S, Yamaguchi-Shinozaki K, Shinozaki K (2022) Arabidopsis TBP-ASSOCIATED FACTOR 12 ortholog NOBIRO6 controls root elongation with unfolded protein response cofactor activity. Proc Natl Acad Sci U S A. 119(6): e2120219119. https://www.pnas.org/doi/10.1073/pnas.2120219119

  Kim et al. found that the transcription cofactor TBP-ASSOCIATED FACTOR 12b (TAF12b) is a key transcription factor acting in unfolded protein response in plant stress response and plant growth, especially root growth.

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)

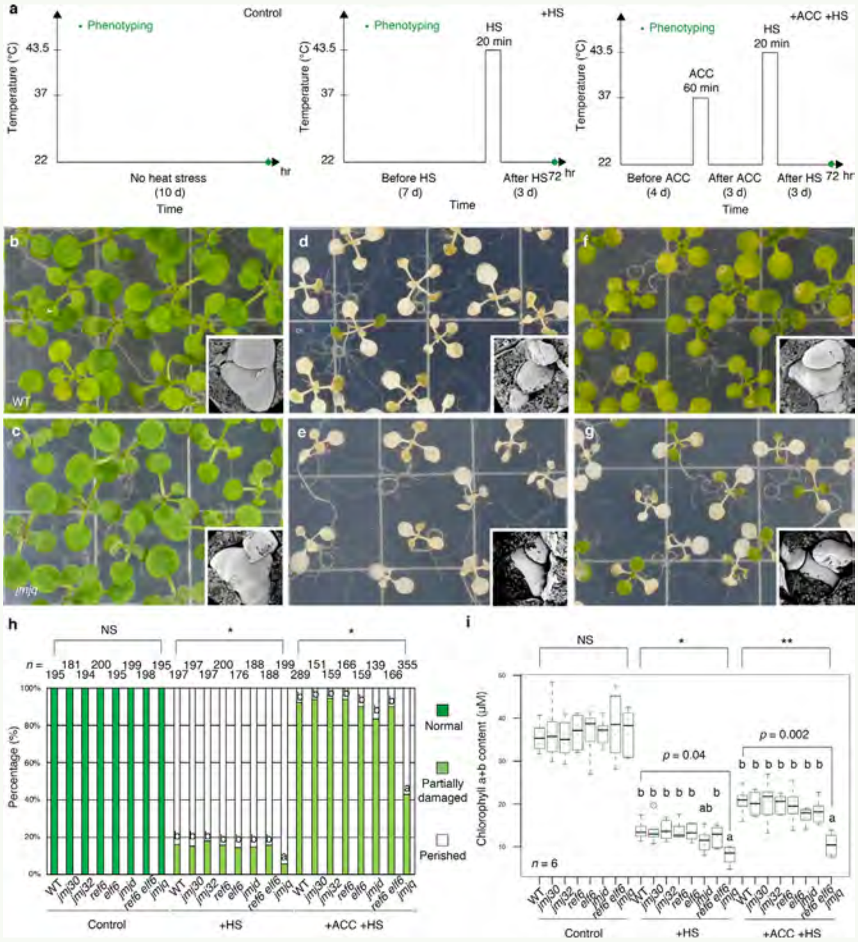

Figure 1: ‘‘H3K27me3 demethylase activity is required for acquired thermotolerance’’. Yamaguchi et al, 2021, *Nature Communications*. https://doi.org/10.1038/s41467-021-23766-w

New Zealand

Lynette Brownfield

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Planned events for 2022 and 2023

- International Congress on Photosynthesis Research July 31-August 5 2022. Dunedin, New Zealand (hybrid event)
- ComBio 2022 September 27-30 2022. Melbourne, Australia (includes the annual meeting for the New Zealand Society of Plant Biologists; in person)
- Plant Science Central July 2023, Massey University, Palmerston North, New Zealand

Selected Publications

- Xu, X., Jibran, R., Wang, Y., Dong, L., Flokova, K., Esfandiari, A., McLachlan, A. R. G., Heiser, A., Sutherland-Smith, A. J., Brummell, D. A., Bouwmeester, H. J., Dijkwel, P. P., & Hunter, D.A (2021) Strigolactones regulate sepal senescence in Arabidopsis, Journal of Experimental Botany, 72; 5462–5477 DOI: 10.1093/jxb/erab199

  The research led by scientists at Massey University (New Zealand) and The New Zealand Institute for Plant and Food Research Limited adds to the understanding the role of hormones play in plant senescence.

- Bulley, S.M.; Cooney, J.M.; Laing, W. (2021) Elevating ascorbate in Arabidopsis stimulates the production of abscisic acid, phaseic acid, and to a lesser extent auxin (IAA) and jasmonates, resulting in increased expression of DHAR1 and multiple transcription factors associated with abiotic stress tolerance. International Journal of Molecular Sciences, 22, 6743. DOI: 10.3390/ijms22136743

  This work from The New Zealand Institute for Plant and Food Research Limited provides further insights into how ascorbic acid can mediate increased abiotic stress tolerance.

- White D.W.R (2022) PEAPOD repressors modulate and coordinate developmental responses to light intensity in Arabidopsis. New Phytologist (online release: https://doi.org/10.1111/nph.18198)

  Research performed in New Zealand at Massey University to describe the possible role of the PPD1 and pPD2 in light signalling.

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)

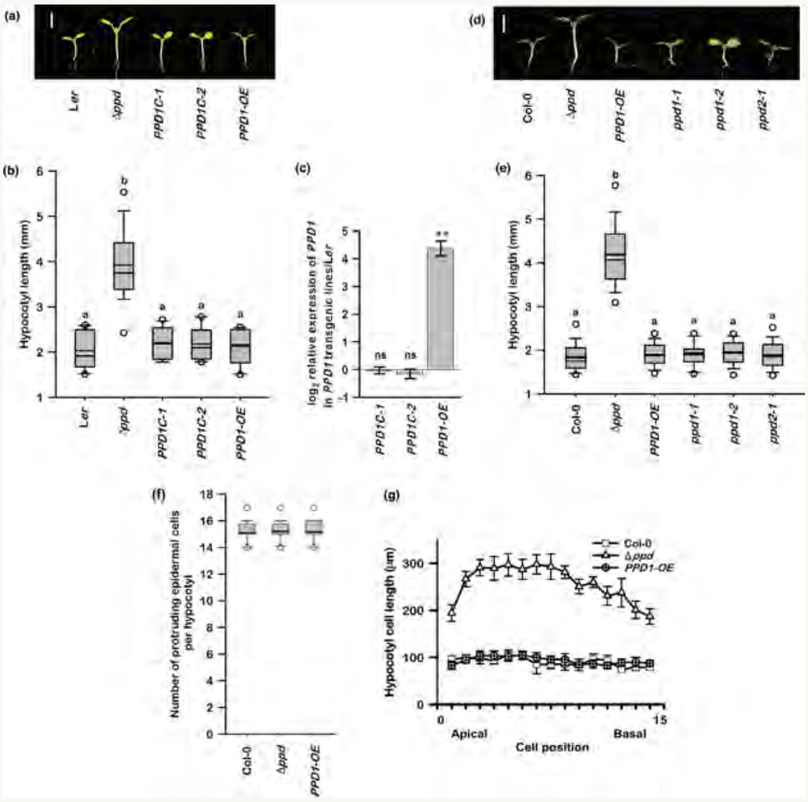

Figure 1: ''PEAPODs (PPDs) regulate seedling hypocotyl length in Arabidopsis thaliana''. White, 2022, *New Phytologist.* https://doi.org/10.1111/nph.18198

Norway

Thorsten Hamann

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Planned events for 2022 and 2023

- Scandinavian Plant Physiology Society Bi-annual conference August 2022, Svalbard: https://spps.se/spps2022/
- 10th International Conference on Plant Peptides and Receptors, 14th to 16th September, Oslo, https://www.plant-peptides-and-receptors.org/

Selected Publications

- William B. Reinar, Vilde O. Lalun, Trond Reitan, Kjetill S. Jakobsen, Melinka A. Butenko. Length variation in short tandem repeats affects gene expression in natural populations of Arabidopsis thaliana. Plant Cell. 2021. 33(7): 2221–2234. DOI: 10.1093/plcell/koab107

  This manuscript investigates elegantly the role of short tandem repeats in regulation of gene expression in Arabidopsis thaliana by combining transcriptomic, modeling and wet lab-based experimental approaches.

- Bacete L, Schulz J, Engelsdorf T, Bartosova Z, Vaahtera L, Yan G, Gerhold JM, Tichá T, Øvstebø C, Gigli-Bisceglia N, Johannessen-Starheim S, Margueritat J, Kollist H, Dehoux T, McAdam SAM and Thorsten Hamann. THESEUS1 modulates cell wall stiffness and abscisic acid production in Arabidopsis thaliana. Proc Natl Acad Sci U S A. 2022 4;119(1): e2119258119. DOI: 10.1073/pnas.2119258119

  This manuscript investigates the role of the cell wall integrity maintenance mechanism in coordinating cellular responses to cell expansion or shrinkage.

Major Funding Sources

- Norwegian Research Council https://www.forskningsradet.no/en/Home_page/1177315753906

Poland

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Planned events for 2022 and 2023

- 8th Central European Congress of Life Sciences, 20-22 June 2022, Krakow, Poland
- 6th Polish Congress of Genetics 27-30, June, Krakow, Poland
- 4th Network Meeting of the UV4Plants Association, 03 – 06 July 2022, Krakow, Poland
- 10th Conference of the Polish Society of Experimental Plant Biology, 20-23 September 2022, Katowice, Poland
- 59th Congress of the Polish Botanical Society, Centenary of the Polish Botanical Society, June 28th 2022, Warsaw, Poland

Selected Publications

- Bieluszewski, T., Sura, W., Dziegielewski, W., Bieluszewska, A., Lachance, C., Kabza, M., Szymanska-Lejman, M., Abram, M., Wlodzimierz, P., De Winne, N., De Jaeger, G., Sadowski, J., Côté, J., and Ziolkowski, P.A. (2022). NuA4 and H2A.Z control environmental responses and autotrophic growth in Arabidopsis. Nature Communications 13, 277. https://doi.org/10.1038/s41467-021-27882-5

  The authors describe the link between molecular regulation of chromatin status and the activation of light-dependent plant responses to stress.

- Gonzalo, L., Tossolini, I., Gulanicz, T., Cambiagno, D.A., Kasprowicz-Maluski, A., Smolinski, D.J., Mammarella, M.F., Ariel, F.D., Marquardt, S., Szweykowska-Kulinska, Z., Jarmolowski, A., and Manavella, P.A. (2022). R-loops at microRNA encoding loci promote co-transcriptional processing of pri-miRNAs in plants. Nature Plants 8, 402-418. DOI: 10.1038/s41477-022-01125-x

  The work describes structural and molecular features that are associated with co-transcriptional pri-miRNA processing in Arabidopsis thaliana.

- Szechyńska-Hebda, M., Lewandowska, M., Witoń, D., Fichman, Y., Mittler, R., and Karpiński, S.M. (2022). Aboveground plant-to-plant electrical signaling mediates network acquired acclimation. The Plant Cell. https://doi.org/10.1093/plcell/koac150

  This very exciting paper, just accepted, describes the phenomenon of electric signal mediated plant to plant communication.

- Zhu, L., Fernández-Jiménez, N., Szymanska-Lejman, M., Pelé, A., Underwood, C.J., Serra, H., Lambing, C., Dluzewska, J., Bieluszewski, T., Pradillo, M., Henderson, I.R., and Ziolkowski, P.A. (2021). Natural variation identifies SNI1, the SMC5/6 component, as a modifier of meiotic crossover in Arabidopsis. Proceedings of the National Academy of Sciences 118, e2021970118. DOI: 10.1073/pnas.2021970118

- Zhu, L., Fernández-Jiménez, N., Szymanska-Lejman, M., Pelé, A., Underwood, C.J., Serra, H., Lambing, C., Dluzewska, J., Bieluszewski, T., Pradillo, M., Henderson, I.R., and Ziolkowski, P.A. (2021). Natural variation identifies SNI1, the SMC5/6 component, as a modifier of meiotic crossover in Arabidopsis. Proceedings of the National Academy of Sciences 118, e2021970118. [DOI: 10.1073/pnas.2021970118](https://doi.org/10.1073/pnas.2021970118)

  The authors report the identification of the Structural Maintenance of Chromosomes SMC5/6 SNI1 factor and decribe its involvement in the regulation of the meiotic recombination process in Arabidopsis.

- Jarzyniak, K., Banasiak, J., Jamruszka, T., Pawela, A., Di Donato, M., Novák, O., Geisler, M., and Jasiński, M. (2021). Early stages of legume-rhizobia symbiosis are controlled by ABCG-mediated transport of active cytokinins. Nat Plants 7, 428-436. [DOI: 10.1038/s41477-021-00873-6](https://doi.org/10.1038/s41477-021-00873-6)

  The authors describe the role of the ABC transporter protein in ATP-dependent cytokinin transport that is essetial for the early steps of nodule formation in legume-rhizobia symbiosis. Non-Arabidopsis work.

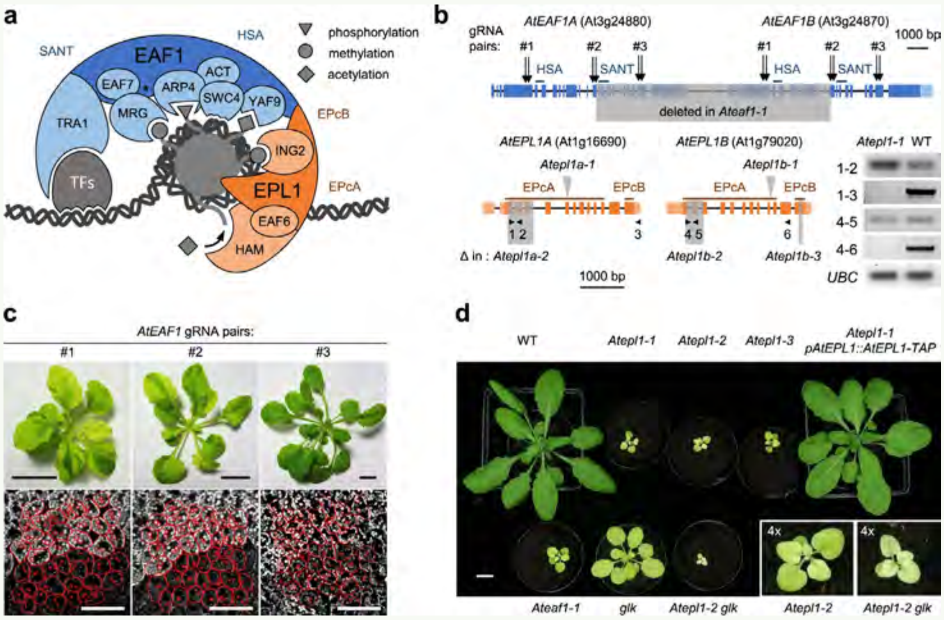

Figure 1: "*Ateaf1* and *Atepl1* mutants as tools for genetic analysis of the plant NuA4 complex". Bieluszewski, Sura, Dziegielewski et al 2022, *Nature Communications*. https://doi.org/10.1038/s41467-021-27882-5

Major Funding Sources

- National Science Centre Poland [https://www.ncn.gov.pl/]
- Foundation for Polish Science [https://www.fnp.org.pl/]
- The National Centre for Research and Development [https://www.ncbr.gov.pl]

Portugal

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University of Porto
scoimbra@fc.up.pt

Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- Evorepro database: a platform dedicated to the visualization and analysis of gene expression and co-expression networks of plants. EVOREPRO (https://evorepro.sbs.ntu.edu.sg/).

- Castro PH, Azevedo H. 2021. SGN, the plant SUMO Gene Network. Project site at the Open Science Framework (https://osf.io/9kfqv/).

Planned events for 2022 and 2023

Outreach events
- International Fascination of Plant Day, 18 May 2022.
- Noite Europeia dos Investigadores, 24 September 2022

Workshops
- 3D Developmental Imaging – EMBO practical courses, 1-9 July 2022, Oeiras, Portugal (https://meetings.embo.org/event/22-3d-dev-imaging)

Conferences
- The III International Meeting of the Portuguese Society of Genetics (IMPSG) will take place at the University of Évora, https://www.impsg2022.uevora.pt/ 27 - 28 June 2022
- Spanish Portuguese Congress on Plant Biology 9 - 12 July 2023. https://bp2021.eu/en/
- Encontro com a Ciência e Tecnologia em Portugal, 16-18 May 2022, Lisboa, Portugal (https://www.encontrociencia.pt/2022/)

Selected Publications

- Julca I, Flores-Tornero M, Proost S, Lindner A-C, Hackenberg D, Steinbachova L, Michaelidis C, Pereira SG, Misra CS, Kawashima T, Borg M, Berger F, Goldberg J, Johnson M, Honys D, Twell D, Sprunck S, Dresselhaus T, Becker JD, & Mutwil M. Comparative transcriptomic analysis reveals conserved transcriptional programsunderpinning organogenesis and reproduction in land plants. 2021 Nature Plants, 7: 1143–1159 https://doi.org/10.1038/s41477-021-00958-2

  This work generated gene expression atlases for various organs and gametes of ten plant species comprising bryophytes, vascular plants, gymnosperms and flowering plants. A comparative analysis of the atlases identified hundreds of organ- and gamete-specific orthogroups and revealed that most of the specific transcriptomes are significantly conserved. Interestingly, our results suggest that co-option of existing genes is the main mechanism for evolving new organs.

- Serrazina, S., Machado, H., Costa, R., Duque, P., Malhó, R. (2021) Expression of Castanea crenata Allene Oxide Synthase in Arabidopsis Improves the Defense to Phytophthora cinnamomi. 2021 Frontiers in Plant Science 12: 628697. doi.org/10.3389/fpls.2021.628697

  This work reports a genetic and functional characterization of the C. crenata AOS (CcAOS) upon its heterologous gene expression in a susceptible ecotype of Arabidopsis thaliana, which contains a single AOS gene. It was found that Arabidopsis plants expressing CcAOS delay pathogen progression and exhibit more vigorous growth in its presence. They also show upregulation of jasmonic acid and salicylic acid-related genes.

- Castro PH, Couto D, Santos MÂ, Freitas S, Lourenço T, Dias E, Huguet S, Marques da Silva J, Tavares RM, Bejarano ER, Azevedo H. SUMO E3 ligase SIZ1 connects sumoylation and reactive oxygen species homeostasis processes in Arabidopsis. 2022 Plant Physiol :189(2):934-954. doi: 10.1093/plphys/kiac085.

  In this study, we explored the SUMO–ROS relationship, using as a model the Arabidopsis (Arabidopsis thaliana) null mutant of the major SUMO-conjugation enhancer, the E3 ligase SAP AND MIZ 1 (SIZ1). We showed that SIZ1 is involved in SUMO conjugate increase when primed with both exogenous and endogenous ROS. Our study connects sumoylation, and specifically SIZ1, to the control of chloroplast functions and places sumoylation as a molecular mechanism involved in ROS homeostatic and signaling events.

- Albuquerque-Martins R, Díez AR, Szakonyi D, Duque P. Assessing Postgermination Development in Arabidopsis thaliana Under Abiotic Stress. 2022 Methods Mol Biol. 2494:207-215. doi: 10.1007/978-1-0716-2297-1_14.

  This work proposes a transfer assay to screen specifically and quickly for post germination phenotypes affected by exogenous ABA in Arabidopsis thaliana. The assay can be applied to different forms of abiotic stress, and we provide tips to score for post germination phenotypes in genotypes exhibiting differential development.

- Belda-Palazón B, Rodriguez PL. Microscopic Imaging of Endosomal Trafficking of ABA Receptors. 2022 Methods Mol Biol; 2462: 59-69. doi: 10.1007/978-1-0716- 2156-1_5.

  In this chapter, we will detail two methods for imaging endosomal trafficking of ABA receptor proteins by confocal microscopy: (a) colocalization of GFP-PYL4 (also known as RCAR10) and CLATHRIN LIGHT CHAIN 2 (CLC2)-mOrange in clathrin-coated vesicles in Nicotiana benthamiana leaf cells and (b) localization of GFP-PYL4 into Wortmannin (WM)-enlarged late endosomes in Arabidopsis thaliana root cells.

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-curieactions.ec.europa.eu/
- Research Organizations such as LAQV Requimte (https://laqv.requimte.pt/), GreenUP (https://www.fc.up.pt/GreenUPorto/pt/), CIBIO(https://cibio.up.pt/en/), GULBENKIAN (https://gulbenkian.pt/fundacao/apresentacao/), ITQB (https://www.itqb.unl.pt/),…and many others, provide recurrent funding to their laboratories.

Singapore

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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- Chae lab developed a new software tool to design gRNA for multiple genomes from multiple accessions, which will be useful for functional genomic studies using pangenomes.
  https://www.biorxiv.org/content/10.1101/2022.03.10.481891v2

Selected Publications

- Shen L., Zhang Y., and Sawettalake N. (2022) A molecular switch for FLOWERING LOCUS C activation determines flowering time in Arabidopsis. Plant Cell 34, 818-833 https://academic.oup.com/plcell/article/34/2/818/6432045

  This study uncovers that CPL3-mediated dephosphorylation of FLX4 protein serves as a key molecular switch in controlling FLC expression for flowering.

- Zhang B, Li C, Li Y, Yu H (2020) Mobile TERMINAL FLOWER1 determines seed size in Arabidopsis. Nature Plants 6: 1146-1157. DOI: 10.1038/s41477-020-0749-5

  This paper reveals a novel mechanisms underlying the control of endosperm cellularization and seed size in plants.

- Wang S, Zhou Z, Rahiman R, Lee GS, Yeo YK, Xin Yang X, Lau OS (2021) Light regulates stomatal development by modulating paracrine signaling from inner tissues. Nature Communications 12, 3403. https://doi.org/10.1038/s41467-021-23728-2

  Communication across tissue layers is involved in the induction of stomatal production in response to light—a fundamental process critical for plant adaptation.

- Tran TM Chng C-P, Pu X, Ma Z, Han X, Liu X, Yang L, Huang C, Miao Y (2022) Potentiation of plant defense by bacterial outer membrane vesicles is mediated by membrane nanodomains. The Plant Cell, Volume 34, Issue 1, January 2022, Pages 395–417, https://doi.org/10.1093/plcell/koab276

Major Funding Sources

- National Research Foundation Singapore (Prime Minister’s Office Singapore) https://www.nrf.gov.sg/
- Ministry of Education, Singapore https://www.moe.gov.sg/
- Singapore Food Agency (SFA) https://www.sfa.gov.sg/
- Temasek Foundation Innovates http://www.temasekfoundation-innovates.org.sg/

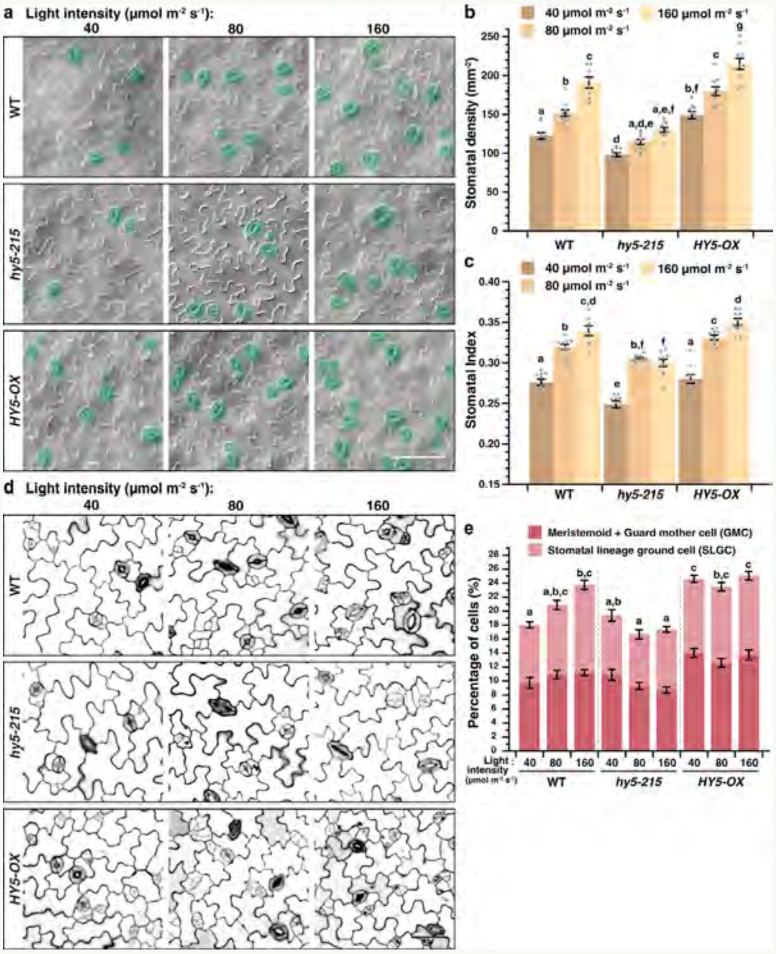

Figure 1: ‘‘Changes in stomatal production in response to light intensities in WT, hy5-215, and HY5-OX (overexpression line of HY5)’’. Wang et al, 2021. *Nature Communications.* https://doi.org/10.1038/s41467-021-23728-2

Spain

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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- The group of Miguel Angel Vega-Palas (IBVF, Sevilla) has generated TAIR10-Tel, a modified version of the Arabidopsis reference genome with additional sequences at most chromosome ends (Farrel et al, Nucleic Acids Res. 2022 50:1449-1464).

Planned events for 2022 and 2023

- XVI Reunión de Biología Molecular de Plantas, Sevilla. September 14-16, 2022. www.bcongresos.com/congresos/rbmp2022/

- International Conference on Plant Proteostasis. Madrid, September 21-23, 2022. plantproteostasis.com/

- Plant Synthetic Biology, Barcelona, September 19-21, 2022. https://www.cragenomica.es/events/plant-synthetic-biology-conference-2022.

- At the Forefront of Plant Research. Barcelona, May 8-10, 2023

- XVI Plant Cell Wall Meeting. Málaga, June 18-22, 2023

Selected Publications

2021 has been a quite productive year for the Arabidopsis community in Spain, both in quantity and quality, and it was hard to select 5 publications. Here, the selection aims to have a broad scope in research focus and methodologies, and is also based on the overall relevance of the work.

- Arteaga N, Savic M, Méndez-Vigo B, Fuster-Pons A, Torres-Pérez R, Oliveros JC, Picó FX, Alonso-Blanco C. MYB transcription factors drive evolutionary innovations in Arabidopsis fruit trichome patterning. Plant Cell. 2021 33:548-565. DOI: 10.1093/plcell/koaa041

  An interesting example of a developmental trait (the formation of trichomes in fruits) that appears to have evolved to adapt to specific climatic conditions and the genetics behind the scenes.

- Perianez-Rodriguez J, Rodriguez M, Marconi M, Bustillo-Avendaño E, Wachsman G, Sanchez-Corrionero A, De Gernier H, Cabrera J, Perez-Garcia P, Gude I, Saez A, Serrano-Ron L, Beeckman T, Benfey PN, Rodríguez-Patón A, Del Pozo JC, Wabnik K, Moreno-Risueno MA. An auxin-regulable oscillatory circuit drives the root clock in Arabidopsis. Sci Adv. 2021 7:eabd4722. DOI: 10.1126/sciadv.abd4722

A major contribution to our knowledge on how the clock works in roots, making use of highly multidisciplinary approaches, to explain how cell division and growth is coordinated with oscillations in gene expression and how external stimuli are perceived and integrated.

- Baile F, Merini W, Hidalgo I, Calonje M. EAR domain-containing transcription factors trigger PRC2-mediated chromatin marking in Arabidopsis. Plant Cell. 2021 33:2701-2715. https://doi.org/10.1093/plcell/koab139

  A clever strategy to get new insights on how the Polycomb Repressive Complexes (PCR) are recruited by transcription factors to their targets, that was able to find a common feature: the presence of an EAR domain in all TF tested that recruit PCR2.

- Cañibano E, Bourbousse C, García-León M, Garnelo Gómez B, Wolff L, García-Baudino C, Lozano-Durán R, Barneche F, Rubio V, Fonseca S. DET1-mediated COP1 regulation avoids HY5 activity over second-site gene targets to tune plant photomorphogenesis. Mol Plant. 2021 14:963-982. DOI: 10.1016/j.molp.2021.03.009

  New views on the importance of proteostasis for the correct activity of HY5, a central factor for light perception, that unveils yet another layer of regulation.

- Merelo P, González-Cuadra I, Ferrándiz C. A cellular analysis of meristem activity at the end of flowering points to cytokinin as a major regulator of proliferative arrest in Arabidopsis. Curr Biol. 2022 32:749-762.e3. https://doi.org/10.1016/j.cub.2021.11.069

  A close view of the meristem at the end of the reproductive period, that provides new insights on the cellular and molecular events that trigger the controlled arrest in flower production, a process still poorly understood.

Major Funding Sources

- In Spain, Arabidopsis research is mainly funded by the State Research Agency (AEI) in competitive calls launched every year (https://www.aei.gob.es/en/). In 2021, around 80 projects to individual laboratories were granted, which is in line with previous years. Additional national calls and regional funding also support other initiatives.

- The health crisis resulting from the COVID-19 pandemic launched the Recovery, Transition and Resilience Plan (PRTR), financed by the Recovery and Resilience Facility (Recovery and Resilience Facility, RRF) of the European Union. The AEI executes PRTR funds directly, and applies them to calls for the years 2020 to 2023. These four years belong to two State Plans for Scientific and Technical Research and Innovation (PEICTI 2017-2020 and PEICTI 2021-2023). While not a major component of the granted projects, some Arabidopsis research has benefited from these additional funds.

- European funding for basic plant research is usually scarce, but several MSCA actions (IF, RISE, or DN) have been awarded to Spanish fellows to work in Arabidopsis. An example of a MSCA-DoctoralNetwork is the recently funded “EpiSeedLink: From seed to seedling: epigenetic mechanisms of priming to design strategies for crop improvement”, where Arabidopsis research is a major component and that brings together 11 partners from 7 european countries.

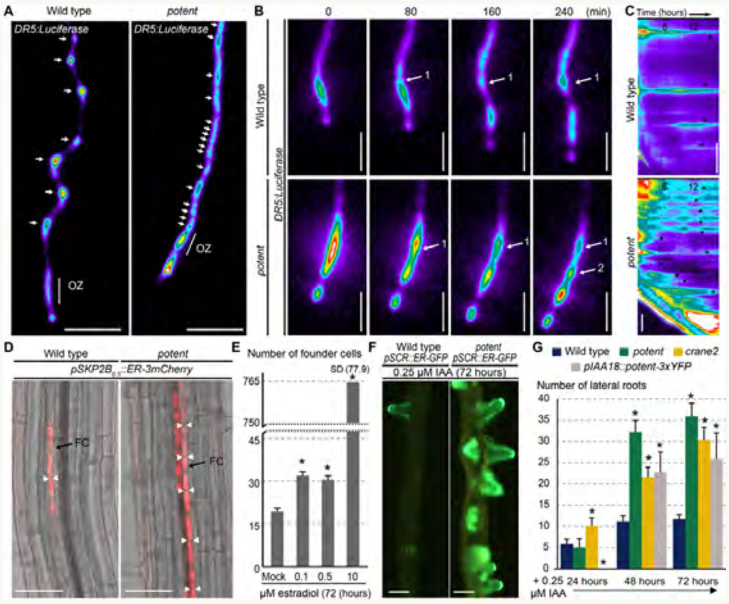

Figure 1: ''The IAA18/POTENT factor regulates the root clock oscillations and LR priming''. Perianez-Rodriguez et al, 2021, *Science Advances*. https://doi.org/10.1126/sciadv.abd4722

Sweden

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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

During this time major funding was granted from the founding bodies, and for new PI to establish themselves in Sweden for instance the European Research Council, Starting Grant to Dr Petr Marhava Swedish University of Agricultural Sciences, Umeå on 'HOT-AND-COLD', "How plants deal with heat and cold: Molecular mechanisms of auxin transport and signaling in response to temperature stress"

The Wallenberg Foundation granted Wallenberg Academy Fellowships 2021 to Dr Derek Lundberg, and Dr Simon Stael at the Swedish University of Agricultural Sciences on plant-bacteria interactions and the healing process of plants that suffer physical damage respectively.

Also, the Swedish Foundation for Strategic Research (SSF) recently awarded several major research grants in the call 'SSF Food, Feed and Forest' for the purpose of plant biotechnology and breeding. Those awarded were mainly focused on tree research but Arabidopsis is an important model organism for several of the awardees.

Other important grants for Arabidopsis research were awarded by funders, such as those shown below in Major Funding Sources.

There are laboratories with funding from Swedish research councils and foundations giving access to core facilities:

- 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 2022 and 2023

- 12th International Conference for Plant Mitochondrial Biology (ICPMB 2022), Malmö, Sweden, May 22-27, 2022, http://icpmb2022.upsc.se/
- The 29th Scandinavian Plant Physiology Society (SPPS) conference (SPPS2022) conference will be held the Longyearbyen, Svalbard, Norway, August 30 – September 2, 2022, https://spps.se/spps2022/
- 4th NordPlant annual meeting, November 30, Lund, Sweden, 2022 https://www.nordplant.org/2022/04/29/nordplant-annual-meeting-2022-30-november-in-lund-sweden/
- Plant Research and Higher Education in Southern Sweden (PlantLink) have activities regularly, they also list meetings and courses https://www.plantlink.se/
- More info can be found at individual centers with Plant research such as, The Linnean Centre for Plant Biology in Uppsala, Sweden https://lcpu.se/
- Umeå Plant Science Centre, Umeå, Sweden, 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
- Fascination of Plants Day, https://plantday18may.org/category/europe/sweden/

Selected Publications

- Svennerstam, H and Jämtgård, S (2022) Timing is everything - obtaining accurate measures of plant uptake of amino acids. New Phytologist 234:311-318. https://doi.org/10.1111/nph.17964

  This recent paper is interesting since it compares methods for determining amino acid uptake and highlights that time is a major factor in determining plant amino acid uptake.

- Minina, EA, Dauphinee AN, Ballhaus F, Gogvadze V, Smertenko AP and Bozhkov PV (2021) Apoptosis is not conserved in plants as revealed by critical examination of a model for plant apoptosis-like cell death. BMC Biology19:100. https://doi.org/10.1186/s12915-021-01018-z

  This paper examines plant cell death of plant cells under heat stress and suggests that those cells undergo necrosis rather than 'apoptosis' of animal cells.

- Zuch DT, Doyle SM, Majda M, X Smith RS, Robert S, Torii KU. (2022) Cell biology of the leaf epidermis: Fate specification, morphogenesis, and coordination. Plant Cell, 34: 209–227. DOI: 10.1093/plcell/koab250

This work adds knowledge on regulation of leaf epidermis cell differentiation.

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 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
- 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 support international scientific exchange
- The major national funding bodies, including 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/, EU https://www.mariecuriealumni.eu/news/european-funding-opportunities-10-websites-you-need-know

Switzerland

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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- Kakui, H., Yamazaki, M., & Shimizu, K. K. (2021). PRIMA: a rapid and cost-effective genotyping method to detect single-nucleotide differences using probe-induced heteroduplexes. Scientific Reports (Vol. 11). https://doi.org/10.1038/s41598-021-99641-x

- Milosavljevic, S., Kuo, T., Decarli, S., Mohn, L., Sese, J., Shimizu, K. K., Shimizu-Inatsugi, & R., Robinson, M. D. (2021). ARPEGGIO: Automated Reproducible Polyploid EpiGenetic GuIdance workflOw. BMC Genomics, 22(1), 1–12. https://doi.org/10.1186/s12864-021-07845-2

Planned events for 2022 and 2023

Conferences

- Lausanne Genomics Days 2022, 16-17 June 2022, Lausanne https://biologie.cuso.ch/?id=2392&tx_displaycontroller[showUid]=6022

- CUSO Biology Symposium 2022 I: Advances in Epigenetics and Epigenomics, 27-29 June 2022, Caux (VD) https://swissplantscienceweb.unibas.ch/en/events/events-details/cuso-biology-symposium-2022-i-advances-in-epigenetics-and-epigenomics/ https://biologie.cuso.ch/?id=2392&L=0&tx_displaycontroller[showUid]=6024

- CUSO Biology Symposium 2022 II: «Bioinformatics» (SIB), 30 June – 01 July 2022, Caux (VD) https://swissplantscienceweb.unibas.ch/en/events/events-details/cuso-biology-symposium-2022-ii-bioinformatics-sib/ https://biologie.cuso.ch/?id=2392&L=0&tx_displaycontroller[showUid]=6385

- PSC Symposium 2021, “From Place to Space: Tracing the Spatial Dimension of Plant Sciences”, 07 Dec 2022, Zurich

- SwissPLANT symposium 2023, 23 - 25 January 2023, Les Diablerets

- LS2 Annual Meeting 2023, 16 - 17 February 2023, Zurich

- International Conference on Evolution in Action, 11 - 15 June 2023, Monte Verità.

Outreach Activities
- PSC Summer School 2022 – Application of Machine Learning in Plant Sciences, 12-16 September 2022, Einsiedeln https://www.plantsciences.uzh.ch/en/teaching/summerschool.html
- Outreach in general https://www.plantsciences.uzh.ch/en/outreach.html
- Plant Science at School https://www.plantsciences.uzh.ch/en/outreach/atschool.html
- MINT-rich Tinkering. Biotinkering for children, young people and school classes (in German) https://www.plantsciences.uzh.ch/de/experimente/mintrichtinkering.html

Selected Publications

- Barbour, M. A., Kliebenstein, D. J., & Bascompte, J. (2022). A keystone gene underlies the persistence of an experimental food web. Science, 376(6588), 70–73. https://doi.org/10.1126/science.abf2232

  The discovery of a "keystone gene" illustrates the need to bridge between biological scales, from genes to ecosystems, to understand community persistence.

- Akiyama, R., Sun, J., Hatakeyama, M., Lischer, H. E. L., Briskine, R. V., Hay, A., Gan, X., Tsiantis, M., Kudoh, H., Kanaoka, M. M., Sese, J., Shimizu, K. K., & Shimizu-Inatsugi, R. (2021). Fine-scale empirical data on niche divergence and homeolog expression patterns in an allopolyploid and its diploid progenitor species. New Phytologist, 229(6), 3587–3601. https://doi.org/10.1111/nph.17101

  This study empirically shows different habitat preference of an allopolyploid and its diploid progenitor species at fine scale in field and associated homolog expression patterns.

- Ursache, R., De Jesus Vieira Teixeira, C., Dénervaud Tendon, V., Gully, K., De Bellis, D., Schmid-Siegert, E., Andersen, T. G., Shekhar, V., Calderon, S., Pradervand, S., Nawrath, C., Geldner, N., & Vermeer, J. E. M. (2021). GDSL-domain proteins have key roles in suberin polymerization and degradation. Nature Plants, 7(3), 353–364. https://doi.org/10.1038/s41477-021-00862-9

- Bjornson, M., Pimprikar, P., Nürnberger, T., & Zipfel, C. (2021). The transcriptional landscape of Arabidopsis thaliana pattern-triggered immunity. Nature Plants, 7(5), 579–586. https://doi.org/10.1038/s41477-021-00874-5

- Podolec, R., Lau, K., Wagnon, T. B., Hothorn, M., & Ulm, R. (2021). A constitutively monomeric UVR8 photoreceptor confers enhanced UV-B photomorphogenesis. Proceedings of the National Academy of Sciences of the United States of America, 118(6). https://doi.org/10.1073/pnas.2017284118

- Highly cited researchers 2021, members of the Swiss Plant Science Web, https://swissplantscienceweb.unibas.ch/en/news/news-details/highly-cited-researchers-2021/

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
- Japan Science and Technology Agency (JST), Core Research for Evolutional Science and Technology (CREST), https://www.jst.go.jp/kisoken/crest/en/
- The Human Frontier Science Program (HFSP), https://www.hfsp.org/

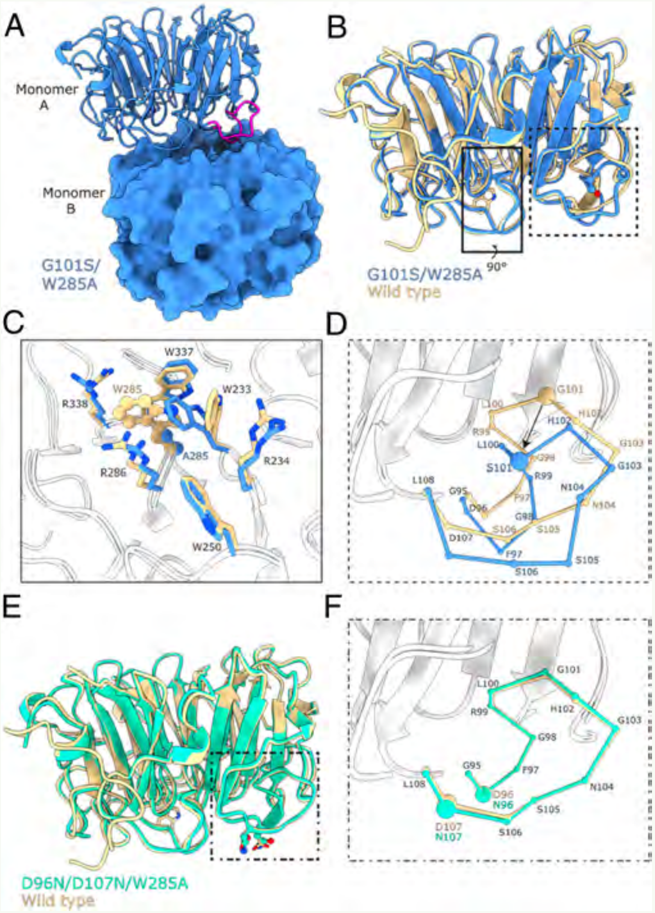
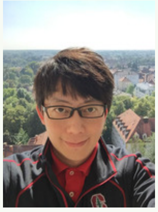


Figure 4: "UVR8^{G101S,W285A} distorts a critical interaction loop at the dimer interface". Podolec et al, 2021. *PNAS.* https://doi.org/10.1073/pnas.2017284118

Taiwan



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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your region in 2021 or early 2022.

- Plants of Taiwan (http://tai2.ntu.edu.tw)
- Orchidstra 2.0 - A Transcriptomics Resource for the Orchid Family (http://orchidstra2.abrc.sinica.edu.tw/orchidstra2/index.php)
- Taiwan Biobank (https://www.twbiobank.org.tw/new_web/)
- Database of Native Plant in Taiwan (http://www.hast.biodiv.tw/Announce/projectContentE.aspx)
- Discover Plants of Taiwan (http://taiwanplants.ndap.org.tw)
- Herbarium of Taiwan Forestry Research Institute (http://taif.tfri.gov.tw/cht/)
- Herbarium School of Forestry and Resource Conservation, National Taiwan University (http://ntuf.cc.ntu.edu.tw)
- Taiwan Rice Insertional Mutants Database

Planned events for 2022 and 2023

- International Workshop on Plant Membrane Biology, Taipei, Taiwan, March, 2023.

Selected Publications

- Hsing-Yi Cho, Mei-Yi Chou, Hsiu-Yin Ho, Wan-Chieh Chen, and Ming-Che Shih. Ethylene modulates translation dynamics in Arabidopsis under submergence via GCN2 and EIN2. Science Advances 2022 Vol 8, Issue 22 DOI: 10.1126/sciadv.abm7863

  This team unveiled that in Arabidopsis under submergence, entrapped ethylene activated downstream pathways to modulate the global translational repression and regulate transcript levels and translation efficiency of specific mRNAs that are required for survival under hypoxia.

- Choun-Sea Lin, Chen-Tran Hsu, Yu-Hsuan Yuan, Po-Xing Zheng, Fu-Hui Wu, Qiao-Wei Cheng, Yu-Lin Wu, Ting-Li Wu, Steven Lin, Jin-Jun Yue, Ying-Huey Cheng, Shu-I Lin, Ming-Che Shih, Jen Sheen, Yao-Cheng Lin, DNA-free CRISPR-Cas9 gene editing of wild tetraploid tomato Solanum peruvianum using protoplast regeneration, Plant Physiology, Volume 188, Issue 4, April 2022, Pages 1917–1930, https://doi.org/10.1093/plphys/kiac022

  This team developed a DNA-free CRISPR-Cas9 genome editing tool based on an optimized protoplast regeneration protocol that creates stable and inheritable diploid and tetraploid regenerants.

- J. Fang, B. Li, L.-J. Chen, V. Dogra, S. Luo, W. Wu. TIC236 gain-of-function mutations unveil the link between plastid division and plastid protein import. Proceedings of the National Academy of Sciences 2022 Vol. 119 Issue 11 Pages e2123353119. DOI: doi:10.1073/pnas.2123353119

Team shed new light on the links between plastid protein import, plastid division, and plant stress responses.

- Toshisangba Longkumer, Chih-Yun Chen, Marco Biancucci, Govinal Badiger Bhaskara, Paul E Verslues, Spatial differences in stoichiometry of EGR phosphatase and Microtubule-associated Stress Protein 1 control root meristem activity during drought stress, The Plant Cell, Volume 34, Issue 2, February 2022, Pages 742–758, https://doi.org/10.1093/plcell/koab290

  Team shows how altering key regulatory genes lets the plant maintain a larger population of dividing cells (larger meristem) during drought and thus maintain higher growth rate.

- Ching-Wen Chiu, Ya-Ru Li, Cheng-Yuan Lin, Hsin-Hung Yeh, Ming-Jung Liu, Translation initiation landscape profiling reveals hidden open-reading frames required for the pathogenesis of tomato yellow leaf curl Thailand virus, The Plant Cell, Volume 34, Issue 5, May 2022, Pages 1804–1821, https://doi.org/10.1093/plcell/koac019

  The team found that the coding capacity of plant virus genomes are underappreciated and will facilitate investigations of other plant viruses and aid in building novel antiviral strategies.

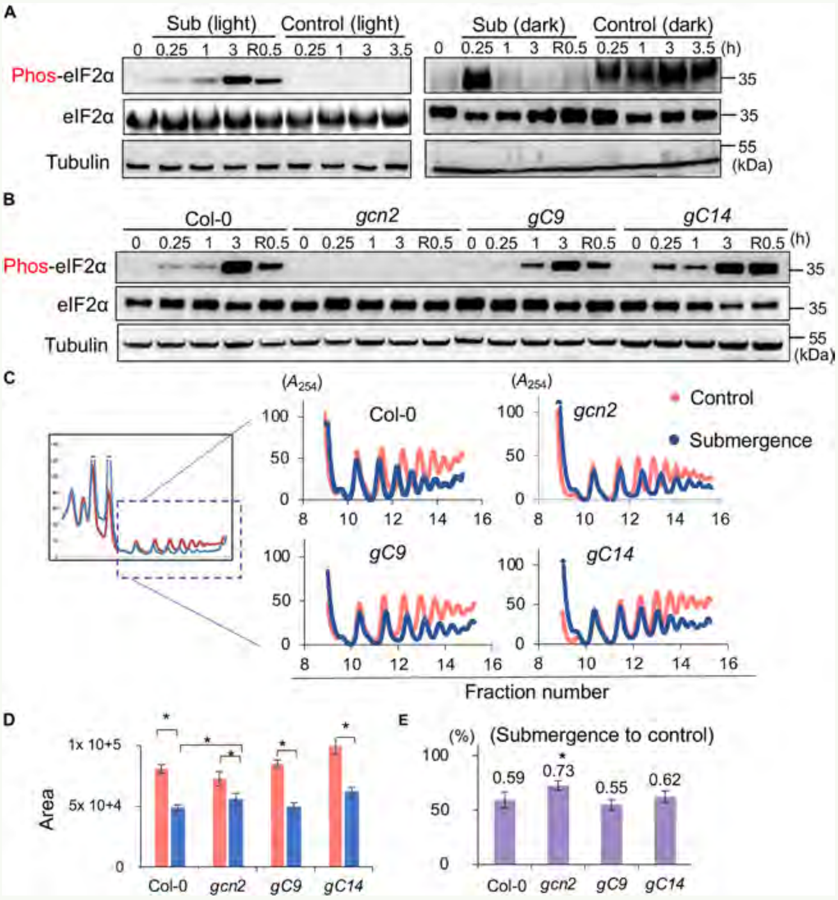

Figure 1: ‘‘GCN2-eIF2α signal is triggered under submergence in Arabidopsis’’. Cho HY et al, 2022, *Science Advances*. DOI: 10.1126/sciadv.abm7863

Major Funding Sources

- Ministry of Science and Technology, Taiwan (https://www.most.gov.tw/?l=en)
- Academia Sinica (https://www.sinica.edu.tw/en)

United Kingdom

Geraint Parry

Arabidopsis Events UK
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Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- Arabidopsis Co-expression Tool
  Zogopoulos VL, Saxami G, Malatras A, Angelopoulou A, Jen CH, Duddy WJ, Daras G, Hatzopoulos P, Westhead DR, Michalopoulos I. Arabidopsis Coexpression Tool: a tool for gene coexpression analysis in Arabidopsis thaliana. iScience. doi: 10.1016/j.isci.2021.102848 https://www.michalopoulos.net/act/

- Plasmodesmata Proteomic Pipeline
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- Novel Arabidopsis Transcriptome, AtRTD3
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- Simuplant Modelling Tool

Collis H, Band LR, Fozard JA, Ghetiu T, Wilson MH, Mellor NL, Bennett MJ, Owen MR. The Virtual Root : Mathematical Modeling of Auxin Transport in the Arabidopsis Root Tip Using the Open-Source Software SimuPlant. Methods Mol Biol. 2022;2395:147-164. doi: 10.1007/978-1-0716-1816-5_8. https://www.simuplant.org/

- Knetminer gene discovery and trait analysis tool
  Hassani-Pak K, Singh A, Brandizi M, Hearnshaw J, Parsons JD, Amberkar S, Phillips AL, Doonan JH, Rawlings C. KnetMiner: a comprehensive approach for supporting evidence-based gene discovery and complex trait analysis across species. Plant Biotechnol J. 2021 Aug;19(8):1670-1678. doi: 10.1111/pbi.13583 https://knetminer.com/

- S-acylation dataset
  Kumar M, Carr P, Turner SR. An atlas of Arabidopsis protein S-acylation reveals its widespread role in plant cell organization and function. Nat Plants. 2022 8(6):670-681. doi: 10.1038/s41477-022-01164-4

- INDEPTH community training and teaching resources
  Tatout C, Mougeot G, Parry G, Baroux C, Pradillo M, Evans D. The INDEPTH (Impact of Nuclear Domains on Gene Expression and Plant Traits) Academy: a community resource for plant science. J Exp Bot. 2022;73(7):1926-1933. doi: 10.1093/jxb/erac005 https://indepth.brookes.ac.uk/indepth-academy/

Planned events for 2022 and 2023

- Sainsbury Laboratory Symposium 2022: Regulatory Dynamics in Development and Evolution. 21-23 September 2022, Cambridge, UK and Online. https://www.slcu.cam.ac.uk/sainsbury_laboratory_symposium

- Biennial AAB Presidential Look-Forward: Nature-based and engineered biology solutions to climate mitigation. 1-2 November 2022, Rothamsted Research and Online. https://web.cvent.com/event/9428dafe-682f-4dc2-9f6b-93de57b486e0/summary

- SEB Annual Conference 2023. 4 – 7 July 2023, Edinburgh, UK. https://www.sebiology.org/events/seb-annual-conference-2023.html

Selected Publications

- Naish M, Alonge M, Wlodzimierz P, Tock AJ, Abramson BW, Schmücker A, Mandáková T, Jamge B, Lambing C, Kuo P, Yelina N, Hartwick N, Colt K, Smith LM, Ton J, Kakutani T, Martienssen RA, Schneeberger K, Lysak MA, Berger F, Bousios A, Michael TP, Schatz MC, Henderson IR. The genetic and epigenetic landscape of the Arabidopsis centromeres. Science. 2021 doi: 10.1126/science.abi7489

  Centromeres are famously challenging to interrogate due to the high level of repeated DNA sequence. In this study Ian Henderson from Cambridge University leads a multinational consortium that uses long-read sequencing to construct the five Arabidopsis centromeres that associate with the Centromere-specific Histone CENH3. They also discover that retrotransposons played a major role in the formation of the centromeres.

- Flannery SE, Pastorelli F, Wood WHJ, Hunter CN, Dickman MJ, Jackson PJ, Johnson MP. Comparative proteomics of thylakoids from Arabidopsis grown in laboratory and field conditions. Plant Direct. doi: 10.1002/pld3.355

  This research led from the University of Sheffield uses quantitative label-free proteomics to demonstrate that field-grown Arabidopsis plants incorporate aspects of both the low and high light acclimation strategies previously observed in laboratory-grown plants. The authors discuss the significance of these alterations in the thylakoid proteome considering the unique set of challenges faced by plants growing under natural conditions.

- Huang W, MacLean AM, Sugio A, Maqbool A, Busscher M, Cho ST, Kamoun S, Kuo CH, Immink RGH, Hogenhout SA. Parasitic modulation of host development by ubiquitin-independent protein degradation. Cell. 2021;184(20):5201-5214.e12. doi: 10.1016/j.cell.2021.08.029

  This study is led from the John Innes Centre and uses Arabidopsis as a model to study how parasites modulate plant defence responses. In this case they show insect-vectored plant pathogenic phytoplasmas take control of several plant developmental processes, causes a witches-broom phenotype, delaying the transition to flowering and prolongs host plant life.

- Hamon-Josse M, Villaécija-Aguilar JA, Ljung K, Leyser O, Gutjahr C, Bennett T. KAI2 regulates seedling development by mediating light-induced remodelling of auxin transport. New Phytol. 2022 235(1):126-140. doi: 10.1111/nph.18110

  Tom Bennett from the University of Leeds leads this study that describes a novel relationship between strigolactone and auxin signalling. This occurs through the modulation of the PIN auxin-transport protein abundance through the activity of the α/β-hydrolase signalling protein KARRIKIN-INSENSITIVE2 (KAI2).

- Krahmer J, Hindle M, Perby LK, Mogensen HK, Nielsen TH, Halliday KJ, van Ooijen G, Le Bihan T, Millar AJ. The Circadian Clock Gene Circuit Controls Protein and Phosphoprotein Rhythms in Arabidopsis thaliana. Mol Cell Proteomics. 2022 ;21(1):100172. doi: 10.1016/j.mcpro.2021.100172

  This University of Edinburgh-led research present a circadian proteomic and phosphoproteomic time series from Arabidopsis thaliana plants under constant light conditions to evaluate any changes that occur is a set of stable proteins whose mRNA levels are not rhythmic. Although only small proportion of the abundance of these proteins was rhythmic a more significant proportion of phospho-sites in these same proteins showed diurnal differences,

Major Funding Sources

- Biotechnology and Biological Sciences Research Council (BBSRC) http://www.bbsrc.ac.uk/
- The Gatsby Charitable Foundation http://www.gatsby.org.uk/
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- 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/

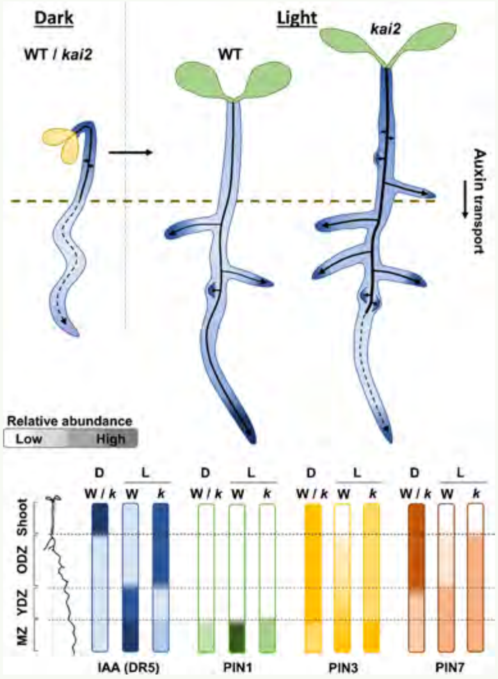

Figure 7: ‘‘A model for KAI2 function in photomorphogenesis’’. Hamon- Josse et al, 2022, *New Phytologist*. https://doi.org/10.1111/nph.18110

United States of America and North American Arabidopsis Steering Committee (NAASC)

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With input from the North American Arabidopsis Steering Committee (NAASC): Jennifer Nemhauser, University of Washington, Seattle; Federica Brandizzi, Michigan State University; Anna Stepanova, NC State University; Siobhan Braybrook, UCLA; Keith Slotkin, Donald Danforth Plant Science Center & Univ. of Missouri-Columbia; Cris Argueso, Colorado State University; Adrienne Roeder, Cornell University; Dior Kelley, Iowa State University; Gloria Muday, Wake Forest University

Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2021 or early 2022.

- Gene expression atlas at single cell resolution in Arabidopsis, DOI: 10.1016/j.devcel.2022.01.008 https://www.sciencedirect.com/science/article/pii/S1534580722000338

- Cuerda-Gil D, Hung YH, Panda K, Slotkin RK. A plant tethering system for the functional study of protein-RNA interactions in vivo. Plant Methods. 2022 Jun 4;18(1):75. doi: 10.1186/s13007-022-00907-w. PMID: 35658900; PMCID: PMC9166424. https://pubmed.ncbi.nlm.nih.gov/35658900/

- SC-ION for network inferences (https://github.com/nmclark2), first published in Clark, N.M., Nolan, T.M., Wang, P. et al. Integrated omics networks reveal the temporal signaling events of brassinosteroid response in Arabidopsis. Nat Commun 12, 5858 (2021). https://doi.org/10.1038/s41467-021-26165-3

- Deepest catalog of Arabidopsis ubiquitinated proteins/peptides: https://www.biorxiv.org/content/10.1101/2021.01.07.425780v1

Planned events for 2022 and 2023

- NAASC are starting to plan ICAR 2024, scheduled to be hosted in-person in North America for the first time since ICAR 2017 took place in St. Louis. ICAR 2020 was scheduled for Seattle, but was postponed, and then converted to ICAR 2021-Virtual, due to the COVID-19 global pandemic. We plan to continue the novel approaches we initiated for ICAR 2020/2021 including
  (1) dedicating the majority of the program to community-proposed and led symposia
  (2) striving for greater diversity and inclusion across several axes (gender, career stage, geography, science topic)
  (3) intentionally centering diversity and inclusion through engaging non-traditional speakers during invited plenary and keynote speaker selection;

(4) developing sessions around bigger mechanistic themes, focusing on the vast utility of resources, data sets, tools and techniques developed by the Arabidopsis community, and application of fundamental discoveries to applied research; and
(5) providing opportunities for participants to present their work.
We will develop new approaches to expand a sense of belonging and will solicit input and participation from the community to guide our priorities.

- NAASC are planning our second community workshop at ICAR to focus on inclusive practices using Arabidopsis for research, teaching and engagement. We held the first workshop at ICAR 2022-Belfast entitled IN PLANTA: INclusive Practices that Leverage Arabidopsis as a Nexus for Training and Application. There were both in-person and online discussion sessions across a diverse range of topics such as: Arabidopsis as a tool for research, teaching & training; Career opportunities & trade-offs: how to prioritize?; Acting as an ally; and More Inclusive Conferences, among others. We will submit a proposal to hold a similar workshop at ICAR 2023-Japan to continue engaging with the community.

- NAASC will compile community input from previous workshops, discussion sessions (such as the ICAR 2021-Virtual Town Hall), and survey data to develop a plan for community-supportive activities for the next ~5 years. At least one workshop is being planned to convene relevant stakeholders to consider community needs and to prioritize our activities. These activities will form the basis of proposals to submit to funders to help support the North American Arabidopsis community and our vital collaborations with the international community. Key areas of focus will include:
  (1) supporting and highlighting the value of fundamental plant biology research;
  (2) providing opportunities, engaging, and increasing inclusion and belonging of members of under-represented groups in US STEM;
  (3) providing opportunities, engaging, and increasing inclusion and belonging of early career researchers; and
  (4) developing approaches to engage all members of the Arabidopsis community to participate in community diversity, equity, and inclusion efforts to ensure that our community is self-renewing, robust, and reflects the true diversity of its members.

Selected Publications

- Montgomery BL, Whittaker JA. 2022. The roots of change: Cultivating equity and change across generations from healthy roots. Plant Cell. 34(7):2588-2593. doi: 10.1093/plcell/koac121. PMID: 35445722; PMCID: PMC9252499.

  This is a clarion call to improve our scientific societies.

- Radin I, Richardson RA, Coomey JH, Weiner ER, Bascom CS, Li T, Bezanilla M, Haswell ES. 2021. Plant PIEZO homologs modulate vacuole morphology during tip growth. Science. 373(6554):586-590. doi: 10.1126/science.abe6310. PMID: 34326243.

  The vacuole is identified as a major site of mechanosensation in plants, and it also identifies a role for PIEZO in this signaling pathway.

- Leydon AR, Wang W, Gala HP, Gilmour S, Juarez-Solis S, Zahler ML, Zemke JE, Zheng N, Nemhauser JL. 2021. Repression by the Arabidopsis TOPLESS corepressor requires association with the core mediator complex. Elife. 10:e66739. doi: 10.7554/eLife.66739. PMID: 34075876; PMCID: PMC8203292.

This paper details the discovery of a mechanism for transcriptional priming in plants, something thought to be limited to metazoans.

- Hossein D, Huang Y-C, Mermaz B, LeBlanc Cl, 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, Couture J-F, Jacob Y. 2022. The histone H3.1 variant regulates TONSOKU-mediated DNA repair during replication. Science. 375(6586):1281-1286. doi: 10.1126/science.abm5320

  This paper provides the first evidence for the "H3 barcode hypothesis" which posits that initial epigenetic decoding occurs via a replication-coupled H3.1 variant.

- Ko, D.K., Brandizzi, F. Transcriptional competition shapes proteotoxic ER stress resolution. 2022. Nat. Plants 8, 481–490. doi.org/10.1038/s41477-022-01150-w.

  This publication focuses on the mechanisms controlling responses to proteotoxic stress and identifies transcriptional regulators that extinguish the function of the first stress responders. This work opens new avenues for modulating energy allocation in stress responses and was possible thanks to the resources that are available to Arabidopsis.

- Dash L, McEwan RE, Montes C, Mejia L, Walley JWW, Dilkes BP, Kelley DR. 2021. slim shady is a novel allele of PHYTOCHROME B present in the T-DNA line SALK_015201. Plant Direct. 5:e00326. doi.org/10.1002/pld3.326.

  This paper details an often overlooked but prevalent phenomenon of Arabidopsis T-DNA lines harboring background mutations, which is important to be aware of.

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

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- 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/

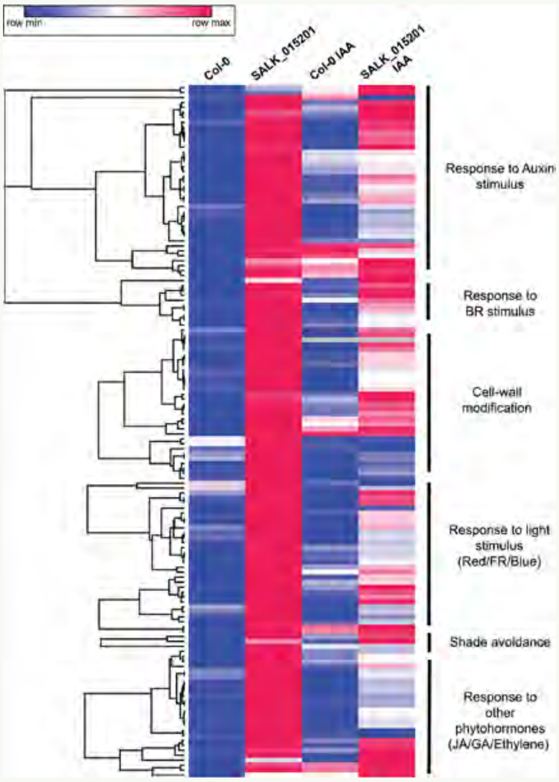

Figure 3: ‘‘Heatmap of enriched genes in SALK_015201 compared to Col-0 identified by GO analysis’’. Dash et al, 2021. *Plant Direct.* https://doi.org/10.1002/pld3.326

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