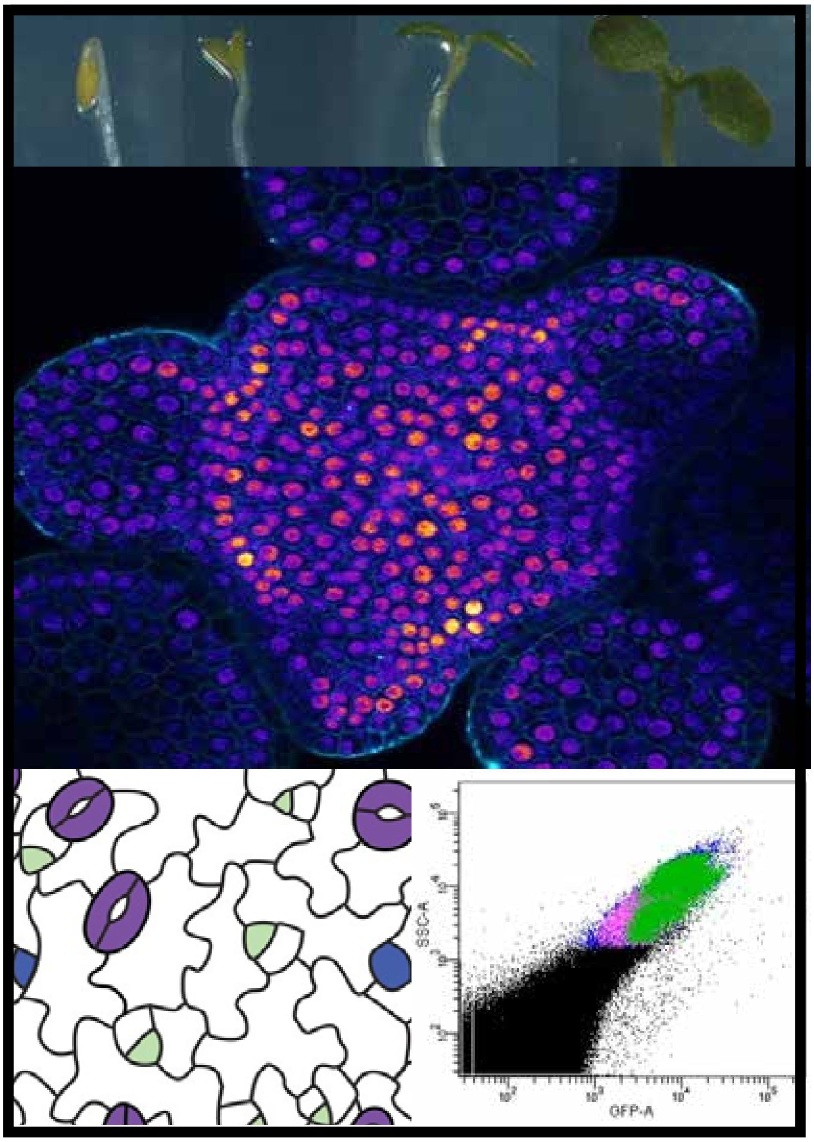
From Bench to Bountiful Harvests

Multinational Arabidopsis Steering Committee (MASC)

Annual Report 2020/2021



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

The MASC report 2020/21 and previous reports are available online at:

> MASC, The Multinational Arabidopsis Steering Committee:
    http://*Arabidopsis*research.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
> GARNet
    http://garnetcommunity.org.uk/reports

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This report has been written by the members of the MASC community including the MASC directors, subcommittee chairs and co-chairs with support of subcommittee members, country representatives, project or resource directors and the wider Arabidopsis community. Throughout the report any references that are highlighted in red include an associated open access figure from that article.

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Annual Report 2020/2021

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Table of Contents

Activities of MASC

MASC web page: www.Arabidopsisresearch.org

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 directors were elected for a range of term lengths. These terms will be for four years once the first round of rotations has ended. 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 2020 Michael Wrzaczek and Barry Pogson rotated off the list of directors and we thank them for their service. The membership of MASC (comprising the members of MASC subcommittees, MASC projects and country representatives) nominated and elected two new directors; Shahid Mukhtar (The University of Alabama at Birmingham) and Yuling Jiao (Institute of Genetics and Developmental Biology, Chinese Academy of Sciences) who will serve as directors until 2024.

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

- 2018-2021: Xuelu Wang (China), Elizabeth Haswell (United States of America)
- 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 late 2021 another two new directors will be elected for a four-year term. In that election we will improve the gender balance on the board of directors as well as maintaining geographical diversity. Currently the directors broadly oversee MASC activities. We will circulate details of the MASC election procedure in the summer of 2021.

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 secretarial activities. From August 2020 Dr Geraint Parry has been paid by MASC Inc to oversee its activities, which remain at a minimal level (anticipated to be ~40 hours in 2020-21) to maintain the activity of the organisation:

- 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 during ICAR meetings

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

The MASC subcommittees, proposed in 2002, were established to help tracking the progress and advances made by the international Arabidopsis community. This report includes contributions from seven subcommittees: Bioinformatics, Epigenetics and Epigenomes, ORFeomics, Natural Variation and Comparative Genomics, Proteomics, Plant Immunity and Systems and Synthetic Biology. **This will be the final report of the ORFeomics subcommittee so we thank Motoaki Seki and Joe Ecker for all their work on this over the past decade.**

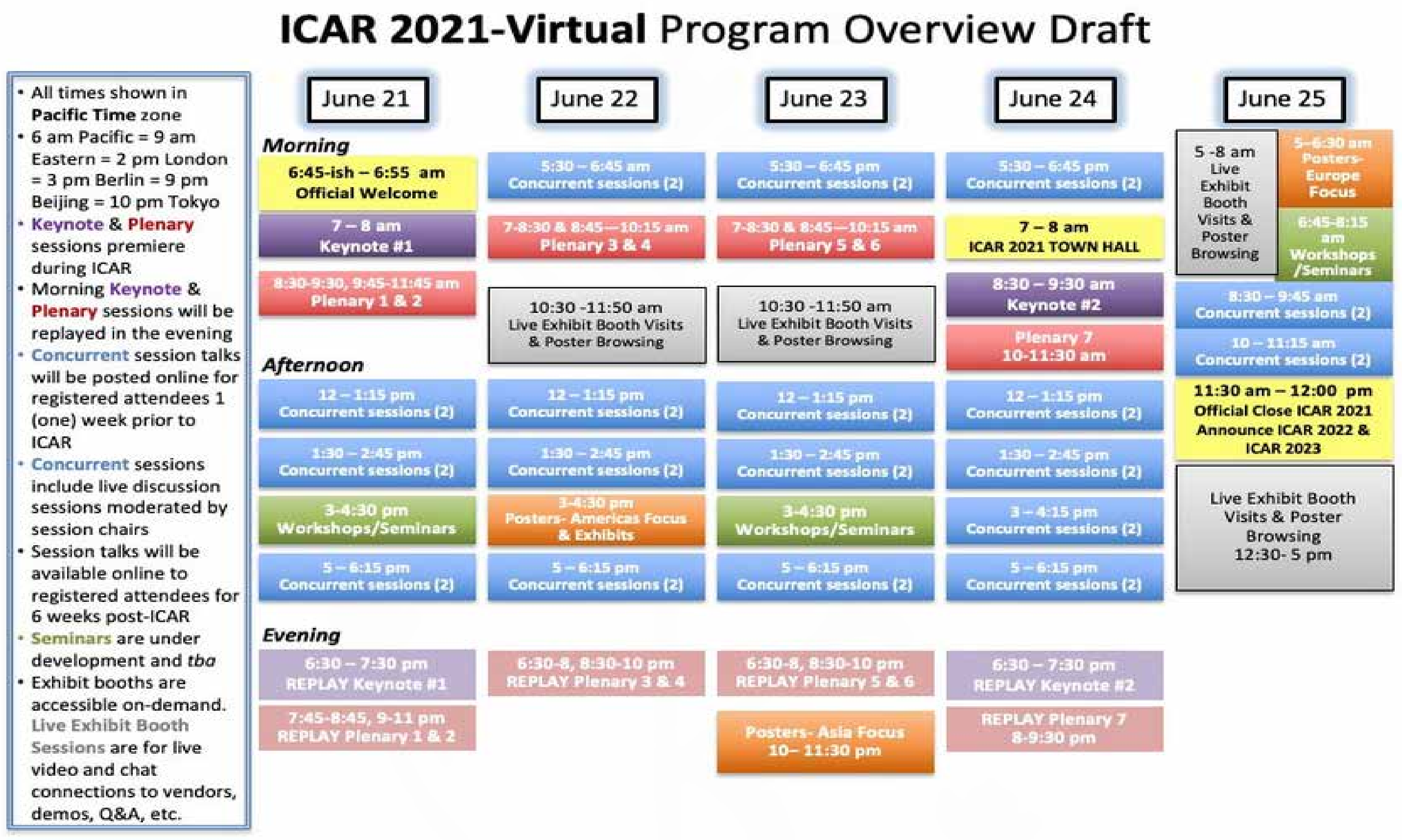
Subcommittees have loose guidelines for their activities:

- Subcommittee chairs are usually required a hold 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 a greater role in the organisations of workshops at ICAR meetings.

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

Country reports provide the bulk of the MASC report and highlight the new resources and publications that have been generated from different parts of the world. In this challenging year we are grateful to the 26 Country representatives that submitted for this report.



ICAR 2021-Virtual Program Overview Draft

- All times shown in **Pacific Time** zone
- 6 am Pacific = 9 am Eastern = 2 pm London = 3 pm Berlin = 9 pm Beijing = 10 pm Tokyo
- **Keynote** & **Plenary** sessions premiere during ICAR
- Morning **Keynote** & **Plenary** sessions will be replayed in the evening
- **Concurrent** session talks will be posted online for registered attendees 1 (one) week prior to ICAR
- **Concurrent** sessions include live discussion sessions moderated by session chairs
- Session talks will be available online to registered attendees for 6 weeks post-ICAR
- **Seminars** are under development and *tba*
- Exhibit booths are accessible on-demand. **Live Exhibit Booth Sessions** are for live video and chat connections to vendors, demos, Q&A, etc.

June 21

Morning
- 6:45-ish – 6:55 am Official Welcome
- 7 – 8 am Keynote #1
- 8:30-9:30, 9:45-11:45 am Plenary 1 & 2

Afternoon
- 12 – 1:15 pm Concurrent sessions (2)
- 1:30 – 2:45 pm Concurrent sessions (2)
- 3-4:30 pm Workshops/Seminars
- 5 – 6:15 pm Concurrent sessions (2)

Evening
- 6:30 – 7:30 pm REPLAY Keynote #1
- 7:45-8:45, 9-11 pm REPLAY Plenary 1 & 2

June 22
- 5:30 – 6:45 am Concurrent sessions (2)
- 7-8:30 & 8:45—10:15 am Plenary 3 & 4
- 10:30 -11:50 am Live Exhibit Booth Visits & Poster Browsing
- 12 – 1:15 pm Concurrent sessions (2)
- 1:30 – 2:45 pm Concurrent sessions (2)
- 3-4:30 pm Posters- Americas Focus & Exhibits
- 5 – 6:15 pm Concurrent sessions (2)
- 6:30-8, 8:30-10 pm REPLAY Plenary 3 & 4

June 23
- 5:30 – 6:45 pm Concurrent sessions (2)
- 7-8:30 & 8:45—10:15 am Plenary 5 & 6
- 10:30 -11:50 am Live Exhibit Booth Visits & Poster Browsing
- 12 – 1:15 pm Concurrent sessions (2)
- 1:30 – 2:45 pm Concurrent sessions (2)
- 3-4:30 pm Workshops/Seminars
- 5 – 6:15 pm Concurrent sessions (2)
- 6:30-8, 8:30-10 pm REPLAY Plenary 5 & 6
- Posters- Asia Focus 10– 11:30 pm

June 24
- 5:30 – 6:45 pm Concurrent sessions (2)
- 7 – 8 am ICAR 2021 TOWN HALL
- 8:30 – 9:30 am Keynote #2
- Plenary 7 10-11:30 am
- 12 – 1:15 pm Concurrent sessions (2)
- 1:30 – 2:45 pm Concurrent sessions (2)
- 3 – 4:15 pm Concurrent sessions (2)
- 5 – 6:15 pm Concurrent sessions (2)
- 6:30 – 7:30 pm REPLAY Keynote #2
- REPLAY Plenary 7 8-9:30 pm

June 25
- 5 -8 am Live Exhibit Booth Visits & Poster Browsing
- 5–6:30 am Posters- Europe Focus
- 6:45-8:15 am Workshops /Seminars
- 8:30 – 9:45 am Concurrent sessions (2)
- 10 – 11:15 am Concurrent sessions (2)
- 11:30 am – 12:00 pm Official Close ICAR 2021 Announce ICAR 2022 & ICAR 2023
- Live Exhibit Booth Visits & Poster Browsing 12:30- 5 pm

For this report we have asked country representatives to provide a perspective on the impact of COVID19 has had on their research communities.

We are extremely grateful to all MASC representatives as they voluntarily give their time toward our activities. All MASC contributors are invited to attend the remote MASC annual meeting that will take place on July21st 2021 2pm GMT. We are happy to invite interested observers to this remote meeting so if you would like further details please contact Geraint Parry (arabidopsisventuk@gmail.com).

The 2020 MASC annual meeting was held virtually on July 21st 2020 and attended by 30 MASC members, which is a higher number than for the live meetings that have recently taken place during ICAR meetings. The MASC annual meeting minutes can be downloaded here: http://arabidopsisresearch.org/images/Documents/Minutes/2020_31st_MASC_Virtual_AGM_Minutes_FINAL.pdf

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

International Conference on Arabidopsis Research (ICAR)

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

For the first time since the mid-1990s the ICAR meeting was unable to take place in 2020, of course due to the COVID19 pandemic. In 2021 ICAR will be a virtual event organised by the North American Arabidopsis Steering Committee, led by Joanna Friesner. This event has attracted a minimum 1000 attendees and will host a remarkable 270+ virtual talks within 7 plenary sessions and an amazing 36 community-selected minisymposia. The organisers have done a superb job of expanding accessibility of this event and the diversity of the selected speakers.

Organisation of these 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:

- 31st ICAR June 21st-25th 2021: Virtual organised by NAASC
http://icar2020.Arabidopsisresearch.org/

- 32nd ICAR, Belfast, UK: June 20th-24th 2022
http://icar2022.Arabidopsisresearch.org/

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

- 34th ICAR, The Americas. 2024

- 35th ICAR, Europe, likely Ghent, Belgium. 2025

We are hopeful that the international community will be able to come back together for a live event in 2022. ICAR2022 is organised by the GARNet network, led by Dr Geraint Parry. This will take place in the International Conference Centre in Belfast, Northern Ireland. The theme of the meeting is *'Come for the Science; Stay for the Stories'* so as to encourage our community to come back for a live meeting and share the stories that haven't been heard for years!

We encourage delegates to enjoy the meeting and then take a holiday in the UK and Ireland; Northern Ireland is the beautiful principle filming location for the Game of Thrones television show.

The MASC Code of Conduct

The MASC directors in collaboration with Joanna Friesner (Executive Director of NAASC) have developed a code of conduct for future ICAR events. This code includes advice about appropriately dealing with harassment and reporting of conference materials.

ICAR conferences will provide a safe and productive environment that promotes equal opportunity and treatment for all participants that is free of harassment and discrimination and allows the sharing of unpublished scientific findings. The code of conduct applies to all registered attendees, speakers, exhibitors, staff, contractors, volunteers, and guests; and it applies both within the ICAR conference venues and in associated events and locations where ICAR conference delegates are present.

The Code of Conduct as be downloaded here: Arabidopsisresearch.org/images/ICAR/MASC_code-of-conduct_ICAR2019.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 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.

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

Current Community Status

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

The Impact of COVID19.

The COVID19 pandemic continues to have tragic consequences for many people across the globe. The presence of numerous lockdowns has placed a significant strain on the livelihoods of many, not least for scientists who have been prevented from attending their workplaces or having their collaborative opportunities curtailed. In addition many of the leading scientists in our community are academics so the often-painful transition to online teaching has significantly impacted the time available to put toward planning, paper-writing or grant applications. In addition, there is no doubt that across the globe these changes have disproportionally negatively affected female scientists, specifically those with younger children who tend to make the majority of the emotional burden of child-rearing, parents of familiies with young children that have had no schooling or daycare available and scientists with significant elder care requirements or families that have been ravaged by COVID19. These factors should be addressed in planned recovery packages.

For a variety of reasons the impact of the pandemic will vary between nations and between institutions within those same nations; for example in the United Kingdom those scientists who work in non-teaching research institutes have been able to sooner return to their workplaces than colleagues in academic institutions. It remains to be seen the impact that this will have on future productivity. Furthermore the ability of national funding bodies to extend periods of support will vary, disproportionally impacting the productivity and future career prospects of PhD students, postdocs and early career faculty.

The inability of scientists to travel to meetings may impact the *ad-hoc* establishing of new collaborations yet the uptake of online communication tools may have had an opposite effect as it has opened up research webinars to a more global audience. Inevitably if unfortunately, the pandemic may make many people focus locally in order to secure their own futures, which may come at the cost of establishing international linkages. We very much hope that the community can come back together live at ICAR2022 to again build upon the excellent collaborative environment that exists within the Arabidopsis community.

Statistics from the ABRC and NASC demonstrate how the pandemic might have impacted lab productivity. The ABRC reports that overall orders were down 30% but that other countries, in particular China, showed larger drops.

However NASC reports that they received an increase in the number and diversity of Arabidopsis seed donations; perhaps a community upside from the pandemic. Virtual projects such as the BAR, TAIR or Gramene could more easily transition to home-working but this had different effects on their productivity. TAIR reports some challenges with maintaining subscription levels due to alterations in University budgets.

All country representatives have reported on the impact of COVID on their own communities. Across the board the message is very similar with delays and reduced occupancy being normal during the past year. There are significant differences in the extent of support for those researchers on short-term contracts such as PhD students and postdoctoral researchers. For example Moritz Nowack reports that in Belgium many young scientists have been hit hard as many of them could not finish projects before their contracts ended.

In Norway PhD students have been eligible for salaried extensions to compensate for COVID problems but this is not the case for postdocs. Hopefully this will not result in more researchers moving away from scientific careers. Fortunately some funding agencies have been able to extend existing contracts; for example Canadian scientists have benefited from a one-year extension to existing grants.

Both Argentine and US country representatives highlight the extra burden that the pandemic has placed on younger female academics. In particular the North American Arabidopsis Steering Committee calls for 'creative and robust institutional and structural efforts to mitigate the expected negative consequences of the COVID-19 pandemic', particularly to protect the most vulnerable researchers.

Cristina Ferrandiz, the Spanish MASC representative highlights a hoped-for-positive consequence of the pandemic, which may be to improve the public understanding of science and the trust of scientists. However it remains to be seen whether the benefits seen in medicinal and vaccine biology will be replicated across the Agrifood sector.

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 is now underway, 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 2000, 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. 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.

In this report MASC subcommittees include 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?

- 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

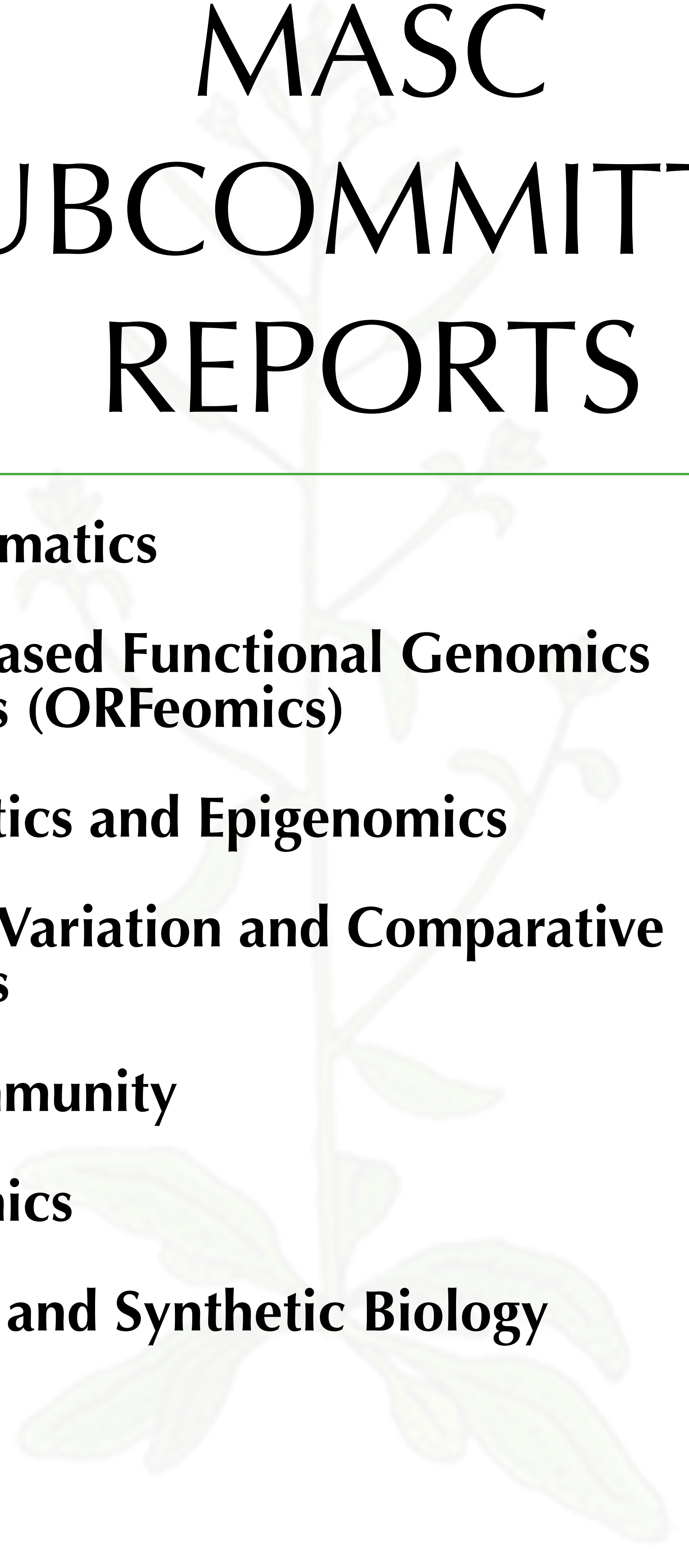
- Ensure that the research recovery from COVID19 is managed in an equitable manner in order to mitigate effects that have disproportionally affected particular groups.

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 Arabidopsis community, particular in the USA, has been in the vanguard of the scientific community taking a proactive role to ensure diversity and inclusion as well as improving plant science outreach activities (Friesner *et al* (2020) Broadening the impact of plant science through innovative, integrative, and inclusive outreach. Plant Direct. https://doi.org/10.1002/pld3.316a). The 4th decadal Roadmap will undoubtedly include recommendations to ensure that everyone has the opportunity to take advantage of the community-tools that are available to support the future of Arabidopsis and plant science research.

MASC aims to publish the 4th decadal Roadmap

MASC SUBCOMMITTEE REPORTS



Bioinformatics

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

Recently developed Open Tools and Resources for Arabidopsis Researchers

Arabidopsis Informatics

As mentioned last year, TAIR, BAR and the National Center for Genome Resources (NCGR) in New Mexico collaborated to ensure that the data and tools formerly provided by Araport remain available to the community. Araport's JBrowse instance migrated to TAIR, Thalemine was redeployed with updated data at the BAR, and a new tool – the Genome Context Viewer – for exploring micro- and macrosynteny in *Arabidopsis thaliana* ecotypes was released by the NCGR. This effort is now described in a paper published in The Plant Cell by Pasha *et al*. (2020).

TAIR

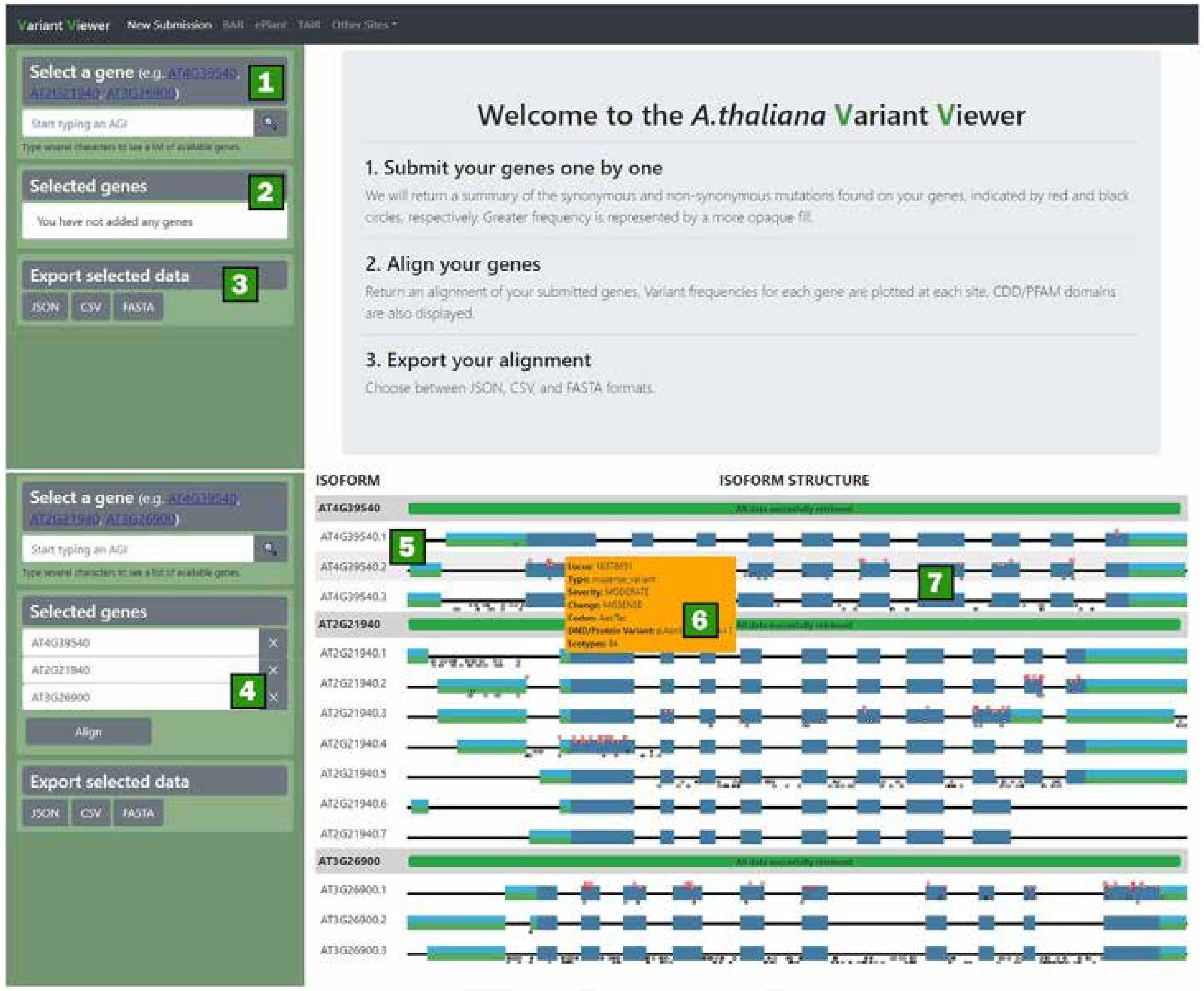
TAIR released a new Synteny Viewer. This tool uses the SynMap tool at CoGE (Lyons and Freeling, 2008) to provide pre-computed syntenic comparisons between *A.thaliana* and genomes from 36 other plant species. New data tracks were added to the Araport JBrowse instance that TAIR resuscitated. New/updated data include TIF-seq and plaNET-seq data from the Marquardt lab (Kindgren *et al*., 2020; Thomas *et al*., 2020), and Ws/Ws-2 polymorphism data from GBrowse. A new tool to enable community curation of gene function called the Generic Online Annotation Tool (GOAT, https://goat.phoenixbioinformatics.org/) was also introduced for collecting Gene Ontology and Plant Ontology annotations from the research community.

TAIR continued to incorporate new Arabidopsis gene function annotations made by curators and members of our community. As of March 2021, around 30% of Arabidopsis genes have at least one experimentally based annotation for GO Molecular Function, GO Biological Process, and GO Cellular Component. And that percentage or higher have GO support based on another annotation method (see TAIR report for exact numbers).

BAR

The Bio-Analytic Resource worked with Ute Roessner's group in Austrialia to develop an Arabidopsis Lipid Map eFP Browser for visualizing the amount of any one of hundreds of lipids across 7 different tissues (Kehelpannala *et al*., 2021). It also worked collaboratively with Patrick Schaefer's group at the University of Warwick to develop a cell-type specific immunity view for roots in ePlant (Rich-Griffin *et al*., 2020).

A Plant Reactome (Tello-Ruiz *et al*., 2018) pathways viewer was added to ePlant (Waese-Perlman *et al*., 2021). The BAR also rolled out two new tools for exploring gene regulatory networks and natural variation: AGENT (Lau *et al*., 2021) and Variant Viewer (Cumming *et al*., 2021), respectively. Large-scale Data Sets and Methods of Note.



Welcome to the *A.thaliana* Variant Viewer

1. Submit your genes one by one

We will return a summary of the synonymous and non-synonymous mutations found on your genes, indicated by red and black circles, respectively. Greater frequency is represented by a more opaque fill.

2. Align your genes

Return an alignment of your submitted genes. Variant frequencies for each gene are plotted at each site. CDD/PFAM domains are also displayed.

3. Export your alignment

Choose between JSON, CSV, and FASTA formats.

The Variant Viewer: an application for viewing variants from the 1001 Genomes Project.

Graphics are rendered using d3.js and plotly.js (see Experimental Procedures). Top: landing page, bottom: output page. Variants are pulled on the fly from the 1001 Genomes Project API (http://tools.1001genomes.org/api) for each gene entered in the search box . Selected genes are displayed as simple gene models and variants are plotted onto models to give an overview of the variants in the gene region. Hover events are triggered allowing users to inspect individual exons, UTRs, coding sequences, and variants . Users are also able to export data for their records .

As mentioned last year, Edward Marcotte's group used co-fractionation mass spectrometry to identify protein complexes in 13 plant species, including Arabidopsis. More than 3 million pairwise interactions were elucidated in this incredible study, which permits the identification of conserved and rewired protein complexes in plants (McWhite *et al*., 2020). The Arabidopsis data consisting of 21,910 interactions have now been loaded into the BAR's Arabidopsis Interactions Viewer database (http://bar.utoronto.ca/interactions2) and into BioGRID.

Also in terms of proteomics, the Kuster group and colleagues released a draft of the Arabidopsis proteome (Mergner *et al*., 2020), encompassing more than 18,000 gene products and 43,000 phosphorylation sites. The data are available in ATHENA and the ProteomicsDB.

The Marquardt Lab's plant native elongating transcripts sequencing (plaNET-seq) method showed transient genome-wide reprogramming of nascent RNAPII transcription during cold, with big implications for understanding plant stress response (Kindgren *et al*., 2020).

Another method, TIF-seq, from the same lab (Thomas *et al*., 2020) identified many transcripts where promoter-proximal RNAPII stalling and premature transcriptional termination could act as checkpoint that governs plant gene expression. As mentioned, these data are available in TAIR's JBrowse instance. scRNA-Seq Search Tools. scRNA-seq data sets continued to be published.

Another tool, the Plant Single Cell RNA-Sequencing Database, for querying such data was published by Ma *et al*. (2020) at https://www.zmbp-resources.uni-tuebingen.de/timmermans/plant-single-cell-browser/, This is in addition to the Wang Lab's Root Cell Atlas search tool at http://wanglab.sippe.ac.cn/rootatlas/ (Zhang *et al*., 2019) and the BAR's eFP Browser (http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi?dataSource=Single_Cell), which provides the ability to query scRNA-seq data from Ryu *et al*. (2019).

The Weigel Lab published a method for performing genome-wide association studies in species using incomplete genomes and a k-mer-based approach (Voichek and Weigel, 2020). They were able to recover significant, known associations for 1,582 phenotypes from 104 Arabidopsis studies but more importantly, they were able to identify new associations in cases where the reference Col-0 genome was missing a chunk of sequence as compared to other ecotypes.

Pedagogy, Policy and Outreach:

The Plant Cell Atlas project (Rhee *et al*., 2019) continued to pick up steam with a well-attended virtual workshop last May. Keep an eye on http://www.plantcellatlas.org/ for updates!

Nicholas Provart and colleagues published a retrospective of 20 years of Arabidopsis genomics and described the amazing advances that the publication of the Arabidopsis genome in 2000 enabled (Provart *et al*., 2020).

Alex Mason and colleagues published a hefty book chapter "Bioinformatic Tools in Arabidopsis Research", covering 32 useful Arabidopsis tools and websites, with step-by-step instructions (Mason *et al*., 2021). TAIR launched a webinar series using Zoom and Voov platforms for 'captive' home audiences. TAIR also continued its partnership with https://www.micropublication.org/, a platform for very short peer-reviewed reports, and this year curated/shepherded 10 Arabidopsis into the Micropublication framework.

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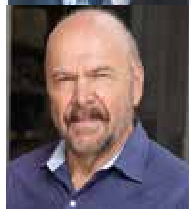
- Waese-Perlman, B. *et al*. (2021). ePlant in 2021: New Species, Viewers, Data Sets, and Widgets. bioRxiv: 2021.04.28.441805

- Zhang, T.-Q., Xu, Z.-G., Shang, G.-D., and Wang, J.-W. (2019). A Single-Cell RNA Sequencing Profiles the Developmental Landscape of Arabidopsis Root. Mol. Plant 12: 648–660.

Clone-Based Functional Genomics Resources (ORFeomics)



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Our subcommittee " Clone-Based Functional Genomics Resources (ORFeomics)" has kept tracking progress made towards the production of full-length cDNAs and open reading frame (ORF) clones for all annotated Arabidopsis protein-coding genes, there are no new large-scale "ORFeomics" projects and no new activities in our subcommittee during 2020-2021. So, we think that we should dissolve our subcommittee.

However, we think that the production of full-length cDNAs and open reading frame (ORF) clones for all annotated Arabidopsis protein-coding genes is so important in the Arabidopsis community, and we hope that the goal will be completed in the future. As our subcommittee can be related with the subcommittee "Systems and Synthetic Biology", that subcommittee will absorb our activity goal (towards the production of full-length cDNAs and open reading frame (ORF) clones for all annotated Arabidopsis protein-coding genes)

Epigenetics and Epigenomics

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Recently developed Open Tools and Resources for Arabidopsis Researchers

Socrates – open-source software for analysis of single cell ATAC-seq data (https://github.com/plantformatics/Socrates)

Recent or Future activities of Subcommittee members

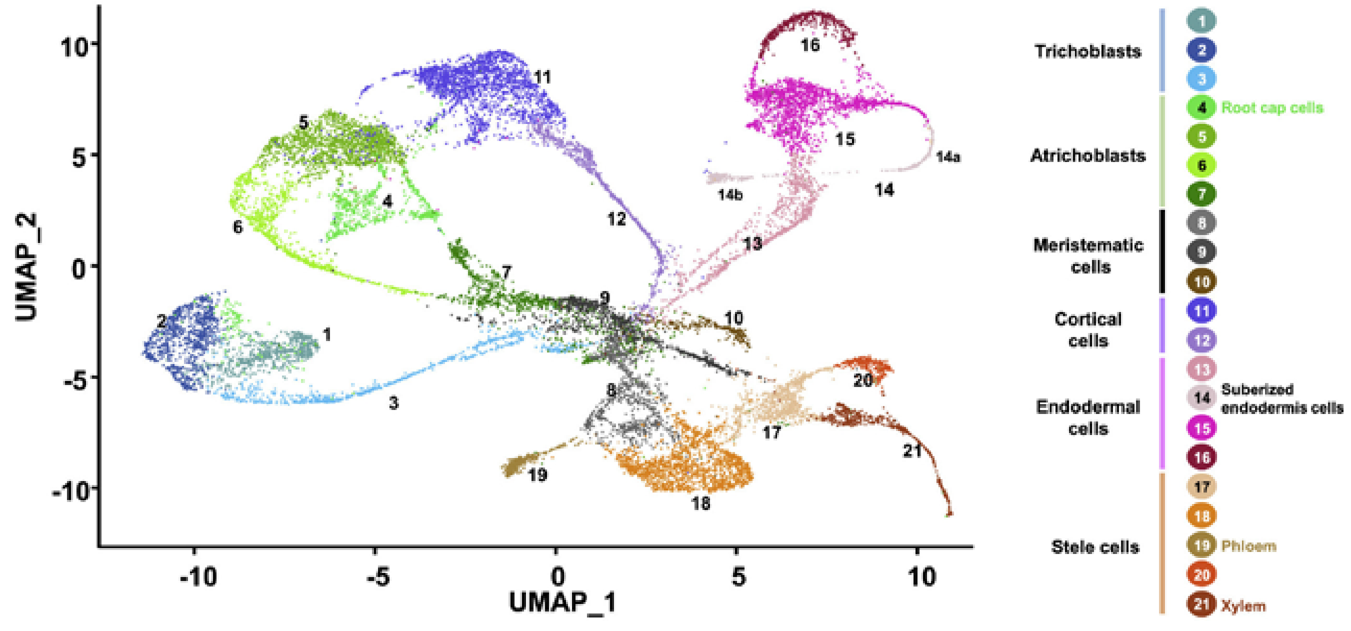
2021: Cold Spring Harbor-Asia Conference: Integrative Epigenetics in Plants, Awaji, Japan December, 2021

Selected Publications

Single-cell epigenome profiling (ATAC-seq studies):

- Farmer *et al* (2021) Single-nucleus RNA and ATAC sequencing reveals the impact of chromatin accessibility on gene expression in Arabidopsis roots at the single-cell level. Molecular Plant https://www.cell.com/molecular-plant/fulltext/S1674-2052(21)00001-0

This study demonstrates the use of single cell RNA and chromatin accessibility to map molecular phenotypes at a single cell resolution. Epigenetic reproduction and memory



Functional annotation of the Arabidopsis root cell-types

(A) Assignment of Arabidopsis root cell types based on the characterization of the expression profile of cell-type and cell-death marker genes.

- Borg *et al* (2020) Targeted reprogramming of H3K27me3 resets epigenetic memory in plant paternal chromatin. Nature Cell Biology https://www.nature.com/articles/s41556-020-0515-y.pdf?origin=ppub

This paper reveals multi-layered epigenetic mechanisms in reprogramming the paternal epigenomes for faithful propagation and reproduction. Epigenetics and cell fate decisions/reprogramming

- Jin *et al* (2021) LEAFY is a pioneer transcription factor and licenses cell reprogramming to floral fate. Nature Communications https://www.nature.com/articles/s41467-020-20883-w

This research highlights the role of LEAFY as a pioneer transcription factor important for cell fate transitions. Genomic editing of intronic enhancers

- Meng *et al* (2021) Genomic editing of intronic enhancers unveils their role in fine-tuning tissue-specific gene expression in *Arabidopsis thaliana*. The Plant Cell https://academic.oup.com/plcell/advance-article/doi/10.1093/plcell/koab093/6187954

This study highlights the presence of important cis-regulatory elements in introns and validates their function using genome editing and reporter assays. Epigenetics and environmental interactions/adaptation

- Jiang J et (2021) UVR8 interacts with de novo DNA methyltransferase and suppresses DNA methylation in Arabidopsis. Nature Plants https://www.nature.com/articles/s41477-020-00843-4

This study uncovered a functional and mechanistic connection between a UV light signaling pathway and DNA methylation and highlights a potential role of DNA methylation in UV adaptation.

Planning for Fourth Decadal Roadmap

We need to identify all epigenetic regulatory elements (*cis* and trans) in all cell types and genotypes under both normal and various stress conditions in *A. thaliana*.

Natural Variation and Comparative Genomics

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Recently developed Open Tools and Resources for Arabidopsis Researchers

AraShare (www.arashare.cn), a stock center to share Arabidopsis seeds among colleagues, was established in China to facilitate research in Arabidopsis.

Recent or Future activities of Subcommittee members

Beside the model species *Arabidopsis thaliana*, there have been many species in the family Brassicaceae and order Brassicales that have been sequenced to facilitate comparative genomics. With respect to natural variation within species, numerous populations have been sequenced or have had pan-genomes made to facilitate population genomics and association studies. With the divide shrinking between “model species” studied by a large consortium and creating genomic resources for any species of interest to a single investigator, the subcommittee is overwhelmed with reporting on all the resources and studies within genera like Arabidopsis and Brassica, let *al*one all the other related species. Our basic understanding of natural variation and genome evolution is exploding along with this research area’s ability to support applied efforts ranging from crop improvement to the conservation of biodiversity.

Selected Publications

- Hepworth J, Antoniou-Kourounioti RL, Berggren K, Selga C, Tudor EH, Yates B, Cox D, Collier Harris BR, Irwin JA, Howard M, Säll T, Holm S, Dean C.. 2020. Natural variation in autumn expression is the major adaptive determinant distinguishing Arabidopsis FLC haplotypes. Elife 9: e57671.

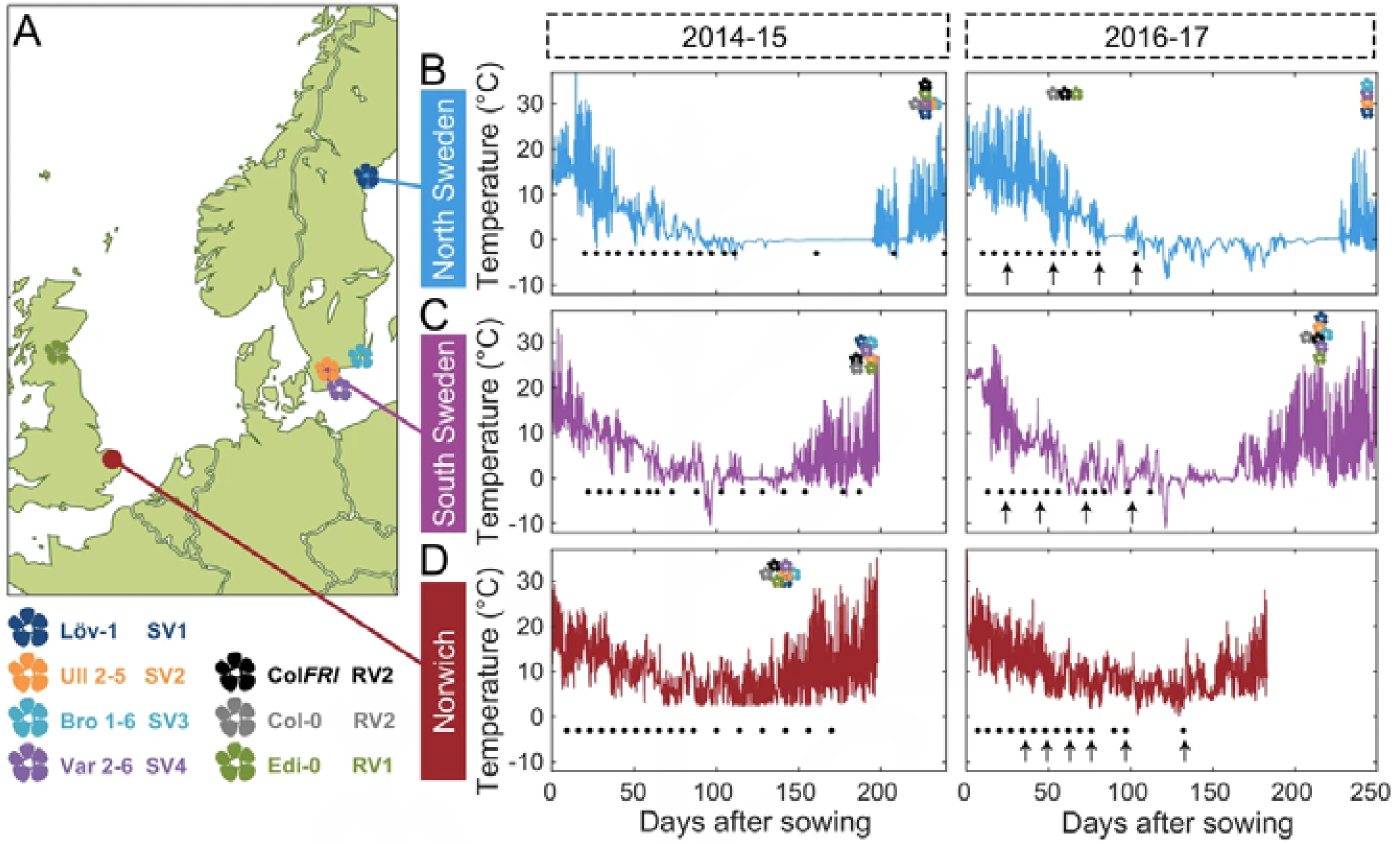
This study reveals how expression variation through non-coding *cis* variation at FLC has enabled Arabidopsis accessions to adapt to different climatic conditions and annual fluctuations

- Tsuchimatsu T, Kakui H, Yamazaki M, Marona C, Tsutsui H, Hedhly A, Meng D, Sato Y, Stadler T, Grossniklaus U, Kanaoka MM, Lenhard M, Nordborg M, Shimizu KK. 2020. Adaptive reduction of male gamete number in the selfing plant *Arabidopsis thaliana*. Nat Commun 11: 2885

This study identified the causal gene of the variation of male gamete number, and support theoretical predictions that reduced investment in male gametes is advantageous in predominantly selfing species

- Voichek Y, Weigel D. 2020. Identifying genetic variants underlying phenotypic variation in plants without complete genomes. Nat Genet 52: 534-540.

This study demonstrates the power of performing GWAS before linking sequence reads to specific genomic regions, which allows the detection of a wider range of genetic variants responsible for phenotypic variation



Field experimental setup.

(A) Map showing locations of field sites (dots) and the origins of five of the accessions (flowers) used in this study. These accessions, with the addition of Col-0, represent the five major and one intermediate (Löv-1) FLC haplotypes identified by Li *et al.*, 2014. The lab genotype Col FRI was also used in this study as a vernalization-requiring reference.
(B–D) Temperature profiles experienced by plants at the three field sites, North Sweden – Ramsta (B), South Sweden – Ullstorp (C) and Norwich, UK (D) (Source data 1, as from Hepworth *et al.*, 2018 and Antoniou-Kourounioti *et al.*, 2018). Flowers above temperature profile indicate the median time of bolting of each of the natural accessions and of Col FRI (legend at bottom left corner).

Black dots below temperature profile indicate the timepoints when plant material was collected for expression analysis. Black arrows below temperature profiles indicate time of transfer to greenhouse with long-day, warm conditions to assess degree of vernalization based on bolting time.

- Wieters B, Steige KA, He F, Koch EM, Ramos-Onsins SE, Gu H, Guo YL, Sunyaev S, de Meaux J. 2021. Polygenic adaptation of rosette growth in *Arabidopsis thaliana*. PLoS Genet 17: e1008748.

This study shows that the growth rate variation is caused by multiple loci of small effect, and tests of adaptive divergence indicate that these differences may reflect adaptation to local environmental conditions

- Zust T, Strickler SR, Powell AF, Mabry ME, An H, Mirzaei M, York T, Holland CK, Kumar P, Erb M, Petschenka G, Gomez JM, Perfectti F, Muller C, Pires JC, Mueller LA, Jander G. 2020

Rapid and independent evolution of ancestral and novel defenses in a genus of toxic plants (Erysimum, Brassicaceae). eLife 9: e51712. The findings describe a system in which plants have naturally evolved an equivalent strategy to escape their main herbivores, and ancestral and novel chemical defenses in Erysimum thus appear to provide complementary rather than redundant functions.

Planning for Fourth Decadal Roadmap

- How can plants and people adapt to the changing climate in a sustainable manner?

- How do we integrate studies across disciplines, evolutionary depth (population biology to cross-clade comparisons), and various ecological challenges to answer these fundamental questions?

- As one initial step, can we better understand evolution in the context of pleiotropy (one gene affecting multiple traits) and polygenic variation (one trait is regulated by multiple genes)?

Plant Immunity

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Recently developed Open Tools and Resources for Arabidopsis Researchers

- PlantPepDB: A manually curated plant peptide database https://www.nature.com/articles/s41598-020-59165-2 PlantPepDB is a manually curated database of plant peptides having different functions and therapeutic activities

- OpenPlantNLR: a research community on plant NLR immune receptors https://zenodo.org/communities/openplantnlr/?page=1&size=20 NLRs (nucleotide-binding leucine-rich repeat) proteins are intracellular immune receptors that constitute the main class of disease resistance (R) genes in plants. The OpenPlantNLR community collects research outputs on plant NLR biology

- The transcriptional landscape of *Arabidopsis thaliana* pattern-triggered immunity. Transcriptomics. (https://doi.org/10.1038/s41477-021-00874-5)

- NLR-Annotator (Plant Physiology, June 2020, Vol. 183, pp. 468–482,; https://doi.org/10.1104/pp.19.01273)

- Bioeffectors as Biotechnological Tools to Boost Plant Innate Immunity: Signal Transduction Pathways Involved. Plants (Basel). 2020 Dec; 9(12): 1731. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7762609/

- NLGenomeSweeper: A Tool for Genome-Wide NBS-LRR Resistance Gene Identification. https://pubmed.ncbi.nlm.nih.gov/32245073/

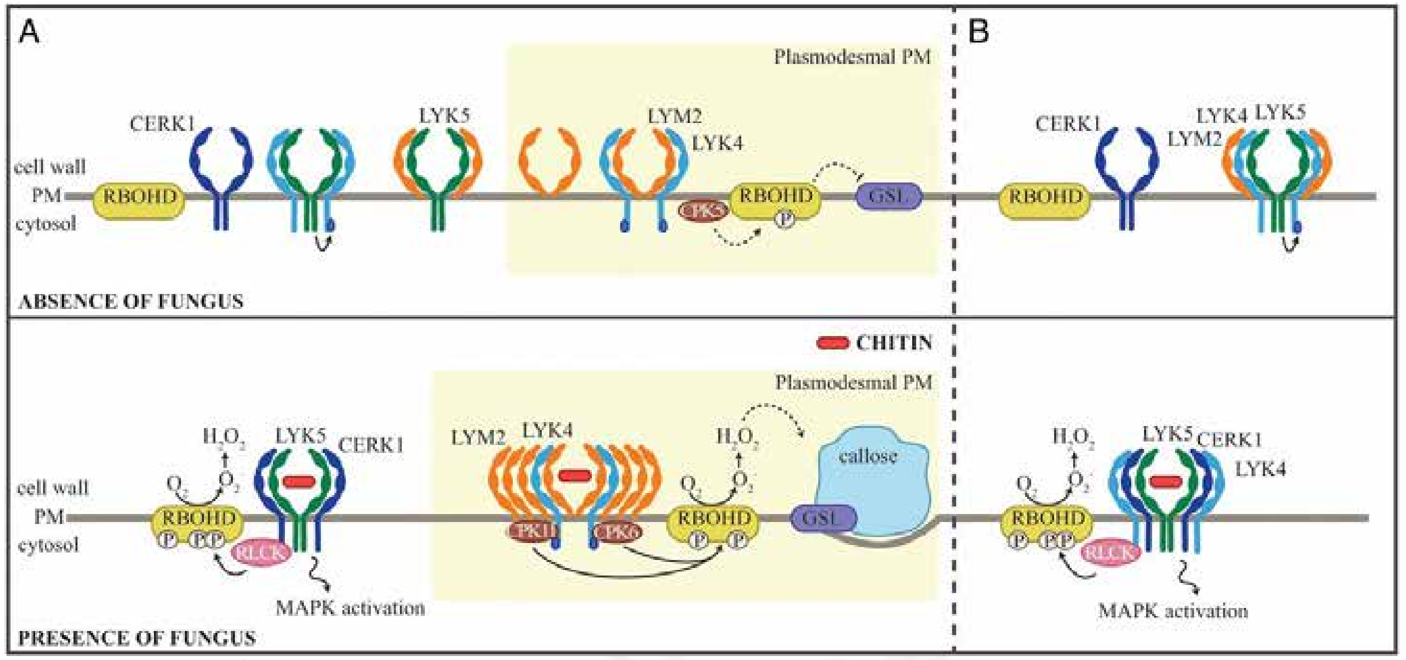
- Monitoring Plant Health with Near-Infrared Fluorescent H 2 O 2 Nanosensors. https://pubmed.ncbi.nlm.nih.gov/32097014/

Recent or Future activities of Subcommittee members

Due to the global COVID-19 situation, most of the last year's conferences were either canceled, postponed, or held in an online (shorter) version. Prior to the lockdown, the subcommittee members Organized and chaired an inaugural workshop on Machine learning and systems biology at Plant and Animal Genome Meeting, San Diego, Jan 2020.

The members of this subcommittee also presented talks in the proteomics workshop at Plant and Animal Genome meeting as well as presented a poster in an education workshop at Plant and Animal Genome Meeting, San Diego, Jan 2020.

However, after the lock-down was enforced, the subcommittee members attended the MPMI virtual seminar series (https://apsjournals.apsnet.org/virtualseminars) and the 2021 IS-MPMI Congress: eSymposia Series (https://www.ismpmi.org/Events/2021Congress/Pages/default.aspx). The members also presented a poster at the Plant Biology Worldwide Summit, July 2020.



Possible mechanisms for LYM2-mediated chitin signaling in the plasmodesmal PM.

This cartoon illustrates two possibilities for some key elements of LysM protein chitin signaling in the PM and plasmodesmal PM. Top represents the relevant associations and localizations we have identified under mock conditions (absence of fungus). Here, LYK5 (green) interacts with LYK4 (light blue), and LYM2 (orange) in the PM and LYK5 mediates modification of a pool of LYK4. This could occur via a population of bipartite complexes (A) or a tripartite LYM2-LYK4-LYK5 complex (B) in the PM. CPK5 negatively regulates callose synthesis in the plasmodesmal PM via a specific phosphorylation pattern (P) (white) of RBOHD. In response to chitin (Lower, presence of fungus), a pool of LYK4 and LYM2 dissociate from LYK5. LYK5 associates with CERK1 (dark blue) (A) or both CERK1 and LYK4 (B) to mediate signaling at the PM, and LYM2 accumulates at plasmodesmata, where it forms a higher-order complex or a signaling platform. This complex recruits LYK4 and CPK6 and -11 (brown) to phosphorylate (P) (white) RBOHD (yellow) at Ser133 and Ser347 and induces callose (blue) synthesis via a glucan synthase-like enzyme (GSL) (purple) to close PD. The PM LYK5-containing complex signals, in part, via RLCKs that phosphorylate (P) (white) RBOHD (yellow) at Ser39, Ser339, and Ser343 (P) (white). While not represented here, RLCKs might constitutively associate with LysM receptor complexes in the PM as for LRR-RKs

Finally, the members also attended CRISPR in the Classroom - Virtual Workshop for Undergraduate Educators. In summary, the combined efforts of subcommittee members have contributed tremendously in the field of plant immunity, enhanced national and international collaborations, contributed in the development of novel and innovative tools, and participated in outreach activities. In summary, the combined efforts of subcommittee members have contributed tremendously in the field of plant immunity, enhanced national and international collaborations, contributed in the development of novel and innovative tools, and participated in outreach activities.

Selected Publications

1. Schultink A, Qi T, Lee A, Steinbrenner AD, Staskawicz B. Structure of the activated ROQ1 resistosome directly recognizing the pathogen effector XopQ. (2020; Science; DOI: 10.1126/science.abd9993)

2. Ma S, Lapin D, Liu L, Sun Y, Song W, Zhang X, Logemann E, Yu D, Wang J, Jirschitzka J, Han Z, Schulze-Lefert P, Parker JE, Chai J. Direct pathogen-induced assembly of an NLR immune receptor complex to form a holoenzyme (2020; Science; DOI: 10.1126/science.abe3069)

3. Wang, W., Withers, J., Li, H., Zwack, P. J., Rusnac, D-V., Shi, H., Liu, L., Yan, S., Hinds, T. R. , Guttman, M., Dong, X., Zheng, N. (2020) Structural basis of salicylic acid perception by Arabidopsis NPR proteins. Nature volume 586, pages311–316

4. Cheval, C., Samwald, S., Johnston, M.G., Keijzer, J.D., Breakspear, A., Liu, X., Bellandi, A., Kadota, Y., Zipfel, C., Faulkner, C. (2020) Chitin perception in plasmodesmata characterizes submembrane immune-signaling specificity in plants. Proc Natl Acad Sci U S A. 117: 9621–9629.

5. Thor, K., Jiang, S., Michard, E., George, J., Scherzer, S., Huang, S., Dindas, J., Derbyshire, P., Leitão, N., DeFalco, T.A., Köster, P., Hunter, K., Kimura, S., Gronnier, J., Stransfeld, L., Kadota, Y., Bücherl, C.A., Charpentier, M., Wrzaczek, M., MacLean, D., Oldroyd, G.E.D., Menke, F.L.H., Roelfsema, M.R.G., Hedrich, R., Feijó, J., Zipfel, C.(2020) The calcium-permeable channel OSCA1.3 regulates plant stomatal immunity. Nature 585:569-573.

Planning for Fourth Decadal Roadmap

- Identification of MAMPs from pathogens and their receptors from plants, and development of resistant crops by the expression of MAMP receptors.

- Identification of avirulent effectors from pathogens and NLR receptors from plants, and development of resistant crops by the expression of NLR receptors.

- How can we collect and standardize imaging data and the images' metadata (not only of published images but also of for example an entire experiment of a published imaging analysis) 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.

- Understanding of uORFs in plant immunity and their roles in crop improvement.

- Integration of diverse -omics in plant-pathogens interactions.

Proteomics

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Recently developed Open Tools and Resources for Arabidopsis Researchers

Members of the subcommittee have been working on an updated portal for the visualization of Arabidopsis MS data ever since the closure of the MASCP Gator. This new portal has now been finalized and is available through the PeptideAtlas: http://www.peptideatlas.org/builds/arabidopsis/

Recent or Future activities of Subcommittee members

The last few years has witnessed several new surveys of Arabidopsis proteins by mass spectrometry. These approaches (deep proteomics) occurred due to the significant improvements in instrumentation, mainly sensitivity, that have occurred over the past 5 years. These data have been re-analyzed and combined into a PeptideAtlas portal that will enable the community to easily visualize peptide coverage on a given Arabidopsis protein. This new portal will enable additional information to be captured (e.g. PTMs, quantitation) about Arabidopsis proteins and is likely to be better supported into the future due to it being hosted by the institute for Systems Biology along with other model system proteomes (e.g. human, Drosophila, C.elegans, etc).

Selected Publications

- Smith S, Zhu S, Joos L, Roberts I, Nikonorova N, Vu LD, Stes E, Cho H, Larrieu A, Xuan W, Goodall B, van de Cotte B, Waite JM, Rigal A, Ramans Harborough S, Persiau G, Vanneste S, Kirschner GK, Vandermarliere E, Martens L, Stahl Y, Audenaert D, Friml J, Felix G, Simon R, Bennett MJ, Bishopp A, De Jaeger G, Ljung K, Kepinski S, Robert S, Nemhauser J, Hwang I, Gevaert K, Beeckman T, De Smet I (2020) The CEP5 Peptide Promotes Abiotic Stress Tolerance, As Revealed by Quantitative Proteomics, and Attenuates the AUX/IAA Equilibrium in Arabidopsis. Mol Cell Proteomics 19: 1248-1262

Showcases the power of quantitative proteomics to identify pathways, in this instance a novel peptide-dependent control mechanism that tunes auxin signaling.

- Bassal M, Abukhalaf M, Majovsky P, Thieme D, Herr T, Ayash M, Tabassum N, Al Shweiki MR, Proksch C, Hmedat A, Ziegler J, Lee J, Neumann S, Hoehenwarter W (2020) Reshaping of the *Arabidopsis thaliana* Proteome Landscape and Co-regulation of Proteins in Development and Immunity. Mol Plant 13: 1709-1732

A further addition to the recent deep proteome analyses of Arabidopsis, this study defines the absolutely quantification of 16000 proteins throughout the plant lifecycle.

- Heinemann B, Kunzler P, Eubel H, Braun HP, Hildebrandt TM (2021) Estimating the number of protein molecules in a plant cell: protein and amino acid homeostasis during drought. Plant Physiol 185: 385-404

A unique look at the balance between protein and amino acid pools in drought stressed Arabidopsis.

- 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: 288-292

Good demonstration of how protein mass spectrometry (phosphoproteomics) can be used to uncover new functions, in this instance phosphorylation of EIN2

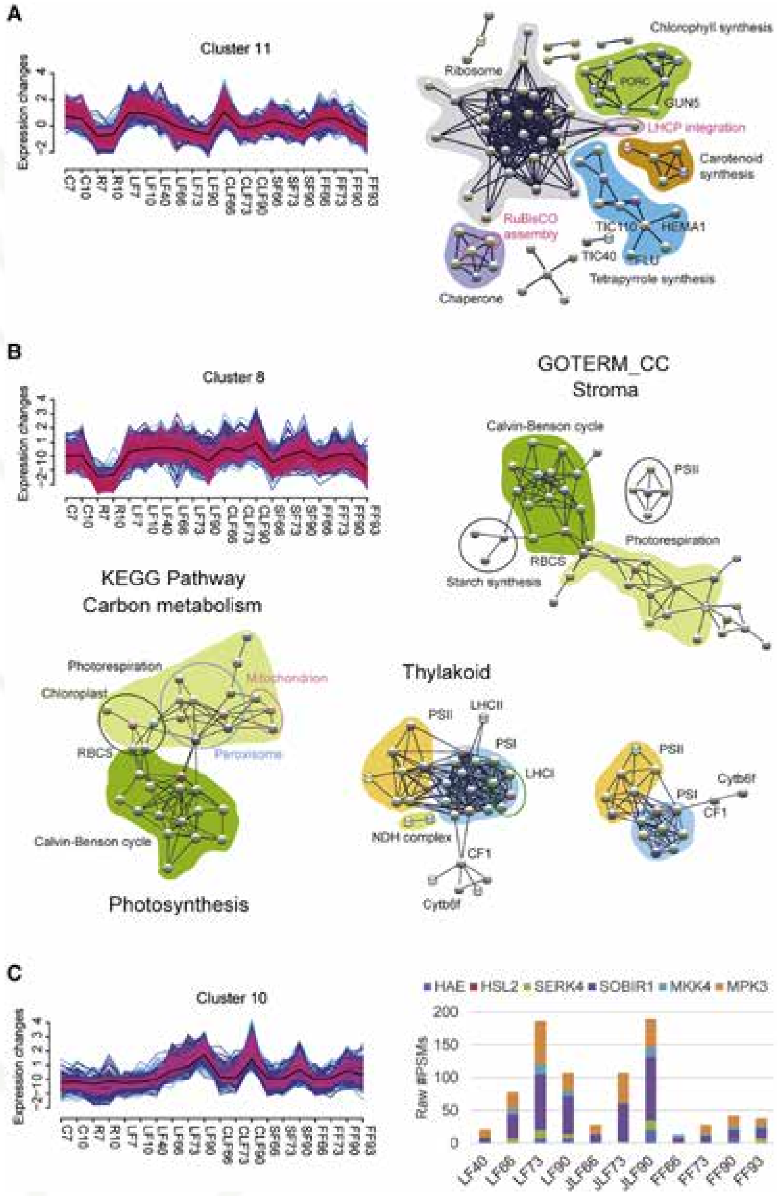
- Tang Y, Huang A, Gu Y (2020) Global profiling of plant nuclear membrane proteome in Arabidopsis. Nat Plants 6: 838-847

Application of emerging technique of proximity-labelling technology coupled to quantitative mass spectrometry to examine the nuclear envelope proteins in Arabidopsis.

Planning for Fourth Decadal Roadmap

Overall: improvements in our ability to better understand protein dynamics within the cell and the plant during development and stress conditions.

- Single cell proteomics
- Dynamics and function of PTMs (stoichiometry, competition)
- Protein turnover
- Whole proteome quantification (simple as RNAseq)
- Improved targeted analysis (simple as qPCR)
- Protein interactions (complexes vs transient interactions)
- Subcellular proteomics. A complete map and dynamics



Proteome Remodeling in the Establishment and Maintenance of Photosynthesis, Degradation of Photosynthetic Apparatus, and Leaf Senescence.
(A) FCM cluster 11. Right panel: physical/functional protein interaction networks generated with the STRING database using all proteins assigned to the GOTERM category Chloroplast (Supplemental Table 12) as the input set. Various biochemical pathways involved in pigment- and photosynthesis-related protein synthesis and chloroplast biogenesis are color coded and indicated.
(B) FCM cluster 8. Right panel: physical/functional protein interaction networks generated with the STRING database using all proteins assigned to the GOTERM categories Stroma, Thylakoid, Carbon metabolism (C Metabolism), and Photosynthesis as input sets (Supplemental Table 13). Light-independent reactions are highlighted in green (Calvin-Benson cycle, dark; photorespiration, light) and light-dependent reactions in orange (photosystem II [PSII]) and blue (photosystem I [PSI]).

- Integration with other technologies for predictive modelling of plant development and response

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Systems and Synthetic Biology

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with support from
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Recently developed Open Tools and Resources for Arabidopsis Researchers

(i) Belcher, M.S., Vuu, K.M., Zhou, A. *et al*. Design of orthogonal regulatory systems for modulating gene expression in plants. Nat Chem Biol 16, 857–865 (2020).

A library of synthetic transcriptional regulators (activators, repressors and promoters) that modulate expression strength in planta.

(ii) Brooks MD, Juang C-L, Katari MS, Alvarez JM, Pasquino H-J, Huang J, Shanks C, Cirrone J, Coruzzi GM. ConnecTF: A platform to integrate transcription factor–gene interactions and validate regulatory networks. Plant Physiology. 185(1). (2021)
A species-independent, web-based platform that integrates genome-wide stdies of TF-target binding, TF-target regulation and other TF-centric omic datasedt and uses these to build and refine validated or inferred gene regulatory networks.

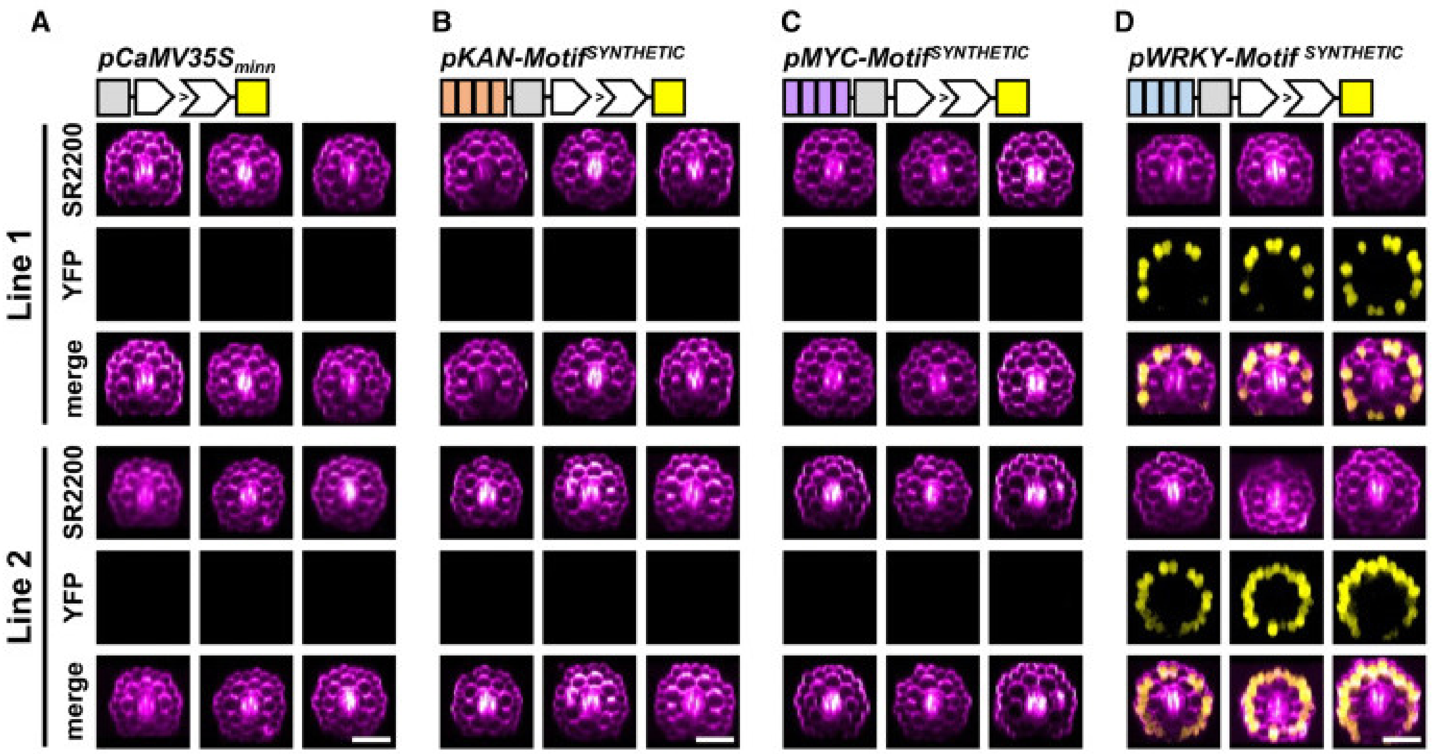
(iii) Cai YM, Carrasco Lopez JA, Patron NJ. Phytobricks: Manual and Automated Assembly of Constructs for Engineering Plants. Methods in Molecular Biology. 2205:179-199.

Phytobricks are standardized DNA parts for plants that can be assembled hierarchically into transcriptional units and multigene constructs. This protocol describes Phytobrick design and construction and their assembly in manual and nanoscale automated one-step reactions as well as high-throughput sequence verification of assembled plasmids.

(iv) Lehmann S., Dominguez-Ferreras A., Huang W., Denby K., Ntoukakis V., Schäfer P. Novel markers for high-throughput protoplast-based analyses of phytohormone signaling.Plos One 15: e0234154 (2020)
The authors generated and validated 18 promoter::luciferase and suggest an experimental setup for high-throughput analysis. They recommended novel markers for the analysis of auxin, abscisic acid, cytokinin, salicylic acid and jasmonic acid responses.

(v) Cirrone J, Brooks MD, Bonneau R, Coruzzi GM, Shasha DE. OutPredict: multiple datasets can improve prediction of expression and inference of causality. Scientific Reports. 10(1):6804. (2020)

Prediction of causal gene regulatory relationships based on time series data as well as known network edges and steady-state data. The method across different species has improved predictive accuracy over other state-of-the-art methods.



“Motif-Only” Synthetic Promoters Reveal Regulatory Functions of Promoter Motifs in Gene Expression in Planta.

Synthetic promoters only consisting of a set of four motifs or motif combinations and a CaMV35S minimal promoter (but lacking any native promoter backbone sequence) were analyzed in plant lines stably expressing the Promoter:LhG4 > pOp6:YFP transactivation system. Except for WRKY-KANADI motif combinations, two independent plant lines were analyzed per promoter construct by confocal microscopy of axial root sections.
(A) to (D) Plant lines expressing the CaMV35S minimal promoter (A), 4× KANADI binding motifs (B), or 4× MYC binding motifs (C) did not activate YFP expression, whereas plant lines expressing 4× WRKY resulted in epidermis-specific YFP expression (D).

Recent or Future activities of Subcommittee members

(i) (Plant session at) 4th German Conference on Synthetic Biology, 24 & 25 September 2020, Virtual

(ii) 4th International Conference on Plant Synthetic Biology, Bioengineering, and Biotechnology October 30 - November 1, 2020, Virtual

(iii) Cold Spring Harbor Network Biology Meeting; March 16-19, 2021; Virtual; Organizers included Pascal Falter-Braun, a member of this subcommittee

(iv) Second iPSB: EMBO Workshop on International Plant Systems Biology: April 26-27, 2021; Main Organizers: Katherine Denby and Miriam Gifford

(v) 31st March 2021 Plantae SynBio, Virtual

Selected Publications

(i) Altmann M, Altmann S, Rodriguez PA, Weller B, Wlorduy Vergara L, Palme J, Marín-de la Rosa N, Sauer M, Wenig M, Villaécija-Aguilar JA, Sales J, Lin CW, Pandiarajan R, Young V, Strobel A, Gross L, Carbonnel S, Kugler KG, Garcia-Molina A, Bassel GW, Falter C, Mayer KFX, Gutjahr C, Vlot AC, Grill. E, Falter-Braun P. Extensive signal integration by the phytoproteome protein network. Nature. 583(7815):271-276.

A systems-level map of the Arabidopsis phytohormone signalling network.

(ii) Alvarez JM, Schinke A-L, Brooks MD, Pasquino A, Leonelli L, Varala K, Safi A, Krouk G, Krapp A, Coruzzi GM. Transient genome-wide interactions of the master transcription factor NLP7 initiate a rapid nitrogen-response cascade. Nature Communications. 11(1157). 2020

Capture of stable and transient TF-target interactions of NLP7, a master regulator of of the nitrogen signaling pathway, using time-series ChIPseq and DamID-seq. These approaches can be applied to validate dynamic GRN models for any pathway of interest.

(iii) Cai YM, Kallam K, Tidd H, Gendarini G, Salzman A, Patron NJ. Rational design of minimal synthetic promoters for plants. Nucleic Acids Research. 48(21):11845-11856. (2020)

Design of a suite of synthetic promoters of different strengths that can regulate the relative expression of output genes in simple genetic devices.

(iv) Rich-Griffin C, Eichmann R, Reitz MU, Hermann S, Woolley-Allen K, Brown PE, Wiwatdirekkul K, Esteban E, Pasha A, Kogel KH, Provart NJ, Ott S, Schäfer P. Regulation of Cell Type-Specific Immunity Networks in Arabidopsis Roots. Plant Cell. 32:2742-2762. (2020)

Identification of gene networks activated by two immunity elicitors (flg22 and Pep1) in epidermis cortex and pericycle cells of Arabidopsis. A tool to analyze paired transcription factor binding motifs was also developed.

(v) Smit ME, McGregor SR, Sun H, Gough C, Bågman AM, Soyars CL, Kroon JT, Gaudinier A, Williams CJ, Yang X, Nimchuk ZL, Weijers D, Turner SR, Brady SM, Etchells JP. A PXY-Mediated Transcriptional Network Integrates Signaling Mechanisms to Control Vascular Development in Arabidopsis. Plant Cell. 32(2):319-335. (2020)

A PXY-mediated transcriptional network was mapped which revealed a feedforward loop incorporating WOX14, TMO6 and LBD4. Thee integrate both auxin and PXY signaling to determine the phloem-procambium boundary in vascular tissue.

Planning for Fourth Decadal Roadmap.

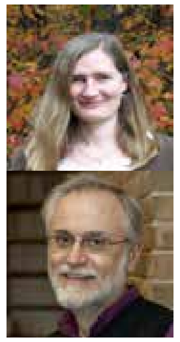
(i) Translation of Arabidopsis research to crop plants – including close relatives like other Brassicas, and other relatives like tomato and more distantly related dicots

(ii) Model-guided predictable engineering of complex traits.

(iii) Spatial and temporal dynamics in plant biology.

MASC PROJECT REPORTS

Arabidopsis Biological Resource Center
https://abrc.osu.edu/



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Recent activities and newly developed tools and/or resources

In 2020 ABRC distributed close to 66,000 samples to 1,305 individuals located in 29 countries. We also provided bulk seed for 4,026 lines to NASC and an additional 3,809 individual samples of seed requested by NASC users. The seed collection is composed of over 500,000 stocks. *Arabidopsis thaliana* seed stocks include large populations of T-DNA, transposon insertion and TILLING mutants, individual well-characterized mutants, natural variants, recombinant inbred and mapping populations, transgenic reporter lines, and RNAi lines and pools. The collection also includes 513 seed stocks from 33 other members of the Brassicaceae. ABRC received donations of 860 seed stocks in 2020. Bulk seed for a further 1,061 seed stocks was received from NASC. Seed donations were mostly composed of characterized mutant lines and other members of the Brassicaceae.

The non-seed portion of the collection numbers over 400,000 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. 23 non-seed resources were added to the collection in 2020, mostly vectors. ABRC has performed quality control testing for 3,497 new and existing stocks, involving either germination testing or verifying stock identity. ABRC outreach served more than 1,220 individuals in 2020 through participation in virtual community events, and collaboration with other STEM units on campus to provide a virtual teacher workshop series and bi-weekly STEM education office hours for educators. We have submitted a 5-year funding proposal to the National Science Foundation (NSF) to partially support the ongoing activities of the center.

Planned future activities

ABRC will continue to solicit donations of new resources with a particular focus on seed resources including multiple (stacked) Arabidopsis mutants and other members of the Brassicaceae. In collaboration with John Sedbrook and his team of researchers we will be curating, propagating, and distributing ca. 600 North American and ca. 350 European wild populations of Thlaspi arvense germplasm (Pennycress) as part of a recent award they received from Joint Genome Institute (DOE) to generate whole-genome sequence for these natural accessions. 500 pennycress EMS mutant lines will also be sequenced by the Sedbrook group and the stocks will be deposited with the ABRC.

Distribution of resources is expected to continue at or above 2020 levels. Quality control testing of new donations and stocks reproduced at ABRC will be carried out at similar levels to 2020. We plan to transition some plasmid stocks to Clonesaver cards to reduce time spent propagating and testing these resources. These cards stabilize DNA without the use of reagents and can be safely stored at room temperature for years. This will also facilitate international distribution as import of live cultures of E.coli is no longer permitted by several countries.

ABRC and NASC collaboration via exchange of seed stock resources and related data will also continue. ABRC outreach in collaboration with local community partners, the Ohio State University (OSU), and the broader plant science research and teaching communities will focus on improving accessibility in our programs and reaching new audiences. ABRC will also present a virtual booth at ICAR 2021.

Please provide a paragraph describing the general impact of the COVID19 pandemic on your activities

The COVID19 pandemic has had a significant negative impact on ABRC's activities as OSU and other research facilities across the world shut down or scaled back research efforts. OSU limited on campus activity from mid-March to early June. During this time, only three of eleven permanent staff members were permitted to continue to work on campus to carry out essential functions such as harvesting seed lines already growing in the greenhouse and maintaining cell cultures. We were also able to continue to fill orders during this period as demand dropped to less than 50% of normal levels.

Orders for the year were substantially reduced with approximately 30% fewer orders than 2019 and 60% fewer samples shipped. The largest impact was seen on orders from China which were down 60% overall for the year. The US and Canada saw a 30% drop in orders and most other countries a 15% reduction. Orders from Japan dropped only 10% in 2020 and Japan overtook China as the second largest consumer of stocks after the US. We have applied for supplemental funding from NSF to counteract the loss of income caused by the reduction in demand for stocks. It was also necessary to reduce staffing levels and raise stock prices in August 2020. As of March 2021, orders have still not returned to pre-pandemic levels and ABRC staff who are able to work from home continue to work remotely. In person outreach events have not yet resumed, but a several virtual events are planned.

Bio-Analytic Resource for Plant Biology (BAR) http://bar.utoronto.ca

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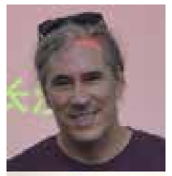

Recent activities and newly developed tools and/or resources

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 A.th.), 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. * 70,944 predicted protein-protein interactions plus 83,626 experimentally determined PPIs and ~2.8 million protein-DNA interactions, which can be explored with our new Arabidopsis Interactions Viewer 2 tool. * 29,180 predicted protein tertiary structures and experimentally determined structures for 402 Arabidopsis proteins.* 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).

The Bio-Analytic Resource worked with Ute Roessner’s group in Austrialia to develop an Arabidopsis Lipid Map eFP Browser for visualizing the amount of any one of hundreds of lipids across 7 different tissues (Kehelpannala *et al*., 2021). It also worked collaboratively with Patrick Schaefer’s group at the University of Warwick to develop a cell-type specific immunity view for roots in ePlant (Rich-Griffin *et al*., 2020). A Plant Reactome (Tello-Ruiz *et al*., 2018) pathways viewer was added to ePlant (Waese-Perlman *et al*., 2021). The BAR also rolled out two new tools for exploring gene regulatory networks and natural variation: AGENT (Lau *et al*., 2021) and Variant Viewer (Cumming *et al*., 2021), respectively. Last but not least, based on the Marcotte Lab’s co-fractionation mass spectrometry to identify protein complexes in 13 plant species, including Arabidopsis (McWhite *et al*., 2020), we loaded the Arabidopsis data consisting of 21,910 interactions into the BAR’s Arabidopsis Interactions Viewer database (http://bar.utoronto.ca/interactions2). The numbers listed above reflect this addition. For non-Arabidopsis researchers, we worked with Robert Schaffer’s group in New Zealand to set up/host an Actinidia eFP Browser, also known as kiwifruit. Check it out here: http://bar.utoronto.ca/efp_actinidia/cgi-bin/efpWeb.cgi (Brian *et al*., 2021). And we also work with Thorsten Schnurbusch’s group and colleagues in Germany to set up a barley floral meristem eFP view (Thiel *et al*., 2021) in our Barley ePlant at http://bar.utoronto.ca/eplant_barley/. New expression views were added for several other species including tomato, soybean and rice.

Planned future activities

A custom eFP view in ePlant for a researcher’s own RNA-seq data is in the works, 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 an image – you can also search to see if it co-occurs with another search term in a figure. Several new ePlants are also planned as part of the Genome Canada project, and an ecosystem viewer will also be developed. The aforementioned AGENT tool was also funded by this grant. The BAR participated in the 2020 American Society of Plant Biology (ASPB) virtual Plant Biology conference, as part of the Plant AgData Outreach booth and in the Plant Bioinformatics workshop.

Please provide a paragraph describing the general impact of the COVID19 pandemic on your activities

We were able to continue developing BAR tools and data sets when BAR staff started working from home. A letter describing a collaborative effort with TAIR and NCGR to rescue/resuscitate Araport was published in The Plant Cell (Pasha *et al*., 2020). Note: the McWhite *et al*. (2020) and Tello-Ruiz *et al*. (2018) publications are not BAR publications.

Brian, L., Warren, B., McAtee, P., Rodrigues, J., Nieuwenhuizen, N., Pasha, A., David, K.M., Richardson, A., Provart, N.J., Allan, A.C., Varkonyi-Gasic, E., and Schaffer, R.J. (2021). A gene expression atlas for kiwifruit (Actinidia chinensis) and network analysis of transcription factors. BMC Plant Biol. 21: 121.

Cumming, M., Esteban, E., Lau, V., Pasha, A., and Provart, N.J. (2021). A ‘Variant Viewer’ for investigating population-level variation in *Arabidopsis thaliana*. bioRxiv: 2021.04.21.440793.

Kehelpannala, C., Rupasinghe, T., Pasha, A., Esteban, E., Hennessy, T., Bradley, D., Ebert, B., Provart, N.J., and Roessner, U. (2021). An Arabidopsis lipid map reveals differences between tissues and dynamic changes throughout development. Plant J.

Lau, V., Woo, R., Pereira, B., Pasha, A., Esteban, E. and Provart, N.J. (2021). AGENT: the Arabidopsis Gene Regulatory Network Tool for Exploring and Analyzing GRNs. bioRxiv: 2021.04.28.441830.

McWhite, C.D. *et al*. (2020). A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. Cell 181: 460-474.e14

Pasha, A., Subramaniam, S., Cleary, A., Chen, X., Berardini, T.Z., Farmer, A., Town, C., and Provart, N.J. (2020). Araport Lives: An Updated Framework for Arabidopsis Bioinformatics. Plant Cell.

Rich-Griffin, C. *et al*. (2020). Regulation of Cell Type-Specific Immunity Networks in Arabidopsis Roots. Plant Cell 32: 2742–2762.

Tello-Ruiz, M.K. *et al*. (2018). Gramene 2018: unifying comparative genomics and pathway resources for plant research. Nucleic Acids Res. 46: D1181–D1189.

Thiel, J. *et al*. (2021). Transcriptional landscapes of floral meristems in barley. Sci. Adv. 7: eabf0832.
Waese-Perlman, B. *et al*. (2021). ePlant in 2021: New Species, Viewers, Data Sets, and Widgets. bioRxiv: 2021.04.28.441805.

EMPHASIS
https://emphasis.plant-phenotyping.eu/

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Julich Plant Phenotyping Centre

Recent activities and newly developed tools and/or resources

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 (2017-2020) supported by the EU project EMPHASIS Prep (Grant Agreement: 739514) to the Implementation Phase (2020-2021) and is supposed to become operational in 2022/2023. EMPHASIS engaged ministry representatives building an Interim General Assembly (IGA), which is open to participation by all European countries that wish to participate in the further development of EMPHASIS and formally sign a "Letter of Intent".

IGA has been making concrete decisions on strategic aspects of EMPHASIS. Currently, representatives from 11 countries are brought together in the IGA (Belgium, Estonia, France, Germany, Israel, Italy, Netherlands, Portugal, Serbia, Switzerland, United Kingdom) to make decisions on user strategies, governance, funding, legal entity, etc. In parallel, "pilot services" have already been developed and implemented during the start-up phase in order to develop and test selected services for EMPHASIS and thus generate concrete added value for the scientific community at an early stage. The "pilot services" include: Field Phenotyping, Innovation, Harmonization, Modeling, Data Management, Training.

Planned future activities

EMPHASIS is expected to enter the operational phase in 2022/2023 with a full portfolio of services. In a distributed pan-European research infrastructure, services will be provided and organized by Service Center(s). The implementation of services is done at national level and the establishment of national nodes involving national funding agencies and ministries is a central part of distributed Research Infrastructures.

Please provide a paragraph describing the general impact of the COVID19 pandemic on your activities

The pandemic has limited a direct interaction with different stakeholders, which is essential in discussion the operations of EMPHASIS. All exchange was moved to web conferences slowing down the development of EMPHASIS.

EPPN2020
https://eppn2020.plant-phenotyping.eu/

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Julich Plant Phenotyping Centre

Recent activities and newly developed tools and/or resources

The EPPN2020 is a H2020 funded research infrastructure project (Grant Agreement: 731013) that provides the European Plant Science community (public and private) with access to phenomics installations chosen for excellence and avoidance of redundancy, with a capacity of hundreds of genotypes and dedicated to innovative non-invasive measurement of traits at different levels of plant organization. It also provides this community with tools, methods and software for organization, storage and joint analysis of experiments at different scales (organ to canopy), time resolutions (minutes to month), for contrasting environmental conditions (current or future). Networking activities establish cooperation and increase integration between facilities involved in EPPN2020 and outside, as well as user groups belonging to academic and private sectors.

EPPN2020 coordinates its activities with the future ESFRI infrastructure EMPHASIS, with the communities of modelling and genomics and with national programs. EPPN2020 has recently finalized the Transnational Access (TNA) scheme enabling 153 experiments at 31 installations. The TNA users were from 37 countries including 16 non-European countries. A procedure with a smooth access was designed based on a web portal that includes information on all available installations, and on a fair and open selection process. Over 80% of the users had no previous cooperation with access providers. 30% of accesses in controlled conditions were based on datasets previously collected in field experiments, which may result in high-level publications. The TNA scheme was complemented by Joint Research Activities, which standardize the good practices in phenomics, via the mapping of current practices, training sessions and the design, test and dissemination of methods, tools and software. Particularly a trans-platform experiment was designed that involved 13 platforms for testing all methods designed in Joint Research Activities, for addressing methodological issues in phenomics and for exchanges with other communities (e.g. genomics or modelling).

Planned future activities

EPPN2020 will end in October 2021, the results and tools developed within the framework of EPPN2020 will be further developed and made available through the Research Infrastructure EMPHASIS.

Please provide a paragraph describing the general impact of the COVID19 pandemic on your activities

The pandemic has reduced the opportunity of the users of Transnational Access to travel to the host institutions and be directly involved in performing the experiments. Additionally, the lockdowns created substantial delays so that the project had to be extended.

Global Plant Council
https://globalplantcouncil.org/

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The Global Plant Council

Recent activities and newly developed tools and/or resources

- Together with the journal “Plants, People, Planet”, The Global Plant Council is holding a new science communication competition on social media called #PlantSciStory2021. Results will be published in late June – early July. Link: https://globalplantcouncil.org/tell-the-world-your-plantscistory2021

- Together with the journal “Frontiers in Plant Science” The Global Plant Council launched a Frontiers Research Topic special call. Among all participants, one Research Topic will be awarded a prize equivalent to three APCs (Article Processing Charges) applicable for Frontiers in Plant Science journal. Link: https://globalplantcouncil.org/ecri/ecri-outreach/frontiers-topics/

- We are accepting a guest post in our blog. We want to help researchers with their writing skills while helping them gain some well-deserved visibility among plant science peers. Link: https://globalplantcouncil.org/ecri/ecri-outreach/ecri-communication-and-dissemination-activity/

- A new working group dealing with Digital Sequence Information (DSI) and Nagoya protocol-derived policies has started.The aim is to raise awareness of the impact these new policies might have on plant scientists and their research. The first panel will take place on the 29th of June at the PBE2021 conference.

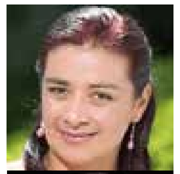
Planned future activities

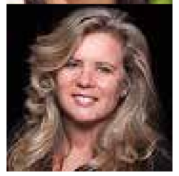
- We have launched a plant science webinar series focusing on transversal (scicomm, ethics…) and high-level topics of interest for plant scientists. We are open to contributions on speakers and topics! Webinars will be recorded and uploaded to our Youtube channel. Link: https://globalplantcouncil.org/webinars/

Please provide a paragraph describing the general impact of the COVID19 pandemic on your activities

COVID19 has forced us to restrict all our activities to online.

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





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Recent activities and newly developed tools and/or resources

Gramene provides open access to plant reference genome assemblies, genetic variation, gene expression, gene functional annotations including curated and projected metabolic and regulatory pathways, and phylogenetic annotations including within species paralogs, lineage specific genes, and ortholog/paralog assignments between species. In collaboration with EnsemblGenomes, Gramene hosts 93 plant reference genomes (almost 4 million genes in total) including three Arabidopsis species (nearly 100,000 genes): *A. thaliana, A. lyrata,* and *A. halleri*. For each reference genome sequence, we provide structural and functional gene annotations including ontology associations and protein domain assignment, genetic and structural variants, phylogenetic trees with orthologous and paralogous gene classification, whole-genome alignments, and synteny maps.

The current gene tree build includes assignment of 122,947 gene families comprising close to 2.9 million genes, supporting homolog and ortholog assignments to the three hosted Arabidopsis species. Access to the data is provided through a graphical user and application programming interface. From the homology tab on the search interface, the gene of interest is anchored by its gene tree assignment, and contains functional and visually informative structural information (e.g., color-coded protein domains and tick marks indicating splice junctions) and interactive features (e.g., ability to select a specific GO term or InterPro domain) to support access to orthologs, paralogs, and homologs that share functional annotations. The search interface and homology view allows custom pruning of the gene trees to selected species of interest, and visualizing sequence conservation to the amino acid level. *A. thaliana* serves as an anchor species within Gramene. *A. thaliana* homologs are displayed as part of the query results within the Gramene search for all species. In addition, *A. thaliana* is used as the dicot model for pairwise DNA level whole-genome alignments collection. Within the past year, the alignments subset for *A. thaliana* grew from 66 to 84, including alignments between *A. thaliana* and each of *A. lyrata* and A. halleri.

In addition, we host alignments between *A. lyrata* and each of Medicago truncatula, *Oryza sativa* (Japonica rice), *Theobroma cacao* (cacao), and *Vitis vinifera* (grapevine); and *A. halleri* to Japonica rice, cacao, and grapevine. Our synteny collection includes synteny maps for *A. thaliana* and each the following four species: *A. lyrata, Brassica rapa*, Japonica rice, and grape; and for *A. lyrata* and grapevine. These maps are based on the gene trees and positional information within the reference assembly. We continue to host 12.9 million Arabidopsis SNPs from the 1001 Arabidopsis Genomes Project. Variants are provided in the context of gene annotation, gene regulation, and protein domain structure, along with predicted functional consequences (e.g. missense variant), and genotypes.

In our continued collaboration with the Expression Atlas project (EMBL-EBI), we provide baseline expression data for 24 species, including *A. thaliana* and *A. lyrata* through both, our Gramene Ensembl genome browser and Plant Reactome pathways interfaces. In addition, we provide direct links to differential gene expression data on the EMBL-EBI Expression Atlas website for a partially overlapping set of 24 species, including *A. thaliana* and *A. lyrata* More recently, EBI Atlas, developed the capacity to host single-cell gene expression data; currently five data sets from four studies are available (Ryu *et al*, 2019; Jean-Baptiste *et al*, 2019; Shulse *et al*, 2019; Turco *et al*, 2019).

In collaboration with Reactome, Gramene hosts 320 metabolic and regulatory pathways curated in Japonica rice and inferred in 106 additional plant species (including the three Arabidopsis species) based on orthology. Reactome pathways are checked and peer-reviewed prior to publication to ensure factual accuracy and compliance with the data model, and a system of evidence tracking ensures that all assertions (which use community standard controlled vocabulary ontologies) are supported by primary literature. Gramene's integrated search capabilities, and interactive views facilitate visualizing gene features, gene neighborhoods, phylogenetic trees, gene expression profiles, and pathways. The views also assist cross-referencing to other bioinformatics resources, including AraPort, TAIR, and NASC for Arabidopsis. Gramene provides tools to support integration of user data sets in context to the reference data. These tools include a sequence assembly converter (which allows the conversion of genomic coordinates between the TAIR9 and TAIR10 genome assemblies), a genetic variant effect predictor, an advanced BioMart-based query interface, data analysis and visualization of OMICS data, multi-species pathway comparisons, and a BLAST/BLAT sequence aligner.

Together these reference comparative genome data and tools enable powerful cross-species comparisons among plants and reference eukaryotic species. Gramene data sets that include Arabidopsis species:

- Structural and functional annotations for 2.2 million gene models in 93 plant reference genomes including three Arabidopsis model species, *A. thaliana, A. lyrata,* and A. halleri, cereal, vegetable, and fruit crops (e.g., Brassicas, Fabaceas, Solanaceas), basal plants and algae.

- 122,947 phylogenetic tree families (built with 93 plant and 5 non-plant species), 382 whole-genome alignments (86 with Arabidopsis species), and 84 synteny maps (5 with Arabidopsis sp.).

- Almost 238 million genetic and structural variants for 14 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).

- Experimental baseline and differential expression data for 972 experiments in 28 plant species, including *A. thaliana* and *A. lyrata*

- v320 reference metabolic and regulatory pathways curated in rice and inferred in 106 additional 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., AraPort, TAIR, 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 coordinates, genetic variant effect predictor, BioMart, Reactome pathways analysis/visualization of OMICS data and multi-species pathway comparisons).

Gramene is committed to open access and reproducible science based on the FAIR (Fair, Accessible, Interoperable and Reusable) data principles. We are a phylogenomic resource, built upon best-of-class open source software, Ensembl, Reactome, and Expression Atlas infrastructure platforms. Gramene has developed a powerful and flexible document-based architecture that enables advanced searching via a web-service accessible by a variety of programming languages; each platform supporting web-based and programmatic access through application programming interfaces (APIs). Extensive use of ontologies, database cross-references, common data formats, metadata, community engagement and open-source software promotes interoperability within the ecosystem of informatics data and services.

Gramene's genome portal utilizes the Ensembl infrastructure and is developed in collaboration with the Ensembl Genomes project (EMBL-EBI); the pathway portal, Plant Reactome (http://plantreactome.gramene.org) utilizes the Reactome infrastructure, and is developed in collaboration with OCIR; the baseline expression data from both, our genomes and pathway browsers, is a collaboration with the Expression Atlas project (EMBL-EBI). Integration across these platforms in Gramene was supported by NSF grant IOS-1127112. More recent work for Gramene has focused on the development of species Pan-genome sites providing access to reference assemblies for multiple accessions of the same species, which facilitates the identification and characterization of common and variable genome regions. Importantly, all our species-specific pan-sites include *Arabidopsis thaliana* as a reference.

Currently the project is solely supported by the USDA-ARS (1907-21000-030-00D).

Ryu KH *et al*. (2019). Single-Cell RNA Sequencing Resolves Molecular Relationships Among Individual Plant Cells. Plant Physiol. 179(4):1444-1456. doi: 10.1104/pp.18.01482.

Jean-Baptiste K, *et al*. (2019) Dynamics of Gene Expression in Single Root Cells of *Arabidopsis thaliana*. Plant Cell. 31(5):993-1011. doi: 10.1105/tpc.18.00785.

Shulse CN, *et al*. (2019) High-Throughput Single-Cell Transcriptome Profiling of Plant Cell Types. Cell Rep. 27(7):2241-2247.e4. doi: 10.1016/j.celrep.2019.04.054.

Turco GM, *et al*. (2019) Molecular Mechanisms Driving Switch Behavior in Xylem Cell Differentiation. Cell Rep. 28(2):342-351.e4. doi: 10.1016/j.celrep.2019.06.041.

Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. Tello-Ruiz MK, Naithani S, Gupta P, Olson A, Wei S, Preece J, Jiao Y, Wang B, Chougule K, Garg P, Elser J, Kumari S, Kumar V, Contreras-Moreira B, Naamati G, George N, Cook J, Bolser D, D'Eustachio P, Stein LD, Gupta A, Xu W, Regala J, Papatheodorou I, Kersey PJ, Flicek P, Taylor C, Jaiswal P, Ware D. Nucleic Acids Res. 2021 Jan 8;49(D1):D1452-D1463.
doi: 10.1093/nar/gkaa979. PMID: 33170273

Planned future activities

With future support, we will continue to maintain and build the Gramene resource aiming to have a minimum of two releases per year: 1) update and expand our reference data collection of plant genomes, genetic variation, gene expression, and standardized comparative annotations, and orthology-based projections; 2) curate single-cell expression data and curate metabolic pathways to Expression Atlas and enrich our Plant Reactome pathways; 3) develop pan-genome resources for maize, rice, sorghum and grapevine; and 4) transform the community through communication and training opportunities.

Please provide a paragraph describing the general impact of the COVID19 pandemic on your activities

Prior to 2020, we held three genome annotation jamborees in conjunction with a major scientific meeting to train plant researchers and members of the plant community—particularly faculty at Primarily Undergraduate Institutions (PUIs)—to curate gene models and develop curriculum modules for their students to partake in Course-based Undergraduate Research Experiences (CUREs). Because of COVID-19 travel restrictions, in 2020, we had to rethink how to host this type of events that would otherwise have been in-person.

In record time, we set up our first virtual annotation jamboree for March 10-12 with the participation of more than two-dozen participants from 13 higher education institutions and the USDA ARS. Participants learned about gene and genome structure, natural variation, gene expression, sequencing technologies, and bioinformatics to eventually assess the quality of computationally predicted gene models using gene annotation tools from their homes. While COVID has presented challenges for traditional outreach, it has also prompted us to rethink opportunities for virtually learning, and created new opportunities to support higher education and remote work.

Nottingham Arabidopsis Stock Centre (NASC)
http://arabidopsis.info/

Sean May
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Director

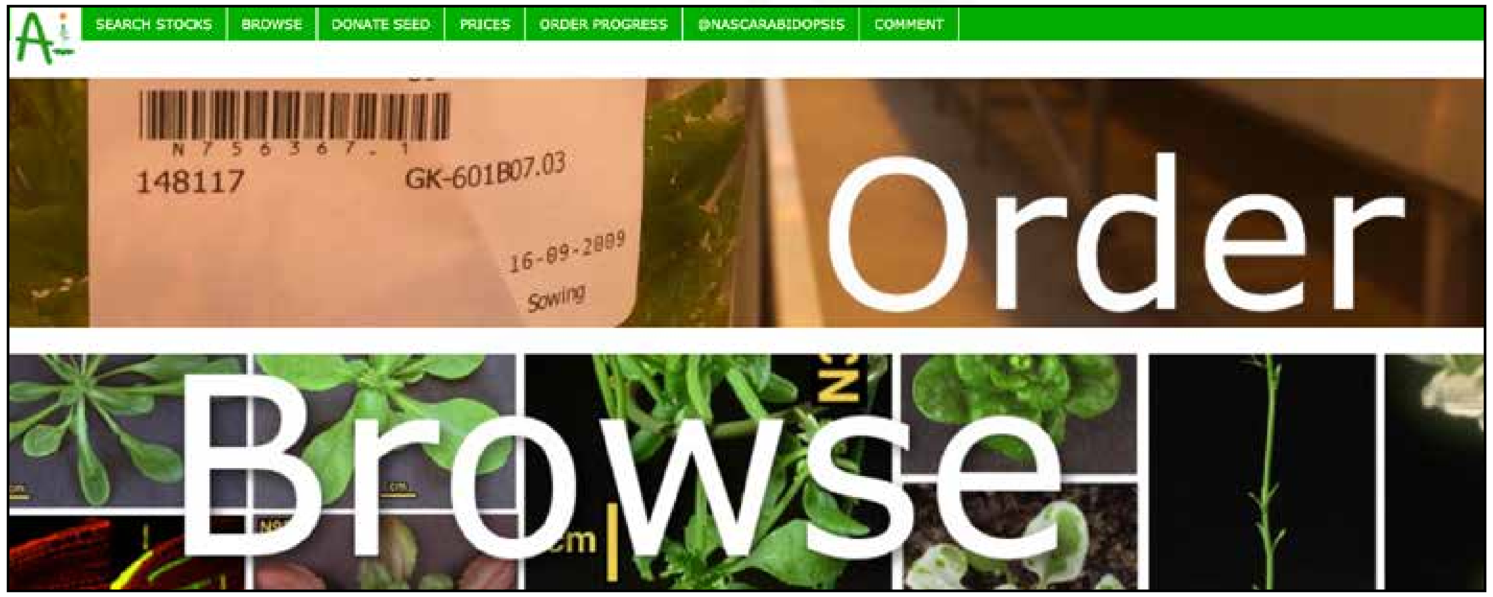
Marcos Castellanos-Uribe
Operations Manager

Recent activities and newly developed tools and/or resources

NASC saw a temporary decline in the numbers of stocks ordered during early 2020. This was particularly noticeable for China during February and some European labs from March as individual groups and departments ramped down their work. That said, orders from countries such as Germany did not noticeably slow, and many institutes worldwide rebounded rapidly in the spring. Most noteworthy was the dramatic resurgence in orders from China from the first week of April 2020.

In terms of numbers of individual stocks delivered for 2020, the highest recipient countries were China, Germany, Sweden, and Switzerland. Orders have remained relatively high throughout the pandemic to a grand total of 68,700 stocks sent in 2020, showing that Arabidopsis research has proven to be a robust area of science even in the 'year of living dangerously / year that time forgot'. During early 2021, outgoing numbers of stocks have been slightly lower than in 'normal' years reflecting the unfortunate 3rd wave across many countries (and associated restrictions).

NASC/ABRC collaboration via exchange of donated and bulked seed stocks and associated data has not been slowed by the pandemic, even if the mail has been. International mail issues have repeatedly impacted ease of stock distribution to many countries during the various lockdown periods. This speed of distribution has been made even more taxing due to an increased need for phytosanitary certification during 2020. If your seeds have taken a little longer to reach you than normal, we apologise. Please do contact us if you have not received seed in a reasonable time and we will follow up. Some especially good news for 2020/21 is that we have enjoyed a larger than normal rate and diversity of new Arabidopsis seed donations into the collection – thank you!



Not all new donations have been Arabidopsis. During lockdown we have co-ordinated with John Sedbrook (Illinois) - representative of the Thlaspi community, to incorporate (new for 2021) a more extensive and diverse Thlaspi collection. On top of the stocks already distributed for many years we now have the following collections [numbers of lines]: Machova_ / Czech Republic [63]; Wrench / UK [7]; Wirth / Germany [29], Galanti European WGS lines [200], Esfahanian / US [260], Sedbrook / Canada [100], with more on the way (e.g. from Russia).

If you know of any Arabidopsis or other model organism lines that would be usefully held at the Stock Centres, please let us know – we may have overlooked them.

In funding news, our 5-year renewal grant was submitted to the BBSRC/UKRI (November 2020, Bioinformatics and Biological Resources Fund) and was successfully funded – a big thank you to everyone involved.

For up-to-date details on stock donations or anything else that you wish to know, please do 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 do contact us - don’t wait for us to come to you.

RIKEN BioResource Research Center
https://web.brc.riken.jp/en/

Masatomo Kobayashi
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Recent activities and newly developed tools and/or resources

RIKEN BRC collects and distributes model plant resources produced in Japan under the support by Japanese government. In 2020, a series of binary vectors deposited from Dr. Tsuyoshi Nakagawa, Shimane University, was added to our Exp-Plant Catalog and distributed to the research community. https://plant.rtc.riken.jp/resource/pdi/pdi_list.html

Planned future activities

We will start distributing some more plant cultured cell lines including that from Arabidopsis. Collection and distribution of mutants and transgenic Arabidopsis lines established in Japan will be continued.

Please provide a paragraph describing the general impact of the COVID19 pandemic on your activities

The outbreak of COVID-19 greatly affects the operation of our project. Due to the state of emergency declared in April, we suspended deposition/distribution of bioresources for 3 months. In addition, international shipment of resource was seriously disturbed due to the temporary suspension of acceptance as well as delivery delays of mail items destined to various countries/territories

The Arabidopsis Information Resource (TAIR)
https://www.arabidopsis.org/

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with input from Tanya Berardini, tberardini@arabidopsis.org; Sabarinath Subramaniam, shabari@arabidopsis.org, Eva Huala, huala@arabidopsis.org

Recent activities and newly developed tools and/or resources

In 2020 we released or updated tools for comparative genomics, genome visualization and functional annotation. We released a new Synteny Viewer. This tool uses pre-computed syntenic comparisons between *A.thaliana* and genomes from 36 other plant species. Users can query for syntelogs using either AGI locus IDs (e.g., AT1G68640), AGI gene model IDs (e.g., AT1G68640.1) or chromosomal location (e.g.1:25769576..25772650). Syntenic comparisons were generated using the SynMap tool at CoGE and syntenic regions are displayed using the CoGE GEvo tool. After taking over the updating and maintenance of JBrowse from the Araport project, we continue to add new data tracks on a regular basis. New/updated data includes TIF-seq and plaNET-seq Data from the Marquardt lab, and Ws/Ws-2 polymorphism data from GBrowse. Please see the JBrowse release notes for more information on the specific updates and changes.

Finally, we released a new tool to enable community curation of gene function called the Generic Online Annotation Tool (GOAT, https://goat.phoenixbioinformatics.org/). GOAT replaces the Arabidopsis- and TAIR-centric TOAST tool for collecting Gene Ontology and Plant Ontology annotations from the research community and offers some significant improvements including the ability to save a submission in progress, sign in using ORCiD, and the ability to annotate any gene from any organism. Future updates will further improve the functionality of the tool. Other activities in the past year include outreach in the form of online webinars, scheduled public data releases and data curation. We took advantage of 'captive' home audiences to launch a webinar series using Zoom and Voov (for users in China) platforms. The recorded webinars are available at our YouTube Channel and on Bilibili (for users in China).

In 2020 as part of our long-term goal to produce a 'gold standard' annotated reference genome, we continued to produce and incorporate new Arabidopsis gene function annotations made by curators and members of our community. As of March 2021, the percentages of protein-coding Arabidopsis genes with GO annotations are as follows: For GO molecular function, 29% have at least one experimentally based annotation, another 30% have no experimental annotation but at least one based on other evidence. For GO biological process 31% have experimentally based annotations and another 26% have annotations based on other evidence. For GO cellular component 35% have experimentally supported annotations, another 55% have annotations based on other types of evidence.

Planned future activities

In 2021 we will continue our functional annotation efforts, adding new data to our database and tools, enhancing the usability of our tools and website, and outreach to broaden access. We continue to prioritize curation of previously 'unknown' genes and capturing 100% of novel gene functions as they are published. As time permits, we are delving into our backlog to identify and capture information that were unable to in previous years.

We plan improvements to the GOAT community curation tool to improve usability. To comply with the directives from the Gene Ontology Consortium, GO annotations from GOAT and TAIR will now be exported in GAF2.2 format. For JBrowse, we plan to continue adding new data including transcriptomic, proteomic and community submitted tracks. Please contact us if you have data that you think would be appropriate to share via JBrowse. We also plan to integrate the new JBrowse2 into TAIR. Planned updates for Synteny Viewer include the addition of viewing options for JBrowse2 and the NCGR Genome Context Viewer. We hope to complete a long-planned overhaul of our Locus page user interface to improve data visibility.

Please provide a paragraph describing the general impact of the COVID19 pandemic on your activities

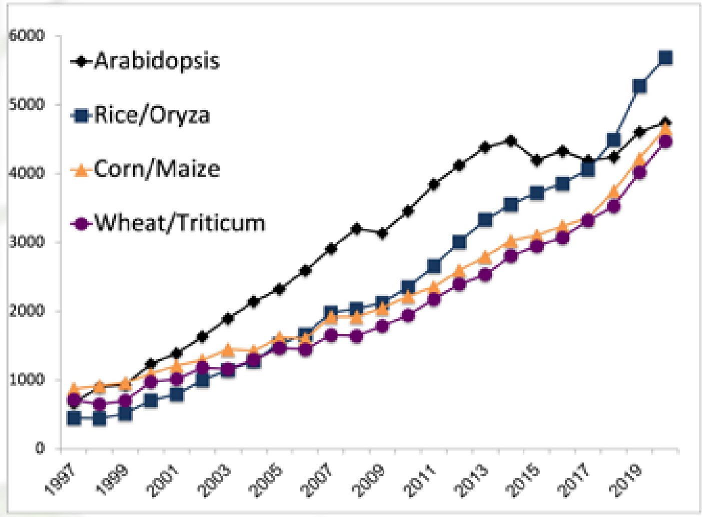
In March 2020, in response to the global shelter in place order, TAIR lifted monthly limits until June 30, 2020 to ensure that researchers working from home were able to access TAIR. Due to the ongoing impacts of COVID19 on the academic community TAIR has experienced downstream effects of reduced university budgets on subscriptions. To reduce costs, Phoenix Bioinformatics, where TAIR is maintained, has made remote work permanent for all employees.

Update on Arabidopsis Publications

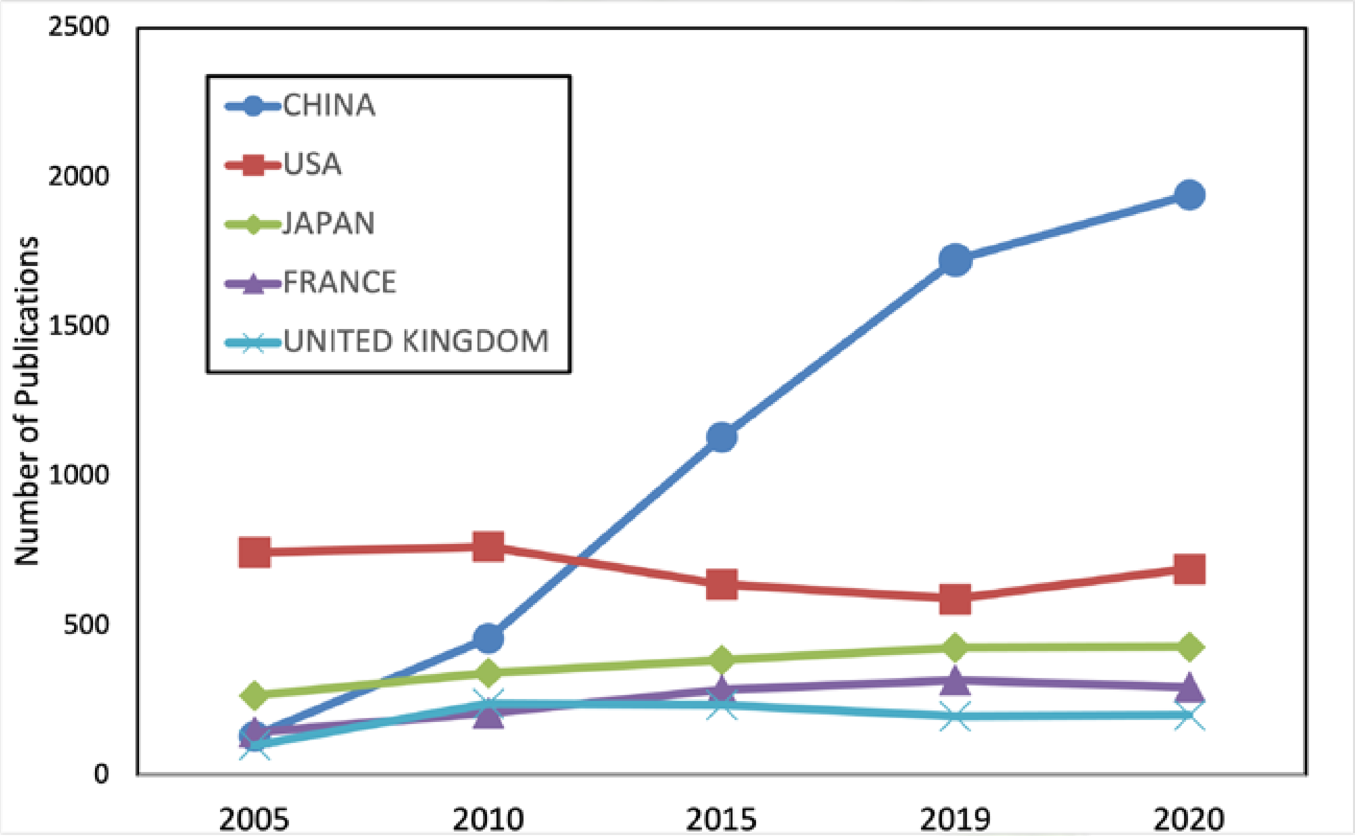
Global Outlook for 2021

In 2020 Arabidopsis remains the second much popular plant included in publications listed on PubMed. However the trend continues in which the increase in the number of Arabidopsis publications is slower than the increases in publications that that feature Rice, Maize or Wheat. This will be final year that 'Arabidopsis publications' stay ahead of 'Maize publications and 'Wheat publications' as global research seemingly moves toward more applied plant science. Another factor in these changes come as a consequence of the technical innovations have allow more 'discovery-led research' to be conducted in non-Arabidopsis plants.

The number of global Arabidopsis publications has risen over the past two years after a seven year period of stability. However the rate of increase is at a slower rate than rise observed in other plant species. Exploring the reasons behind the rapid increase in the number of 'rice publications' is outside the remit of this report. However over the last 3 years there has been a more rapid rise in the number of 'CRISPR and rice' rather than 'CRISPR and Arabidopsis' publications. Gene editing technology is maybe different to other genomic techniques since its uptake has happened concurrently in many experimental systems as its effectiveness isn't significantly impacted by genomic size.



Papers published in Pubmed journals globally with Arabidopsis, Rice/Oryza, Corn/Maize or Wheat/Triticum in the Title/Abstract.

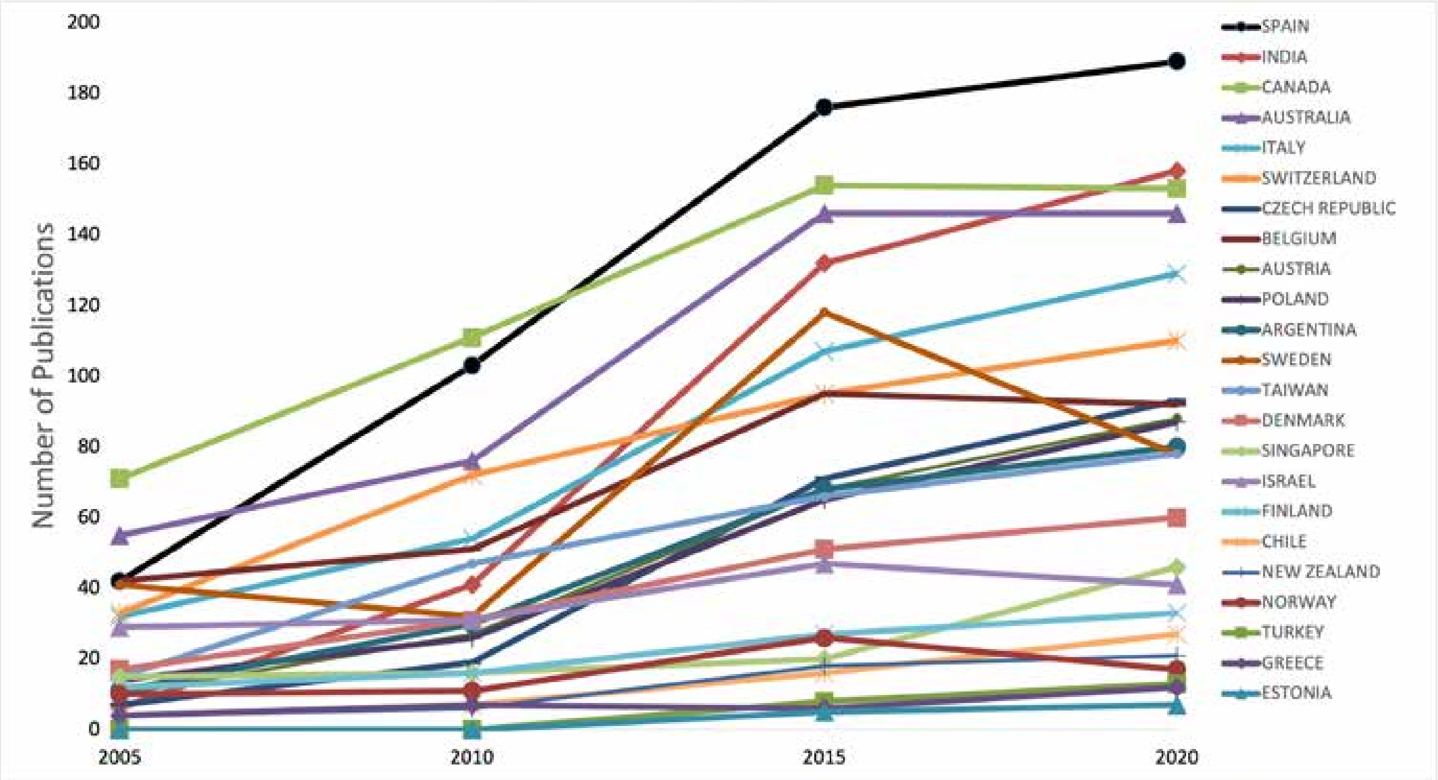


Papers published in Pubmed journals between 2005-2020 vwith Arabidopsis in the Title/Abstract. Globally these countries have the highest number of publications of those included in this MASC report..

Country Outlook

The 'Arabidopsis publications' from China have again impressively increased from 2019 -> 2020 albeit at a slower rate. These number of outputs is remarkable and drives the global positive trend in the number of Arabidopsis publications. It remains to be seen whether this slower increase continues over the coming years but the trend from other countries suggests that this will be the case. The other nations included in this report with the highest number of publications continue to show a plateau in these numbers, reflecting the global trend outside of China and a few other countries.

Looking at the number of 'Arabidopsis publications' for other nations included in this report it shows that the majority of nations show an absolute increase in the number of published papers since 2015. However some countries have shown a larger rise, including India where the number of papers rose to ~150 in 2020, up from <40 papers in 2010. Hopefully this is a sign that improved laboratory facilities will support a continued increase of productivity over coming years.



Papers published in Pubmed journals between 2005-2020 with Arabidopsis in the Title/Abstract. These countries are included in this edition of the MASC report.

MASC COUNTRY REPORTS

Argentina

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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 2020 or early 2021

Funding was mostly directed to COVID-19 projects and tools were focused on providing regional solutions for pandemic related issues. If those tools will be available or provide solutions for Arabidopsis researchers, we will know soon.

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

Research activities in the whole country were stalled by COVID19. With very few exceptions, most research centers, universities and institutes remained in lockdown until the end of the year, meaning scientists couldn't access their workplaces for months. On top of that, schools were closed for the school year, adding an extra burden to families, especially to women scientists. This will affect the scientific community in general for years to come.

Planned events for 2021 and 2022

- XXXIII Argentinian meeting of Plant Physiology (Reunión Argentina de Fisiología Vegetal), September 13-17, 2021, Santa Fe, Argentina. https://rafv2020.wixsite.com/santa-fe

- XXXVIII Jornadas Argentinas de Botánica (Argentinian Botany Meeting), September 6-8 2021, Entre Ríos, Argentina. Virtual. https://botanicaargentina.org.ar/xxxviii-jornadas-argentinas-de-botanica-entre-rios-2021/

- XLIX Congreso Argentino de Genética / XVIII Congreso Latinoamericano de Genética (Argentinian / Latin American Genetics joint conference), October 5-8, 2021, Valdivia, Chile. https://alagenet.org/alag2021/

- 2° Reunión Argentina de Biología de Semillas (Seed Biology Argentinian Network meeting), October 2021, Salta, Argentina. https://redargentinasemillas.weebly.com/reuniones.html

- LVII Reunión Anual de la SAIB (Argentinian Society for Research in Biochemistry and Molecular Biology, 57th annual meeting), November 1-4, 2021. http://www.saib.org.ar/sites/default/files/SAIB-Circular_1_2021.pdf

- The ARG Plant Women network offers weekly virtual seminars and monthly professional development workshops (in Spanish). https://argplantwomen.weebly.com/.

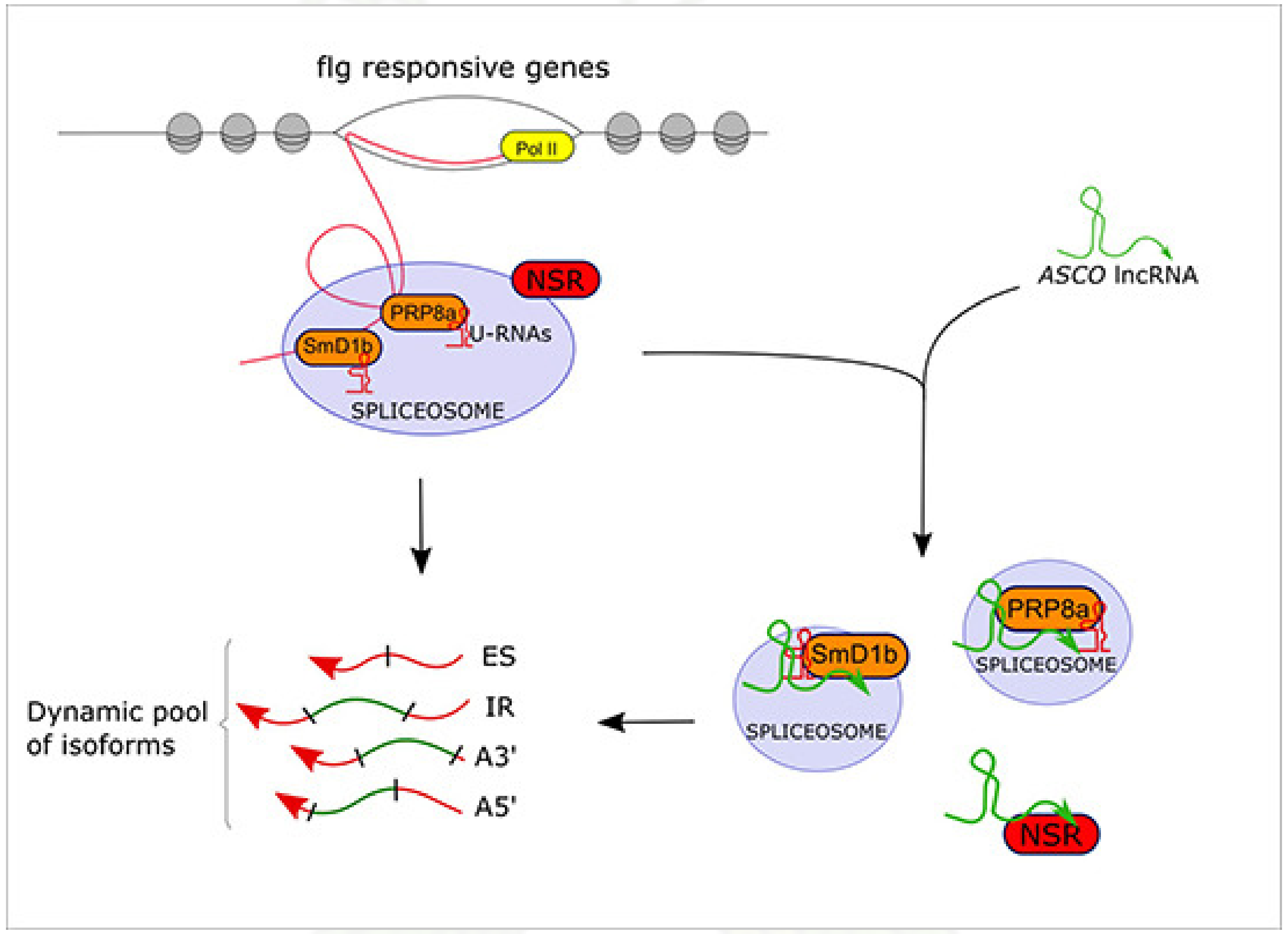
Selected Publications

- “Single-stranded oligodeoxynucleotides induce plant defence in *Arabidopsis thaliana*”Laila Toum, Gabriela Conti, Francesca Coppola Guerriero, Valeria P Conforte, Franco A Garolla, Sebastián Asurmendi, Adrián A Vojnov, Gustavo E Gudesblat. 2020. Annals of Botany, 126 413–422, https://doi.org/10.1093/aob/mcaa061

Publication from a recently established group showing the potential use of effectors as defense inducers (with applications in agriculture) using Arabidopsis as study model.

- “The Arabidopsis lncRNA ASCO modulates the transcriptome through interaction with splicing factors” Richard Rigo, Jérémie Bazin, Natali Romero-Barrios, Michaël Moison, Leandro Lucero, Aurélie Christ, Moussa Benhamed, Thomas Blein, Stéphanie Huguet, Céline Charon, Martin Crespi, Federico Ariel. 2020. EMBO Reports, 21:e48977 https://doi.org/10.15252/embr.201948977

An international collaborative project led by an awarded early career researcher.



The Arabidopsis lncRNA ASCO is bound by multiple splicing factors, including spliceosome core components. ASCO deregulation modulates alternative splicing of specific genes, thus shaping the global transcriptome and plant response to flagellin.

- The Arabidopsis lncRNA ASCO is recognized by multiple splicing factors.
- ASCO deregulation affects the alternative splicing of a specific subset of genes.
- ASCO deregulation alters the Arabidopsis response to flagellin.

- “Pathogenicity and toxicity of Fusarium tucumaniae and Fusarium crassistipitatum to soybean and *Arabidopsis thaliana*” Romina G. Rosati, Rocío S. Ramos, María M. Scandiani, Alicia G. Luque, Claudia P. Spampinato. 2021. Plant Pathology, 70: 407-416 (first published September 2020) https://bsppjournals.onlinelibrary.wiley.com/doi/full/10.1111/ppa.13286

A publication of an all-women team describing the use of Arabidopsis as a tool to study pathogens of regional importance for agricultural production.

- “*Arabidopsis thaliana* SURFEIT1-like genes link mitochondrial function to early plant development and hormonal growth responses” Diana E. Gras, Natanael Mansilla, Carina Rodríguez, Elina Welchen, Daniel H. Gonzalez. 2020. The Plant Journal, 103: 690-704. https://onlinelibrary.wiley.com/doi/full/10.1111/tpj.14762

A very elegant study of a senior researcher and his group.

Major Funding Sources

- Agencia Nacional de Promoción de la Investigación, el Desarrollo Tecnológico y la Innovación (Agencia I+D+i), Ministerio de Ciencia, Tecnología e Innovación.
There is a yearly call for proposals, unfortunately it was not opened during 2020 (the last call was on November 2019, results were announced in mid-February; the new call is open now until mid-March) http://www.agencia.mincyt.gob.ar/frontend/agencia/convocatorias

- Consejo Nacional de Ciencia y Tecnología (CONICET). There was a proposal call for pluriannual grants during 2020 (last time opened was 2017). https://convocatorias.conicet.gov.ar/proyectos-pip/

- Some universities (such as Universidad de Buenos Aires, Universidad Nacional de Quilmes, Universidad Nacional del Litoral, etc) and provincial science agencies (Santa Fe, Córdoba, Buenos Aires, Chubut) open calls for proposals.

- Other sources are foundations such as Fundación Bunge y Born. I’m not sure though how much they provide support to the Arabidopsis community as calls from these sources are open to all disciplines.

- Argentinian scientists have access to some international funding sources such as the ICGEB grant calls (https://www.icgeb.org/activities/grants/).

Australia

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Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

Whilst Australia has had relatively low numbers of infection, the pandemic has affected most academic, industry and government based research facilities at varying degrees. States such as Victoria underwent lock-down for up to 6 months, delaying many research projects, whilst Western Australia, with almost no community transmission did not experience any significant lock-downs. Nevertheless, we have all felt the downstream consequences ranging from minor shipment delays, increased teaching and carers loads from online teaching/learning, to major university restructures due to economic losses from the lack of international students. Strict travel bans has generally prevented travel across states (and internationally) resulting in almost all conferences and symposiums cancelled and/or rescheduled.

Planned events for 2021 and 2022

- 13th International Congress on Plant Molecular Biology (IPMB), Cairns Convention Centre, Queensland, 23-27 Oct 2022. https://ipmb2022.org/ ASPS 2021.

- The annual Australian Society of Plant Biologists meeting for 2021 will be a hybrid conference spread across multiple locations Australia wide (www.asps.org.au).

- 25th November 2021. COMBIO 2022 Melbourne Convention and Exhibition Centre. Annual national conference that includes several symposia dedicated to plant research. This conference incorporated the annual Australian Society of Plant Biologists meeting for 2022. 27-30th September 2022. http://www.combio.org.au

Selected Publications

1. Roman, A., *et al.*, Superoxide is promoted by sucrose and affects amplitude of circadian rhythms in the evening. Proc Natl Acad Sci U S A, 2021. 118(10).

Here researchers have identified that reactive oxygen species (ROS) act as a metabolic signal associated with sugar levels, which acts on the circadian oscillator in the evening in Arabidopsis.

2. Sun, Y.K., *et al.*, Divergent receptor proteins confer responses to different karrikins in two ephemeral weeds. Nat Commun, 2020. 11(1): p. 1264.

Researchers have identified the residues near the karrikin receptor, KAI2 active site that are required for ligand selectivity, highlighting the diversification of KAI2 and the differential responses to fire smoke.

Seedling and rosette phenotypes of two independent transgenic lines of Arabidopsis homozygous for KAI2pro:GFP-BtKAI2 transgenes. Seedlings were 7 days old and rosettes 22 days old. Scale bars: 5 mm

3.Xu, B., *et al.*, GABA signalling modulates stomatal opening to enhance plant water use efficiency and drought resilience. Nat Commun, 2021. 12(1): p. 1952.

Researchers have identified that the non-protein amino acid _-aminobutyric acid (GABA) can act as a signaling molecule to reduce stomatal opening, improving water use efficiency and drought tolerance

Major Funding Sources

- Fundamental and translational research can be funded by the Australian Research Council (www.arc.gov.au)

- Translational research is funded by the Grains Research Development Corporation (http://grdc.com.au)

- Industry collaborations can be funded by the Australian Research Council Linkage Programs (www.arc.gov.au)

Austria

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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 2020 or early 2021

PHENOplant was funded by the FFG and final construction work finished in early 2021 at the GMI. The new platform is designed for mid-size crop plants as well as Arabidopsis and is fully integrated into a state-of-the-art walk-in phytotron providing highly homogeneous plant growth conditions. Furthermore, the platform will allow precise environmental simulations across different climate zones as well as controlled plant stress experiments. Within the planned infrastructure, plants will be transported on conveyor belts from the growth area to the imaging cabinets equipped with high-tech sensors. Apart from 3D RGB imaging, morphometric parameters, and color classifications derived from top- and side-view RGB imaging, the infrastructure will deliver data on PAM chlorophyll fluorescence which is used for monitoring abiotic and biotic stresses that affect photosynthetic mechanisms (e.g. drought-, heat-, and light stress, nutrient deficiencies, heavy metal toxicities, fungal infections etc.). Hyperspectral imaging (VNIR and SVIR) will provide additional complex data on crop condition and health.

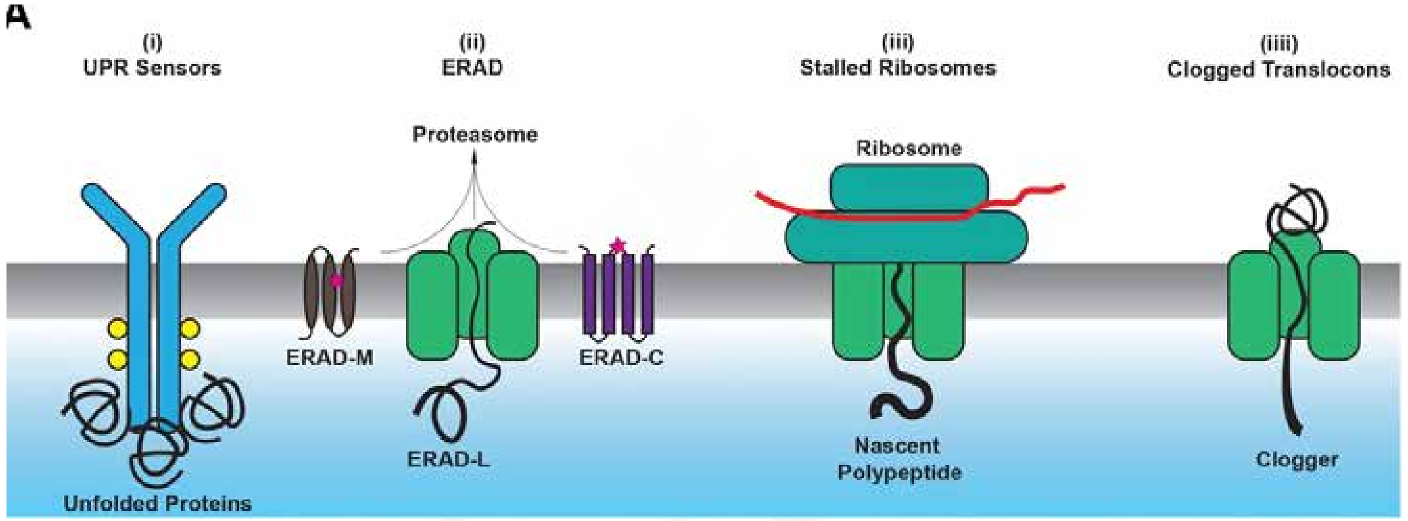
Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

This year has been extraordinarily challenging. However, thanks to outstanding initiatives developing SARS-CoV2-testing pipelines at the Campus Vienna BioCenter/GMI as well as at the Department of Applied Genetics and Cell Biolology (DAGZ) of the University of Natural Resources and Life Sciences, Vienna regular PCR/LAMP tests 2-3 times weekly have allowed to continue doing research but with reduced laboratory hours.

Planned events for 2021 and 2022

In 2020, most of our outreach activities moved online:
- The GMI provided teachers with an online-learning- and game tool “GMI4kids” and participated in the ZOOM-childrens’ University, broadcasted podcasts (within the academy’s podcast-series “makro-mikro”).

- Furthermore, the GMI published several “science for the public”-films via their youtube channel. In addition, the GMI developed a new outdoor game, an extension to “Botanic Quest” – ND-quest. This is a quiz around some of the natural monuments in Vienna. It had been developed together with the City of Vienna and proved to be ideal for people of all ages during the pandemic.



C53 is not activated by associating with UPR sensors. Cartoon depicting the four scenarios we tested to understand the mechanism of activation of C53. doi: 10.7554/eLife.58396

Selected Publications

- Borg M, Jacob Y, Susaki D, LeBlanc C, Buendía D, Axelsson E, Kawashima T, Voigt P, Boavida L, Becker J, Higashiyama T, Martienssen R, Berger F. (2020) Targeted reprogramming of H3K27m;3 resets epigenetic memory in plant paternal chromatin. Nat Cell Biol, Bd. 22 (6), S. 621-629. DOI: 10.1038/s41556-020-0515-y

This works describes a novel mechanism that enables plants to reset epigenetic states with specialized histone variants.

- Stephani M, Picchianti L, Gajic A, Beveridge R, Skarwan E, Sanchez de Medina Hernandez V, Mohseni A, Clavel M, Zeng Y, Naumann C, Matuszkiewicz M, Turco E, Loefke C, Li B, Dürnberger G, Schutzbier M, Chen HT, Abdrakhmanov A, Savova A, Chia KS, Djamei A, Schaffner I, Abel S, Jiang L, Mechtler K, Ikeda F, Martens S, Clausen T, Dagdas Y. (2020) A cross-kingdom conserved ER-phagy receptor maintains endoplasmic reticulum homeostasis during stress. Elife, 9:e58396. doi: 10.7554/eLife.58396.

This work was a large collaboration involving all 4 institutes at the Vienna BioCenter, detailing the discovery of a cross-kingdom conserved ER autophagy receptor.ATM controls meiotic DNA double-strand break formation and recombination and affects synaptonemal complex organization in plants

- Kurzbauer MT, Janisiw MP, Paulin LF, Prusén Mota I, Tomanov K, Krsicka O, Haeseler AV, Schubert V, Schlögelhofer P. Plant Cell. 2021 doi: 10.1093/plcell/koab045.

ATM is essential to limit the number of meiotic double-strand breaks and affects chromatin loop size and synaptonemal complex length and width.

Major Funding Sources

- Austrian Science Fund (FWF) https://www.fwf.ac.at/

- European Research Council (ERC) https://erc.europa.eu/ - Vienna Science and Technology Fund (WWTF) https://www.wwtf.at/

- Austrian Research Promotion Agency (FFG) https://www.ffg.at/en

Belgium

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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 2020 or early 2021

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

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

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

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

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

The impact of COVID-19 on academic research and training of scientists in Belgium has been, and continues to be, severe. Several country-wide lockdowns reduced work efficiency drastically. To guarantee work safety, staff presence in institutes was reduced to as much as 30% of normal occupancy. Remote work from home was obligatory for periods of time. No face-to-face meetings have happened for lengthy periods of time, and regular seminars and lectures have been cancelled altogether for some time before online formats had been set up. Also undergrad students had to largely switch to online courses, and hands-on training in the lab was drastically reduced. Young scientists with short-term contracts (PhD students, postdocs) were hit hard as many of them could not finish projects before their contracts ended.

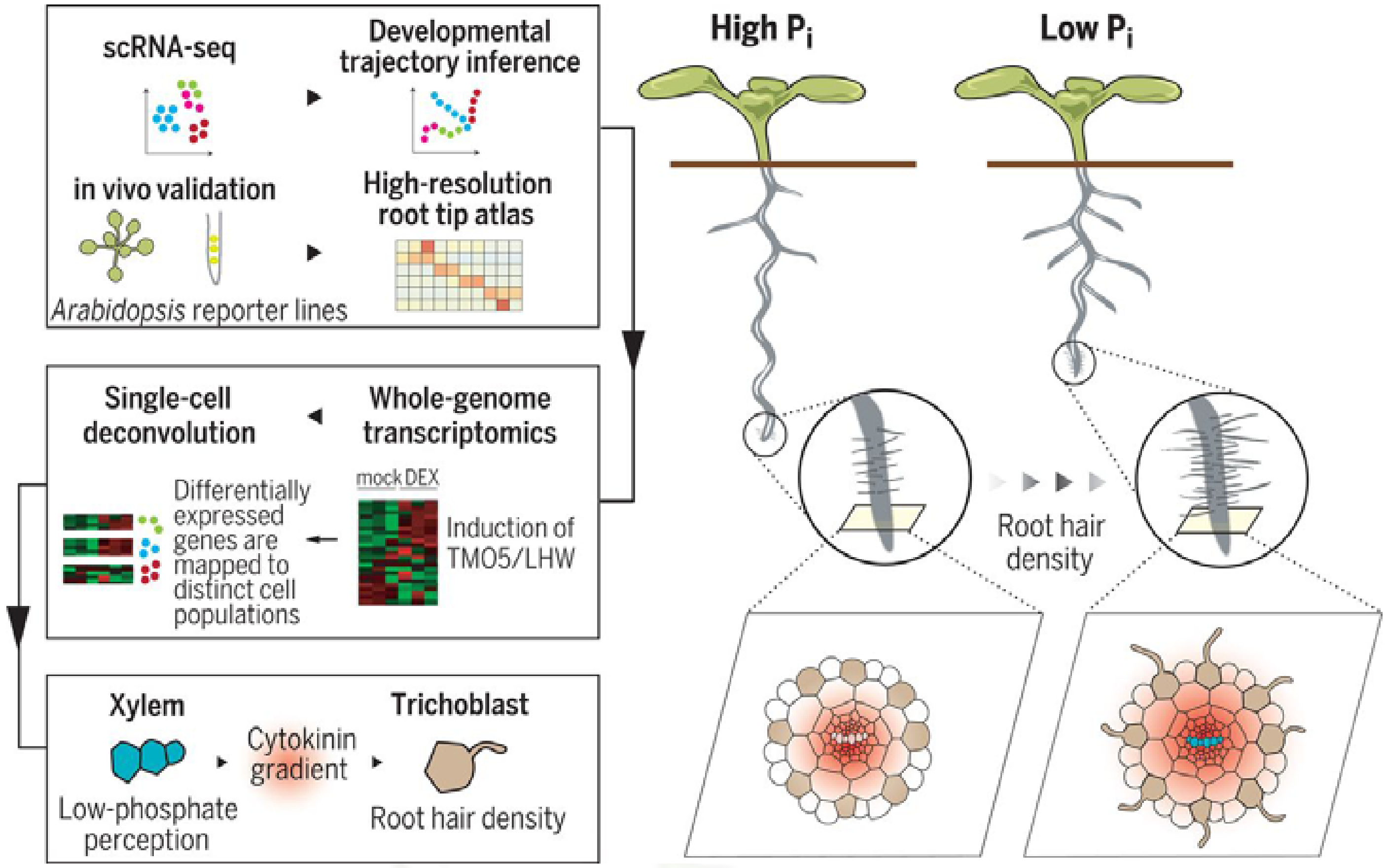
Finally also private life has suffered – for expats it was very difficult, or for periods of time impossible, to visit partners or family in other countries. Social life has been severely reduced, which is again especially hard for expats with a limited local social and family bonds. Parents of young children had to combine work with childcare and homeschooling for many months. Especially for foreigners without local family support, and for couples with both partners working full time, this situation was, and continues to be, difficult to manage.

Planned events for 2021 and 2022

- 72nd ISPCI International Congress of Crop Protection (ONLINE) May 18, 2021 Ghent, Belgium https://www.ugent.be/bw/plants-and-crops/iscp/en

- Plant Science for Climate Emergency (ONLINE) June 7-9, 2021 Ghent, Belgium https://www.vibconferences.be/events/plant-science-for-climate-emergency

- SEB Annual Meeting 2021 June 29 – July 2, 2021 Antwerp, Belgium https://www.sebiology.org/events/event/seb-antwerp-2021 - GCC2021



Vascular transcription factors guide epidermal responses.
A validated high-resolution single-cell gene expression atlas of the Arabidopsis root was intersected with TMO5/LHW target genes, uncovering an enrichment of epidermal-restricted expression patterns. By activating local cytokinin biosynthesis, the vascular TMO5/LHW complex was shown to regulate epidermal root hair density in response to the availability of phosphate. scRNA-seq, single-cell RNA-sequencing; mock, untreated condition; DEX, dexamethasone; Pi, inorganic phosphate.

– Galaxy Community Conference July 5-12, 2021 Gent, Belgium https://www.vibconferences.be/events/gcc2021

- Genome Engineering and Synthetic Biology (ONLINE) September 22-24, 2021 https://www.vibconferences.be/events/genome-engineering-and-synthetic-biology-virtual-4th-edition

- 4th International Brassinosteroid Conference August, 17-19 2022 Ghent, Belgium (meeting website will be set up soon)

Selected Publications

De Clercq I, Van de Velde J, Luo X, Liu L, Storme V, Van Bel M, Pottie R, Vaneechoutte D, Van Breusegem F, Vandepoele K.Nat Plants. 2021 Apr;7(4):500-513. doi: 10.1038/s41477-021-00894-1

- Integrative inference of transcriptional networks in Arabidopsis yields novel ROS signalling regulators.

Wendrich JR, Yang B, Vandamme N, Verstaen K, Smet W, Van de Velde C, Minne M, Wybouw B, Mor E, Arents HE, Nolf J, Van Duyse J, Van Isterdael G, Maere S, Saeys Y, De Rybel B.Science. 2020 Nov 13;370(6518):eaay4970. doi: 10.1126/science.aay4970. Epub 2020 Sep 17.

- Complementary information about Arabidopsis DNA motifs, open chromatin, transcription factor-binding and expression-based regulatory interactions were combined using a supervised learning approach to generate an integrated gene regulatory network (iGRN), correctly inferring known functions for 681 transcription factors and predicted hundreds of new gene functions. Vascular transcription factors guide plant epidermal responses to limiting phosphate conditions.

Canher B, Heyman J, Savina M, Devendran A, Eekhout T, Vercauteren I, Prinsen E, Matosevich R, Xu J, Mironova V, De Veylder L.Proc Natl Acad Sci U S A. 2020 Jul 14;117(28):16667-16677. doi: 10.1073/pnas.2006620117. Epub 2020 Jun 29

- By generating and exploiting a high-resolution single-cell gene expression atlas of Arabidopsis roots, an enrichment of TARGET OF MONOPTEROS 5/LONESOME HIGHWAY (TMO5/LHW) target gene responses in root hair cells was revealed, and shown to increase root hair density during low-phosphate conditions by modifying both the length and cell fate of epidermal cells.Rocks in the auxin stream: Wound-induced auxin accumulation and ERF115 expression synergistically drive stem cell regeneration.

Fernandez AI, Vangheluwe N, Xu K, Jourquin J, Claus LAN, Morales-Herrera S, Parizot B, De Gernier H, Yu Q, Drozdzecki A, Maruta T, Hoogewijs K, Vannecke W, Peterson B, Opdenacker D, Madder A, Nimchuk ZL, Russinova E, Beeckman T.Nat Plants. 2020 May;6(5):533-543. doi: 10.1038/s41477-020-0645-z. Epub 2020 May 11.

- A combination of cellular imaging and in silico modeling demonstrates that wound-induced vascular stem cell death obstructs the polar auxin flux, and causes auxin to accumulate in the endodermis, which grants the endodermal cells the capacity to undergo periclinal cell division to repopulate the vascular stem cell pool.GOLVEN peptide signalling through RGI receptors and MPK6 restricts asymmetric cell division during lateral root initiation.

Liu D, Kumar R, Claus LAN, Johnson AJ, Siao W, Vanhoutte I, Wang P, Bender KW, Yperman K, Martins S, Zhao X, Vert G, Van Damme D, Friml J, Russinova E.Plant Cell. 2020 Nov;32(11):3598-3612. doi: 10.1105/tpc.20.00384. Epub 2020 Sep 21.

- Endocytosis of BRASSINOSTEROID INSENSITIVE1 Is Partly Driven by a Canonical Tyr-Based Motif.

Wei P, Demulder M, David P, Eekhout T, Yoshiyama KO, Nguyen L, Vercauteren I, Eeckhout D, Galle M, De Jaeger G, Larsen P, Audenaert D, Desnos T, Nussaume L, Loris R, De Veylder L.Plant Cell. 2021 Jan 25:koab005. doi: 10.1093/plcell/koab005.

- Arabidopsis casein kinase 2 triggers stem cell exhaustion under Al toxicity and phosphate deficiency through activating the DNA damage response pathway.

He H, Denecker J, Van Der Kelen K, Willems P, Pottie R, Phua SY, Hannah MA, Vertommen D, Van Breusegem F, Mhamdi A.Plant Cell. 2021 Mar 13:koab079. doi: 10.1093/plcell/koab079. Online ahead of print.

- The Arabidopsis Mediator Complex Subunit 8 Regulates Oxidative Stress Responses

Wang J, Yperman K, Grones P, Jiang Q, Dragwidge J, Mylle E, Mor E, Nolf J, Eeckhout D, De Jaeger G, De Rybel B, Pleskot R, Van Damme D.Proc Natl Acad Sci U S A. 2021 Apr 13;118(15):e2023456118. doi: 10.1073/pnas.2023456118.

- Conditional destabilization of the TPLATE complex impairs endocytic internalization.

Major Funding Sources

- Flanders Institute for Biotechnology (VIB; www.vib.be

- European Union Framework Programs (cordis.europa.eu/)

- Belgian Federal Science Policy Office (www.belspo.be)

-Research Foundation – Flanders (FWO; http://www.fwo. be/en/index.aspx)

- Fonds de la Recherche Scientifique (FNRS; http://www.frs-fnrs.be)

-European Research Council (http://erc.europa.eu/)

Canada

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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 2020 or early 2021

The Bio-Analytic Resource has added a number of new resources:

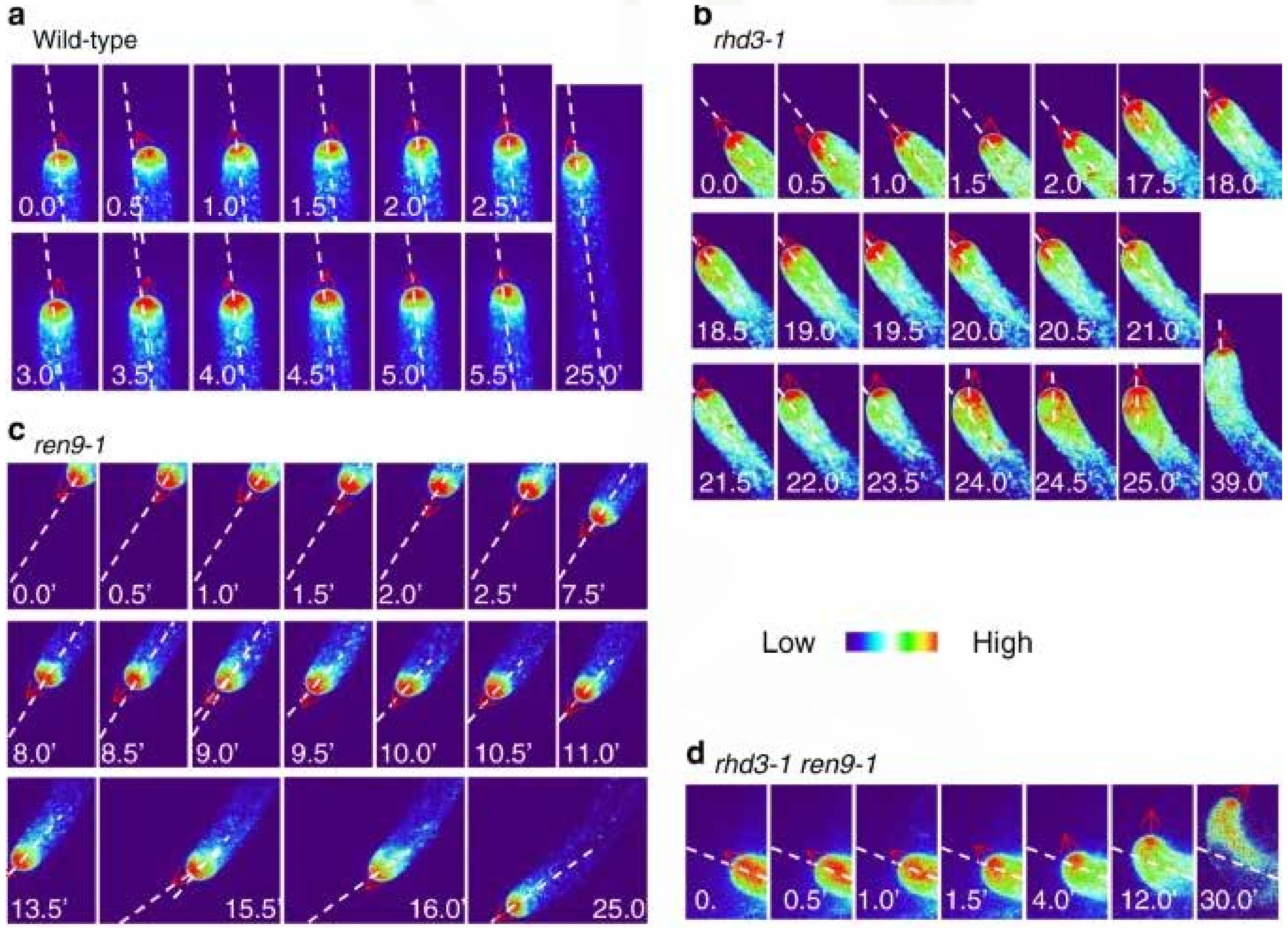
- An Arabidopsis Lipid Map eFP Browser

- A Cell-type specific immunity viewer for roots in ePant.

- Plant Reactome pathways viewer in ePlant.

- A new tool called AGENT for exploring gene regulatory networks and another, Variant Viewer, for natural variation.

- Protein complex information based on mass spectrometry has been integrated into the Arabidopsis Interactions Viewer database.



Heatmap of the targeting of YFP-RAB-A2a in a root hair of wild-type (a), rhd3-1 (b), ren9-1 (c), and rhd3-1 ren9-1 (d)

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

In response to the pandemic, the three main funding agencies, including the Natural Sciences and Engineering Research Council of Canada (NSERC) which funds most Arabidopsis research in Canada, extended the period for use of research grants as well as for scholarships and fellowships. In addition, they provided funds for a one-year extension of existing grants. Funding supplements to support students, postdoctoral fellows, and research support personnel were also provided to help mitigate the impact.

Selected Publications

- Provart NJ, Brady SM, Parry G, Schmitz RJ, Queitsch C, Bonetta D, Waese J, Schneeberger K, Loraine AE. Anno genominis XX: 20 years of Arabidopsis genomics. Plant Cell. 2020 Dec 29:koaa038. doi: 10.1093/plcell/koaa038. Epub ahead of print. PMID: 33793861.

This review provides an overview of the advances that have been made in Arabidopsis twenty years after the publication of its genome sequence.

- Sun J, Zhang M, Qi X, Doyle C, Zheng H. Armadillo-repeat kinesin1 interacts with Arabidopsis atlastin RHD3 to move ER with plus-end of microtubules. NatCommun. 2020 Nov 2;11(1):5510. doi: 10.1038/s41467-020-19343-2. PMID: 33139737; PMCID: PMC7606470.

In this paper the authors identify ARK1 (armadillo-repeat kinesin1) via an enhancer screen of an rdh3 mutant which, like RDH3, impacts the movement of the endoplasmic reticulum on microtbules.

- Bunsick M, Toh S, Wong C, Xu Z, Ly G, McErlean CSP, Pescetto G, Nemrish KE, Sung P, Li JD, Scholes JD, Lumba S. SMAX1-dependent seed germination bypasses GA signalling in Arabidopsis and Striga. Nat Plants. 2020 Jun;6(6):646-652. doi:10.1038/s41477-020-0653-z. Epub 2020 May 25. PMID: 32451447.

This is an elegant study where they authors are able to show that strigolactone dependent germination can bypass the dominant gibberellin dependent germination pathways by negative regulation or inactivation of SUPPRESSOR OF SMAX2 1 (SMAX1).

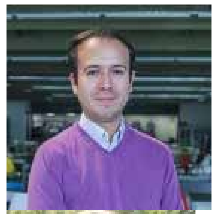
Major Funding Sources

- 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



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Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

The COVID19 pandemic has had a great impact on Chilean research and researchers. The first quarantine led to the interruption of several ongoing projects and delayed the start of new ones. In addition, it impacts the trade system, so reagents and other materials needed for research were scarce and new orders take a significant amount of time to be delivered. Since this quarantine comprised near a 4-month period, it also has an impact in the preparation of reports for projects on its final year of operation and the generation of data for new proposals to be submitted in future calls. Actually, the National Agency for Investigation and Development (ANID) offered an extension for projects in its final year, in order to help researchers to overcome the difficulties to perform research activities. Nowadays, Chilean scientific community is back to the laboratories and trying to retake the research activities as fast as its possible.

Planned events for 2021 and 2022

From April 2021 to January 2022 Plant Biology Colloquiums: A series of virtual meetings hosted by the Chilean Society of Plant Biologists. It included several symposiums for instance 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 Abiotic Stress.

Organizer: Chilean Society of Plant Biologists (https://www.biologiavegetal.cl/)

Guests :Claudia Muñoz (Universidad Andres Bello, Chile), Adrian Moreno (Universidad Andres Bello, Chile), Carlos Figueroa (Universidad de Talca, Chile)Raúl Herrera (Universidad de Talca, Chile) Lee Meisel (INTA, Universidad de Chile, Chile)Anita Arenas (Universidad Austral de Chile, Chile), Jose Ugalde (University of Bonn, Germany), Paula Pimentel (CEAF, Chile)

Selected Publications

- Saez-Aguayo S, Parra-Rojas JP, Sepúlveda-Orellana P, Celiz-Balboa J, Arenas-Morales V, Sallé C, Salinas-Grenet H, Largo-Gosens A, North HM, Ralet MC, Orellana A. (2021) Transport of UDP-rhamnose by URGT2, URGT4, and URGT6 modulates rhamnogalacturonan-I length. Plant Physiol. Apr 2;185(3):914-933. doi: 10.1093/plphys/kiaa070.(https://academic.oup.com/plphys/article-abstract/185/3/914/6054815?redirectedFrom=fulltext)

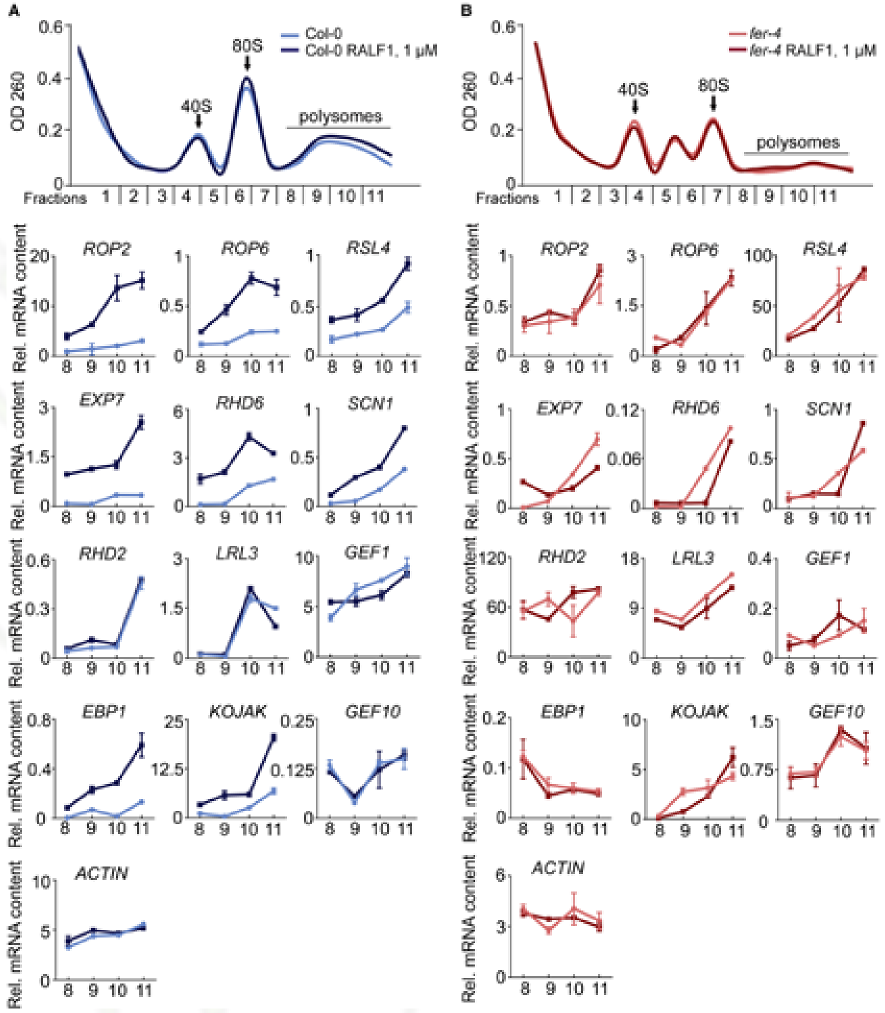
The absence of UDP-Rhamnose transporters has an impact on cell wall polysaccharide synthesis affecting rhamnogalacturonan-I and xylan, reinforcing the role of nucleotide sugar transporters on cell wall biosynthesis.

- Zhu S, Estévez JM, Liao H, Zhu Y, Yang T, Li C, Wang Y, Li L, Liu X, Pacheco JM, Guo H, Yu F. (2020) The RALF1-FERONIA Complex Phosphorylates eIF4E1 to Promote Protein Synthesis and Polar Root Hair Growth. Mol Plant. May 4;13(5):698-716. doi: 10.1016/j.molp.2019.12.014.(https://www.sciencedirect.com/science/article/pii/S1674205219304319)

The link between RALF1–FERONIA signaling, and protein synthesis constitutes a novel component regulating cell expansion in these growing polar cells

- Silva-Sanzana C, Estevez JM, Blanco-Herrera F. (2020) Influence of cell wall polymers and their modifying enzymes during plant-aphid interactions. J Exp Bot. Jun 26;71(13):3854-3864. doi: 10.1093/jxb/erz550.(https://academic.oup.com/jxb/article/71/13/3854/5673625)

This review highlights the different hypotheses, perspectives, and evidence supporting cell wall polymers and modifying enzymes as relevant plant traits for aphid resistance/susceptibility.



RALF1 Affects the Translation of RH Tip Growth-Related Gene Transcripts. (A and B) Top: ribosome profiles. Fractions (8–11) containing mRNAs associated with polysomes are indicated with a black line. Bottom: RT-qPCR results for polysome-associated mRNAs. At least three biological replicates of (A)–(B) were performed with similar results.

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 2020 or early 2021.

- AraShare: A community biological resource center
http://www.arashare.cn/
- Plant Transcriptional Regulatory Map (includes updated PlantTFDB and additional resources)
http://plantregmap.cbi.pku.edu.cn/
- AHD2.0: Arabidopsis hormone database 2.0
https://bigd.big.ac.cn/ahd/
- LSD3.0: Arabidopsis leaf senescence database 3.0
https://bigd.big.ac.cn/lsd/
- PlantGSEA: a gene set enrichment analysis toolkit for plant community
http://structuralbiology.cau.edu.cn/PlantGSEA/
- PsRobot: Plant small RNA analysis toolbox
http://omicslab.genetics.ac.cn/psRobot/
- Shoot cell type-specific expression ebrowser
http://jiaolab.genetics.ac.cn/shootapex.html

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

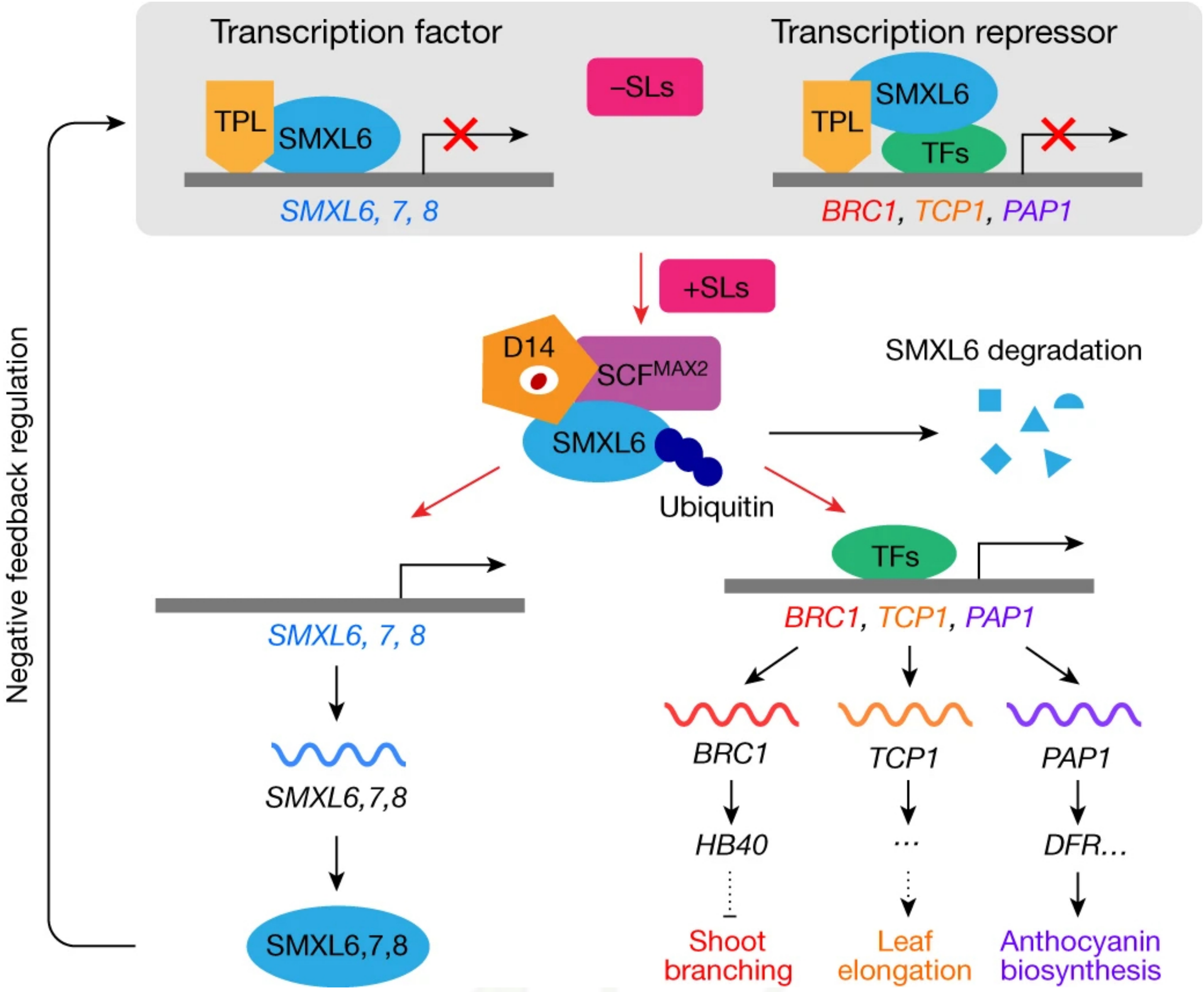
COVID19 outbreak started in Wuhan in late January during the Lunar New Year holidays. A countrywide lock down followed up that stopped or at least slowed down research in the majority of universities and research institutions. For about a semester, graduate and undergraduate students stayed at home so that laboratories were mostly closed. Nevertheless, quite a few research groups with expertise in sequence analysis and molecular evolution participated in COVID19 pandemic studies. Since summer, the pandemic was contained. Life resumed normal as well as laboratory research, although temporarily interfered by the occasional identification of new cases in a few cities. In October, we were pleased to see the annual National Congress of Plant Biology to take place as usually, although about half of the attendees selected the online option.

Planned events for 2021 and 2022

- 2020 National Congress of Plant Biology, October 11-14, 2020, Shenzhen, Guangdong

- 5th Forum of Young Plant Scientists, November 26-29, 2020, Changzhou, Jiangsu (http://plantyouth2020.csp.escience.cn/)

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



In the absence of strigolactones (SLs; top), SMXL6 plus TPL bind directly to the promoters of SMXL6, 7, 8 and repress their expression, functioning as a repressive transcription factor (TF). Meanwhile, SMXL6 can also form a complex with unknown transcription factors that are expected to recognize and bind to the promoters of BRC1, TCP1 or PAP1, repressing their transcription as well. In the presence of SLs, D14 binds SLs (white and red circle within D14) and promotes the formation of the D14–SCFMAX2–SMXL6 complex, triggering the ubiquitin-mediated degradation of SMXL6. This relieves the transcriptional repression of SMXL6, 7, 8. Newly synthesized SMXL6 proteins in turn repress transcription, forming a negative feedback loop. The degradation of SMXL6 also releases its transcriptional repression of BRC1, TCP1 and PAP1, thus activating signalling cascades that repress shoot branching, promote leaf elongation and enhance anthocyanin biosynthesis, respectively.

Selected Publications

- Wang L, Wang B, Yu H, Guo H, Lin T, Kou L, Wang A, Shao N, Ma H, Xiong G, Li X, Yang J, Chu J, Li J. (2020) Transcriptional regulation of strigolactone signalling in Arabidopsis. Nature 583(7815): 277-281.

By identifying strigolactone early-responsive genes, this study clarifies how shoot branching, leaf development, and anthocyanin biosynthesis are regulated.

- Wu H, Li B, Iwakawa HO, Pan Y, Tang X, Ling-Hu Q, Liu Y, Sheng S, Feng L, Zhang H, Zhang X, Tang Z, Xia X, Zhai J, Guo H. (2020) Plant 22-nt siRNAs mediate translational repression and stress adaptation. Nature 581(7806): 89-93.

This study identified large amount of 22 nt siRNAs generated by coding sequences, which interferes with translation, and promotes resistance to stress conditions.

- Wu H, Qu X, Dong Z, Luo L, Shao C, Forner J, Lohmann JU, Su M, Xu M, Liu X, Zhu L, Zeng J, Liu S, Tian Z, Zhao Z. (2020) WUSCHEL triggers innate antiviral immunity in plant stem cells. Science 370(6513): 227-231.

By showing WUSCHEL inhibits ribosome maturation, which is required for virus proliferation, this study explains why shoot apical meristem is resistant to virus infection.

Major Funding Sources

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

- Ministry of Science and Technology (MOST). (http://www.most.gov.cn/eng/programmes1/index.htm)

Czech Republic

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

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

All research centers of both universities as well as academy of sciences are affected by different degrees of lock-down measures so that experimental activity was differentially hampered in different locations and times. It is impossible to assess how big is overall negative impact.

Planned events for 2021 and 2028

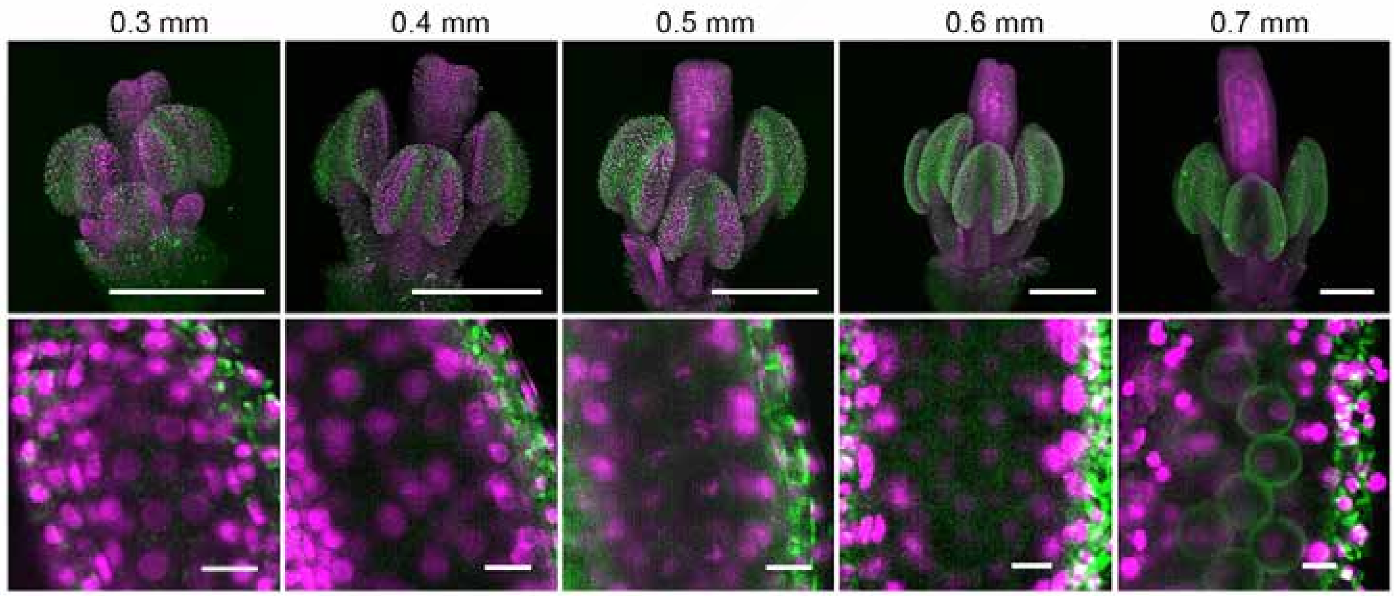
- 26th ICSPR Plant Reproduction conference June 20-24, 2022, at Prague (Czech Republic)

- 7th European Workshop on Plant Chromatin 2022 (EWPC 2022), Pr_honice, Prague, Date: 18.05.2022 - 20.05.2022

Selected Publications

- Valuchova S, Mikulkova P, Pecinkova J , Klimova J, Krumnikl M, Bainar P, Heckmann S, Tomancak P, Riha K. Imaging plant germline differentiation within Arabidopsis flowers by light sheet microscopy. Elife 9:e52546. doi: 10.7554/eLife.52546. 2020

New approach allowing detailed in vivo microscopy monitoring of Arabidopsis flower and germline development by light sheet microscopy is described.



Maximum intensity projections (MIPs) of micrographs of HTA10:RFP flowers dissected from buds of the indicated sizes (upper panel, scale bar 200 µm). A detailed image of a single anther lobe with PMCs and microspores is shown in the lower panel (scale bar 10 µm). HTA10:RFP in magenta, 488 nm autofluorescence in green.

- Kubiasová K, Montesinos JC, Samajová O, Nisler J, Mik V, Semerádová H, Plíhalová L, Novák O, Marhav_ P, Cavallari N, Zalabák D, Berka K, Dole_al K, Galuszka P, Samaj J, Strnad M, Benková E, Plíhal O, Spíchal L. Cytokinin fluoroprobe reveals multiple sites of cytokinin perception at plasma membrane and endoplasmic reticulum. Nat Commun. 11(1):4285. doi: 10.1038/s41467-020-17949-0. PMID: 32855390; PMCID: PMC7452891. 2020

Fluorescently labelled cytokinin pools of the ER-located cytokinin receptors can enter the secretory pathway and reach the PM in cells of the root apical meristem

- Mandáková T, Hlousková P, Koch MA, Lysak MA. Genome Evolution in Arabideae Was Marked by Frequent Centromere Repositioning. Plant Cell. 32(3):650-665. doi: 10.1105/tpc.19.00557. Epub 2020 Jan 9. PMID: 31919297; PMCID: PMC7054033. 2020

Centromere repositioning is proposed as the key mechanism differentiating overall conserved homoeologous chromosomes across the crown-group Arabideae subclades.

Major Funding Sources

Both major funding agencies for basic research

- Czech Science Foundation (GACR) and Ministry of Education of CR (MSMT CR) regularly support projects based on the use of Arabidopsis as a model plant.

1. Czech Science Foundation/GA_R, Prague (http://www.gacr.cz)

2. Ministry of Education, Youth and Sports of Czech Republic, Prague (http://www.msmt.cz/research-and-development-1) Both institutions support also bilateral projects with selected countries.Targeted or applied research is since recently supported also by the Technology Agency of the Czech Republic (TACR) and Arabidopsis model is accepted as a driver for applications.

3. Technology Agency of the Czech Republic (http://www.tacr.cz/english/)4. Ministry of Agriculture, National Agency for Agricultural Research (NAZV) might support projects using Arabidopsis as a driver for the applied research (http://eagri.cz/public/web/mze/poradenstvi-a-vyzkum/vyzkum-a-vyvoj/narodni-agentura-pro-zemedelsky-vyzkum/)

Estonia

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University of Tartu, Institute of Technology

Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2020 or early 2021

We continually update and improve the custom-built gas-exchange systems designed for measuring stomatal conductance, transpiration and photosynthesis in whole Arabidopsis rosettes and in leaves in controlled and adjustable conditions. Air temperature, air composition (humidity, CO2, O3 etc) and light conditions can be manipulated throughout the experiment and several plants can be recorded in parallel.

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

The COVID19 pandemic has resulted in reduced personal contacts, as everywhere. We have been able to continue laboratory work throughout the pandemic with measures in place for distancing and limiting the number of people present in the workplace, while encouraging working from home as much as possible. There has been active participation in virtual webinars and shifting of focus to data analysis and writing. Nevertheless, the lack of in-person discussions has left a mark on research progress.

Planned events for 2021 and 2022

The New Phytologist next generation scientists meeting organized by New Phytologist Foundation originally planned for 2020 will take place in Estonia at the first possible instance, likely in a hybrid virtual and in-person format. (https://www.newphytologist.org/nextgenevents/2020)

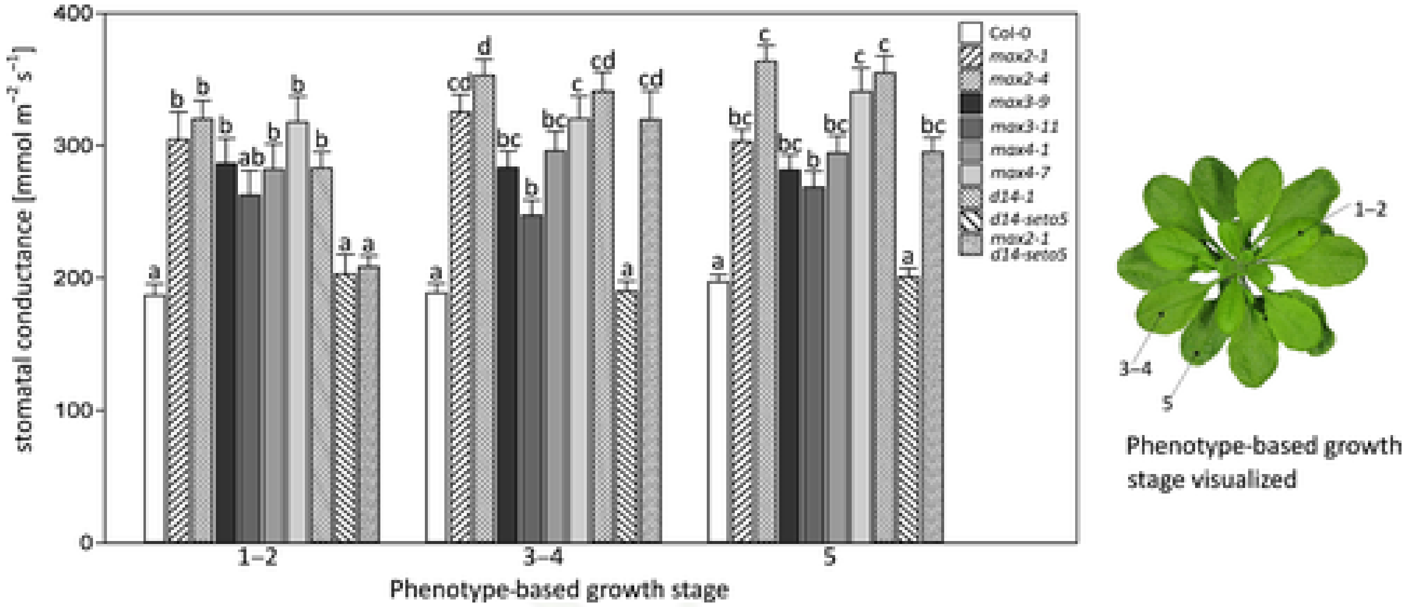
Selected Publications

- Kalliola M, Jakobson L, Davidsson P, Pennanen V, Waszczak C, Yarmolinsky D, Zamora O, Palva ET, Kariola T, Kollist H, Brosche M. (2020) Differential role of MAX2 and strigolactones in pathogen, ozone, and stomatal responses. Plant Direct 2020;4:1–14. DOI: 10.1002/pld3.20

Collaboration with researchers from Finland indicates a role for MAX2 in stomatal responses to environmental stimuli:

- Mõttus J, Maiste S, Eek P, Truve E, Sarmiento C. (2021). Mutational Analysis of *Arabidopsis thaliana* ABCE2 Identifies Important Motifs for its RNA Silencing Suppressor Function. Plant Biology, 23 (1), 21_31. DOI: 10.1111/plb.13193.

Analysis of mutant versions of the ABCE2 protein enabled identification of its motifs that are required for suppressing RNA silencing:



The stomatal conductance of strigolactone biosynthesis and perception mutants measured with a porometer from leaves of different developmental stages. The error bars represent standard error of the mean. 2–3 leaves per each growth stage was measured from each plant, and altogether, a minimum 20 plants were measured from each plant line. The phenotype-based growth stage is determined in the article by Boyes *et al.*, (2001) in which numbers indicate the growth stage: 1 indicates leaf production, 3 rosette growth, and 5 inflorescence emergence. We used the plants for analysis before they reached the stage 5.10 (i.e., before the first flower buds were visible). In statistical analysis, we conducted a logarithmic transformation on the data and then univariate analysis of variance combined to Tukey HSD post hoc test

- Hõrak H, Fountain L, Dunn JA, Landymore J, Gray JE (2021) Dynamic thermal imaging confirms local but not fast systemic ABA responses. Plant, Cell & Environment 44: 885–899. DOI: 10.1111/pce.13973.

Leaf temperature imaging indicates a lack of fast systemic ABA-induced stomatal closure in Arabidopsis but identifies a small slow response.

Major Funding Sources

- Estonian Research Council, www.etag.ee

- Centres of Excellences funded by European Regional Development Fund, coordinat-ed in Estonia by Archimedes Foundation, www.archimedes.ee

Finland

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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 2020 or early 2021

Arabidopsis research at the Finnish National Plant Phenotyping Infrastructure (https://www2.helsinki.fi/en/infrastructures/national-plant-phenotyping) has enjoyed funding for implementing FAIR data management standards together with European and Nordic colleagues to enable future open science data.

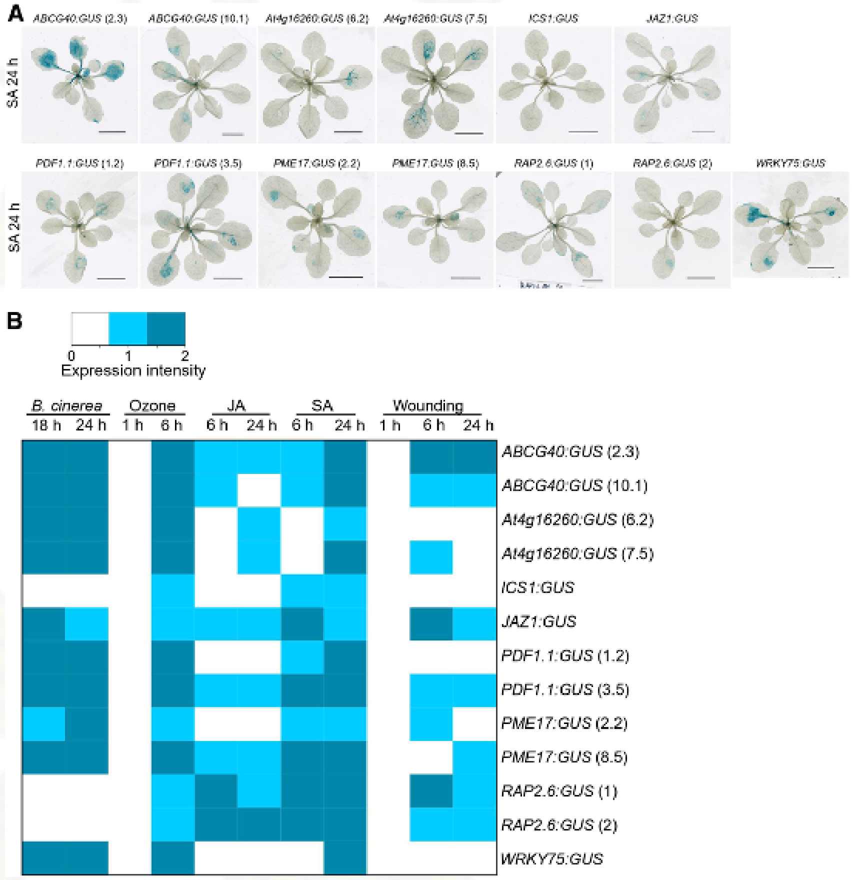
Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

From March 2020 onwards, University of Helsinki and other universities in Finland first went from partial lockdown to full lockdown during May. From June 2020, labwork has again been possible with a maximum number of people assigned per each lab and office. Face masks are mandatory in University premises. We have been using online calendars to make bookings for the rooms in advance. Remote work and teaching has been strongly recommended whenever possible. Overall, Covid-19 has slowed down laboratory work variably. Lab and team meetings have been held remotely through Zoom, and this has worked adequately, although everybody is eager to have physical team meetings again. Everyone is also looking forward to attending physical conference meetings: virtual meetings are informative, however they are lacking social interaction, which is essential for most of us.

Selected Publications

1. Wang X, Ye Y, Lyu M, Ursache R, Löytynoja A, Mähönen AP. An inducible genome editing system for plants. Nature Plants 2020 Jul;6(7):766-772. doi: 10.1038/s41477-020-0695-2

Tissue-specific induction of Cas9 enable precise genome editing in somatic tissues



Visualization of stress marker gene expression with promoter β-glucuronidase (GUS) staining. A, Representative pictures of the salicylic acid (SA) treatment (500 µM, 24 h) in all promoter:GUS lines. B, Summary of treatment-specific GUS expression at early and late timepoints. The displayed average of three repeats is calculated from stain intensity score values (0 = no staining, 1 = faint staining, 2 = strong staining) determined by visual evaluation.

2. Kimura S, Hunter K, Vaahtera L, Tran HC, Citterico M, Vaattovaara A, Rokka A, Stolze SC, Harzen A, Meißner L, Wilkens MMT, Hamann T, Toyota M, Nakagami H, Wrzaczek M. CRK2 and C-terminal Phosphorylation of NADPH Oxidase RBOHD Regulate Reactive Oxygen Species Production in Arabidopsis. Plant Cell. 2020 Apr;32(4):1063-1080. doi: 10.1105/tpc.19.00525.

This work revealed a new layer of regulation in plant ROS production

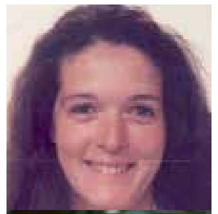
3. Vuorinen K, Zamora O, Vaahtera L, Overmyer K, Brosché M. Dissecting Contrasts in Cell Death, Hormone, and Defense Signaling in Response to Botrytis cinerea and Reactive Oxygen Species. Mol Plant Microbe Interact. 2021 Jan;34(1):75-87. doi: 10.1094/MPMI-07-20-0202-R

Arabidopsis double and triple mutants deficient for salicylic acid, jasmonic acid and ethylene signaling was generated and is available for the Arabidopsis community.

Major Funding Sources

Academy of Finland: https://www.aka.fi/en/ Jane and Aatos Erkko Foundation: http://www.jaes.fi.

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 2020 or early 2021

- 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/ in the embryo.

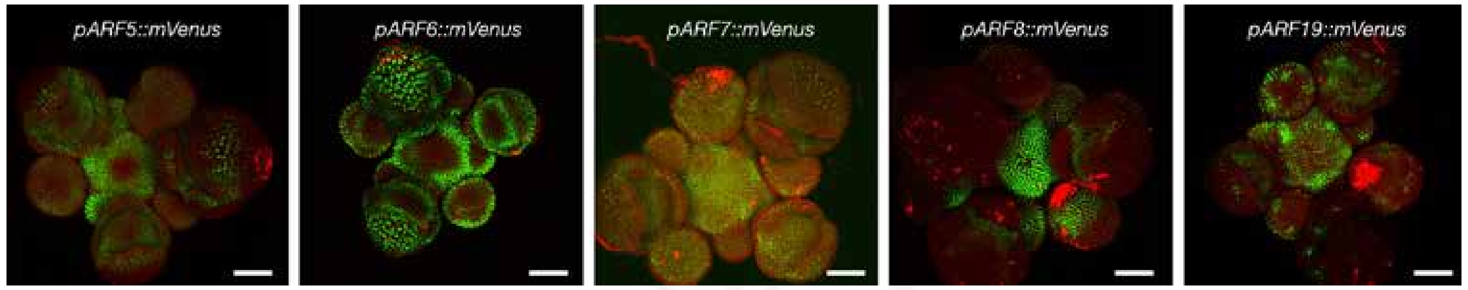
Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

COVID19 has heavily impacted our laboratories in 2020. For half of the year (two periods from mid-March to mid-May and September to December), laboratory activities were greatly reduced and a lot of biological material was lost, which impacted all experiments, especially those on crop species. The government, institutions or laboratories provided some support to many PhD or Master students to complete their thesis by providing them with an additional 2 or 3 months of salary/scholarship. But this is not enough to fully make up for the lost time. Moreover, since March, all researchers have to work at home as much as possible, which complicates and slows down their work considerably.

Planned events for 2021 and 2022

- Some institutions have started series of webinars among which the SPS network (https://www6.inrae.fr/saclay-plant-sciences_eng/with) more than 30 online seminars also available as video (https://www6.inrae.fr/saclay-plant-sciences_eng/Events/Online-SPS-Seminars) or the AFBV (French association for Plant Biotech, https://www.biotechnologies-vegetales.com/les-webinaires-afbv-2021/)

- Most of the events have been postponed to 2021



Expression of class A ARF genes in the shoot (SAM) reported using long promoters containing sequences 5′ and 3′ of the ATG (pARF::mVenus).Scale bars, 50 µm. Experiments were performed at least three times with similar results.

Selected Publications

- Pectin homogalacturonan nanofilament expansion drivesmorphogenesis in plant epidermal cells. (2020) Haas KT, Wightman R, Meyerowitz EM, Peaucelle A. Science. 367(6481):1003-1007. doi: 10.1126/science.aaz5103.

The extracellular cell wall can actively shape the cell it contains without relying on turgor pressure.

- A network of transcriptional repressors modulates auxin responses (2021) Truskina, J *et al*. Nature, 589, 11. Doi 10.1038/s41586-020-03066-x.

The default configuration of open chromatin enables a network of transcriptional repressors to regulate expression levels of class A ARF proteins and modulate auxin signalling output throughout development.

- A two-way molecular dialogue between embryo and endosperm is required for seed development Doll, NM *et al*. (2020) Science, 367, 6476, 431, DOI: 10.1126/science.aaz4131.

Subtilase-mediated processing of the embryo-derived TWS1 sulfated peptide precursor, releases an active peptide, triggering GASSHO-dependent cuticle reinforcement in the embryo.

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

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Greece

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Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

While 2020 was a peculiar year with a lot of obstacles and restrictions due to COVID19 pandemic, the research activity in Greece remained active.

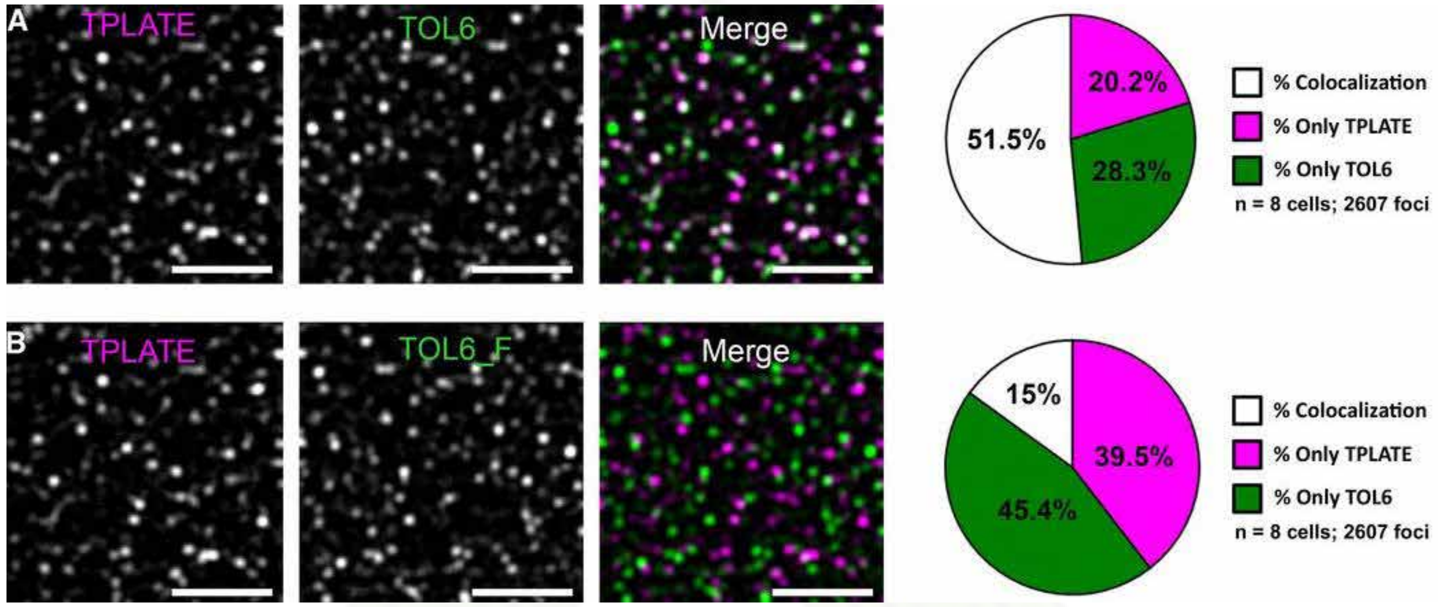
Selected Publications

[1] Arora D, Abel NB, Liu C, Van Damme P, Yperman K, Eeckhout D, Vu LD, Wang J, Tornkvist A, Impens F, Korbei B, Van Leene J, Goossens A, De Jaeger G*, Ott T*, Moschou PN*, Van Damme D* (2020) Establishment of Proximity-dependent Biotinylation Approaches in Different Plant Model Systems. Plant Cell 32:3388-3407. (*equal senior)

Approaches for in vivo interactome mining were established using abortive biotin ligases. These approaches were applied in different plant systems including tomato, tobacco, and Arabidopsis.

[2] Samakovli D, Roka L, Plitsi PK, Kaltsa I, Daras G, Milioni D, Hatzopoulos P (2020) Active BR signalling adjusts the subcellular localisation of BES1/HSP90 complex formation. Plant Biol (Stuttg) 22:12 9-133

The formation of a complex between BES1 and HSP90 under control conditions and active BR signaling was studied. The interaction of HSP90 with BES1 regulates BR-dependent gene expression.



TOL6, TOL9, and SCAMP5 Can Be Confirmed as Novel TPC Interactors.
(A) and (B) Representative spinning-disk dual-color images and corresponding quantification of colocalization (%) between TPLATE and TOL6. TPLATE-TagRFP endocytic foci at the plasma membrane were compared with TOL6-Venus foci (A) as well as horizontally flipped TOL6-Venus (TOL6_F) channel images as a control (B). Eight movies from three individual plants, and in total 2607 foci, were analyzed.

[3] Samakovli D, Tichá T, Vavrdová T, Ove_ka M, Luptov_iak I, Zapletalová V, Kucha_ová A, K_enek P, Krasylenko Y, Margaritopoulou T, Roka L, Milioni D, Komis G, Hatzopoulos P, _amaj J (2020) YODA-HSP90 Module Regulates Phosphorylation-Dependent Inactivation of SPEECHLESS to Control Stomatal Development under Acute Heat Stress in Arabidopsis. Molecular Plant 13:612-633.

HSP90s play a crucial role in transducing heat-stress response through the YODA cascade regulating stomata formation.

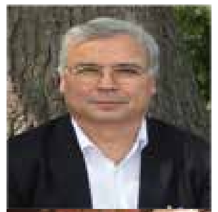
Major Funding Sources

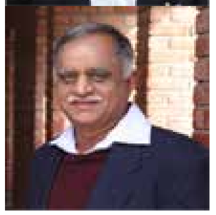
-General Secretariat for Research & Innovation, GSRI: http://www.gsrt.gr

-Hellenic Foundation for Research & Innovation, HFRI: https://www.elidek.gr

-Ministry of Development & Investments: https://www.espa.gr/

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 2020 or early 2021

Almost all the Arabidopsis labs have generated mutants and genetic resources related to plant development, metabolism, biotic and abiotic stress tolerance, symbiosis etc. Realizing the importance of a model system like Arabidopsis for plants, the Society of Plant Biochemistry and Biotechnology (SPBB) brought out a special issue of the Journal of Plant Biochemistry and Biotechnology entitled, "Advances in Plant Biology: Impact of Arabidopsis Research"(https://link.springer.com/journal/13562/volumes-and-issues/29-4).

This issue carries several comprehensive reviews written by pioneers in the field on role of light in plant development, various aspects of biotic and abiotic stresses biology etc. A majority of articles are from Indian labs, which provide a flavour of the work being carried out and the expertise available related to Arabidopsis and plant biology in India. We are sure that the readers of this special issue of JPBB on Arabidopsis will find it a very useful resource.

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

Several labs across the country were completely shut down from March to September 2020. All the students including postgraduate and postdoctoral fellows were asked to vacate campus accommodation in several universities and Institutes. Even later as and when new Covid cases were identified in and around a lab, the labs were closed. Such intermittent closure of labs has severely hampered research activities across the country.

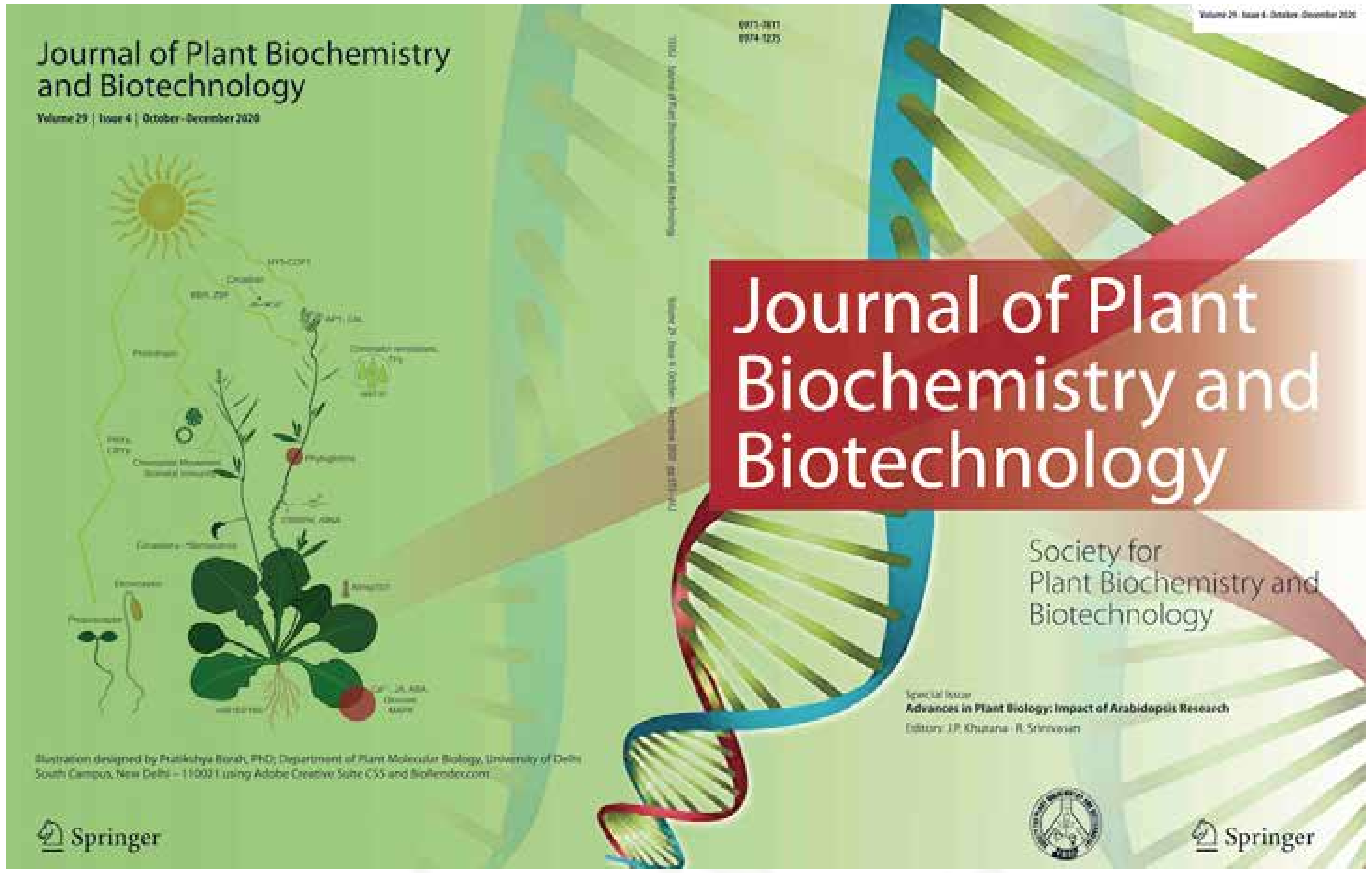
Planned events for 2021 and 2022

A few conferences/ workshops are being planned by SPBB and Indian Plant Physiology Society during 2021 and 2022. However, because of the recent wave of Covid and the uncertainties involved the exact details have not been finalized

Selected Publications

- Majumdar P, Karidas P, Siddiqi I and Nath U (2020) The ubiquitin-specific protease TNI/UBP14 functions in ubiquitin recycling and affects auxin response. Plant Physiol. 184:1499-1513

This article shows that a Mutation in TARANI/ UBIQUITIN-SPECIFIC PROTEASE 14(TNI/UBP14) leads to reduced auxin response and widespread auxin-related phenotypic defects in *Arabidopsis thaliana*.



Journal of Plant Biochemistry and Biotechnology

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Journal of Plant Biochemistry and Biotechnology

Society for Plant Biochemistry and Biotechnology

Special Issue

Advances in Plant Biology: Impact of Arabidopsis Research

Editors: J.P. Khurana · R. Srinivasan

Springer

- Sharma A, Badola PK, Bhatia C, Sharma D and Trivedi PK (2020) Primary transcript of miR858 encodes regulatory peptide and controls flavonoid biosynthesis and development in Arabidopsis. Nature Plants 6:1262–1274

This article provides evidence for the role of a peptide encoded by a microRNA transcript in a metabolic process in plants.

- Yadukrishnan P, Rahul PV, Ravindran N, Bursch K, Johansson H, Datta S. (2020). CONSTITUTIVELY PHOTOMORPHOGENIC1 promotes ABA-mediated inhibition of post-germination seedling establishment. Plant J. 103: 481-496

This article shows that the light signaling protein COP1 positively regulates ABA signaling by promoting the binding of ABI5 with its target promoters and inhibiting seedling establishment.

Major Funding Sources

- Council of Scientific and Industrial Research (CSIR), New Delhi http://www.csirhrdg.res.in/
- Department of Biotechnology (DBT), Government of India http://dbtindia.nic.in/index.asp
- Department of Science &Technology (DST), Government of India http://www.dst.gov.in/scientific-programme/serindex.html
- Council of Scientific and Industrial Research (CSIR), New Delhi http://www.csirhrdg.res.in/
- Indian Council of Agricultural Research (ICAR), New Delhi http://www.icar.org.in/
- University Grants Commission, New Delhi https://www.ugc.ac.in/

Israel

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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 2020 or early 2021

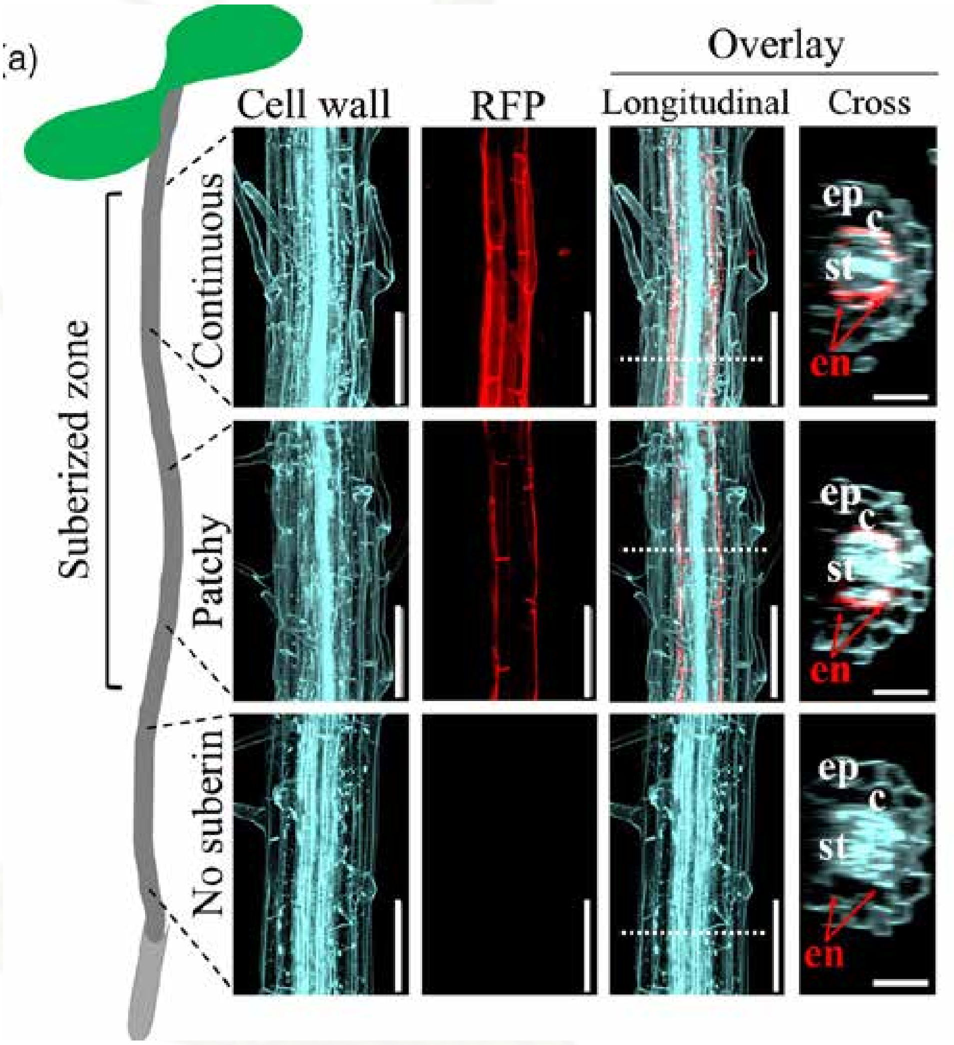
The Position and Complex Genomic Architecture of Plant T-DNA Insertions Revealed by 4SEE Krispil R (2020), DOI: 10.3390/ijms21072373 Present a genomic method for detection of the entire scope of T-DNA locations. 4SEE is a high resolution method based on chromosome conformation capture technology to map the position of any point of interest in plant genomes. Application of 4SEE in several characterized transgenic Arabidopsis lines mapped unannotated T-DNA insertions and their associated chromosomal rearrangements including inversions and translocations.

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

Universities like the rest of the public sector suffered from pandemic. Because public schools were mainly online during 2020, the ability of working parents, even from home was seriously compromised. Other than that, the Universities maintained a skeleton crew of 30% to maintain and 100% of teaching was online.

Planned events for 2021 and 2022

- International Conference on Plant Biology, Physiology, Ecology, Physiology and Plant Science ICPBPEPPS on November 29-30, 2022 in Jerusalem, Israel https://waset.org/plant-biology-physiology-ecology-physiology-and-plant-science-conference-in-november-2022-in-jerusalem.



SUB is expressed in endodermal cells displaying patchy or continuous suberization.

(a) Confocal laser scanning microscopy (CLSM) images showing endodermis-specific expression of red fluorescent protein (RFP) driven by the native 50 upstream region of the SUB gene (pAtSUB::RFP) in the Arabidopsis root. Root cell layers are highlighted using Calcofluor white (cyan). Note the RFP signals (647 nm) detected in patchy and continuous suberized root zones but not in the non-suberized zone. Overlay longitudinal Z projection images represent merged cell wall and RFP signals, where dashed lines in these images reresent root areas presented in overlay cross-section views (right panels). Bars represent 50 μm.

Selected Publications

"One step closer to understand the formation of the root endodermal barrier": Cohen, H., Fedyuk, V., Wang, C.H., Wu, S. and Aharoni, A. (2020) SUBERMAN regulates developmental suberization of the Arabidopsis root endodermis. Plant J, 102, 431-447.

"Corelation between high free methionine and the accumulation of stress-associated metabolites." Girija, A., Shotan, D., Hacham, Y. and Amir, R. (2020) The Level of Methionine Residues in Storage Proteins Is the Main Limiting Factor of Protein-Bound-Methionine Accumulation in Arabidopsis Seeds. Front Plant Sci, 11.

Major Funding Sources

- ISF: https://www.isf.org.il

- BSF and NSF-BSF: https://www.bsf.org.il/

- ERC: https://erc.europa.eu/

- GIF: http://www.gif.org.il/Pages/default.aspx

Italy

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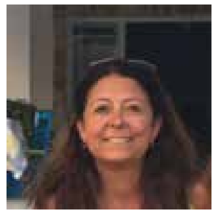


Please describe any new experimental resources and/or software tools available to Arabidopsis researchers that have been initiated or funded in your country in 2020 or early 2021

- NoMinor (NoM) mutants, knocked-out for genes encoding for the three monomeric subunits of PSII antenna proteins (CP29, CP26 and CP24)

- Characterization of two Arabidopsis polymorphisms, the SALK_059908C and of SM_3_25823, named respectively, pme17-2 and pme17-3

- Single and multiple Arabidopsis T-DNA insertion lines, CRISPR-cas9 mutants, overexpressing lines and marker lines, RNA-seq data of inflorescences/Methods for Digital PCR and Polysomes profiles on Arabidopsis sample (described in Cucinotta *et al.*, 2020 and Di Marzo *et al.*, 2020)

- Switch Miner, a software for identifying genetic network utilizing transcriptome data, in Arabidopsis gave optimal preliminary results

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

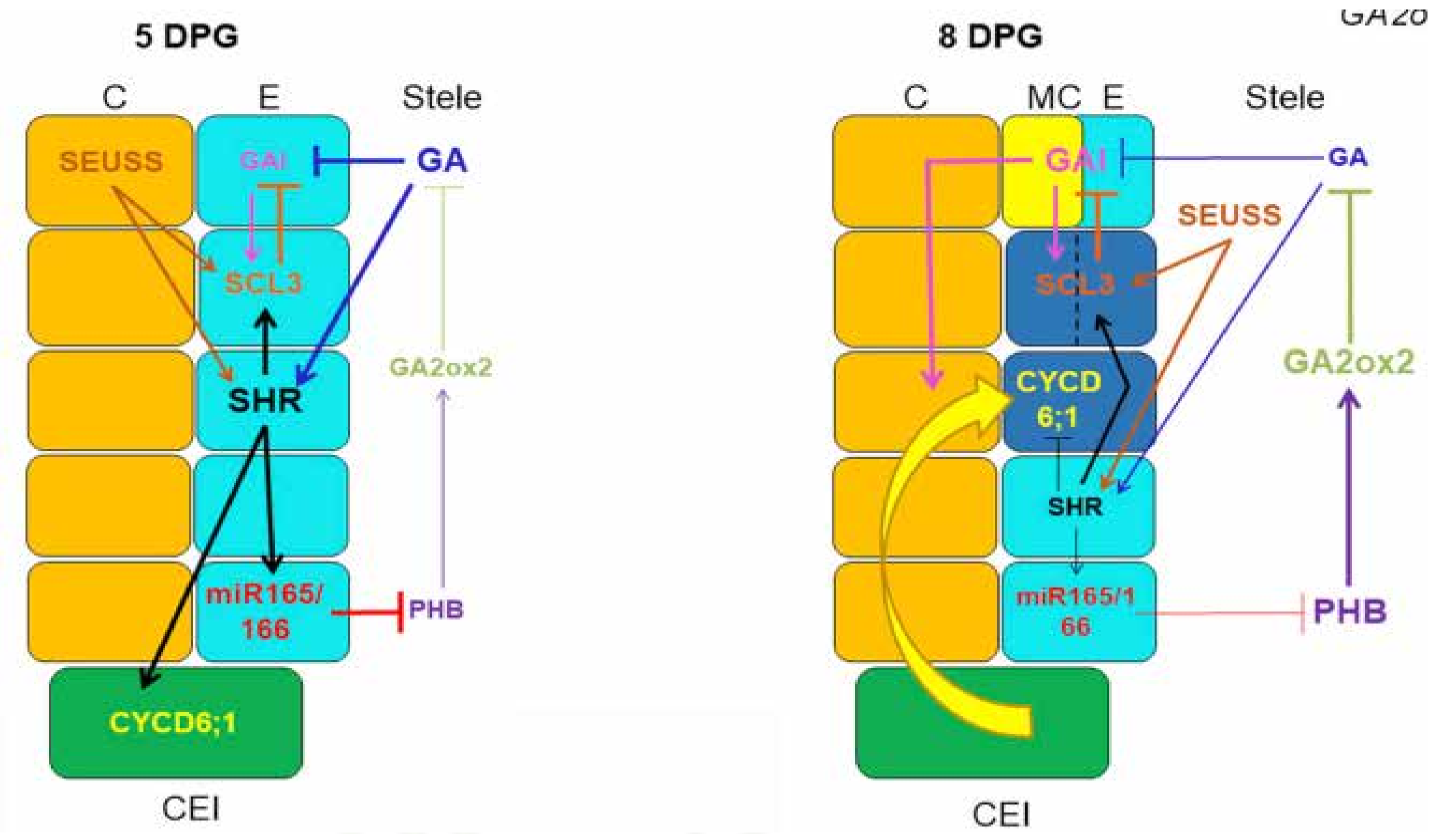
The COVID19 emergency had a large impact on plant research. In Italy, from March 2020 to May 2020, Universities and research centers were closed. Since mid-June 2020 labs were reopened, but only a small number of our PhD students and Postdocs could come into the labs per day. These restrictions had a great impact on the everyday lab activity, slowing down data production and decreasing interaction between lab members. Another issue was related with the international collaborations and exchanges, made impossible by closure of the borders. This inevitably slowed down many research projects

Planned events for 2021 and 2022

1.EMBO workshop-International plant systems biology-(Venice, Italy) 26-27 April 2021 Virtual

2. Joint conference by FESPB & EPSO Plant Biology Europe 2021 (Turin, Italy) 28th June to 1st July 2021, Virtual

3. Plant Calcium Signaling conference (Milan, Italy) July 20224.116° Conference of Italian Botany Society (Virtual, September 2021)



Model: PHB levels increase between 5 and 8 dpg, resulting in increased GA2ox2 expression. Increased GA2ox2 levels promote the degradation of GAs in the vasculature, stabilizing GAI protein. GAI directs the accumulation of CYCD6;1 in the endodermis, promoting MC formation. Decrease levels of GAs after 5 dpg dampens SHR levels that regulate miR165 and 166 and SCL3 that in turn attenuate PHB expression and GAI activity, respectively. Orange, cortex (C); cyan, endodermis (E); yellow, middle cortex (MC); green, cortex/endodermis initial (CEI); blue, periclinally dividing cells (dashed line). Yellow arrow indicates the CYCD6;1 switch.

Selected Publications

- Bertolotti G., Unterholzner S.J., Scintu D., Salvi E., Svolacchia N., Di Mambro R., Ruta V., Linhares Scaglia F., Vittorioso P., Sabatini S., Costantino P., Dello Ioio R. (2021) Current Biology Jan 25;31(2):420-426. (IF 9.6)

This paper is the result of the collaboration of different groups (Italian and Brazilian Universities), that have been coordinated by a young Italian scientist and deals with developmental biology- one of the major area on which Arabidopsis research is focused on in Italy)

- Guardini, Z., Bressan, M., Caferri, R., Bassi, R., & Dall'Osto, L. (2020). Identification of a pigment cluster catalysing fast photoprotective quenching response in CP29. Nature Plants, 6(3), 303-313 (IF 13.2)

The research group from the University of Verona has analyzed the process by which plants protect themselves from excess light, an important step in understanding the use of energy by plants)

- Marmiroli M, Lepore GO, Pagano L, d'Acapito F, Gianoncelli A, Villani M, Lazzarini L, White JC, Marmiroli N. 2020 The fate of CdS Quantum Dots in plants as revealed by Extended X-ray Absorption Fine Structure (EXAFS) analysis. Environ. Sci. Nano 7, 1150–1162. (IF 7.9)

This applied research paper, in collaboration between University and CNR deals with cadmium tolerance and provides important insight into understanding the fate of nanoparticles in plants and in the environment)

Major Funding Sources

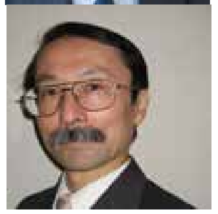
Italian funding:

- Ministero dell'Università e della Ricerca (MIUR) https://www.miur.gov.it/
- Sapienza Universit y of Rome https://www.uniroma1.it
- University 'Roma Tre' https://scienze.uniroma3.it/
- University of Milan: PIANO DI SVILUPPO DI ATENEO https://www.unimi.it
- Regione Lazio http://www.lazioinnova.it

International funding:

- H2020-MSCA-RISE-2020. Mechanisms of Apomictic Developments.
- H2020-MSCA-ITN-2015-GA. Solar Energy to Biomass - Optimisation of light energy conversion in plants and microalgae
- H2020-MSCA-RISE-2015.Exploring the molecular control of seed yield in crops.
- H2020-MSCA-RISE-2015. Sexual Plant Reproduction – Seed formationMSCA-ITN-2015-ETN - Marie Sk_odowska-Curie Innovative Training Networks (ITN-ETN),
- PRIMA_2020. Partnership for Research and Innovation in the Mediterranean Area https://prima-med.org/Private funding
- Armenise Harvard Foundation Consolidator Granthttps://armeniseharvard.org/
- Fondazione Cariplo (WAKE-APT)https://www.fondazionecariplo.it/

Japan



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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 2020 or early 2021

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

- PRIMe Platform for RIKEN Metabolomics (http://prime.psc.riken.jp/).

Arabidopsis metabolomics platform publicly available platform resources:

•Widely targeted metabolomics (in Drop Met, http://bit.ly/2HU2ACI) •AtMetExpress Arabidopsis metabolome expression database (http://bit.ly/1P2YByw)

•LC-MCS Branch (http://bit.ly/1P2Zhnt) PRIMe Web Applications

•MeKO Metabolite Profiling Database for Knock-Out Mutants in Arabidopsis (MeKO) (http://bit.ly/1QQBWYl)

•PRIMeLink integrates 3 above databases (AtMetExpress, MS2T and ReSpect) for bi-directional search from gene or metabolite (http://bit.ly/1RCX4Bc)

•ReSpect RIKEN MSn Spectral database for phytochemicals (http://bit.ly/1P2ZaIv)

• HiFi Heteroatom-containing Ion Finder (http://bit.ly/1nBxjJ6)

•PlaSMA Plant Specialized Metabolome Annotation(http://plasma.riken.jp/)Distribution and Redistribution

•Drop Met mass-spec based metabolome analyses (http://bit.ly/1LVEfwq)

Other RIKEN CSRS developed tools and resources:
•AtGenExpress Arabidopsis Gene Expression profile database (http://bit.ly/1P2YT8v)

•KNApSacK Comprehensive species-metabolite relationship database (http://bit.ly/1LfFkyZ) (NAIST)

•Plant-PrAS (Plant-Protein Annotation Suite) database of physicochemical and structural properties, and novel functional region in plant proteomes (http://plant-pras.riken.jp/)

•MassBank Public repository of mass spectral data for sharing spectra among research communities (http://www.massbank.jp/en/about.html)

•Plant-PrAS (Plant-Protein Annotation Suite) (http://plant-pras.riken.jp/)

- RIPPS (RIKEN Plant Phenotyping System) (https://academic.oup.com/pcp/article/59/10/2030/5043525)

- The Chloroplast Function Database III (https://plant.rtc.riken.jp/color/c/index.html)_Arabidopsis nuclear-encoded chloroplast protein mutant seeds(https://epd.brc.riken.jp/en/archives/4909)

• Arabidopsis sORF Database HanaDB-At (http://hanadb01.bio.kyutech.ac.jp/hanadb-at/)

• Hormone-like peptides in Arabidopsis (http://hanadb01.bio.kyutech.ac.jp/peptide/)

•Hormonome platform and RIKEN Plant Hormone Research Network_(http://hormones.psc.riken.jp/)
RIKEN National Science Institute - BioResource Research Center (BRC) (https://epd.brc.riken.jp/en/)

•Arabidopsis seeds, cDNA, and plant cultured cells: Exp-Plant catalog (https://plant.rtc.riken.jp/resource/index.html)•Resource information (https://epd.brc.riken.jp/en/)

•National BioResource Project (http://nbrp.jp/index.jsp)

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

- KOMICS Kazusa Metabolomics Database portal (http://www.kazusa.or.jp/komics/en/)

- MassBase: a plant metabolome database (http://bit.ly/1Rlf9Dd)

- MS-MS Fragment Viewer database (http://bit.ly/1QWjPUm)_Plant GARDEN Plant Genome And Resource Database ENtry (https://plantgarden.jp)

- PGDBj Plant Genome DataBase Japan (http://pgdbj.jp/?ln=en)

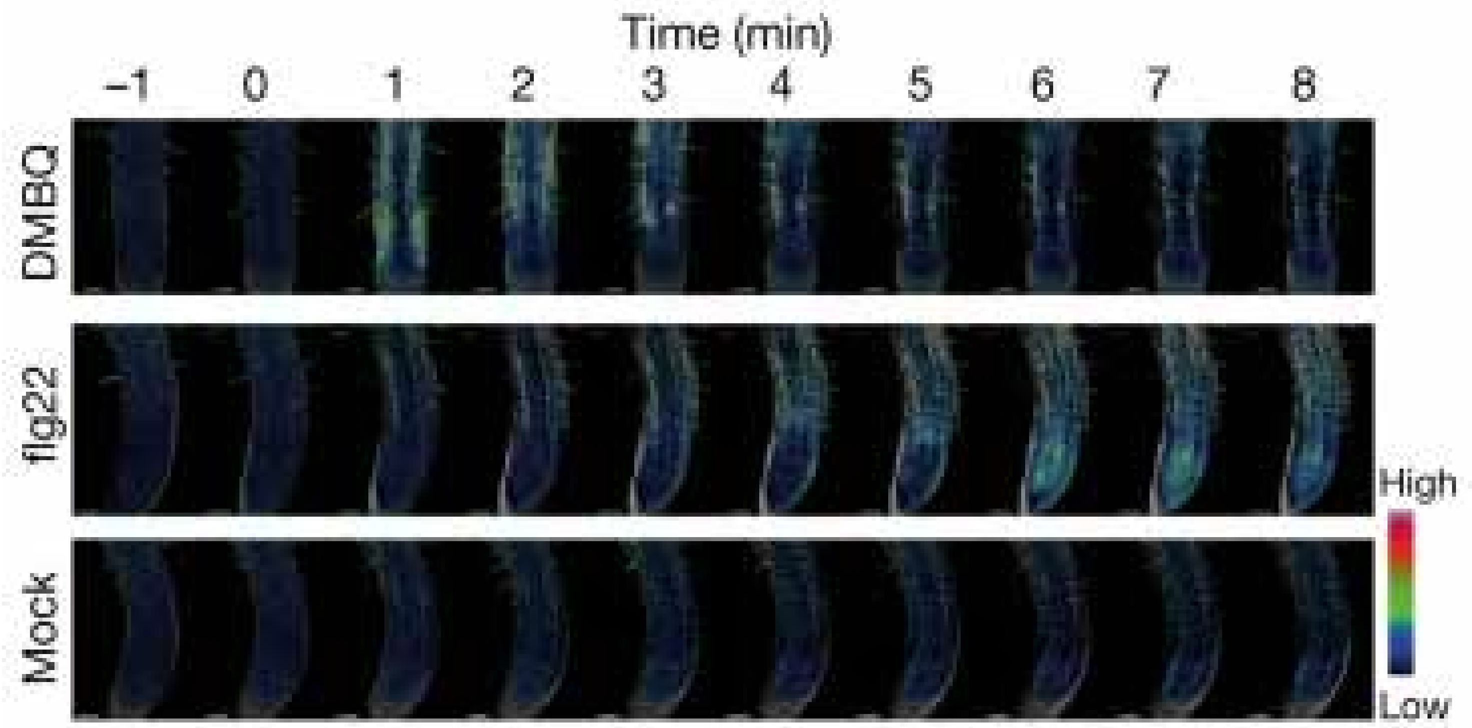
- Kusaki DB: a database to assess existence and completeness of orthogroups in plant species(http://pgdbjsnp.kazusa.or.jp/app/kusakidb) (https://hub.docker.com/r/ghelfi/kusakidb)_KaPPA-View4 for integration of transcriptome and metabolome data on metabolic maps (http://kpv.kazusa.or.jp/)

- CoP: a database for plant co-expressed gene network (http://webs2.kazusa.or.jp/kagiana/cop0911/)

- RnR: a database for regulatory network in T87 cultured cells of *Arabidopsis thaliana* (http://webs2.kazusa.or.jp/kagiana/rnr0912/indexff.htm)

National Institute for Basic Biology (http://www.nibb.ac.jp)_nekko: a portal site for Rhizophagus irregularis genome (http://nekko.nibb.ac.jp)

- Japanese Morning Glory Genome Database: (http://ipomoeanil.nibb.ac.jp)_The Plant Organelles Database 3: (http://podb.nibb.ac.jp/Organellome/)_PHYSCObase: (http://moss.nibb.ac.jp/physco.html)



[Ca2+]cyt dynamics in the root of Arabidopsis seedlings expressing R-GECO1, in response to 5 µM DMBQ, 1 µM flg22 or dimethyl sulfoxide (DMSO) control. A montage of fluorescence images was obtained from Supplementary Videos 1–3. Kymographs are in Extended Data Fig. 1. Scale bars, 50 µm.

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

COVID19 has greatly affected our research in terms of style and activity. Although we did not get into full-lockdown in Japan, plant science-related annual meetings (Botanical Society of Japan, Japanese Society of Plant Physiologists, Japanese Society for Plant Biotechnology, etc.) were postponed or held online. Researchers have explored the new research style using web communication under the pandemic of COVID19.

Planned events for 2021 and 2022

- Mar. 14-16, 2021: 62rd Annual Meeting of JapaneseSociety of Plant Physiologists (on line meeting). Matsue. (https://jspp.org/annualmeeting/62/e_greeting.php)

- May 28 2021: International RIKEN Symposium on Sustainable Resource Science “Hope for the Future” (on line meeting)

- Dec. 13-16, 2021: Cold Spring Harbor Asia Conference “Integrative Epigenetics in Plants”, Awaji Yumebutai Conference Center- Mar. 22-24, 2022: 63rd Annual Meeting of Japanese Society of Plant Physiologists. Tsukuba.

Selected Publications

- Laohavisit, A., Wakatake, T., Ishihama, N., Mulvey, H., Takizawa, K., Suzuki, T. and Shirasu, K. “Quinone perception in plants via leucine-rich-repeat receptor-like kinases”, Nature 587, 92–97. Doi: 10.1038/s41586-020-2655-4

Identification of a novel leucine-rich-receptor-like kinase provides insights into the role of quinone signalling for the haustorium formation in parasitic plants and for plant immunity in nonparasitic plants.

- Notaguchi M, Kurotani KI, Sato Y, Tabata R, Kawakatsu Y, Okayasu K, Sawai Y, Okada R, Asahina M, Ichihashi Y, Shirasu K, Suzuki T, Niwa M, Higashiyama T.(2020) Cell-cell adhesion in plant grafting is facilitated by beta-1,4-glucanases. Science 369, 698-702. doi: 10.1126/science.abc3710

Surprising ability of tobacco in hetero-grafting and its molecular mechanism were shown, providing huge impact both in basic and applied biology

- Kidokoro, S., Hayashi, K., Haraguchi, H., Ishikawa, T., Soma, F., Konoura, I., Toda, S., Mizoi, J., Suzuki, T., Shinozaki, K. and Yamaguchi-Shinozaki, K.“Posttranslational regulation of multiple clock-related transcription factors triggers cold-inducible gene expression in Arabidopsis”, Proc. Natl. Acad. Sci. USA 118, e2021048118Doi:10.1073/pnas.2021048118

Elucidation of the mechanisms of DREB1 expression in response to cold stress provides huge impact both in basic and applied plant stress biology.

Major Funding Sources

RIKEN is 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)

New Zealand

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Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

At the end of March 2020 New Zealand went into lockdown for approximately seven weeks in response to COVID19. During this time most research institutes closed with only essential maintenance work permitted and researchers and students required to work from home. Following this lockdown, community transmission of COVID19 has remained low in New Zealand and research institutes have been open. However, the Auckland region saw two outbreaks requiring a return to lockdown for 1-2 weeks in August 2020 and February 2021, closing research institutes in Auckland, while instiues in the rest of the country remained open, but with some restrictions.

The research community has also been impacted by the cancelation of at least one funding round, restrictions on international travel imposed by many research institutions and restrictions on international researchers entering New Zealand. Additionally, there has been delays on the delivery of consumable items and equipment from international suppliers.

Planned events for 2021 and 2022

- Plant Science Central Conference, July 6-8 2021, Palmerston North, New Zealand. In-person event planned with some virtual presentations for international speakers.

- Queenstown Research Week including a satellite in Applied Genetics in Breeding Technologies, Aug 30 to Sept 2 2021, Queenstown, New Zealand

- 16th congress of the Federation and Asian and Oceanian Biochemists and Molecular Biologists (partnering with the New Zealand Society of Plant Biologists), November 22-25 2021, Christchurch, New Zealand. In-person event planned with some virtual presentations for international speakers.

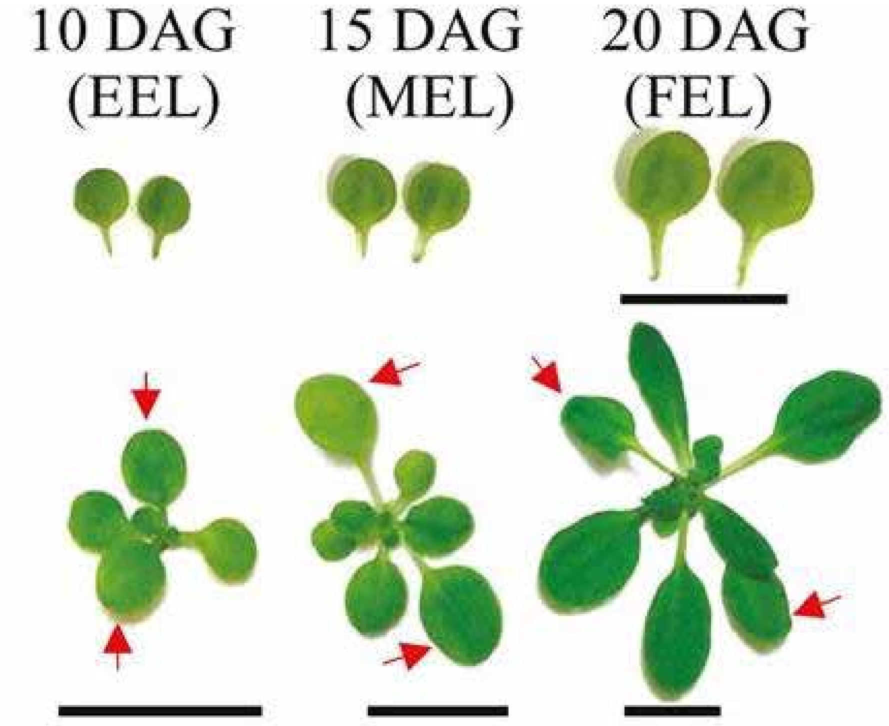
- International Congress on Photosynthesis Research; August 6th-12th 2022, Rotorua Energy Events Centrehttps://www.photosynthesis-research.org/ispr-news/asia-oceania/2019/international-congress-on-photosynthesis-research-2020/

Selected Publications

These articles highlight the diverse research using Arabidopsis that occurs in New Zealand.

1. Miebach, M., Schlechter, R.O., Clemens, J., Jameson, P.E. and Remus-Emsermann M.N.P. (2020) Litterbox-A gnotobiotic zeolite-clay system to investigate Arabidopsis–microbe interactions. Microorganisms 8, 464. https://doi.org/10.3390/microorganisms8040464

This manuscript describes a new soilless medium with improved aeration compared to an agar-based medium and reduced cross-contamination between phyllosphere and rhizosphere to support studies into plant-microbe interactions.



First rosette leaf pair expansion. (A) Arabidopsis WT first rosette leaf pairs detached from plants at 10, 15, and 20 days after germination (DAG). Scale bar=10 mm.

2. Kanojia, A., Gupta, S., Benina, M., Fernie, A.R., Mueller-Roeber, B., Gechev, T. and Dijkwel, P.P. (2020) Developmentally controlled changes during Arabidopsis leaf development indicate causes for loss of stress tolerance with age. Journal of Experimental Botany, 71, 6340–6354. https://doi.org/10.1093/jxb/eraa347

This collaborative effort between New Zealand and European scientists proposes that age-related changes that lead to scenescence in Arabidopsis also result in reduced stress tolerance.

3. Williams, M.A.K., Cornuault, V., Irani, A.H., Symonds V., Malmström, J., An, Y., Sims, I.M., Carnachan, S.M., Sallé, C. and Noth, H. (2020) Polysaccharide structures in the outer mucilage of Arabidopsis seeds visualized by AFM. Biomacromolecules 21, 1450-1459. DOI: 10.1021/acs.biomac.9b01756

This manuscript describes the use of atomic force microscopy to show that rhamnogalacturonan I from the mucilage of Arabidopsis seedlings can form surprisingly long versions that can self assemble into a range of structures.

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)

- The Agricultural and Marketing Research and Development Trust (AGMARDT: http://agmardt.org.nz/).

Norway

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Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

The COVID pandemic initially brought both education and research to a halt at universities and research institutes in Norway. While education overall adapted quite quickly to online teaching, research was in a different situation due to subject-specific challenges (laboratory vs. season-dependent, field-based research). Different institutions had also very different policies governing return to laboratory-based research activities, which was not helpful for the community as a whole. In addition, the policies supporting PhD students and postdoctoral researchers differed significantly. While PhD students are eligible for salaried extensions to compensate for problems caused by COVID, this is not the case for postdoctoral researchers with obvious negative consequences. Publication outputs seem to have increased similarly like the number of grant applications submitted to the research council. Unfortunately, there´s no reliable data available regarding possible gender-specific impacts of COVID on the Norwegian plant biology research community.

Planned events for 2021 and 2022

The Norwegian Plant Biology community will be hosting the biannual conference of the Scandinavian Plant Physiology Society at the end of August on Svalbard. Currently the conference is scheduled to go ahead in person

Selected Publications

- The Role of a Glucosinolate-Derived Nitrile in Plant Immune Responses. Ting HM, Cheah BH, Chen YC, Yeh PM, Cheng CP, Yeo FKS, Vie AK, Rohloff J, Winge P, Bones AM, Kissen R. Front Plant Sci. 2020: 11: 257. doi: 10.3389/fpls.2020.00257. eCollection 2020.

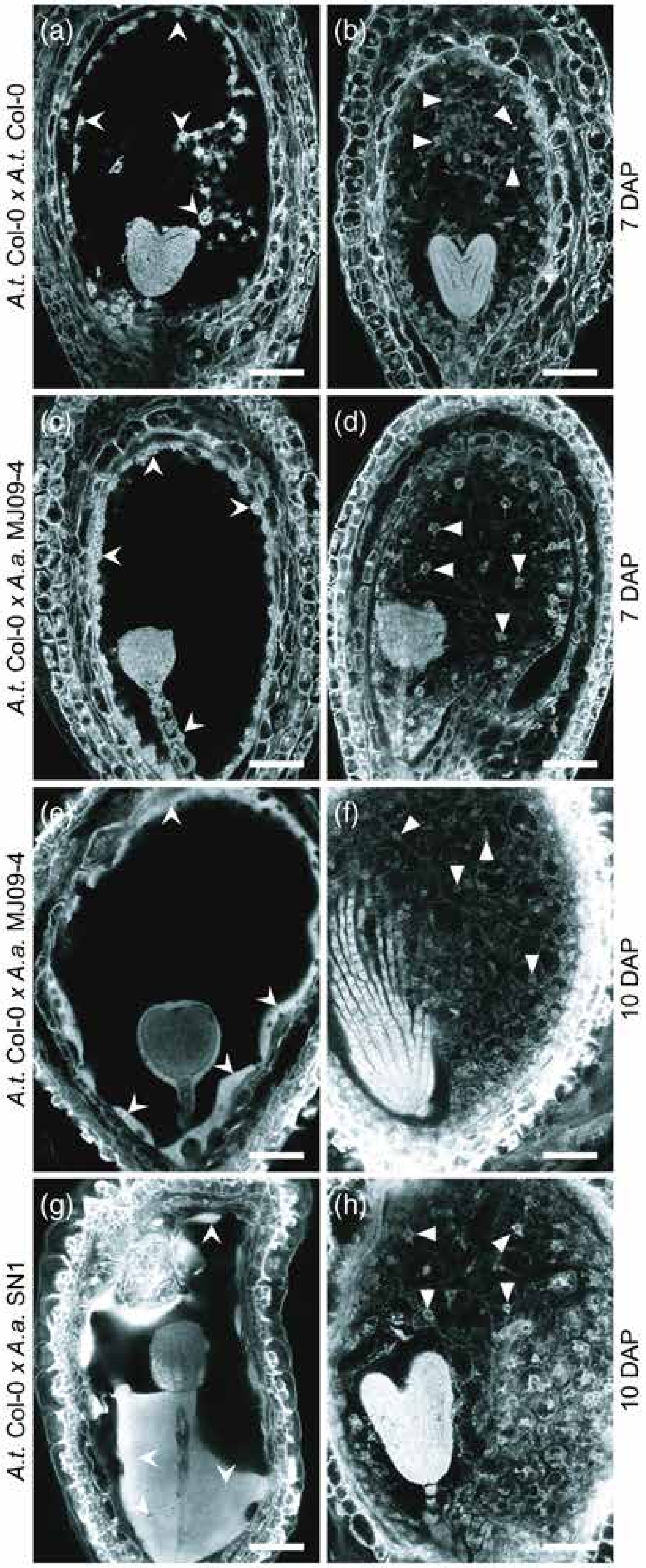
The article presents the results of a thorough and diligent investigation into the role of nitriles, whose role in plant defense is still not well understood.

- Genetic variation and temperature affects hybrid barriers during interspecific hybridization. Bjerkan KN, Hornslien KS, Johannessen IM, Krabberød AK, van Ekelenburg YS, Kalantarian M, Shirzadi R, Comai L, Brysting AK, Bramsiepe J, Grini PE. Plant J. 2020:122-140. doi: 10.1111/tpj.14523.

The article investigates elegantly the impact of genetic diversity and temperature on hybridization barriers between Arabidopsis arenosa, *A. lyrata,* and *A. thaliana* using AGL36-like genes.

- Metagenomic analysis of historical herbarium specimens reveals a post-mortem microbial community. Bieker VC, Sánchez Barreiro F, Rasmussen JA, Brunier M, Wales N, Martin MD. Mol Ecol Resour. 2020: 20(5):1206-1219. doi: 10.1111/1755-0998.13174.

The article presents interesting insights into opportunities to leverage knowledge from existing museum herbaria and highlights relevant pitfalls.



Variation in endosperm cellularization between *A. thaliana* and A. arenosa hybrids.

(a–h) Confocal scanning laser micrographs of endosperm cellularization in hybrid seeds visualized by Feulgen staining. For all crosses, both non-cellularized and cellularized endosperm is observed and micrographs representative for each class are presented in the left and right panels respectively. Open arrowheads point to syncytial endosperm nuclei while closed arrowheads point to cellularized endosperm nuclei. Scale bar = 50 µm. (a and b) *A. thaliana* control 7 days after pollination (DAP) typically at the embryo late heart stage in which most seeds display complete endosperm cellularization (b). (c, d) *A. thaliana* × A. arenosa MJ09 hybrid seeds at 7 DAP. Embryo development is slower compared with *A. thaliana* controls. Both non-cellularized (c) and cellularized endosperm (d) was frequently observed. (e, f) *A. thaliana* × A. arenosa MJ09 hybrid seeds at 10 DAP. Only a few seeds fail to cellularize (e) and most seeds exhibit completed endosperm cellularization (f). (g, h) *A. thaliana* × A. arenosa SN1 hybrid seeds at 10 DAP. A higher fraction of seeds display syncytial stage endosperm (g) compared with A. arenosa MJ09 hybrid seeds (e, f), but some have completed endosperm differentiation (h).

Major Funding Sources

Norwegian Research Councilhttps://www.forskningsradet.no/en/Home_page/1177315753906

Poland

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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 2020 or early 2021

Polish researchers Hanna Cwiek-Kupczynska and Pawel Krajewski were involved in the preparation of the new version of a metadata standard for the documentation of phenotyping datasets. MIAPPE 1.1 structures the metadata (which may consist of images, other binary data, tabular files, etc.).

The new MIAPPE 1.1 standard also provides the opportunity to store environmental conditions data. The work has been published this year in the New Phytologist:Papoutsoglou, E.A., Faria, D., Arend, D., Arnaud, E., Athanasiadis, I.N., Chaves, I., Coppens, F., Cornut, G., Costa, B.V., _Cwiek-Kupczynska H., Droesbeke, B., Finkers, R., Gruden, K., Junker, A., King, G.J., Krajewski, P., Lange, M., Laporte, M.-A., Michotey, C., Oppermann, M., Ostler, R., Poorter, H., Ramirez-Gonzalez, R., Ramsak, Z., Reif, J.C., Rocca-Serra, P., Sansone, S.-A., Scholz, U., Tardieu, F., Uauy, C., Usadel, B., Visser, R.G.F., Weise, S., Kersey, P.J., Miguel, C.M., Adam-Blondon, A.-F. and Pommier, C. (2020) Enabling reusability of plant phenomic datasets with MIAPPE 1.1. New Phytologist, 227, 260-273.

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

Due to the COVID19 pandemic schools and universities in Poland switched to remote learning mode. Shift work or remote systems of work have been implemented in Polish research institutes. The international mobility of scientists has significantly decreased, and many projects that included tasks to be performed in cooperation with groups from outside of Poland have been delayed. All these aspects significantly hampered the progress of experimental work. It is remarkable that most meetings (including internal meetings, lab meetings etc.) and conferences are held remotely. This has its pros and cons. An obvious positive aspect is the possibility of participating in large international conferences without the need to cover high travel and accommodation costs. However, it remains an open question to what extent does an on-line conference compares to on-site conferences? So far in these difficult conditions, scientists in Poland have continued their work, carry out projects and publish. Let us hope that the difficult time will pass and we will be able to work at full steam again.

Planned events for 2021 and 2022

•10th Polish Society of Experimental Biology (PSEB) Conference; Katowice, Poland; September 20–23, 2021 (virtual)[https://ptber.org.pl/default/en/conferences/10th-conference/]

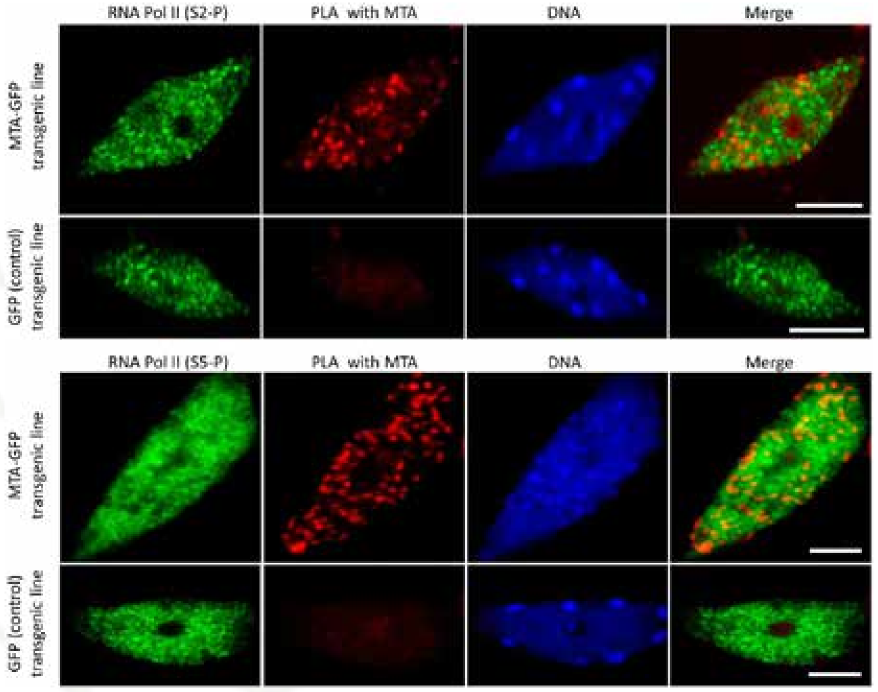
•2nd National Conference on the Anatomy and Histology of Plants organized by the Polish Botanical Society (PBS); September 7-8, 2021 (virtual)[https://pbsociety.org.pl/default/ii-krajowa-konferencja-anatomia-i-histogeneza-roslin-dzis-i-jutro-7-8-09-2021-r-zgloszenia/]

•Plant Applied Genetics- challenges of the XXI century, 22-24 September 2021, Warsaw [http://kghibr.sggw.pl/genetyka2021/]

Selected Publications

- Bhat, S.S., Bielewicz, D., Gulanicz, T., Bodi, Z., Yu, X., Anderson, S.J., Szewc, L., Bajczyk, M., Dolata, J., Grzelak, N., Smolinski, D.J., Gregory, B.D., Fray, R.G., Jarmolowski, A. and Szweykowska-Kulinska, Z. (2020) mRNA adenosine methylase (MTA) deposits m6A on pri-miRNAs to modulate miRNA biogenesis in *Arabidopsis thaliana*. Proceedings of the National Academy of Sciences, 117, 21785-21795

The authors found that mRNA adenosine methylase (MTA) co-transcriptionally introduces m6A into a set of *A. thaliana* miRNA precursors stimulating their biogenesis via interactions with early-stages miRNA biogenesis protein Tgh, affecting pri-miRNA secondary structure and in consequence enhancing recruitment of Microprocessor to pri-miRNAs.



PLA shows the interaction between MTA and RNA Pol II phosphorylated at Serine 2 and Serine 5. Positive PLA signals (red spots in the second column) can be seen only in cells containing the MTA–GFP transgene, but not in control cells expressing GFP alone. RNA Pol II is represented in green. DNA is stained with HOECHST (blue). (Scale bars, 5 µm.)

- Pastorczyk, M., Kosaka, A., Pislewska-Bednarek, M., Lopez, G., Frerigmann, H., Kulak, K., Glawischnig, E., Molina, A., Takano, Y., and Bednarek, P. (2020). The role of CYP71A12 monooxygenase in pathogen-triggered tryptophan metabolism and Arabidopsis immunity. New Phytologist, 225, 400-412.

The authors provide new insights into pathogen-triggered changes in tryptophan metabolism; they describe the role of the CYP71A12 monooxygenase in the biosynthesis of indole_3_carboxylic acid (ICA) and the consequence of the disturbance of this regulatory module to defense response in Arabidopsis.

- Zmienko, A., Marszalek-Zenczak, M., Wojciechowski, P., Samelak-Czajka, A., Luczak, M., Kozlowski, P., Karlowski, W.M. and Figlerowicz, M. (2020) AthCNV: A Map of DNA Copy Number Variations in the Arabidopsis Genome. The Plant Cell, 32, 1797-1819

Based on the analysis of short-read sequencing data released by the 1001 Genomes Consortium, Zmienko *et al*. created a comprehensive atlas of copy number variations (CNVs) and large indels in the Arabidopsis genome, showed the impact of local genomic context (e.g. CNV overlap with genes and transposable elements) on CNV distribution and demonstrated the usefulness of gene-associated CNVs as markers for population structure analysis and genome-wide association studies.

Major Funding Sources

NCN National Science Centre Poland [www.ncn.gov.pl]
NCN supports basic research in Poland.
In 2020 projects using Arabidopsis as a model received apr. €3,270,358

Singapore

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Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

In Singapore, we had a “circuit breaker” measures, abbreviated as CB, during 7 April, 2020 – 1June 2020. The measures mandated a stay-at-home order by the Government of Singapore, however they allowed essential research staff to regularly visit the labs to sustain minimal research activities. The measures were effective so that research activities could slowly resume after the CB with staggering working hours and safe-distancing among researchers. As of Dec 28, 2020, the measures were lifted to a phase in which general research activities could be performed to the level comparable to pre-Covid19 days. We still stay vigilant to keep the safe-distancing rule, temperature logging, mask-wearing and on-line meetings to avoid crowding.

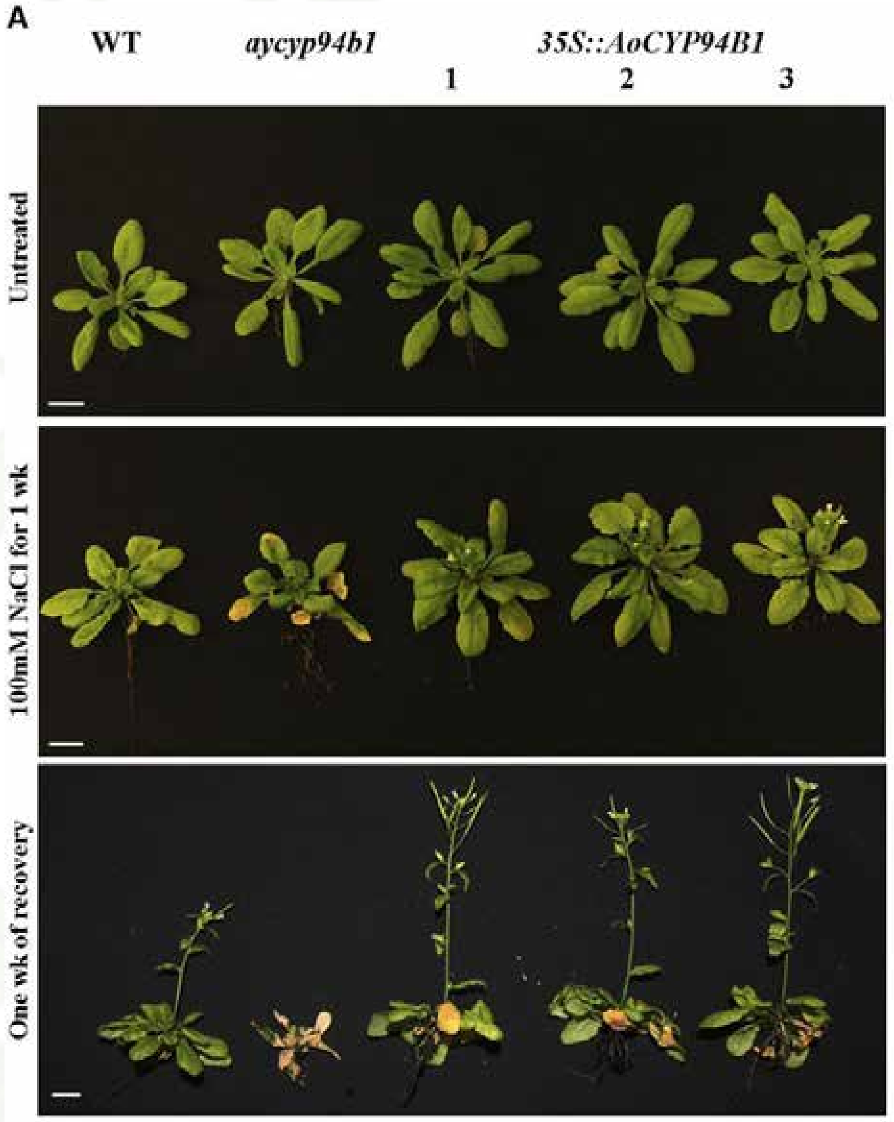
Planned events for 2021 and 2022

Due to Covid-19, most local in-person conferences were all canceled or switched to virtual events.

Selected Publications

1) Mobile TERMINAL FLOWER1 determines seed size in Arabidopsis. Zhang B, Li C, Li Y, Yu H. Nature Plants (2020) Sep;6(9):1146-1157. doi: 10.1038/s41477-020-0749-5. Epub 2020 Aug 24.

TFL1 is a novel mobile regulator generated in the chalazal endosperm, which moves to the peripheral endosperm to control seed size under the regulation by a group of small GTP-binding Ras-related nuclear proteins.



Heterologous expression of AoCYP94B1 increases salt tolerance and regulates Na+ accumulation in Arabidopsis plants. A, Growth response to salt (100 mm NaCl for 1 week) of the wild type (WT), atcyp94b1, and three independent lines of 35S::AoCYP94B1 heterologously expressed in the mutant background was monitored in 1-month-old, soil-grown Arabidopsis plants in the untreated and salt-treated conditions and after 1 week (wk) of recovery in normal water. Scale bar = 10 mm.

2) Regulation of CYP94B1 by WRKY33 controls root apoplastic barrier formation leading to salt tolerance. Krishnamurthy P, Vishal B, Ho WJ, Lok CJF, Lee F, Kumar PP.Plant Physiology (2020) 184:2199-2215.doi:https://doi.org/10.1104/pp.20.01054

This work identifies a cytochrome p450 gene from mangrove as a key factor to generate apoplastic barrier in roots for salinity adaption.

3) Genetics of autoimmunity: an evolutionary genetics perspective. Wan WL, Kim ST, Castel B, Charoennit N, Chae E. New Phytologist (2021) 229(3):1215-1233 doi: 10.1111/nph.16947

A commissioned article for Tansley review series provides a comprehensive overview on hybrid necrosis and immune system incompatibilities in plants.

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 Innovateshttp://www.temasekfoundation-innovates.org.sg/

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 2020 or early 2021

- Crisanto Gutiérrez’s lab (CBM, Madrid) has developed a highly useful tool (PlaCCl), a unique sensor with three fluorescent reporters that allows spatiotemporal visualization of cell cycle progression and works in a variety of organs (Desvoyes *et al*, 2020, Nature Plants 6, 1330-1334)

- A work led by A. Carbonell (IBMCP, Valencia) presents two different strategies based on artificial sRNAs that can be used to finely modulate the degree of silencing of endogenous and exogenous target genes (López-Dolz L *et al*, Nucleic Acids Res. 2020, 48, 6234-6250).

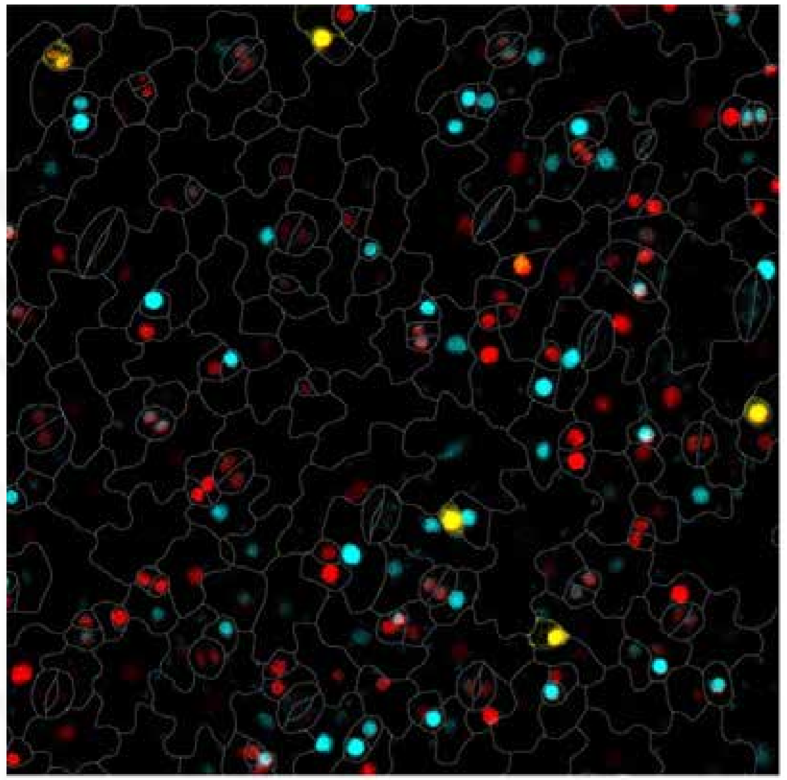
Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

As many other countries, Spain has been badly hit by COVID-19, with severe restrictions in mobility and in the capacity to access workplaces for months. This has had an understandable negative effect on the progress of many projects, with the reduced bench hours, the loss of biological material and the uncertainty of working conditions and its subsequent impact on planning. Possibly, the situation has been particularly stressful for those researchers working under pressure to advance their careers in a finite time framework (aspiring PhD candidates close to term, young postdocs on fellowships or trying to acquire international experience, young PIs at early stages of their careers, etc.), but fortunately some measures have been taken by Spanish funding agencies and universities/research institutions to mitigate some of these problems. However, these problems have been general consequences of the pandemics, not particularly worse for the Arabidopsis community.

In fact, the Spanish scientific production focused on Arabidopsis research has been very similar to that of previous years, and hopefully, the overall impact in this aspect will be minimal. On the other hand, Spanish Arabidopsis researchers have a strong tradition of international collaborations that have been more difficult in this context, but again, this should be easily overcome if the situation improves as expected. On the bright side, the pandemics has reinforced to a certain point public trust and interest in science and, while still biomedical research is perceived as the most important, all fields should benefit of this awareness and, hopefully, will be translated into new and better funding instruments in the next years.

Planned events for 2021 and 2022

In Nov 2020, the XV National Meeting of Plant Molecular Biology, a major event bringing together most of the plant labs in Spain, and specially the Arabidopsis community, was held online with a high level of participation and scientific quality. In the next years, several meetings have been planned, some of them postponed from 2020, hoping for the chance of in-person attendance. This volatile scenario has caused that, for some of them, the precise details of the organization (dates, location, program) are still missing.



Confocal image of leaf epidermal cells expressing the PlaCCI marker, which contains in a single construct pCDT1a::CDT1a-eCFP, pHTR13::HTR13-mCherry and pCYCB1;1::NCYCB1;1-YFP.
This allows simultaneous identification of cells in different phases of cell cycle: G1 in cyan, S+earlyG2 in red and lateG2+M (prophase and metaphase) in yellow. The marker is described in Desvoyes *et al*, 2020, Nature Plants 6, 1330-1334.

- BP2021: XXIV Reunión de la Sociedad Española de Biología de Plantas and XVII Congreso Hispano-Luso de Biología de Plantas, 7 y 8 de julio de 2021. Online. https://bp2021.eu/

- ”Understanding plant responses to climate changes: redox-based strategies” organized by L.M. Sandalio, F van Breusegem, F.J. Cejudo. 21-23 September, 2021. Baeza, Spain

- “Joint Meeting for Plant and Human Sulfur Biology and Glucosinolates “, organized by C. Gotor y L.C. Romero, 26-30 September, 2021, Sevilla, Spain. https://www.s-bio-glucosinolate2020.com/index

- “Workshop in Molecular Mechanisms controlling flowering”, organized by C. Ferrándiz and F. Madueño. Expected June 2022, location to be announced.

- International Plant Proteostasis Meeting, organized by V. Rubio, F. Theodolou, B. Orosa and M. Trujillo. Madrid, 2022, exact dates to be announced.As for outreach, the Arabidopsis community is present in many initiatives, for instance:The cycle of conferences “Qué sabemos de…”, organized by CSIC; Fascination of Plants day activities; etc.

Selected Publications

- Chen WW, Takahashi N, Hirata Y, Ronald J, Porco S, Davis SJ, Nusinow DA, Kay SA, Mas P. A mobile ELF4 delivers circadian temperature information from shoots to roots. Nature Plants, 6:416-426.

A highly interesting study that opens new views on clock functioning and how a long-distance shoot-to-root dialogue works and transmits information of ambient temperature to the underground organs.

- Esteve-Bruna, D., Carrasco-López, C., Blanco-Touriñán, N., Iserte, J., Calleja-Cabrera, J., Perea-Resa, C., Úrbez, C., Carrasco, P., Yanovsky, M. J., Blázquez, M. A., Salinas, J., & Alabadí, D. (2020).

Prefoldins contribute to maintaining the levels of the spliceosome LSM2-8 complex through Hsp90 in Arabidopsis. Nucleic Acids Research, 48, 6280–6293. Prefoldins were originally identified as aids for actin and tubulin folding in the cytosol, but new regulatory roles of these proteins in the nucleus are being uncovered across kingdoms. In this work, a novel function of prefoldins in regulating mRNA splicing is described

- Laureano-Marín AM, Aroca Á, Pérez-Pérez ME, Yruela I, Jurado-Flores A, Moreno I, Crespo JL, Romero LC, Gotor C. (2020) Abscisic Acid-Triggered Persulfidation of the Cys Protease ATG4 Mediates Regulation of Autophagy by Sulfide. Plant Cell: 32:3902-3920

Autophagy is a key process for the degradation and recycling of cytoplasmic components in eukaryotes, which plays a crucial role in plant growth and stress responses. This work sheds new light on how hydrogen sulfide regulates this process in conjunction with abscisic acid.

Major Funding Sources

In Spain, Arabidopsis research is mainly funded by the State Research Agency in competitive calls launched every year. In 2020, around 75 projects to individual laboratories were granted, which is in line with previous years.

Additional national calls and regional funding also supports other initiatives.PLANTGROWTH, a large individual competitive grant from the ERC AdG program to Crisanto Gutiérrez (CBM, Madrid) is active since 2019, focusing on understanding and exploiting genome replication, cell division and epigenetics to design improved plant growth strategies.European funding for basic plant research is usually scarce, but several MSCA actions (IF, RISE, etc) have been awarded to Spanish fellows to work in Arabidopsis.

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 2020 or early 2021

During this time major funding was granted by the Swedish Foundation for Strategic Research (SSF) in Agenda 2030 Research (ARC) Centers on Future Advanced Technology for Sustainability. The project “Re-designing photosynthesis for future food security” with Åsa Strand from UPSC as main applicant, more info here https://www.upsc.se/about-upsc/news/5929-new-funding-to-re-design-photosynthesis-and-increase-crop-productivity.html

SSF has selected Eleni Stavrinidou, research fellow in the Laboratory of Organic Electronics, for research into bioelectronic components for plants as one of 20 Future Research Leaders recieving SEK 12 million in a five-year period and the opportunity to participate in a leadership programme https://liu.se/en/research/electronic-plants

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

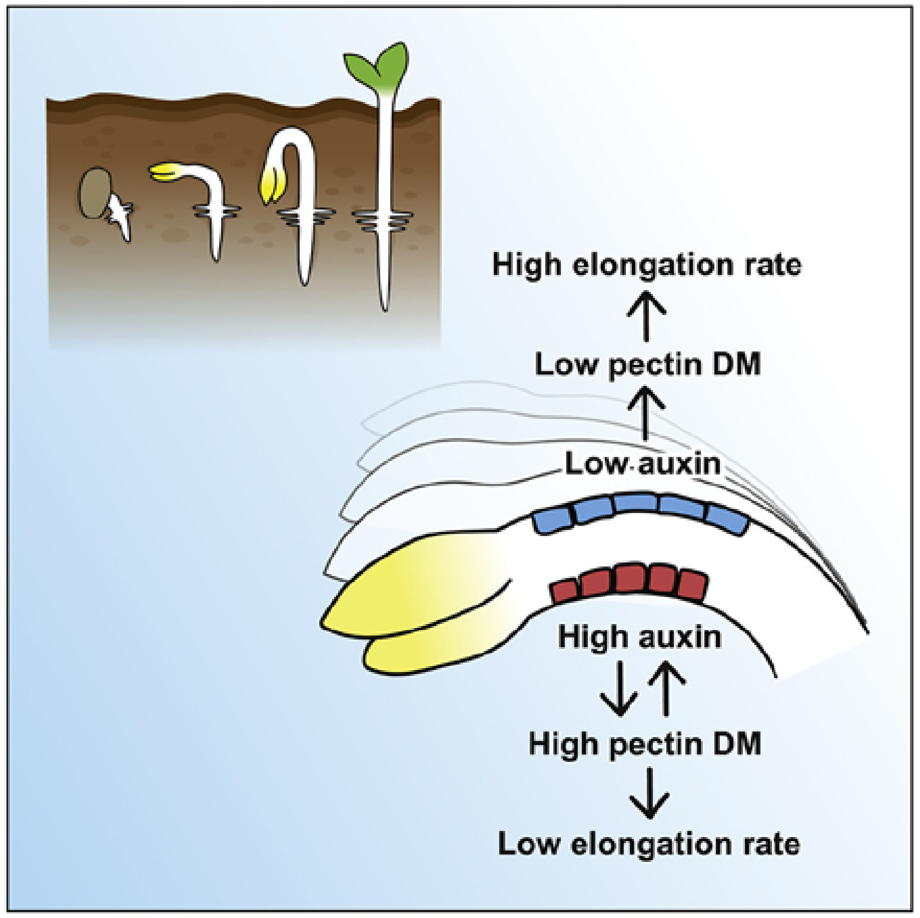
- Max Lab hosted by Lund University; https://www.maxiv.lu.se/Dedictated to high-throughput, nanovolume characterization and crystallization of biological macromolecules
- Science for Life Laboratory (SciLifeLab) is a national resource center dedicated to large scale research in molecular biosciences 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 Swedenhttps://www.plantlink.se/The Linnean Centre for Plant Biology in Uppsalahttps://lcpu.se/

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

Although Sweden did not experience a full-scale lockdown, activities have been hampered by covid-19 restriction to limit spread and a large part of our work have been operated remotely, unless necessary.

Planned events for 2021 and 2022

- 15th Nordic Photosynthesis Congress (NPC15) 5-8 October 2021 Gothenburg, Sweden, http://www.npc15.se/



- Scandinavian Plant Physiology Society (SPPS2021) conference will be held the 24-27th of August 2021 in Longyearbyen, Svalbard, Norway, https://spps.se/spps2021/

- Webinar Series by Physiologia Plantarum and the Scandinavian Plant Physiology Society firs event 20 May 2021 bit.ly/3e1xk72

- Plant Research and Higher Education in Southern Sweden (PlantLink) have activities regularly, 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

- This paper is interesting since it help advance knowledge on how tissue bending is coordinated during development. Mechanochemical feedback mediates tissue bending required for seedling emergence (2021) Jonsson, K.; Lathe, R.S.; Kierzkowski, D.; Routier-Kierzkowska, A.-L.; Hamant, O.; Bhalerao, R.P. Current Biology 31:1154-1164

- This highly cited paper shows that Polymerase IV function is necessary for pollen development in Capsella and highlighting that different mechanisms may be at play in related species. Polymerase IV Plays a Crucial Role in Pollen Development in Capsella (2020)Wang, Z.X. ; Butel, N.; Santos-Gonzalez, J. (Santos-Gonzalez, Juan)[1,2] ; Borges, F. ; Yi, J.; Martienssen, R.A.; Martinez, G. ; Kohler, C. Plant Cell 32: 950-966

- This work adds knowledge on regulation of photoprotection in photosystems, essential for plant adaptation and fitness. An atypical short-chain dehydrogenase-reductase functions in the relaxation of photoprotective qH in Arabidopsis (2020) Amstutz, C.L.; Fristedt, R.; Schultink, A.; Merchant, SS; Niyogi, K.K.; Malnoe, A. Nature Plants 6:154-166

Major Funding Sources

The Swedish Research Council (VR); http://www.vr.seVR 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.sePromotes sustainable growth by funding needs-driven research and the development of effective innovation systems

- The Swedish Research Council Formas; http://www.formas.seSupports research (rather applied) and need-driven research in the areas Environment, Agricultural Sciences and Spatial Planning

- The Wallenberg Foundations; http://www.wallenberg.org/enPrivate foundations supporting researcher initiated basic research as well as larger centers of excellence devoted to functional genomics and other strategic areas

- 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.comPrivate foundations devoted to support scientific research in Northern Sweden

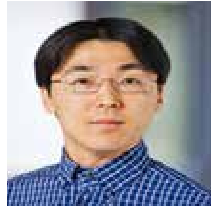
- Stiftelsen Olle Engkvist Byggmästare; http://engkviststiftelserna.se/A private foundation supporting basic science

- Sven and Lily Lawski's foundation for research in Natural Sciences (Biochemistry and Genetics); http://www.lawskistiftelsen.se/A private foundation supporting basic science

All major 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 aimed at specific research areas.

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.

Switzerland



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Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

Like many labs worldwide, we experienced massive challenges due to the restrictions announced in relation to COVID19 . We have lost many months of work because many plants had to be thrown away and therefore experiments could not be conducted to the end. This will also have an impact on our publications in 2021 and future years. As an indirect effect, some kits and consumables are not available - especially NGS library kits, PCR plates or filter tips are in shortage. Due to this shortage, research will be delayed.

Planned events for 2021 and 2022

Conferences:

Conferences and meetings based on the CUSO network (Universities from Western Switzerland) https://biologie.cuso.ch/molecular-plant-sciences/welcomeE.g.)

Plant Development – a Combined on-Site and Virtual Workshop, 03 Sep 2021, University of Lausanne, Lausanne

-PSC Symposium 2021, Patterns in Nature and Plant Sciences, 08 Dec 2021, ETH Zurich, Zurich-https://www.plantsciences.uzh.ch/en/outreach/conferences/patterns.html-SwissPLANT Symposium, 24 - 26 Jan 2022,

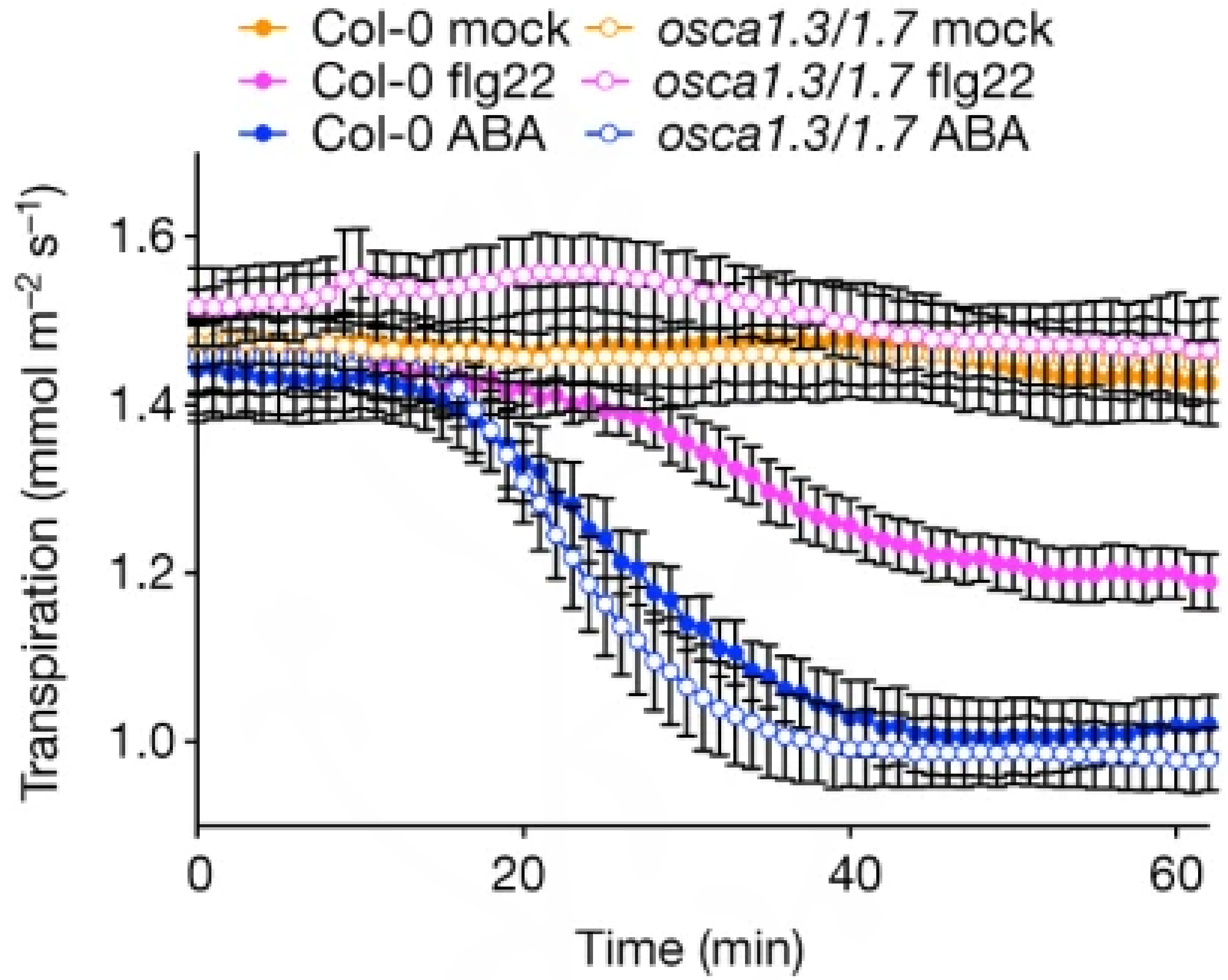
Les Diablerets
https://swissplantscienceweb.unibas.ch/en/swissplant/Summer schools-(Not exclusively for Arabidopsis)

Summer Schools in Plant Sciences
https://swissplantscienceweb.unibas.ch/en/education/summer-schools/

Outreach Activities

- Plant Science at SchoolContinuing Education Program in Plant Sciences for Secondary School Teachers Over the past four years, this program has become a national example of successful collaboration between researchers, teachers and regional learning centers.http://www.plantsciences.uzh.ch/outreach/atschool.html

- PSC Discovery Program for Youth – new Agora project In collaboration with educators of the ETH MINT Lernzentrum, the Zurich-Basel Plant Science Center (PSC) offers workshops for school classes at the secondary school level.http://www.plantsciences.uzh.ch/de/outreach/discovery.htmlhttp://www.snf.ch/en/funding/science-communication/agora/Pages/default.aspx



Leaf transpiration recorded in excised intact leaves of wild-type and osca1.3/1.7 plants. Stimuli were added to the solution at the petioles at concentrations of 10 µM flg22 and 10 µM ABA, with 0.01% ethanol as control. Data are mean ± s.e.m. for n = 4 (Col-0 mock, osca1.3/1.7 flg22 and Col-0 ABA) or n = 5 (osca1.3/1.7 mock, Col-0 flg22 and osca1.3/1.7 ABA) leaves. The experiment was performed twice with similar results.

Selected Publications

- Nat Commun. 2020 Jun 8;11(1):2885. doi: 10.1038/s41467-020-16679-7.Adaptive reduction of male gamete number in the selfing plant *Arabidopsis thaliana*Tsuchimatsu T., Kakui H., Yamazaki M., Marona C., Tsutsui H., Hedhly A., Meng D., Sato Y., Städler T., Grossniklaus U., Kanaoka M. M., Lenhard M., Nordborg M., Shimizu K. K.

This study clearly showed the natural selection on the gamete number by analysing the natural variations; the results along with the used technique might help to design the agricultural and livestock breeding.

- Nat Commun. 2020 Mar 12;11(1):1323. doi: 10.1038/s41467-020-15133-y.Cryptochrome-mediated blue-light signalling modulates UVR8 photoreceptor activity and contributes to UV-B tolerance in ArabidopsisTissot N., Ulm R.

Photoreceptors for both visible light and UV-B regulate UV-B tolerance through an intricate interplay allowing the integration of diverse sunlight signals.

- Nature . 2020 Sep;585(7826):569-573. doi: 10.1038/s41586-020-2702-1The calcium-permeable channel OSCA1.3 regulates plant stomatal immunityThor K., Jiang S., Michard E., George J., Scherzer S., Huang S., Dindas J., Derbyshire P., Leitão N., DeFalco T. A., Köster P., Hunter K., Kimura S., Gronnier J., Stransfeld L., Kadota Y., Bücherl C. A., Charpentier M., Wrzaczek M., MacLean D., Oldroyd G. E. D., Roelfsema R. G., Hedrich R., Menke F. L. H., Feijó J., Zipfel C.

This study identifies a long sought-after calcium-permeable channel involved in stomatal immunity and its regulatory mechanism.

Highly cited researchers 2020, members of the Swiss Plant Science Web
https://swissplantscienceweb.unibas.ch/en/news/details/highly-cited-researchers-2020/

Major Funding Sources

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

b. European Research Council (ERC), https://erc.europa.eu/

c. ERA-CAPS SICOPID: http://www.eracaps.org/joint-calls/era-caps-funded-projects/era-caps-third-call-%E2%80%93-2017/activation-and-regulation-plasma

d. Syngenta (Plant Science Center - Syngenta Fellowship), https://www.plantsciences.uzh.ch/en/research/fellowships/syngenta.html

e. Horizon 2020https://ec.europa.eu/programmes/horizon2020/en

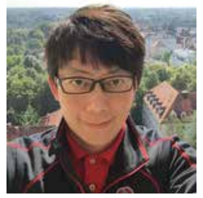
f. State Secretariat for Education, Research, and Innovation (SERI), https://www.sbfi.admin.ch/sbfi/en/home.html

g. University Research Priority Program of Evolution in Action: From Genomes to Ecosystems (directors: Beat Keller, Ueli Grossniklaus, Kentaro K. Shimizu, University of Zurich) http://www.evolution.uzh.ch/en.html

h. Japan Science and Technology Agency (JST), Core Research for Evolutional Science and Technology (CREST)https://www.jst.go.jp/kisoken/crest/en/

i. The Human Frontier Science Program (HFSP) https://www.hfsp.org/

Taiwan



Cheng-Hsun Ho,
Agricultural Biotechnology Research Center (ABRC) of Academia Sinica
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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 2020 or early 2021

1. Plants of Taiwan (http://tai2.ntu.edu.tw)

2. Orchidstra 2.0 - A Transcriptomics Resource for the Orchid Family (http://orchidstra2.abrc.sinica.edu.tw/orchidstra2/index.php)

3. Taiwan Biobank (https://www.twbiobank.org.tw/new_web/)

4. Database of Native Plant in Taiwan (http://www.hast.biodiv.tw/Announce/projectContentE.aspx)

5. Discover Plants of Taiwan (http://taiwanplants.ndap.org.tw)

6. Herbarium of Taiwan Forestry Research Institute (http://taif.tfri.gov.tw/cht/) Herbarium School of 7. Forestry and Resource Conservation, National Taiwan University (http://ntuf.cc.ntu.edu.tw)

7. Taiwan Rice Insertional Mutants Database

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

Even Taiwan was in 2020 and is still one of the safest places in the world in 2021 from COVID19 pandemic (only ~a thousand of confirmed Covid-19 cases), the biggest impact of COVID19 in the year 2020 and 2021 is it is still too risk to travel around the world. Thus, the way via face-to-face to exchange the ideas and up-to-date scientific discoveries to the international scientific community is still not available. Moreover, the number of international researchers and speakers be invited to Taiwan for their researches and seminars, respectively, have been largely reduced. However, the people and research community in Taiwan are keeping their promise to help in all and many different ways.

Planned events for 2021 and 2022

1. International Conference on the History of the Five Dynasties Period
Website: https://www1.ihp.sinica.edu.tw/Bulletin/Events/1743/Detail

Selected General Publications

1. Chen FY, Jung HW, Tsuei CY, Liao JC. Converting Escherichia coli to a Synthetic Methylotroph Growing Solely on Methanol. Cell. 2020 Aug 20;182(4):933-946.e14. doi: 10.1016/j.cell.2020.07.010. Epub 2020 Aug 10. PMID: 32780992.

”a combination of basic research and applied research at a high level” and achieving “a world-leading breakthrough research in the field of bio-energy”

2. Chen, YH., Huang, TY., Lin, YT. *et al*. VPS34 K29/K48 branched ubiquitination governed by UBE3C and TRABID regulates autophagy, proteostasis and liver metabolism. Nat Commun 12, 1322 (2021). https://doi.org/10.1038/s41467-021-21715-1

"This study provides a new insight into the treatment of fatty liver. "

3. Leung, TF., Jiang, D., Wu, MC. *et al*. Isolable dicarbon stabilized by a single phosphine ligand. Nat. Chem. 13, 89–93 (2021). https://doi.org/10.1038/s41557-020-00579-w

"This finding would generate a new paradigm of chemical reactivity in carbon and silicon group.

Major Funding Sources

1. Ministry of Science and Technology, Taiwan (https://www.most.gov.tw/?l=en)

2. Academia Sinica (https://www.sinica.edu.tw/en)

Turkey

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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 2020 or early 2021

Initiation of a collection for *Arabidopsis thaliana* ecotypes from Turkey.

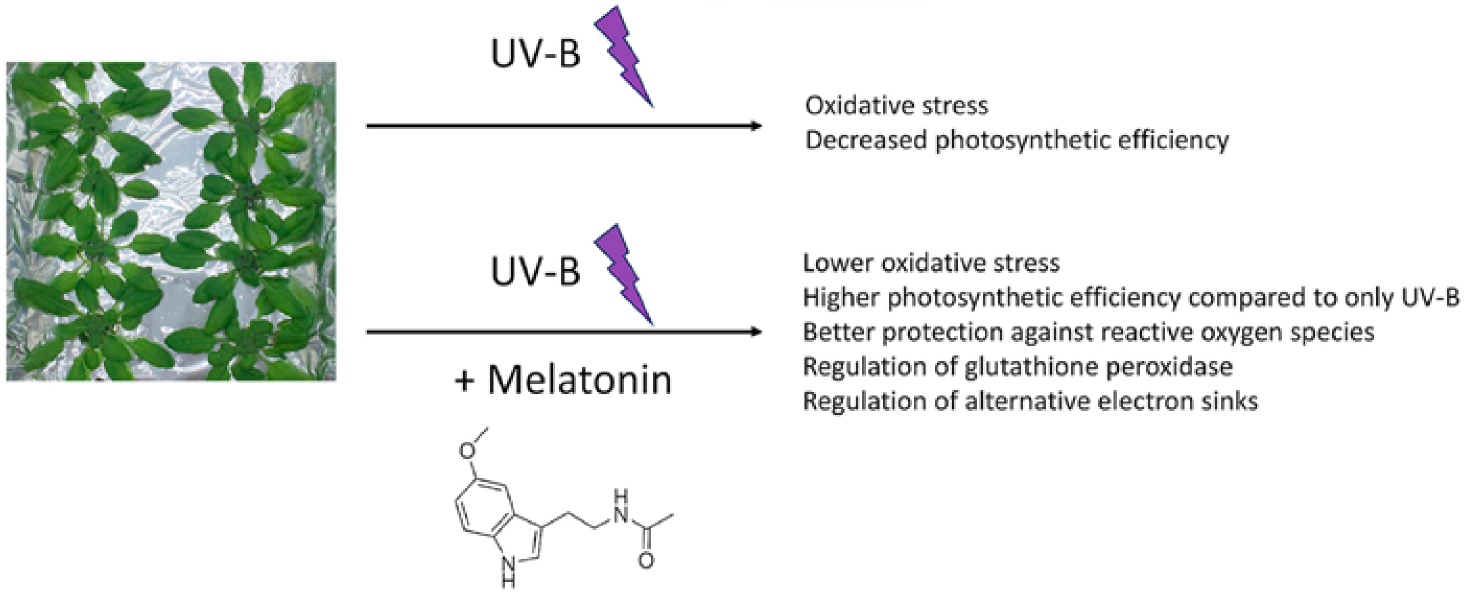
Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

The COVID-19 pandemic has been a challenge for scientists in Turkey due to lock-downs, problems in worldwide logistics and initiation of distance learning. For plant science, and other branches of science that deal with living organisms, it was challenging to grow and maintain biological material, which hindered the progress of research. Restrictions and precautions in the laboratory and personnel space made it impossible to do studies that require a high level of manpower and cooperation. Graduate students had to stall most of their research and extra time has been granted for their studies by the Council of Higher Education of Turkey. Moreover, academic staff had to adapt distance-learning technologies, which required effort diverted from science. The ambiguity of the course of events made it very difficult to make decisions related to teaching and grading of courses. As of May 2021 distance learning is being used for three semesters in a row. There seems to be no decrease in publication output in the short term, however, labs are publishing data that has been obtained before the pandemic and this will probably have a negative impact on publication output post-pandemic due to the gap in efforts for obtaining data.

Planned events for 2021 and 2022

- 4th National Plant Physiology Symposium (UBFS2021) https://ubfs2020.aku.edu.tr/ (postponed from 2020 to 2021)

- Fascination of Plants Day 2021-22, Symposias held at Ege University (18 May).



Selected Publications

Total of 11 publications has been published as of 16.05.2021 that uses Arabidopsis as plant material

- Acet, T., & Kadıo_lu, A. (2020). SOS5 gene-abscisic acid crosstalk and their interaction with anti-oxidant system in *Arabidopsis thaliana* under salt stress. Physiology and Molecular Biology of Plants, 26(9), 1831-1845

- Haskirli, H., Yilmaz, O., Ozgur, R., Uzilday, B., & Turkan, I. (2021). Melatonin mitigates UV-B stress via regulating oxidative stress response, cellular redox and alternative electron sinks in *Arabidopsis thaliana*. Phytochemistry, 182, 112592

- Ozgur, R., Uzilday, B., Bor, M., & Turkan, I. (2020). The involvement of gamma-aminobutyric acid shunt in the endoplasmic reticulum stress response of *Arabidopsis thaliana*. Journal of Plant Physiology, 253, 153250.

Major Funding Sources

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

United Kingdom

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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 2020 or early 2021

- New fluorescent auxin probes visualize tissue-specific and subcellular distributions of auxin in Arabidopsis https://nph.onlinelibrary.wiley.com/doi/10.1111/nph.17183

- 1,135 Ionomes reveals the global pattern of leaf and seed mineral nutrient and trace element diversity in *Arabidopsis thaliana* https://onlinelibrary.wiley.com/doi/10.1111/tpj.15177 https://ffionexplorer.nottingham.ac.uk/ionmap/

- KnetMiner: a comprehensive approach for supporting evidence-based gene discovery and complex trait analysis across species.https://onlinelibrary.wiley.com/doi/10.1111/pbi.13583

- 3D RNA-seq: a powerful and flexible tool for rapid and accurate differential expression and alternative splicing analysis of RNA-seq data. https://www.tandfonline.com/doi/full/10.1080/15476286.2020.1858253

- Arabidopsis antibody resources for functional studies in plantshttps://www.nature.com/articles/s41598-020-78689-1

- Computational tools for serial block electron microscopy reveal plasmodesmata distributions and wall environments http://www.plantphysiol.org/content/early/2020/07/23/pp.20.00396.longhttp://mib.helsinki.fi/downloads.html

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

The impact of COVID19 on the UK scientific community varied depending the type of institution in which the research is conducted. Many university research labs were closed from March-October 2020 whilst labs in many Research Institutes were often able to return to work soon after the first lockdown ended in May 2020. As such this may have a significant effect in research productivity over the coming years. On the return to labs researchers have needed to limit numbers and observe social distancing. This has required additional planning but should not greatly impact productivity.

The majority of UK research funding comes from UKRI research councils. UKRI is distributing funding of up to £180 million to support research and technical staff whose projects have been disrupted. Universities and organisations will receive COVID-19 allocations and will be able to provide the majority of funded projects with an extension in funding.

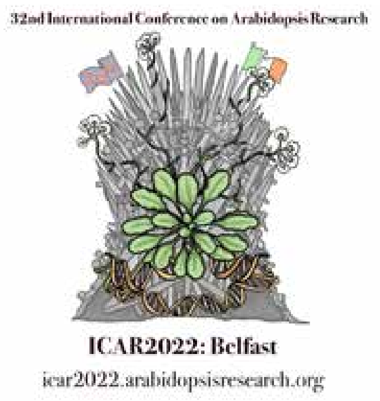
UK PhD students take between 3-4years to complete their studies and UKRI-funding for students in their final year of study was extended by 6 months. Other PhD students were able to apply for a three-month extension on a case-by-case basis. The UK is slowly opening up in May 2021 although social distancing will remain until into the summer and beyond.

University researchers expect difficulty in travelling overseas during the majority of 2021 so will likely be limited to virtual or UK based meetings until 2022. We very much hope to welcome the international community to the UK next year for ICAR2022 in Belfast.

Planned events for 2021 and 2022

- The #UKPlantSciPresents webinar series has had 20+ events since May2020 and will continue in September 2021. These events provide a forum for (mostly) UK-based Arabidopsis researchers to promote their research. Over the past year 3500+ delegates have attended these webinars. The recording of webinars can be viewed here: http://blog.garnetcommunity.org.uk/ukplantscipresents-webinars

- ICAR2022 will be held in Belfast between 20-24 June 2022 where we hope to bring together the Arabidopsis community for the first time since 2019 in Wuhan. Professor Dame Caroline Dean, Professor Keiko Torii and Professor Liam dolan will provide keynote talks and we have scheduled six exciting plenary sessions. **Applications are now open to organise a two-hour concurrent session so we encourage the community to take advantage of this opportunity. All information can be found here:** http://icar2022.arabidopsisresearch.org/



Selected Publications

- Pandey BK, Huang G, Bhosale R, Hartman S, Sturrock CJ, Jose L, Martin OC, Karady M, Voesenek LACJ, Ljung K, Lynch JP, Brown KM, Whalley WR, Mooney SJ, Zhang D, Bennett MJ (2021) Plant roots sense soil compaction through restricted ethylene diffusion. Science. doi: 10.1126/science.abf301

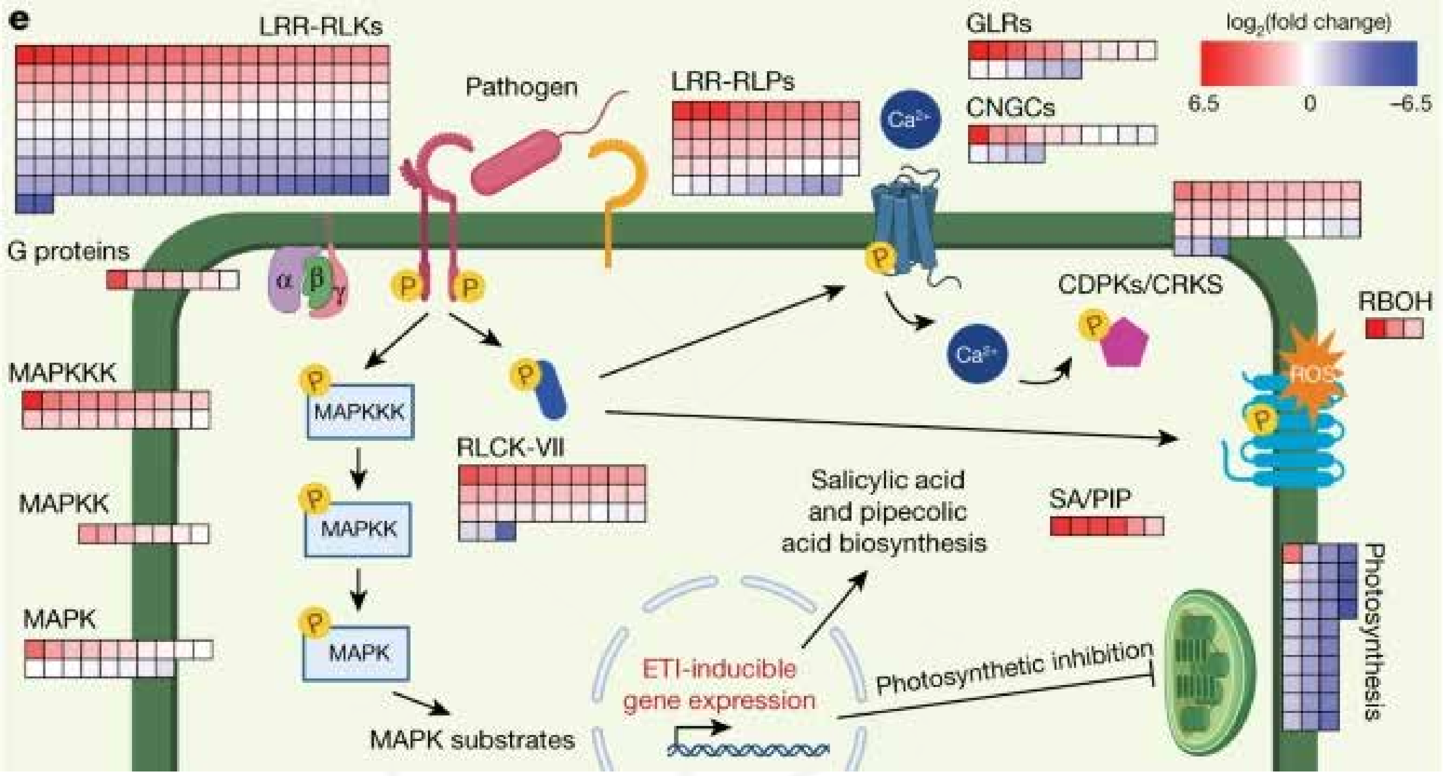
This manuscript uses a mix of molecular genetics and CT imaging to demonstrate that ethylene insensitive mutants are able to grow better through compacted soil than wildtype plants. This suggests a mechanism in which compacted soils prevents the diffusion of ethylene, thus inhibiting root growth.

- Yang W, Cortijo S, Korsbo N, Roszak P, Schiessl K, Gurzadyan A, Wightman R, Jönsson H, Meyerowitz E (2021) Molecular mechanism of cytokinin-activated cell division in Arabidopsis. Science doi: 10.1126/science.abe2305.

This research provides a more detailed explanation of the role of cytokinin in promoting cell proliferation. The authors show that in the Arabidopsis shoot apical meristem, cytokinin regulates cell division by promoting nuclear shuttling of the transcription factor Myb-domain protein 3R4 (MYB3R4) at the G2-to-M transition. An engineered nuclear-restricted MYB3R4 mimics the cytokinin effects of enhanced cell proliferation and meristem growth.

- Ngou BPM, Ahn HK, Ding P, Jones JDG (2021) Mutual potentiation of plant immunity by cell-surface and intracellular receptors. Nature. doi: 10.1038/s41586-021-03315-7.

This manuscript analyses interactions between the two distinct immune systems in Arabidopsis; cell-surface receptors and intracellular receptors. Activation of either immune system alone is insufficient to provide effective resistance against a bacterial pathogen. Thus, immune pathways activated by cell-surface and intracellular receptors in plants mutually potentiate to activate strong defences against pathogens.



RNA sequencing (RNA-seq) results showing the upregulation of PTI signalling pathway components during ETIAvrRps4.

Heat maps represent the expression level of PTI signalling pathway genes, salicylic acid (SA) and pipecolic acid (PIP) biosynthesis pathway genes and photosynthetic pathway genes at 4 h after the induction of ETIAvrRps4. Red, upregulation; blue, downregulation. CDPKs, calcium-dependent protein kinases; CNGCs, cyclic nucleotide-gated channels; CRKs, cysteine-rich receptor-like kinases; GLRs, glutamate-like receptors; LRR-RLKs, leucine-rich-repeat receptor-like protein kinases; LRR-RLPs, leucine-rich repeat receptor-like proteins; RLCK-VII, receptor-like cytoplasmic kinase subfamily VII. All experiments were repeated at least three times with similar results. Data represent log2-transformed fold changes in gene expression (normalized against expression of the corresponding genes before ETIAvrRps4 activation).

- Parry G, Benitez-Alfonso Y, Gibbs DJ, Grant M, Harper A, Harrison CJ, Kaiserli E, Leonelli S, May S, McKim S, Spoel S, Turnbull C, van der Hoorn RAL, Murray J (2021) How to build an effective research network: lessons from two decades of the GARNet plant science community. J Exp Bot. doi: 10.1093/jxb/eraa397.

For the past twenty years the GARNet network has supported the UK plant science community, with a particular focus on Arabidopsis. GARNet funding ended in 2020 and this manuscript provide a GARNet perspective on what it takes to develop an effective research network.

Major Funding Sources

- Biotechnology and Biological Sciences Research Council (BBSRC) http://www.bbsrc.ac.uk/

- The Gatsby Charitable Foundation http://www.gatsby.org.uk/

- European Research Council http://ec.europa.eu/research/era/index_en.htm

- Natural Environment Research Council http://www.nerc.ac.uk

- The Gates Foundation http://www.gatesfoundation.org/

- The Leverhulme Trust: https://www.leverhulme.ac.uk/

- The Newton Fundhttps://www.newtonfund.ac.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 2020 or early 2021

1. Brumos J, Zhao C, Gong Y, Soriano D, Patel AP, Perez-Amador MA, Stepanova AN, Alonso JM. An Improved Recombineering Toolset for Plants. Plant Cell. 2020 Jan;32(1):100-122. doi: 10.1105/tpc.19.00431. Epub 2019 Oct 30. PMID: 31666295; PMCID: PMC6961616.

The authors developed an improved recombineering-based tagging system to tag or edit plant genes using bacterial artificial chromosomes that can be introduced back into the plant genome and demonstrated the system's utility by generating translational reporter fusions for a large set of auxin-related genes.

2. Madison I, Melvin C, Buckner E, Williams C, Sozzani R, Long T. MAGIC: Live imaging of cellular division in plant seedlings using lightsheet microscopy. Methods Cell Biol. 2020; 160:405-418. doi: 10.1016/bs.mcb.2020.04.004. Epub 2020 May 30. PMID: 32896331

The authors developed an imaging technique for seedlings that involves simultaneous imaging of at least 4 samples to enable data acquisition at a high temporal resolution, while overcoming several challenges of imaging using existing microscopy techniques.

3. Buckner E, Madison I, Melvin C, Long T, Sozzani R, Williams C. BioVision Tracker: A semi-automated image analysis software for spatiotemporal gene expression tracking in *Arabidopsis thaliana*. Methods Cell Biol. 2020; 160:419-436. doi: 10.1016/bs.mcb.2020.04.017. Epub 2020 Jun 5. PMID: 32896332.

The authors developed a procedure for analyzing 3D microscopy images to track and gather quantitative spatiotemporal gene expression data in living Arabidopsis seedlings.

Please provide a paragraph describing the general impact of the COVID19 pandemic on the scientific community in your country

The COVID-19 pandemic has been highly challenging to US scientists with inequities and disparities in impact. Significant negative impacts were felt by researchers who have dependents and for whom a lack of external dependent-care has been unavailable. There has been a disproportionate impact on younger scientists for whom there are expiration dates on funding lines, and mothers of young children who generally have borne the brunt of additional labor of childcare and home schooling. For parents and other child caregivers, the pandemic was particularly disastrous because children were home, daycare centers and summer camps were often closed, and school was remote/online. Some early data suggest that mothers were the most affected: the proportion of female authors on preprints, submissions and publications dropped, and mothers suffered a 33% larger reduction in research hours, while simultaneously taking on more household and childcare duties than fathers did (Langin, K. (2021).

The pandemic hit academic mothers especially hard, new data confirm. Science. doi: 10.1126/science.caredit.abh0110). The impact of COVID-19 on faculty of color was further exacerbated by the explosion of racial unrest that erupted during the peak of the pandemic, and continues to this day. The long-term career repercussions of the COVID-19 pandemic are difficult to predict but we expect that there will likely be significant ripple effects for years, and the effects will disproportionally affect women and people of color. Repercussions range from reduced academic productivity that may be reflected in years of disrupted research-publish-successful grant funding cycles, to attrition of women scientists and people of color from academia (and other careers) as a result of compounded societal stresses and the unbearable additional labor from the COVID-19 pandemic atop the existing challenges of research, education, service, and mentorship that are already required of most academic plant scientists.

Like many, US scientists adopted and learned to use existing software to allow remote work and teach teaching, with Zoom as a primary example. Most research labs experienced a complete shutdown with remote work for ~3 months (mid-March to mid-June 2020). Some labs were allowed to maintain their plants, yet some biological resources were lost. Many projects involving genetics were severely delayed. The shift suddenly to teaching online took tremendous effort to rework courses on the fly. Re-opening research labs, usually at partial capacity, required many weeks of paperwork and complex rotation schedules to be developed by most faculty.

Many people have had to work in shifts, so they may only get half days in the lab and limited access to necessary equipment; this has been seriously detrimental to research progress. NAASC calls for creative and robust institutional and structural efforts to mitigate the expected negative consequences of the COVID-19 pandemic, particularly on early-career scientists, mothers, and people of color. In the absence of such measures, we can predict a tragic and significant loss of highly talented and diverse members of the plant science community.

Planned events for 2021 and 2022

The 31st International Conference on Arabidopsis (ICAR, 21-25 June, 2020) was scheduled for Seattle, Washington, USA in July, 2020. NAASC (ICAR organizers) postponed the conference to 2021 due to Covid-19 pandemic, and then converted it to a virtual meeting due to uncertainties on global vaccination efforts and travel restrictions (http://icar2020.arabidopsisresearch.org).

The program (under development since fall, 2017) is the most diverse and democratically-developed in ICAR history. There are 23 invited platform speakers, including two Keynote Speakers and 21 Plenary Speakers, and 36 community-proposed and organized mini-symposia that will feature up to 252 additional speakers.

The theme of ICAR 2021-Virtual is "ARABIDOPSIS as a NEXUS for INNOVATION, APPLICATION, and IMPACT"; innovative approaches for the meeting include:Diversity and Inclusion: People and Science

• Confirmed Keynote Speakers, Drs. Detlef Weigel and Joanne Chory, are true pioneers in plant biology research. We chose them for their significant, exciting, and cross-cutting science and messages that exemplify the meeting theme to the big societal challenges we are facing.

• We developed an exciting and diverse list of plenary speakers in alignment with the conference theme by flipping the typical process: first, we developed a speaker list of those we would like to speak, regardless of topic, and once confirmed, we grouped them into sessions. This approach put the emphasis on finding exciting speakers that have a new breakthrough to present and enabled us to address our diversity, equity and inclusion objectives at a global level

• Another first for ICAR: we invited innovative mini-symposia topics from the community and received 100+ submissions for 36 slots. We reserved, in advance, at least 25% to be led by students and postdocs; we have been fundraising to provide all session organizers with budgets to recruit speakers. •We created the DiversifyPlantSci list (https://tinyurl.com/DiversifyPlantSci) to promote a global plant sciences community that reflects the diversity of all its members. The online resource is a list of plant biologists from under-represented groups, to increase diversity and inclusion by expanding beyond personal networks. This list has been used to develop invited speaker lists from some sessions

• We surveyed the global Arabidopsis community at multiple points to give input into the programs of (first) ICAR 2020, and later, ICAR 2021. A large number of speakers on our invited "short list" came from community input

• After pivoting to ICAR 2021-Virtual, we solicited community input again; based on community priorities we added live interactive discussion sessions to mini-symposia. Activities post-ICAR 2021: NAASC are coming to the end of a 5-year NSF* funding award that underpins all our community-supporting efforts. In parallel with the current major effort to organize ICAR 2021-Virtual, NAASC have been developing plans for future community activities with the intent to apply for funding support. NAASC have engaged in discussions over the past 2 years internally, as well as with external collaborators. We held a 3-day online workshop in summer 2020, (rescheduled due to Covid-19) with invited assessors and evaluators from the community to review our recent efforts and provide assessments on our progress and recommendations for future efforts.

*NAASC activities are funded in part by NSF Award No. 1518280; Any opinions, findings, & conclusions or recommendations expressed in this material are those of the author(s) & do not necessarily reflect the views of the National Science Foundation.

Selected Publications

1) Friesner, J, Colón_Carmona, A, Schnoes, AM, *et al*. Broadening the impact of plant science through innovative, integrative, and inclusive outreach. Plant Direct. 2021; 5:e00316. https://doi.org/10.1002/pld3.316a)

We highlight this NAASC-led white paper as a valuable community resource; it describes the broad context where science outreach is performed, the specific challenges faced by plant scientists, and outlines basic concepts in the design, evaluation and dissemination of outreach activities and provides case studies for their implementation; finally, it charts a course to make to make outreach more innovative, integrative and inclusive.

Advancing outreach in plant science through Inclusion, Innovation and Integration. Successful outreach programs thrive when a holistic approach is taken. Inclusive programs are crafted with awareness of the demographic, cultural and institutional contexts they exist in. Innovative programs use the state of the art organizational models in their design and devise a means of evaluating their effectiveness through assessments appropriate to their scale. Integrative programs communicate their outreach efforts across labs and institutes to disseminate and share what works. All of these activities need to be supported by an ecosystem of funding from the government, universities and private foundations that recognize excellence across these areas

2) Montgomery BL. Planting Equity: Using What We Know to Cultivate Growth as a Plant Biology Community. Plant Cell. 2020 Nov; 32(11):3372-3375. https://www.doi.org/10.1105/tpc.20.00589.a)

We highlight this important work, the first in a new series of Letters that focus on anti-Black racism globally; the author "draws analogies between how we think about plant and human communities and encourages a collective shift in academia from "gatekeeping" to "groundskeeping" practices, specifically with respect to facilitating successful outcomes for Black and other People of Color and underrepresented groups in the scientific community."

3) Shigenaga AM, Kroh GE, Argueso CT. Plant Disease & Climate Change: A Classroom Exercise Emphasizing Scientific Collaboration. The American Biology Teacher. 2021 March; 83 (3): 174–179. https://doi.org/10.1525/abt.2021.83.3.174a)

We highlight this publication on a model-learning college classroom exercise on rice susceptibility to a bacterial pathogen because it incorporates two important approaches: improving student understanding of the interactions between abiotic and biotic factors that decrease crop production, compounded by climate change, and the importance of communication between fields to produce solutions to major issues.

Major Funding Sources

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Additional support from:
- US Department of Agriculture (USDA): http://www.usda.gov/US
- Department of Energy (DOE): http://energy.gov/
- National Institutes of Health (NIH): http://www.nih.gov/
- National Aeronautics and Space Administration (NASA): http://www.nasa.gov/

Private Sources:
- Howard Hughes Medical Institute (HHMI)- alone and partnered with several other organizations, support a number of prominent US Arabidopsis researchers and educators:
(1) HHMI Faculty Scholars (current or past NAASC Scholars: Siobhan Brady, Jose Dinneny, Elizabeth Haswell, and Jennifer Nemhauser): http://www.hhmi.org/programs/biomedical-research/faculty-scholars
(2) HHMI Investigators (past NAASC Investigators: Dominique Bergmann, Philip Benfey, Joanne Chory, Jeff Dangl, Xinnian Dong, Joe Ecker, Elliot M. Meyerowitz, and Keiko Torii) http://www.hhmi.org/programs/biomedical-research/investigator-program
(3) HHMI Professors (past NAASC Professors: Richard M. Amasino and Bonnie Bartel) https://www.hhmi.org/developing-scientists/hhmi-professors

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