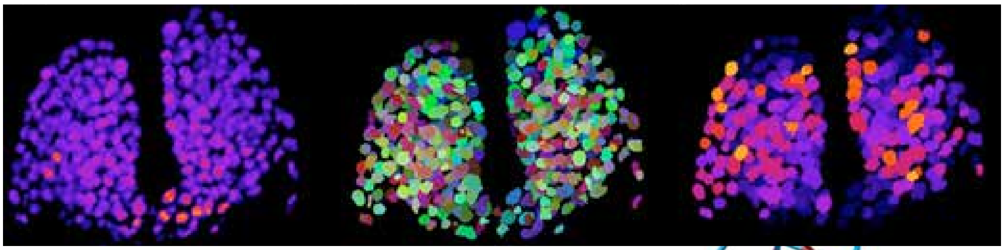
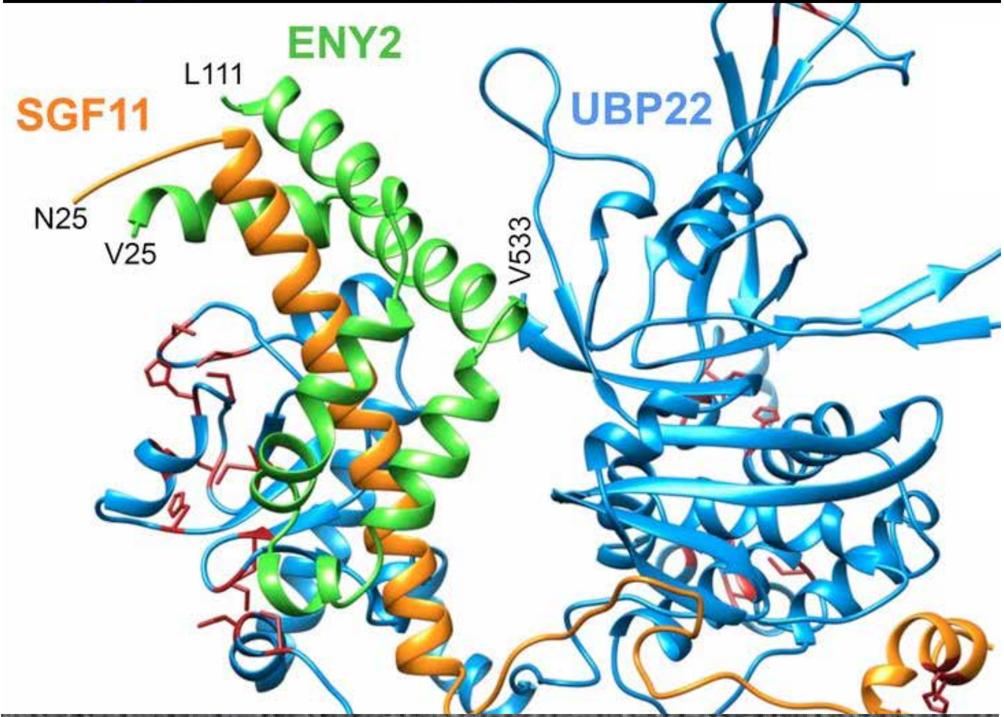
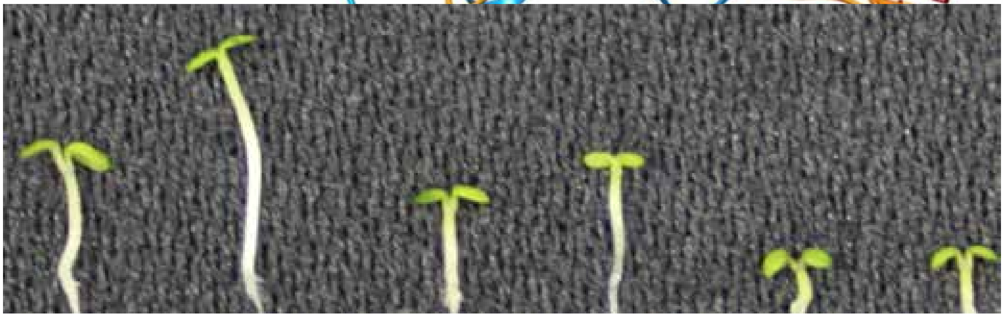
From Bench to Bountiful Harvests

Multinational Arabidopsis Steering Committee (MASC)

Annual Report 2018/2019







The Multinational Arabidopsis Steering Committee

Annual Report 2018/2019

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Cover images taken from Open Access publications

Top Image: https://elifesciences.org/articles/39298
Middle Image: https://elifesciences.org/articles/37892
Bottom Image: https://www.sciencedirect.com/science/article/pii/S1534580717310791

Further information can be found on the MASC website: www.*Arabidopsis*research.org

The MASC report 2018/19 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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Acknowledgements

MASC is grateful to all authors for their contribution to the MASC annual report 2018/2019.

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 figure from that article.

MASC thanks the organisers of ICAR2019 for their contribution from their meeting that has in part allowed the preparation and printing of this document.

Table of Contents

Executive Summary and Analysis

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 then MASC would be unable to prepare this document that aims to track of the progress and challenges of the global Arabidopsis community. MASC are delighted to welcome the Global Plant Council as a new Project contributor as well as five Country Representatives who have submitted new reports from Estonia, Poland, Saudi Arabia, Singapore and Taiwan.

Within this document you can read about the many ways in which Arabidoposis research remains healthy. This is evidenced by continued increase in the number of Arabidopsis stocks distributed by the three global stock centres, the high level of quality Arabidopsis publications and the growth in Arabidopsis research in countries with a developing research infrastructure.

However the community has been dealt a blow with the uncertain future of the Araport resource after the US National Science Foundation (NSF) did not agree to follow-on funding. Araport was developing as a catch-all resource for Arabidopsis bioinformatic resources and have recently integrated the BAR ePlant resource for the visualisation of plant data across multiple levels.

Members of International Arabidopsis Informatics Consortium (IAIC) are in discussions regarding future options for Araport. In the short-term this will involve hosting the Thalemine portion of Araport at the University of Toronto and the JBrowse portion at TAIR, albeit with no provision for extra development. Therefore a global effort is needed to ensure that there is continued development of software 'widgets' that can integrate newly developed software tools into a centralised resource.

IAIC recommended the formation of an Arabidopsis Super-Portal that brings together available Arabidopsis-facing community resources. The early-stages of this portal is now hosted at TAIR (https://conf.Arabidopsis.org/display/COM/Resources) and it will provide a central location for the significant number of research tools developed with Arabidopsis as the model organism and that are underpinned by continued work in that area.

History of MASC

MASC started in the early 1990's when scientists from several countries formed an *ad hoc* committee to promote large-scale research with Arabidopsis. The ultimate goal was the understanding of physiological, biochemical and developmental processes of flowering plants at the molecular level, employing Arabidopsis as a model system. In order to reach this long-term goal a commitment from the global Arabidopsis community was essential. Therefore, actively engaged researchers developed 'The Multinational Coordinated Arabidopsis - Genome Research Project' in 1990.

Over time this changed through different versions of MASC, which in the current and hopefully long-lasting version is registered in Canada as a not-for-profit organisation. This should ensure smooth transitions between board members and hopefully provide some small amount of financial support for future ICAR meetings, which are a key component of the *Arabidopsis* year. MASC and the Arabidopsis community are working toward the third decade-long roadmap document entitled 'From Bench to Beautiful Harvests' (Lavagi *et al.*, 2012, Plant Cell, 24:2240-7). The 2018/2019 annual MASC report is the 7th published under the current road map.

The major goal stated in this roadmap is to obtain in-depth knowledge of how the genome is translated into a continuum of processes, from the single molecule to cells and tissues, the whole organism, within populations and fields of plants. There is clear progress across each of these areas but perhaps most gratifying is in the range of community-facing resources that are available for people to use. These range from the well-established genome and transgenic tools such as TAIR or SIGnAL through to newly released software such as Plant PTM Viewer (https://dev.bits.vib.be/ptm-viewer/index.php) and the Viva Visualising Variation tool (http://bser1.bse.vt.edu:3838/).

In 2017 MASC evolved into the not-for-profit MASC Inc. includes non-paid positions for the President (Nicholas Provart), Treasurer (Siobhan Brady) and Secretary (Geraint Parry). These officers are supported by a Board of eight Directors who oversea general activities. After 2020 MASC directors will fulfil 4-year terms of office that will often coincide with their involvement in the organisation of an ICAR meeting or with the development of a new community grant. In 2020 the terms of two directors, Michael Wrzaczek and Barry Pogson, will end so MASC will be looking for candidates to take over their roles. Please consider applying if you would like to be involved with MASC activities.

MASC Subcommittees

Eight MASC Subcommittees have been tasked with monitoring progress as well as discussing future directions in each of their respective fields of Arabidopsis research. This annual report includes submissions from seven subcommittees whilst the submission from the Phenomics community is included in the project report that covers the range of currently available phenotyping-focussed grants.

It is hoped that members of each subcommittee are in a position keep in close contact with the community and promote international cooperation. The activity of each subcommittee is largely determined by the motivation of their leaders to arrange events both at ICAR meetings and elsewhere. Members of the Systems and Synthetic Biology subcommittee led organisation of a Systems Biology meeting in September 2018 in Roscoff, France whilst members of the Natural Variation and Comparative Genomics subcommittee have committed to arranging a workshop session at ICAR2020 in Seattle.

The seven subcommittees that have contributed to the 2018- 2019 annual MASC report are as follows:

- Bioinformatics (page 12)
- ORFeomics (page 14)
- Epigenetics and Epigenomes (page 14)
- Metabolomics (page 17)
- Natural Variation and Comparative Genomics (page 18)
- Proteomics (page 20)
- Systems and Synthetic Biology (page 21)

MASC is open to discuss the evolution of the current subcommittees and community members are welcome to suggest if there is a need for a new subcommittee. In this case please contact the permanent members of MASC (Nicholas Provart, Siobhan Brady or Geraint Parry) to discuss your ideas. Suggestions will be gratefully received and likely approved so the next step in the official formation of new subcommittee would be to assemble a group of individuals knowledgeable in the area who could contribute to the submission to the annual report as well as becoming involved in the organisation of subcommittee-related meetings and workshops at ICAR meetings.

Arabidopsis Community Projects and Resources

A key component of the mature Arabidopsis research community is the variety of resources that have been developed over of the course of the past 20 years. These community projects, stock centres and bioinformatic resources enable researchers to fully integrate their research from its initial phenotypic description through to full multi-omic characterisation.

Toward the end of 2018 the International Arabidopsis Informatics Consortium (IAIC) published a White paper in Plant Direct (https://onlinelibrary.wiley.com/doi/full/10.1002/pld3.109) that formulated a number of recommendations to enable the future growth of Arabidopsis resources especially in light of the challenges with continued funding of Araport. These recommendations include establishment of a centralized annotation authority to coalesce annotation from new groups, establish a consistent naming scheme, distribute this format regularly and frequently, and encourage and enforce its adoption. In addition efforts should be made to set out community-established guidelines and standards for data and metadata formats alongside a searchable, central repository for analysis and visualization tools.

On May 10th 2019 the Arabidopsis Biological Research Center launched a new ordering website that is independent of TAIR and offers access to stock data, ordering, payment and donation information. Relatedly the RIKEN stock centre has developed Exp-Plant Catalog that provides information about our Arabidopsis resources including natural accessions, individual mutants and transgenic lines, transposon-tagged lines, full-length cDNA clones, ORF clones of transcription factor genes, and genomic DNA clones to the community. This catalog will soon include new Arabidopsis Transcription Factor – Glucocorticoid Receptor mutant seeds and insertional mutants of Arabidopsis Nuclear-Encoded Chloroplast Proteins.

MASC Director Nicholas Provart continues to lead the expansion of the Bio-Analytic Resource (BAR) with the integration of cell-type specific meristem data in collaboration with MASC China representative Yuling Jiao. Excitingly the Arabidopsis ePlant framework is now aiding other research communities with the development of 15 other ePlants, including establishment of new resources for wheat, tomato and maize in 2018.

MASC is now a member of the Global Plant Council (GPC) so we are delighted that they have submitted a project report. The GPC is a coalition of national, regional and international societies and affiliates representing plant, crop and agricultural and environmental sciences across the globe (http://globalplantcouncil.org/).

DOI: 10.1002/pld3.109

WHITE PAPER

Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future

International Arabidopsis Informatics Consortium*

Global collaboration across plant science is no-better exemplified by the activities of the International phenotyping community that have been awarded a set of large multi-country grants that encourage integration between users. Perhaps more importantly they also provide access to phenotyping facilities by researchers who do not have the means at the home institution (https://www.plant-phenotyping.org/).

Finally we include a final report from the Germany DFG Priority Programme 1529 "Adaptomics". This program has supported more than 20 projects, many of which were of a collaborative nature, over two consecutive funding periods of 3 years at Universities and Research Institutions mostly in Germany between 2011 and 2018. The central scientific objective of ADAPTOMICS was to obtain fundamental insights into the molecular solutions that plant species use to grow in different environmental circumstances. The program focused on Brassicaceae species outside *Arabidopsis thaliana* and so took advantage of the uniquely advanced molecular understanding of this model Brassicaceae species.

If the leaders of any other relevant programs would like them to be highlighted in the MASC report then please contact the secretary, Geraint Parry.

All community resources can be found on pages **29-35**.

Country Highlights

MASC is supported by individual countries through the selection of representatives that each year report on the progress that there colleagues have made. They provide an important commentary on the prospects for Arabidopsis research in their individual countries.

As reported above we are delighted to include inaugural country reports from Estonia, Poland, Saudi Arabia, Singapore and Taiwan alongside follow-up reports from 27 other countries.

It can be challenging to recruit Country representatives so if you work in a country not included in this report then please get in contact with Geraint Parry (geraint@garnetcommunity.org.uk) to put yourself forward for this position.

Providing an update for the global community not only highlights the outstanding work that is occurring in your home country but also provides an easy reference point that can be important in discussions with potential funders and other interested parties.

In particular it would be excellent to recruit new country representatives for the Netherlands and Mexico. MASC would like to thank Marcelo Yanovsky for providing the Argentinian report over the past few years.

The Country reports can be found on pages **40-97**.

Activities of MASC

MASC web page: www.Arabidopsisresearch.org

MASC Inc has now been incorporated as a not-for-profit in Canada for over a year. This requires non-paid positions for the 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 will ultimately 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. This is a list of the inaugural board of directors and the length of their terms:

- 2018-2020: Michael Wrzaczek (Finland), Barry Pogson (Australia)
- 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)

From 2020 two new directors will be elected for four term years. Primarily appointments these will aim to improve the gender balance on the board of directors as well as maintaining geographical diversity. Currently the directors have a very light role broadly overseeing MASC activities.

The lack of any full-time positions mean that MASC activities remain minimal in order to just maintain the activity of the organisation. These activities are important given the historical importance of the MASC activities over the past 50 years.

The three main MASC activities are:

- Preparation of the MASC Annual Report
- Hosting the MASC annual meeting
- Overseeing the organisation of the International Conference on Arabidopsis Research (ICAR)

This MASC report was assembled by Dr Geraint Parry who also organises the MASC annual meeting. Dr Parry fulfills this role in addition to his current position as the GARNet coordinator in the UK (http://garnetcommunity.org.uk/). It is hoped that this role will continue for the foreseeable future, taking advantage of the full-time funding provided to the UK plant science community by the Biotechnology and Biological Sciences Research Council (BBSRC).

This MASC annual report includes submissions from four new countries and two new report resources. These new submissions have resulted from either the individual project leaders contacting members of the MASC committee or by recruitment by Dr Parry. However there are still gaps in the submissions and we would hope to restore reports from those countries who haven't submitted for a few years or more new countries that have any Arabidopsis research.

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. As there is no specific funding for the MASC coordinator, Dr Parry continues to manage these limited MASC activities:

- 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 the ICAR

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

The MASC subcommittees, proposed in 2002, were established to help tracking the progress and advances made by the international Arabidopsis community. This report includes contributions from seven of the eight current subcommittees: Bioinformatics, Epigenetics and Epigenomes, ORFeomics, Metabolomics, Natural Variation and Comparative Genomics, Proteomics and Systems and Synthetic Biology. The activities of the Phenomics subcommittee are captured within the project report from International Plant Phenotyping projects.

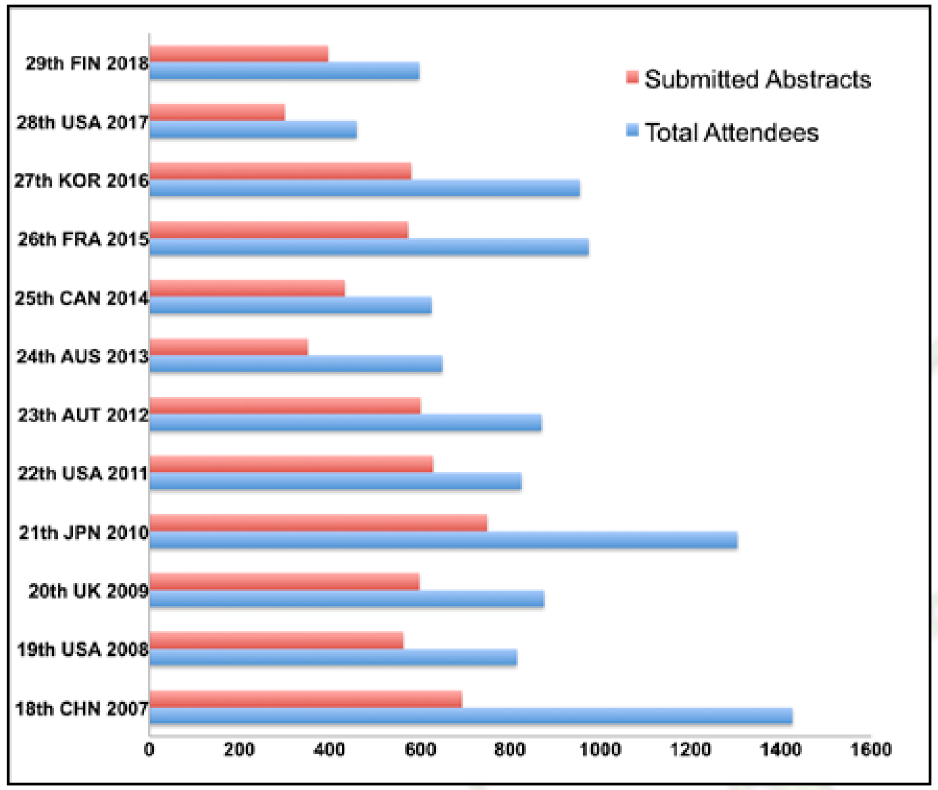

Figure 1. Number of attendees (blue) and number of posters presented (red) at the International Conference on Arabidopsis Research since 2007, when information about posters became available.

The requirements for a subcommittee to be considered active were formulated in 2009:

- Submission of an annual report
- Input at MASC annual meetings
- MASC subcommittee chair has to be nominated with a 3-year minimum term to provide continuity
- Co-chairs could help promote activity of the subcommittee
- MASC subcommittee chairs/co-chairs should confirm leadership annually. If necessary, new subcommittee chairs should be found
- Chair/co-chair should confirm and represent the interest of subcommittee members.

Over the next few years the MASC directors will encourage sub-committee members to take a greater role in the organisations of workshops at ICAR meetings or at independent events.

All representative of subcommittees, projects or countries are invited to attend the MASC annual meeting that takes place at the ICAR meeting. In 2019 the MASC Annual meeting will be held on Monday June 17th at 19.00 in the Hongkong room at the Eurasia Convention Centre in Wuhan, during ICAR2019. We are happy to invite interested observers to this meeting so if you would like further details please contact Geraint Parry (geraint@garnetcommunity.org.uk).

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

International Conference on Arabidopsis Research (ICAR)

Over the past decade the flagship ICAR meeting has rotated though global locations in Asia, North America and Europe. However the board of directors is more than happy to consider other global locations if there is a need to take the ICAR meeting to previously under-represented locations. Organisation of these meetings relies upon a committed local organising committee who might engage a conference management company to deal with the meeting details.

These are the locations for upcoming ICAR meetings:

- 30th ICAR, Wuhan China: June 16th-21st 2019:
http://icar2019.*Arabidopsis*research.org/

- 31st ICAR, Seattle, USA July 6th-10th 2020:
http://icar2020.*Arabidopsis*research.org/

- 32nd ICAR, Belfast, UK, June 2021: June 21st-25th 2021
http://icar2021.*Arabidopsis*research.org/

- 33rd ICAR, Asia. 2022
- 34th ICAR, The Americas. 2023
- 35th ICAR, Europe. 2024

The 29th International Conference on *Arabidopsis* Research (ICAR) was held in Turku, Finland between 25th-29th June 2018 where the organising committee was led by MASC director Michael Wrzaczek. The total number of attendees was 599, which included 396 delegates who submitted abstracts. This 63% abstract submission rate is exactly the same as the average over the past 10 years.

This was a second consecutive meeting with lower than expected attendance and this can be likely explained due to competition from a set of major plant science meetings that were occurring in Europe during Summer 2018. However and as usual, the meeting included a series of outstanding keynote speakers, plenary and concurrent sessions. The keynote speakers were Alison Smith, Dominique Bergmann and Tetsuya Higashiyama.

In 2018 there was another strong selection of submitted workshops during ICAR2018. There were 14 total workshops including one entitled 'Seeing the invisible – young researchers pre-senting fluorescent based sensors as potent analytical tools' organized by PhD students Maike Breiden and Vilde Olsson.

The North American *Arabidopsis* Steering Committee (NAASC) are the organisers of ICAR2020 and have committed to extending the opportunities for delegates to contribute to the meeting organisation. Proposals are invited for mini-symposia, recommendations for session topics and nominations for invited speakers and input into conference accessibility.

Please make your recommendations before July 31st 2019 at https://www.surveymonkey.com/r/5ZHYMYS

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 has two broad functions.

Firstly it 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 latest tools and publications from each of those subcommittees, resources or countries.

These resources can be found here:

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

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

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

If you would like to suggest any changes or content to be added to the MASC website then please contact Geraint Parry (geraint@garnetcommunity.org.uk).

Reports of the MASC Subcommittees

Bioinformatics

Compiled by Nicholas Provart (nicholas.provart@utoronto.ca) with input from MASC Bioinformatics Subcommittee members and the wider *Arabidopsis* community. 30 April 2019.

Arabidopsis Informatics – TAIR: Staff at The Arabidopsis Information Resource (TAIR) have continued updating Arabidopsis gene data in TAIR from published literature over the past year. From March 2018-Feb 2019, TAIR added 4,431 experimental Gene Ontology (GO) and Plant Ontology (PO) annotations generated by TAIR curators, TAIR community, UniProt and Gene Ontology Consortium (GOC) to the database. A total of 558 articles were used to annotate to 1,696 distinct loci. We added 3,783 articles of which 2,302 were linked to 3,921 genes. We curated 849 new gene symbols, 164 alleles, 304 phenotypes and added/updated 5,867 gene summaries. We processed 610 annotations provided by 89 community members spanning 99 papers. TAIR database is updated weekly and the most up to date annotations are accessible via TAIR's website and tools (www.*Arabidopsis*.org).

TAIR also continues to provide quarterly public releases of year-old datasets (https://www.*Arabidopsis*.org/download/index-auto.jsp?dir=/download_files/Public_Data_Releases). The 18th public release from TAIR contains cumulative curated data sets up to March 31, 2018. Educators can continue to request access to the "full" version of TAIR for teaching purposes. We look forward to integrating JBrowse into TAIR in the coming year

Araport.org: Unfortunately, the U.S. National Science Foundation did not provide renewed funding for Araport.org, leaving its future uncertain. At a meeting Maryland in March 2019, curators and informaticians from several resources, including TAIR and the BAR met to decide a path forward. It was decided that the Thalemine functionality of Araport.org would move to the BAR, while its JBrowse instance would be moved to TAIR – stay tuned for an update to this seemingly never-ending saga.

The **BAR (Bio-Analytic Resource)** received new funding from Genome Canada to expand the popular ePlant tool to incorporate ecosystem-level data.

DNA and RNA resources: John Brown's lab in Dundee looked at the how the Arabidopsis transcriptome responds at the level of alternative splicing, showing that hundreds of genes exhibit alternative splicing in response to cold (Calixto *et al*., 2018).

Marcus Schmid's group used INTACT to isolate phloem companion cell-specific transcriptomes and DNA for epigenomic analyses, identifying MRF1 as a regulator of flowering (You *et al*., 2019).

Hiroshi Kudoh's group (Nagano *et al*., 2019) used a wild *Arabidopsis thaliana* relative (*A. halleri*) to study the dynamics of variation in transcriptome expression weekly over two years (and bihourly on the four equinoxes/solstices), to identify 2,879 seasonally-oscillating genes (and 7,185 diurnally-oscillating ones).

Kenichi Tsuda and colleagues used RNA-seq to show rapid transcriptional reprogramming mediated by phytohormone signaling in the effector-triggered immunity response (Mine *et al*., 2018). Last, Detlef Weigel's group used a 16S sequencing-based approach to show stable associations between diverse Pseudomonas pathogen sublineages and wild *Arabidopsis thaliana* strains over evolutionary timescales (Karasov *et al*., 2018).

Gene regulatory networks (GRNs)/codes: The 2019 Nucleic Acids Research database issue (Rigden and Fernández, 2019) contains updates or reports on several plant databases. Of note here: the PlantPAN database for reconstructing transcriptional regulatory networks from ChIP-seq experiments was updated to version 3.0, and now encompasses TF ChIP-seq data for 82 regulatory factors in *Arabidopsis* (Chow *et al*., 2019).

1001 Genomes Data: The Wright Lab at Virginia Tech released ViVa: Visualizing Variation in the *Arabidopsis* 1001 genomes project (Hamm *et al*., 2018) http://plantsynbiolab.bse.vt.edu/ViVa.

Protein Resources: The Plant PTM Viewer from the Gevaert's Lab at the University of Gent (Willems *et al*., 2019) permits exploration of 370,000 PTM (post-translational modification) sites for 19 types of protein modifications in proteins from five different plant species. It can be accessed and encompasses more than 100,000 PTMs in *Arabidopsis*!
https://www.psb.ugent.be/webtools/ptm-viewer/

A new Arabidopsis Interactions Viewer (AIV2) was released by the Provart Lab (Dong *et al*., 2019). The authors also predicted almost 10,000 protein-protein interactions (PPIs) using a docking algorithm, and have worked with BioGRID to incorporate 42,605 experimentally-determined PPIs into the new interface, along with 2.8M protein-DNA interactions. The new AIV2 is available at http://bar.utoronto.ca/interactions2.

Georgia Drakakaki's group published a cool study based on arrayed antibodies to identify the glycan contents of post-Golgi vesicles ((Wilkop *et al*., 2019). Youssef Belhkadir's group at GMI in Austria together with a number of colleagues published a leucine-rich repeat receptor kinase cell surface interaction network (CSILRR) of 567 interactions between the extracellular domains of 225 LRR-RKs (Smakowska-Luzan *et al*., 2018). These data are available in the AIV2 mentioned earlier.

New Plant Bioinformatics Course: The Provart lab released a 6 module course on Cousera.org called "Plant Bioinformatics" (https://www.coursera.org/learn/plant-bioinformatics/), which one can audit for free, or receive a certificate for, for a small fee. This hands-on course is broadly about exploring online tools for mining plant data, but given that most data come from *Arabidopsis*, the course provides lots of insight for this species, too. The course covers plant genomic databases, and useful sites for info about proteins; expression analysis; coexpression tools; promoter analysis; functional classification and pathway vizualization; and network exploration (PPIs, PDIs, GRNs).

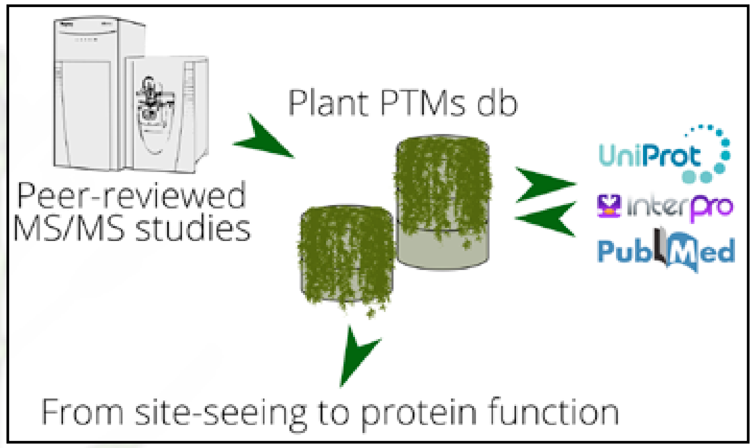

Figure 2. Plant PTM Viewer is a centralized resource for plant post-translational modifications(PTMs) intuitive for wet- and dry-lab scientists. https://www.psb.ugent.be/webtools/ptm-viewer/submit.php

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Clone-Based Functional Genomics Resources (ORFeomics)

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Open Tools and Resources for Arabidopsis Researchers

We prepared the updated list of Full-length cDNA and ORF clones that are available from Resource Centers (Please see Table 1). The revised ones are shown in red.

Recent activities of Subcommittee members.

Keeping tracking progress made towards the production of full-length cDNAs and open reading frame (ORF) clones for all annotated Arabidopsis protein-coding genes.

Future Activities of the Subcommittee.

ORFeomics subcommittee would like to propose a new project to collect all ORF (full-length cDNA) clones from every Arabidopsis protein-coding gene so as to test protein-protein, protein-DNA and protein-RNA interactions.

Our recent search showed that now about 23,000 Arabidopsis protein-coding genes have been isolated as Full-length cDNA (ORF) clones. One of the last unexplored continents of Arabidopsis are the remaining 5,000 protein-coding genes. After that, only the non-coding genes remain to be isolated.

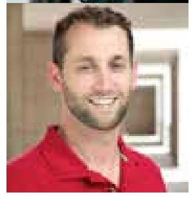
With the completion of isolating all 28,000 Arabidopsis protein-coding genes, comprehensive analysis of plant gene function will become possible by various functional analyses using transgenic and protein expression approaches.

The human whole ORFeome project is already ongoing. Arabidopsis is a model plant, thus this will represent the first big plant ORFeome project. On completion it might be possible to start synthetic biology using the whole gene set of Arabidopsis to allow functional studies of corresponding proteomes.

Selected Publication

Yazaki, J., Galli, M., Kim, A. Y., & Ecker, J. R. (2018). Profiling interactome networks with the HaloTag-NAPPA in situ protein array. Current Protocols in Plant Biology, 3, e20071. doi: 10.1002/cppb.20071

Epigenetics and Epigenomics



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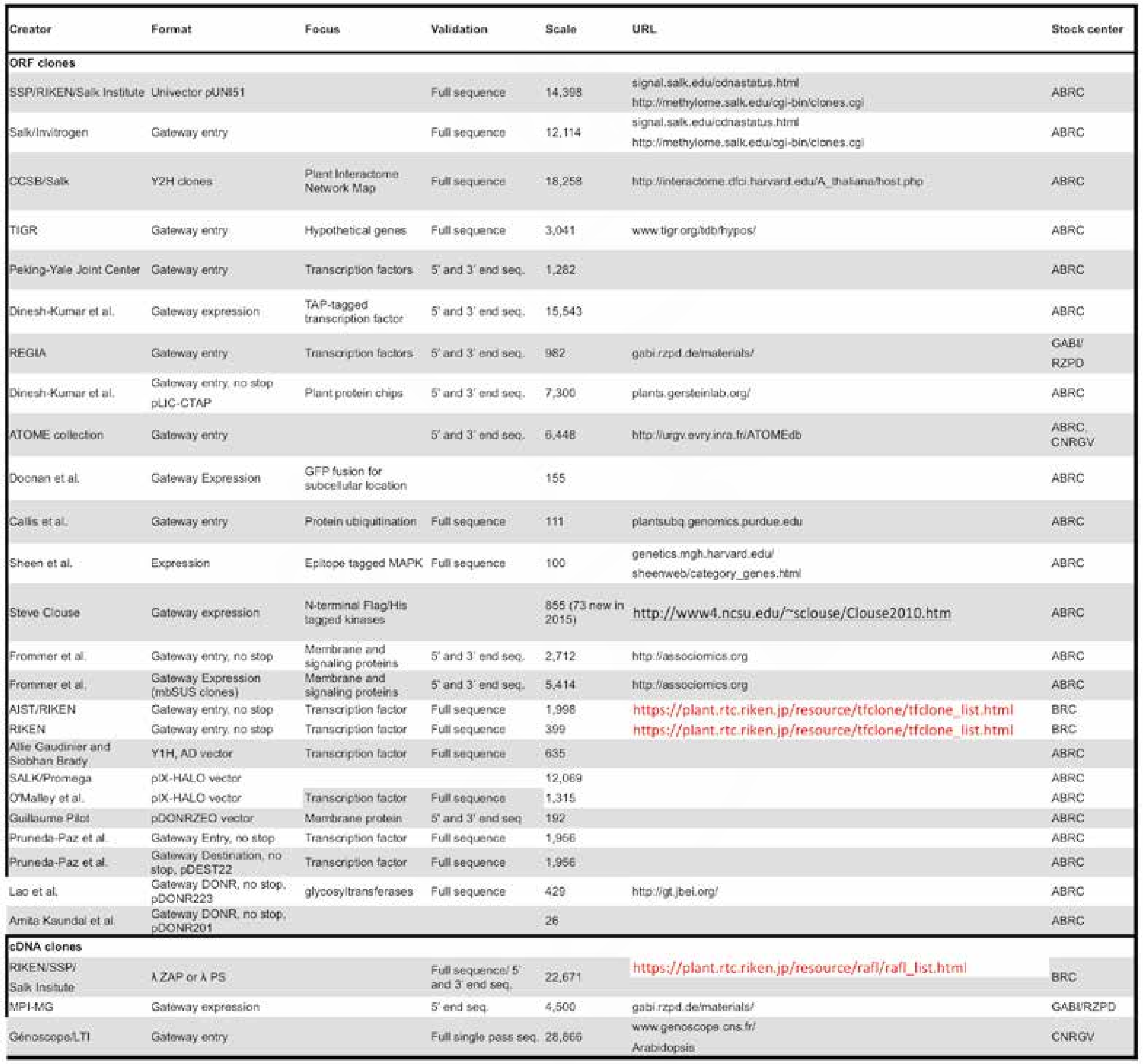
Open Tools and Resources for Arabidopsis Researchers

CoGe browsers for Arabidopsis, maize and soybean - online servers for plant epigenomic data

Recent activities of Subcommittee members.

The Epigenetics and Epigenomics Subcommittee members organized and participated several epigenetic sections associated with various international conferences in 2018. These were held at Plant Genomes Conference and Gordon Research Conference in US, ASPB meeting in Canada, ICAR and plant epi/genetics symposium in Finland, International Plant Molecular Biology meeting in France, Uppsala Transposable symposium in Sweden, Plant Genomes in a changing environment in UK, Agricultural Bioscience International Conference, and Cold Spring Harbor Asia meeting in China. The Subcommittee members have also organized laboratory workshop on cell type-specific nuclei purification by INTACT at Frontiers and Techniques in Plant Science at CSHL.

The combined activities of Subcommittee members have enhanced the appreciation of the importance of epigenetic regulation in plant biology, boosted the interests, and strengthened international collaborations and coordination to understand the roles and regulation of plant epigenetics/epigenomics. The epigenetic research has also attracted a large amount of interests from the media and general public.



Creator	Format	Focus	Validation	Scale	URL	Stock center
ORF clones						
SSP/RIKEN/Salk Institute	Univector pUNI51		Full sequence	14,398	signal.salk.edu/cdnastatus.html http://methylome.salk.edu/cgi-bin/clones.cgi	ABRC
Salk/Invitrogen	Gateway entry		Full sequence	12,114	signal.salk.edu/cdnastatus.html http://methylome.salk.edu/cgi-bin/clones.cgi	ABRC
CCSB/Salk	Y2H clones	Plant Interactome Network Map	Full sequence	18,258	http://interactome.dfci.harvard.edu/A_thaliana/host.php	ABRC
TIGR	Gateway entry	Hypothetical genes	Full sequence	3,041	www.tigr.org/tdb/hypos/	ABRC
Peking-Yale Joint Center	Gateway entry	Transcription factors	5' and 3' end seq.	1,282		ABRC
Dinesh-Kumar et al.	Gateway expression	TAP-tagged transcription factor	5' and 3' end seq.	15,543		ABRC
REGIA	Gateway entry	Transcription factors	5' and 3' end seq.	982	gabi.rzpd.de/materials/	GABI/ RZPD
Dinesh-Kumar et al.	Gateway entry, no stop pLIC-CTAP	Plant protein chips	5' and 3' end seq.	7,300	plants.gersteinlab.org/	ABRC
ATOME collection	Gateway entry		5' and 3' end seq.	6,448	http://urgv.evry.inra.fr/ATOMEdb	ABRC, CNRGV
Doonan et al.	Gateway Expression	GFP fusion for subcellular location		155		ABRC
Callis et al.	Gateway entry	Protein ubiquitination	Full sequence	111	plantsubq.genomics.purdue.edu	ABRC
Sheen et al.	Expression	Epitope tagged MAPK	Full sequence	100	genetics.mgh.harvard.edu/ sheenweb/category_genes.html	ABRC
Steve Clouse	Gateway expression	N-terminal Flag/His tagged kinases		855 (73 new in 2015)	http://www4.ncsu.edu/~sclouse/Clouse2010.htm	ABRC
Frommer et al.	Gateway entry, no stop	Membrane and signaling proteins	5' and 3' end seq.	2,712	http://associomics.org	ABRC
Frommer et al.	Gateway Expression (mbSUS clones)	Membrane and signaling proteins	5' and 3' end seq.	5,414	http://associomics.org	ABRC
AIST/RIKEN	Gateway entry, no stop	Transcription factor	Full sequence	1,998	https://plant.rtc.riken.jp/resource/tfclone/tfclone_list.html	BRC
RIKEN	Gateway entry, no stop	Transcription factor	Full sequence	399	https://plant.rtc.riken.jp/resource/tfclone/tfclone_list.html	BRC
Allie Gaudinier and Siobhan Brady	Y1H, AD vector	Transcription factor	Full sequence	635		ABRC
SALK/Promega	pIX-HALO vector			12,069		ABRC
O'Malley et al.	pIX-HALO vector	Transcription factor	Full sequence	1,315		ABRC
Guillaume Pilot	pDONRZEO vector	Membrane protein	5' and 3' end seq	192		ABRC
Pruneda-Paz et al.	Gateway Entry, no stop	Transcription factor	Full sequence	1,956		ABRC
Pruneda-Paz et al.	Gateway Destination, no stop, pDEST22	Transcription factor	Full sequence	1,956		ABRC
Lao et al.	Gateway DONR, no stop, pDONR223	glycosyltransferases	Full sequence	429	http://gt.jbei.org/	ABRC
Amita Kaundal et al.	Gateway DONR, no stop, pDONR201			26		ABRC
cDNA clones						
RIKEN/SSP/ Salk Insitute	λ ZAP or λ PS		Full sequence/ 5' and 3' end seq.	22,671	https://plant.rtc.riken.jp/resource/rafl/rafl_list.html	BRC
MPI-MG	Gateway expression		5' end seq.	4,500	gabi.rzpd.de/materials/	GABI/RZPD
Génoscope/LTI	Gateway entry		Full single pass seq.	28,866	www.genoscope.cns.fr/ Arabidopsis	CNRGV

Table 1. List of available ORF Resources. Revised numvers are shown in Red

Future Activities of the Subcommittee.

The Epigenetics and Epigenomics Subcommittee members plan to organize epigenetic section in conjunction with several international meetings, including Plant & Animal Genomes Conference in San Diego, Japanese Society of Plant Physiologists 60th Annual Meeting, ICAR2019 in China, European workshop on plant chromatin in MPI Cologne, CSHL Frontiers and Techniques in Plant Science, and Symposium on Impact of Nuclear Domains On Plant Phenotypes in Spain.

WThe subcommittee members will also organize the European workshop on plant chromatin and laboratory workshop on cell type-specific nuclei purification by INTACT at Frontiers and Techniques in Plant Science at CSHL in 2019.

Conferences and Workshops

- Plant & Animal Genomes Conference, San Diego, CA, January 2018 (Session on Epigenomics of Plants International Consortium)

- Institut Jean-Pierre Bourgin symposium, Versailles, France, March 2018 (Session on Epigenomics)

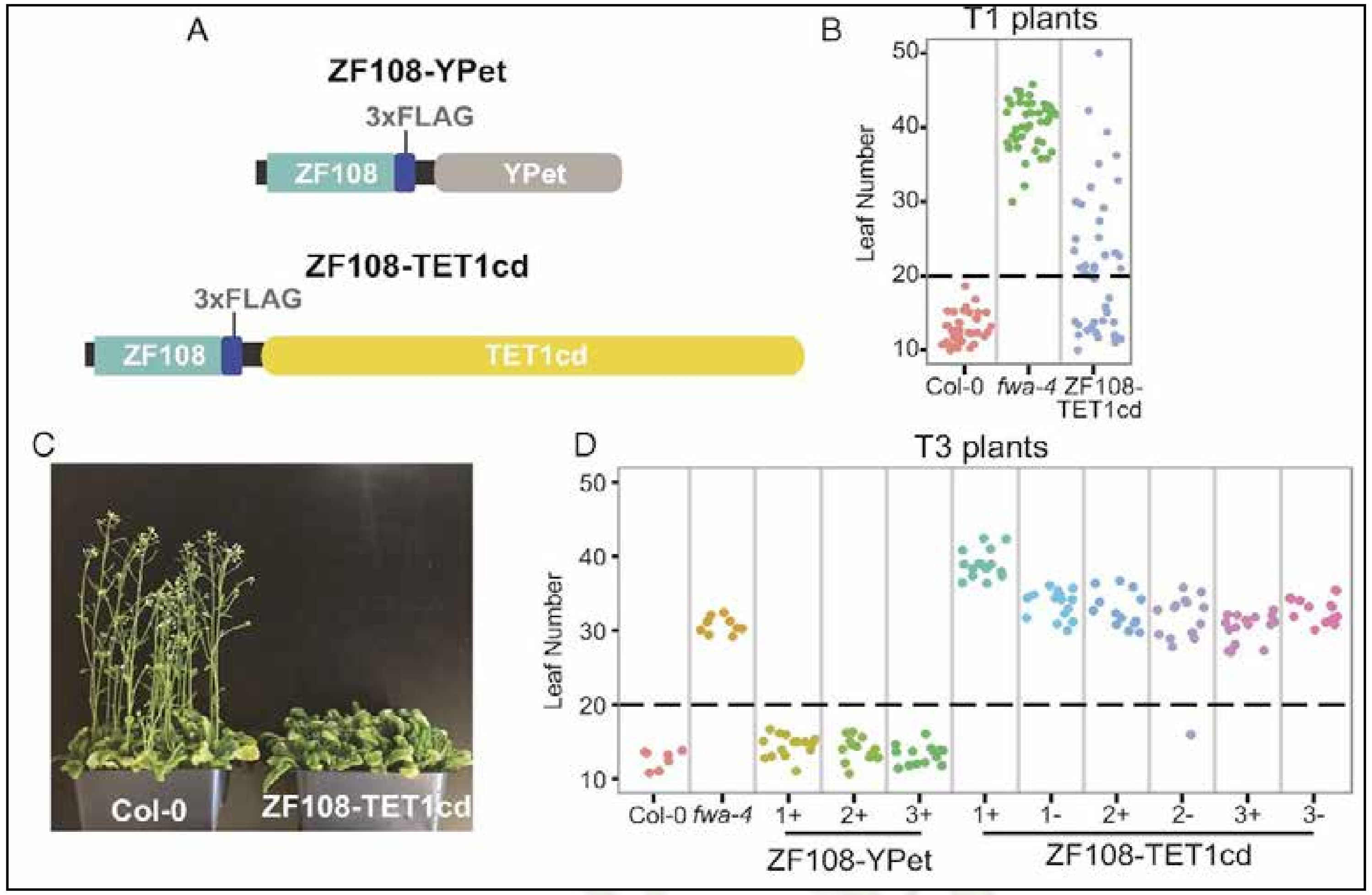


Figure 3: ZF108–TET1cd expression causes heritable late flowering and FWA up-regulation. (A) Schematic representation of the ZF108–YPet (Upper) and the ZF108–TET1cd fusions (Lower). (B) Flowering time of Col-0, fwa-4, and ZF108–TET1cd T1 plants. (C) Col-0 plants and a representative ZF108–TET1cd T3 line grown side by side to illustrate the differences in flowering time. (D) Flowering time of Col-0, fwa-4, three independent lines containing ZF108–YPet and three independent lines of ZF108–TET1cd. For each independent ZF108–TET1cd line, two different T3 populations were scored, one containing the ZF108–TET1cd transgene (+) and one that had the transgene segregated away in the T2 generation (–). For B and D, individual plants are depicted as colored dots. Leaf number corresponds to the total number of rosette and caulinar leaves after flowering. All plants above the dashed line are considered late flowering.

- Cold Spring Harbor Asia meeting on Chromatin, Epigenetics & Transcription, Suzhou, China, April 2018 (Section on Epigenetic inheritance and Plant Epigenetics)
- Gordon Research Conference, Plant Molecular Biology. Holderness, NH, June 2018 (Session on Epigenetics)
- Midwest Chromatin & Epigenetics meeting, West Lafayette, IN, June 2018 (Session on Plant Epigenetics)
- CSHL Frontiers and Techniques in Plant Science, CSHL, NY, June 2018
- American Society for Plant Biologist, Montreal, Canada, July 2018 (Session on Plant Epigenetics)
- 29th International Conference on *Arabidopsis* Research, Turku, Finland, June 2018 (Session on Epigenetics)
- International Plant Molecular Biology meeting, Montpellier, France, August 2018 (Session on plant Epigenetics)
- Agricultural Bioscience International Conference, Weifang, Shangdong, China, September 2018 (Session on plant Epigenetics)
- International plant epi/genetics symposium, Angers, France, October 2018
- UW-Madison Epigenetics symposium, Madison, WI, October 2018
- 2nd Uppsala Transposon symposium, Uppsala, Sweden, October 2018
- Plant Genomes in a changing environment, Cambridge, UK, October 2018

- Plant & Animal Genomes Conference, San Diego, CA, January 2019 (Session on Plant Epigenetics & Epigenomics)
- Japanese Society of Plant Physiologists 60th Annual Meeting, Nagoya, Japan, March 2019 (Session on inheritance and rewriting of cellular memory in plants)

- 30th International Conference on *Arabidopsis* Research, Wuhan, China, June 2019 (Plenary and concurrent sessions on Epigenetics)
- European workshop on plant chromatin, MPI Cologne, June 2019
- CSHL Frontiers and Techniques in Plant Science, CSHL, NY, June 2018

- Symposium on Impact of Nuclear Domains On Plant Phenotypes, Madrid, Spain, December 2019 http://www.sebiology.org/events/event/impact-of-chromatin-domains-on-plant-phenotypes

- Plant Epigenetics, Japan (hosted by Keiko Sugimoto and Toshiro Ito) Date:TBD 2020

Selected Publications

1) Targeted DNA demethylation of the *Arabidopsis* genome using the human TET1 catalytic domain (PNAS, 2018)

2) Paternal easiRNAs regulate parental genome dosage in *Arabidopsis* (Nature Genetics, 2018)

3) Epigenetic activation of meiotic recombination near *Arabidopsis thaliana* centromeres via loss of H3K9me2 and non-CG DNA methylation (Genome Research, 2018)

4) Partial maintenance of organ-specific epigenetic marks during plant asexual reproduction leads to heritable phenotypic variation (PNAS, 2018)

5) Embryonic epigenetic reprogramming by a pioneer transcription factor in plants (Nature, 2018)

Metabolomics

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Recently developed Open Tools and Resources for *Arabidopsis* Researchers

http://plasma.riken.jp/
PlaSMA – Plant Specialized Metabolome Annotation
The comprehensive structural characterization in mass spectrometry-based plant metabolome using the advanced computational mass spectrometry with fully 13C-labeled plant materials and MS/MS spectral information.

https://pubs.acs.org/doi/suppl/10.1021/acs.analchem.8b04096/suppl_file/ac8b04096_si_001.pdf
MetNet – R aiding metabolite annotation
The metabolite network prediction from high-resolution mass spectrometry data - MetNet uses both structural and quantitative information on high-resolution mass spectrometry-based metabolomics data for network inference and enables the annotation of unknown analytes. (Naake and Fernie, 2019, Anal Chem. 91, 1768-1772)

https://www.ebi.ac.uk/metabolights/MTBLS528
Data resource: Metabolomics data deposited in MetaboLights (MTBLS528) - the natural variance of the Arabidopsis floral secondary metabolites (Tohge et al., 2018, Scientific Data, 5, 180051)

Recent activities of Subcommittee members.

Since metabolomics is an important component of Arabidopsis omics, a continuous goal of this subcommittee will be to promote metabolomics research of Arabidopsis leading to functional genomics and systems biology. Full integration of Arabidopsis-based metabolomics research with the activity of the Metabolomics Society <http://www.metabolomicssociety.org/> is also an important goal of this subcommittee. Several members of the subcommittee are involved in drawing up the plant biology specific documentation for the Metabolomics Society. In addition this committee will aim to establish a mechanism that allows the dissemination of metabolomics datasets to the wider Arabidopsis community and encourage and facilitate initiatives for the integration of metabolomic datasets with other omic datasets. This will involve depositing metabolomic data in a usable format for data integration.

Future Activities of the Subcommittee.

The subcommittee discussion will be taken not only in the occasion of ICAR annual meeting but also in the occasions of several other metabolomics-related meetings, where the subcommittee members can join. The web interface will provide user with a user-friendly tool to search for *Arabidopsis thaliana* metabolomics data in available databases. In addition, the people in plant metabolomics community actively provide open tools and resources useful for Arabidopsis researchers as indicated above

Conferences, Workshops and Training events

2018/6/18-22
MU Metabolomics Workshop, Metabolomics Center, University of Missouri, US

2018/6/24-28
Metabolomics 2018 (In partnership with The Plant Metabolomics Forum), Seattle, Washington, US

2018/7/8-13
The 23rd International Symposium on Plant Lipids, Yokohama, Japan

2018/11/19-20
Multi-omics approach in plant systems biology 2018, Bangkok, Thailand

2019/6/16-21
Gordon Research Conference, Plant Metabolic Engineering, Castelvecchio Pascoli, Italy

2019/6/23-27
Metabolomics 2019, The Hague, The Netherlands

Selected Publications

Ohnishi, M., *et al.*, Molecular components of Arabidopsis intact vacuoles clarified with metabolomic and proteomic analyses. Plant Cell Physiol., 59, 1353–1362 (2018)

Higashi, Y., *et al.*, HEAT INDUCIBLE LIPASE1 remodels chloroplastic monogalactosyldiacylglycerol by liberating □-linolenic acid in Arabidopsis leaves under heat stress. Plant Cell, 30, 1887-1905 (2018)

da Fonseca-Pereira, P., *et al.*, The Mitochondrial Thioredoxin System Contributes to the Metabolic Responses Under Drought Episodes in Arabidopsis. Plant Cell Physiology, 60, 213-229 (2018)

Wu, S., *et al.*, Mapping the *Arabidopsis* metabolic landscape by untargeted metabolomics at different environmental conditions. Molecular Plants, 11, 118-134 (2018)

Tsugawa, H., *et al.*, A cheminformatics approach to characterize metabolomes in stable isotope-labeled organisms. Nature Methods, DOI : 10.1038/s41592-019-0358-2, *in press* (2019)

Natural Variation and Comparative Genomics

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We are currently expanding the subcommittee membership and diversifying the leadership over the coming year. Please contact Chris Pires (piresjc@missouri.edu) or Brian Dilkes (bdilkes@purdue.edu) if you are interested in participating in preparing the next report or attending organizational meetings (e.g., ICAR 2020).

Recently developed Open Tools and Resources for Arabidopsis Researchers

ViVa: Visualizing Variation in the *Arabidopsis thaliana* 1001 genomes project.
Published at bioRxiv http://dx.doi.org/10.1101/488395 and Plant Direct (in press). The tool is available on the web (plantsynbiolab.bse.vt.edu/ViVa).
Questions can be directed to R. Clay Wright (wrightrc@vt.edu)

Brassibase (brassibase.cos.uni-heidelberg.de) is a developing knowledge system for Brassicaceae taxonomy, systematics, evolution, and available germplasm resources and specimen collections. The knowledge base includes cross-referenced information on acurate enumeration of all species, genera and tribes, chromosome numbers, genome sizes, morphological characters, and biological traits.

The Bio-Analytic Resource (BAR, bar.utoronto.ca) identifies novel aspects of plant biology, especially in the area of plant stress biology. Several members of the Brassiceae have BAR links (e.g., *Arabidopsis thaliana, Camelina sativa,* and *Eutrema salsugineum*). Gene Slider is a tool for visualizing orthologous DNA sequences, including over 90,000 conserved non-coding regions across the Brassicaceae.

Gramene database (www.gramene.org), in collaboration with EMBL-EBI's Plants Ensembl, provides genomics data access to researchers to search and customize genome browser tracks. The upload data tool allows uploading and visualizing user data on the genome browser, and a variant effect prediction tool allows users to predict SNP consequences from their own data.

Recent activities of Subcommittee members.

Aside from publishing research on natural variation, the subcommittee has identified a key hurdle to resolve: the need for open public availability of seeds/germplasm. While numerous publications have emerged on natural variation, the access to seeds used in studies remains a barrier. The subcommittee aims to improve the availability of seeds, particularly for crop wild relatives, in public seed repositories (e.g., ABRC).

Given recent advances in genome-enabled methods, there is also an opportunity to better leverage herbarium and garden resources (e.g., ancient DNA studies that can be integrated with other 'omics studies).

The committee aims to draft a proposal on community guideline for making data public in standard formats (along with metadata) with international standards (e.g., European Variation Archive).

Recent activities of Subcommittee members.

The subcommittee plans to meet at ICAR 2020 in Seattle (July 6-10, 2020).
Please contact Chris Pires (piresjc@missouri.edu) for details.

In addition, at least one proposal for a session at ICAR 2020 that focuses on highlighting exciting discoveries across the diversity of the Brassicaceae. The goal is to encourage Arabidopsis researches to take advantage of the datasets and model systems being developed across the Brassicaceae that can be used to gain novel insight into processes being studied in Arabidopsis.

Please contact Katie Greenham (greenham@umn.edu) and Pat Edger (pedger@gmail.com) for details.

Conferences, Workshops and Training events

The annual Plant and Animal Genome (PAG) meeting in San Diego is a primary location for researchers on this subcommittee to meet.

The subcommittee plans to meet at ICAR 2020 in Seattle (July 6-10, 2020), and one or more sessions are being organized that are related to this subcommittee.

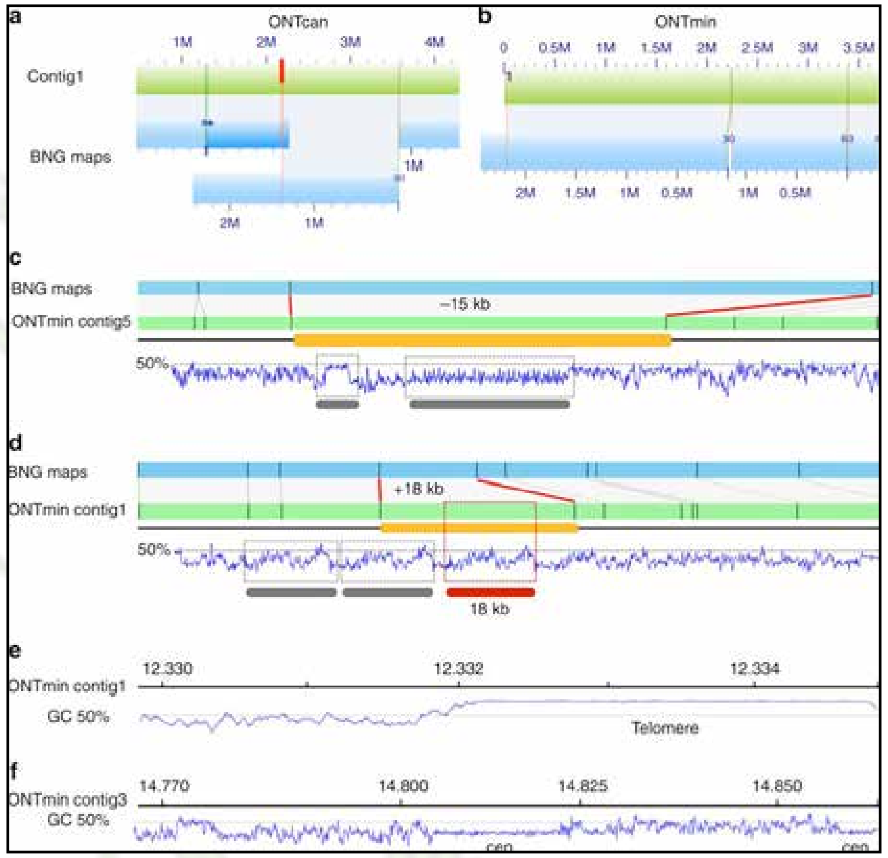

Figure 4: Bionano Genomics maps identify mis-assemblies and hard to assemble regions in the Oxford Nanopore MinION assembly. BNG cmap_30 (blue; marked as 30) identified a a chimeric ONTcan contig 1 (green) and b the correct assembled contig 1 in the ONTmin assembly (green). The chimeric position is indicated with a red bar. c A collapsed region in ONTmin contig 5, in which approximately 15 kb sequences are missing from one of the two potential repeat regions as identified by the GC pattern (gray bars). In contrast, d shows a falsely duplicated region of approximately 18 kb, with the duplicated repeat region highlighted (red bar, 18 kb). e ONTmin assembly resolves various telomere regions, for example after 12.332 Mb on contig 1, as outlined by a GC plot (blue line). f ONTmin also resolves short centromere arrays as shown toward the end of contig 3 (blue, GC plot)

Selected Publications

Aller EST *et al.* 2018. Comparison of the relative potential for genetic and epigenetic variation to contribute to plant defense evolution. G3 8(5)1733-1746

Fulgione A and Hancock AM. 2018. Archaic lineages broaden our view on the history of *Arabidopsis thaliana*. New Phytologist 219: 1194-1198.

Lafon-Placette C *et al.* 2018. Paternally expressed imprinted genes associate with hybridization barriers in Capsella. Nature Plants 4: 352-357.

Michael TP *et al.* 2018. High contiguity *Arabidopsis thaliana* genome assembly with a single nanopore flow cell. Nature Communications 9: 541.

Nikolov LA *et al.* 2019. Resolving the backbone of the Brassicaceae phylogeny for integrating trait diversity. New Phytologist 222: 1638-1651.

Proteomics

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http://www.masc-proteomics.org/

Recently developed Open Tools and Resources for *Arabidopsis* Researchers

The subcommittee has been committed to the task of data centralization and visualization. Over the past year, we have transitioned the non-synonymous SNP data currently housed at 1001Proteomes to the ePlant resource.

The SUBA database has been expanded to contain a new module (Multiple Marker Abundance Profiling) that provides an estimate of organelle distribution from a list of AGIs as the result of a proteomic survey.
http://suba.live/toolbox-app.html

Recent activities of Subcommittee members.

The members of the proteomics subcommittee (MASCP) maintain a range of online resources with a focus on collating data associated with *Arabidopsis* proteins. Many of these resources house extensive proteomic data from experiments conducted on Arabidopsis and other species. They provide a visual interface to these data and many are linked through a central repository, the MASCP Gator.
http://gator.masc-proteomics.org/

Future Activities of the Subcommittee.

As part of data and resource consolidations, the subcommittee will port proteomic data into ePlant to provide information about proteins e.g. abundance, protein evidence and post-translational modifications.

Selected Publications

Linthwaite VL, Janus JM, Brown AP, Wong-Pascua D, O'Donoghue AC, Porter A, Treumann A, Hodgson DRW, Cann MJ (2018) The identification of carbon dioxide mediated protein post-translational modifications. Nat Commun 9: 3092

Pu Y, Walley JW, Shen Z, Lang M, Briggs SP, Estelle M, Kelley D (2019) Quantitative early auxin root proteomics identifies GAUT10, a galacturonosyltransferase, as a novel regulator of root meristem maintenance. Mol Cell Proteomics https://doi.org/10.1074/mcp.RA119.001378

Van Leene J, Han C, Gadeyne A, Eeckhout D, Matthijs C, Cannoot B, De Winne N, Persiau G, Van De Slijke E, Van de Cotte B, Stes E, Van Bel M, Storme V, Impens F, Gevaert K, Vandepoele K, De Smet I, De Jaeger G (2019) Capturing the phosphorylation and protein interaction landscape of the plant TOR kinase. Nat Plants 5: 316-327

Wong MM, Bhaskara GB, Wen TN, Lin WD, Nguyen TT, Chong GL, Verslues PE (2019) Phosphoproteomics of Arabidopsis Highly ABA-Induced1 identifies AT-Hook-Like10 phosphorylation required for stress growth regulation. Proc Natl Acad Sci USA 116: 2354-2363

Zeng W, Ford KL, Bacic A, Heazlewood JL (2018) N-glycan micro-heterogeneity in glycoproteins of Arabidopsis. Mol Cell Proteomics 17: 413-421

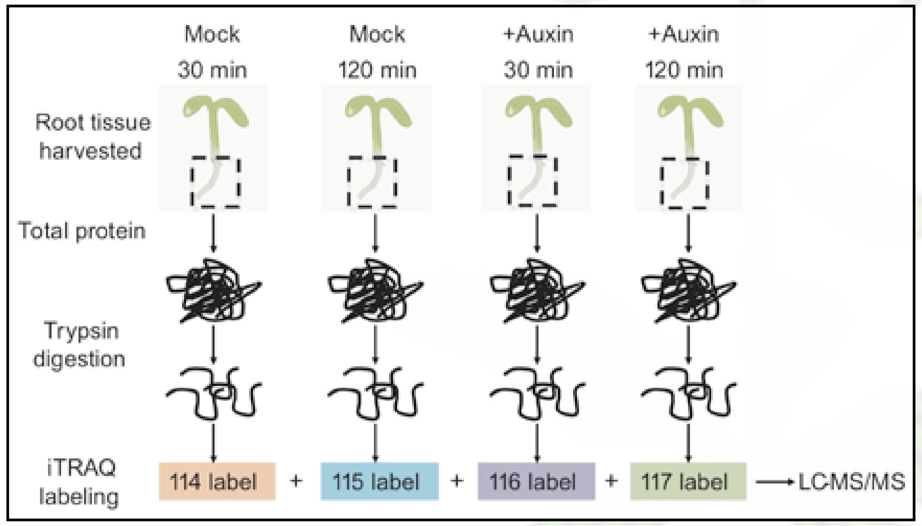

Figure 5. Quantitative proteomic analysis of early auxin responsive proteomes in *Arabidopsis* roots identifies ~300 differentially expressed proteins. (A) Schematic of the experimental workflow. Five day-old wild-type seedlings were treated with 1 uM indole- 3-acetic acid ("auxin") or an equivalent volume of solvent control ("mock") for 30 min and 120 min and dissected roots were processed for proteome profiling using 4-plex iTRAQ labeling as diagramed. This was repeated three more times for a total of four multiplexed 2D-LC-MS/MS runs

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Systems and Synthetic Biology

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Recently developed Open Tools and Resources for Arabidopsis Researchers

- Dong *et al.* (2019) Plant Physiology. Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/ New Molecular Interactions Viewer. 1789(4):1893-1907.
- Crozet *et al* (2018) ACS Synthetic Biology Birth of a Photosynthetic Chassis: A MoClo Toolkit Enabling Synthetic Biology in the Microalga Chlamydomonas reinhardtii ACS Synthetic Biology 7 (9), pp 2074–2086
- Pollak *et al* (2019) Loop Assembly: a simple and open system for recursive fabrication of DNA circuits New Phytologist 222; 628-640
- Ravendran *et al* (2019) CyanoGate: A modular cloning suite for engineering cyanobacteria based on the plant MoClo syntax Plant Physiology DOI: https://doi.org/10.1104/pp.18.014
- BOOK: Plant Genome Editing with CRISPR Systems (2019) Methods in Molecular Biology Volume 1917, Editor: Yiping Qi https://doi.org/10.1007/978-1-4939-8991

Conferences, Workshops and Training events

- Gordon Conference on Plant Molecular Biology: Dynamic Plant Systems June 10-15, 2018; Chair, Gloria Coruzzi (NYU); Vice-chair , Rob McClung (Dartmouth)

- 1st International Plant Systems Biology Meeting: iPSB2018 https://sites.google.com/site/iplantsystemsbiol/pictures

- EMBO Meeting: Integrating Systems Biology - From Networks to Mechanisms to Models. Heidelberg, April 2018 - organizers: Pascal Falter-Braun, Sandra Orchard, Sorina Popescu, Luis Serrano, Claudia Falter;

- SynBio 'Crossing Kingdoms', an international event bringing together scientists from the microbial, animal and plant field. 16-18 April 2018, Sainsbury Laboratory at the University of Cambridge, UK

- Open Plant Forum. 13-26 July 2018, Norwich, UK

- AIChE 2nd International Conference on Plant Synthetic Biology, Bioengineering, and Biotechnology. November 29 - December 1, 2018. Clearwater, Florida, USA

- Banbury Center: Revolutionizing Agriculture with Synthetic Biology, 2-5 December, 2018, Cold Spring Harbor, NY, USA

- International Association for Plant Biotechnology Congress, 19-24 August, Dublin, Ireland

Training - Plant Synthetic Biology

- Synbiosys Summer School, Copenhagen Plant Sciences Centre, Denmark, August 2018
- The Synthetic and Systems Biology Summer School (SSBSS) Robinson College, University of Cambridge, UK, July 2017
- GARNet Plant gene editing workshop, March 2018, University of Bristol, UK
- Synthetic Biology Summer School, 2-6 July 2018 University of Essex, UK

Future Conferences or Workshops:

The Subcommittee is planning the 2nd International Plant Systems Biology in 2020, iPSB2020 in Venice! More details will be released shortly

Selected Publications

Gaudinier *et al* (2018) Transcriptional regulation of nitrogen-associated metabolism. Nature 563(7730):259-264

Lai *et al* (2018) Building Transcription Factor Binding Site Models to Understand Gene Regulation in Plants Molecular Plant DOI:https://doi.org/10.1016/j.molp.2018.10.010

Luo *et al* (2018) Dynamic DNA methylation: In the right place. At the right time. Science 361:1336-1340.

South *et al* (2019) Synthetic glycolate metabolism pathways stimulate crop growth and productivity in the field Science 363; 6422

Varala *et al* (2018) Temporal transcriptional logic of dynamic regulatory networks underlying nitrogen signaling and use in plants. Proc Natl Acad Sci U S A. 115(25):6494

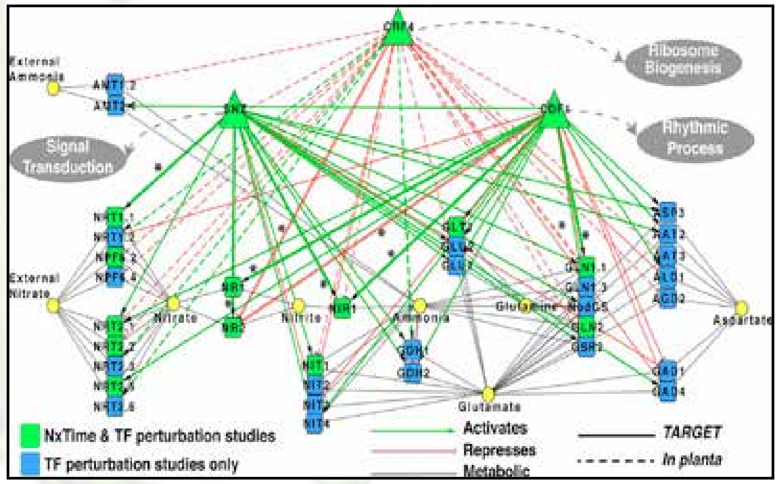
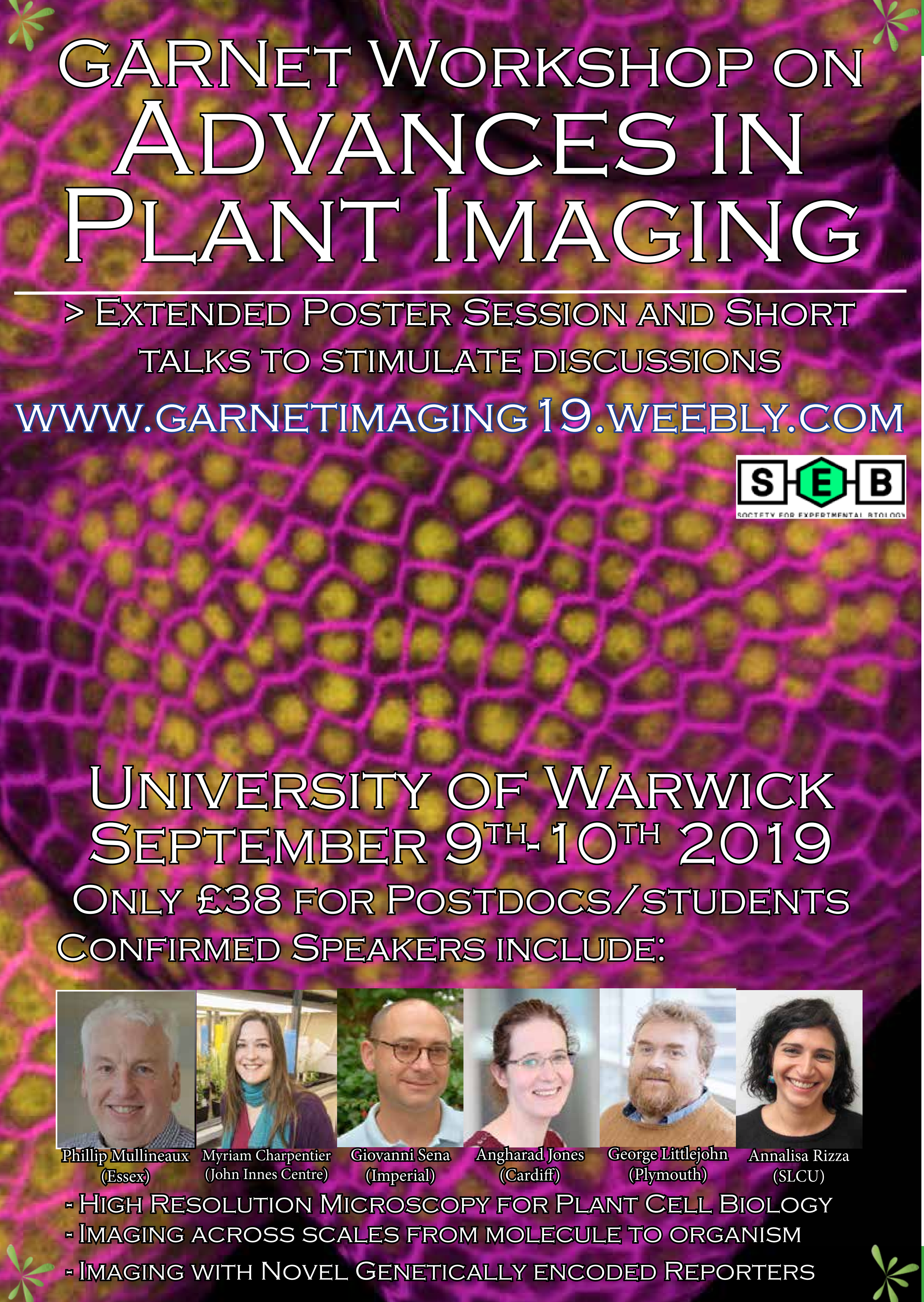


Figure 6. Three TFs—CRF4, SNZ, and CDF1—regulate 53% of the N-uptake/assimilation pathway genes. A time-based machine learning approach DFG was used to infer TF-target influence in an N-response GRN in shoots (Methods). Validated genome-wide targets of three TFs in this GRN—CRF4, SNZ, and CDF1—are shown to regulate 53% (35/65) genes in the N-uptake/assimilation pathway. TF edges to N-responsive genes (green nodes) that are predicted by the GRN and validated by TF perturbations are shown by asterisks and thicker edge width. Gray circles indicate other cellular processes validated to be regulated by these three TFs.



Arabidopsis Community Projects and Resources

The Arabidopsis community has always been very open, so today researchers and funding bodies can look back on more than 20 years of strong international collaboration and data sharing. The efforts of the Arabidopsis community have always been guided by long term plans, which have led to the establishment of many Arabidopsis community projects and resources:

The Arabidopsis genome research project (1990-2001) led to the completion of the Arabidopsis genome. During this decade two out of three stock and resource centers ABRC (Arabidopsis Biological Resource Center, US) and NASC (Nottingham Arabidopsis Stock Center, UK) were founded.

The Multinational Coordinated Arabidopsis Functional Genomics Project (2002-2011) led to the functional annotation of most of the Arabidopsis genes, in that at least providing expression data for them. Alongside, The Arabidopsis Information Resource (TAIR) was founded in 2001 to meet the needs of the growing Arabidopsis research community.

From Bench to Bountiful Harvests (2012-2021) aims to obtain in-depth knowledge of how the genome is translated into a continuum of processes, from the single molecule to cells and tissues, the whole plant, plant populations, and fields of plants, to be able to build a predictive model of an Arabidopsis plant.

The directors of Arabidopsis community projects and resources have been contributing to the MASC reports for several years, by presenting their respective goals, progress and news. Since 2014, general plant projects and resources have also been included, reflecting the growing connections between researchers focussing on different plant species.

Resource and Stock Centers

Arabidopsis Biological Resource Center (ABRC)
(page 24)

Nottingham Arabidopsis Stock Centre (uNASC)
(page 25)

RIKEN BioResource Center (BRC)
(page 25)

The Arabidopsis Information Resource (TAIR)
(page 26)

International Arabidopsis Informatics Consortium (IAIC)
(page 27)

Plant Projects and Resources with Strong Participation of the Arabidopsis Community

Bio-Analytic Resource for Plant Biology (BAR)
(page 29)

Adaptomics Project (page 31)

International Plant Phenotyping Resources (page 32)

Gramene (page 33)

Global Plant Council (page 35)

Besides the above listed projects and resources, there are many other international and multinational initiatives with major contributions from Arabidopsis researchers

Following a recommendation from IAIC, a new online repository has been established that lists major online software tools:

https://conf.*Arabidopsis*.org/display/COM/Resources

These pages include a curated set of bioinformatics and data resources that have been compiled by members of the International Arabidopsis Informatics Consortium (IAIC) and curators at TAIR. This is not a comprehensive list; if you know of a resource that you think should be included, please send us an email.

Search within these pages for Arabidopsis community bioinformatics tools and data resources. You can use labels for data types such as 'proteomics' or 'gene_expression' or actions such as data submission or data analysis.

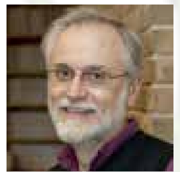
Browse by subject portals

Epigenomics Resources
Education and Outreach Resources
General Databases
Gene Expression/Transcriptomics Resources
Metabolomics Resources
Proteomics Resources
Stock Centers (DNA, Seeds, other Physical Resources)

Resource and Stock Centers

The Arabidopsis Biological Resource Center (ABRC)

www.abrc.osu.edu



David Somers
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ABRC Director

Emma Knee
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ABRC Associate Director

Recent Open Tools and Resources for *Arabidopsis* Researchers

In 2018 ABRC distributed close to 100,000 samples to 2,245 individuals located in 50 countries. Close to 50% of these samples were seed lines of insertion mutants. We also sent over 8,000 seed lines to NASC, either as bulk seed for distribution by NASC, or as individual aliquots for NASC users where we were not able to provide bulk seed. In return, ABRC received bulk seed for over 6000 stocks from NASC. The seed collection is now composed of more than 535,000 stocks.

The non-seed collection includes individual clones, and libraries from *Arabidopsis thaliana* and several other members of the Brassicaceae numbering almost 450,000 stocks as well as vectors, host strains, antibodies, cell lines and education resources. Most of the *A. thaliana* seed stocks donated in 2018 were T-DNA insertion mutant lines. These include lines from the GABI- Kat collection donated by B. Weisshaar through NASC and lines derived from the SALK institute T-DNA insertion population that have been characterized to some extent and were donated by R. Last. We also received a number of well characterized mutant and transgenic lines as well as seed stocks of other members of the Brassicaceae including accessions of *Boechera stricta* from T. Mitchell-Olds.

Distribution of seed pools expressing amiRNAs designed to target functionally redundant genes for forward genetic screening began this year. These were developed and donated by J. Schroeder and F. Hauser and were amplified at ABRC prior to release. Vectors added to the collection include CRISPR/Cas9 vectors from D. Weigel. ABRC has performed quality control testing of 6,684 lines in 2018 including germination testing and verifying stock identity.

ABRC ARABIDOPSIS BIOLOGICAL RESOURCE CENTER
THE OHIO STATE UNIVERSITY

Planned future activities of your project or resource.

ABRC will continue to solicit donations of Arabidopsis seed resources and to expand the stock collection to other resources and species. In particular, we are emphasizing a new focus on "legacy collections" – donations of collections of seed stocks from retiring researchers or from those switching away from Arabidopsis as their main research organism. We have recently taken possession of such collections from Rob Last and David Meinke and are in the process of curating and amplifying their donations. Distribution is expected to continue at the current levels, as is quality control testing. ABRC and NASC continue to collaborate sharing seed stock resources and related data.

On May 10th we released a new web site and database to replace the ordering system currently hosted by TAIR. The new site allows access to stock data, ordering, payment and donation information as well as general information about Arabidopsis and ABRC. All stock information will continue to be available in the TAIR web site through ongoing collaboration between ABRC and TAIR. After the release of the new web site and database we plan to develop an application programming interface (API) to allow TAIR, NASC and others easy access to stock data.

Conferences, Workshops and Training events

ABRC organized a booth at ICAR 2018 in conjunction with NASC, and participated in a data resources booth at Plant Biology 2018. Jelena Brkljacic presented plans for our new website and database in a workshop at PAG XXVII. ABRC outreach and education ran booths at two local events, the Science Education Council of Ohio's annual conference and the Center of Science and Industry Teacher Resource Fair. ABRC also organized a Teacher workshop at Ohio State to familiarize local teachers with our *Arabidopsis* based teaching resources. In 2019 ABRC and NASC will organize a booth together at ICAR in Wuhan, China and will again participate in the data resources booth at Plant Biology in San Jose, California.

Additional Information

The ABRC published an education paper, Price, C.G., Knee, E.M., Miller, J.A., Shin, D., Mann, J.W., Crist, D.K., Grotewold, E., and Brkljacic, J. (2018) Following Phenotypes: An Exploration of Mendelian Genetics using *Arabidopsis* plants. American Biology Teacher, 80(4):291-300.

We are very grateful to Dr. Jelena Brkljacic for her many years of dedicated service as ABRC Associate Director and welcome Dr. Emma Knee as our new Associate Director.

The Nottingham Arabidopsis Stock Centre (uNASC)

http://www.*Arabidopsis*.info

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

Marcos Castellanos-Uribe
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marco.castellanos@nottingham.ac.uk

In 2018 we sent over 120,000 tubes of seed worldwide to 49 countries (even more nations than last year). This year's top five receiving countries (in descending order), are the UK, Germany, China, Japan and France. The biggest donor of stocks by far is Germany (for yet another year) and we are now receiving large numbers of the final stocks from the GABI-KAT project - with many, many thanks to Bernd Weisshaar for such unstinting service to the community over the years.

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.

See you in Wuhan!

Arabidopsis.info

RIKEN BioResource Center (RIKEN BRC)

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

Masatomo Kobayashi
(RIKEN coordinator)

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

We have developed the Exp-Plant Catalog that provides the information of our Arabidopsis resources including natural accessions, individual mutants and transgenic lines, transposon-tagged lines, full-length cDNA clones, ORF clones of transcription factor genes, and genomic DNA clones to the community. In addition, a list of cultured cell lines such as Arabidopsis T87 cells and Tobacco BY-2 cells are also available from the Catalog.

Exp-Plant catalog:
https://plant.rtc.riken.jp/resource/index.html

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

Planned future activities

We are going to add some new resources such as Arabidopsis Transcription Factor – Glucocorticoid Receptor mutant seeds and insertional mutants of Arabidopsis Nuclear-Encoded Chloroplast Proteins to the Exp-Plant Catalog.

Conferences, Workshops and Training events

The 11th Asian Network of Research Resource Centers (ANRRC) International Meeting will be held in Philippines in this autumn.

Additional Information

The RIKEN BRC is a member of National BioResource Project (NBRP) funded by the Japanese government. Not only Arabidopsis but also rice, wheat, barley, lotus/glycine, tomato, morning glory, chrysanthemum and algae resources are preserved and provided through the project.

Project HP: http://nbrp.jp/index.jsp

RIKEN BRC

Arabidopsis Informatics and Data Sharing Resources

The Arabidopsis Information Resource (TAIR)

www.*Arabidopsis*.org

Leonore Reiser
TAIR curator
lreiser@phoenixbioinformatics.org

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

Activities

The primary activity of TAIR is functional annotation of the Arabidopsis genome, with an emphasis on literature curation, to produce a 'gold-standard' reference genome dataset. From March 2018-Feb 2019, TAIR added 4431 experimental Gene Ontology (GO) and Plant Ontology (PO) annotations generated by TAIR curators, TAIR community, UniProt and Gene Ontology Consortium (GOC) to the database. A total of 558 articles were used to annotate to 1696 distinct loci. We added 3783 articles of which 2302 were linked to 3921 genes. We curated 849 new gene symbols, 164 alleles, 304 phenotypes and added/updated 5867 gene summaries.

We processed 610 annotations provided by 89 community members spanning 99 papers. TAIR database is updated weekly and the most up to date annotations are accessible via TAIR's website and tools (www.Arabidopsis.org). TAIR also continues to provide quarterly public releases of year-old datasets (https://www.*Arabidopsis*.org/download/index-auto.jsp?dir=/download_files/Public_Data_Releases).

In the past year we have made many changes to the back end of TAIR that have significantly reduced downtime, as well as performance improvements to speed page loading. Other changes to enhance the data and user experience include (1) integration of the Bio Analytic Resource (BAR) eFP expression brower into TAIR locus pages, and (2) the complete integration of Araport 11 genome annotation into all of our tools (e.g. SeqViewer/GBrowse/Bulk downloads).

New tools and Resources

Phoenix Bioinformatics, which maintains TAIR, has developed a new tool for inferring gene function called Phylogenes (www.phylogenes.org), in collaboration with the PANTHER project at the University of Southern California (USC). Phylogenes displays phylogenetic trees of gene families along with related data to facilitate inference of function for unknown genes. The first release contains 29 plant species across a wide taxonomic range, along with 10 non-plant, well-annotated reference genomes.

Community Engagement

To assist the International Arabidopsis Informatics Consortium (IAIC) in gathering and disseminating information, we created a directory of public community resources for plant biology (https://conf.*Arabidopsis*.org/display/COM/Resources) to begin cataloging databases, stock centers, datasets, analytic tools and other resources of use to the Arabidopsis and plant research community. We encourage people to contact us (curator@*Arabidopsis*.org) to suggest resources to be included and shared widely with the research community.

To complement our social media outreach on Twitter (@tair_news) and Facebook (https://www.facebook.com/tairnews/), we have also started a TAIR blog (https://conf.*Arabidopsis*.org/blog/) to share interesting news and insights from a curator's perspective.

Planned future activities of your project or resource.

In the coming year we plant to continue our literature based functional annotation of the *Arabidopsis* genome, to produce weekly updates to the TAIR database and quarterly public releases of bulk data sets. We plan additional improvements to TAIR's underlying software and interfaces to improve usability. Additional enhancements/tools we hope to add in the coming year include extending JBrowse with additional tracks from Araport and an improved community curation tool.

Conferences, Workshops and Training events

TAIR staff presented at ICAR2018 (Making Published Data FAIR) and ICAR2019 (Arabidopsis Bioinformatics Resources), ASPB 2018 (Plant Bioinformatics Resources), and will co-organize the workshop for ASPB 2019. TAIR/Phoenix Staff led workshops at PAG2019 on (1) Data Resource Sustainability, (2) Arabidopsis Bioinformatics Resources, and ran an annotation training workshop (3) Functional Annotation Hands-On Most Ever Fun Session.

In addition to workshops and trainings we co-authored two papers both of which broadly deal with topics of best practices around data management/data sharing/FAIR data.

1.Reiser L, Harper L, Freeling M, Han B, Luan S (2018) FAIR: A Call to Make Published Data More Findable, Accessible, Interoperable, and Reusable. Mol Plant. 11(9):1105-1108. doi: 10.1016/j.molp.2018.07.005.

2.Harper L, Campbell J, Cannon EKS, Jung S, Poelchau M, Walls R, Andorf C, Arnaud E, Berardini TZ, Birkett C, Cannon S, Carson J, Condon B, Cooper L, Dunn N, Elsik CG, Farmer A, Ficklin SP, Grant D, Grau E, Herndon N, Hu ZL, Humann J,Jaiswal P, Jonquet C, Laporte MA, Larmande P, Lazo G, McCarthy F, Menda N, Mungall CJ, Munoz-Torres MC, Naithani S, Nelson R, Nesdill D, Park C, Reecy J,Reiser L, Sanderson LA, Sen TZ, Staton M, Subramaniam S, Tello-Ruiz MK, Unda V,Unni D, Wang L, Ware D, Wegrzyn J, Williams J, Woodhouse M, Yu J, Main D (2018) AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. Database (Oxford). doi: 10.1093/database/bay088.

Additional Information

We gratefully acknowledge the support of the research community for their data contributions, suggestions for improvement and financial support.

tair

International Arabidopsis Informatics Consortium (IAIC)

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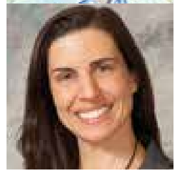

Joanna D. Friesner
IAIC Assistant
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North American Arabidopsis Steering Committee

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

The Arabidopsis community, and other scientific communities that use Arabidopsis resources in their work, rely on the publicly shared community resources developed over the past several decades. Valuable resources accessed by researchers, both in the public and private sectors, include reference genomic sequence data and newer resources. Many of these have been generated by the community over the past 15 years, and at an increasing rate, as technological advances and subsequent reductions in costs to generate data sets have led to a rapid increase in the number and type of data sets in the public sphere.

In 2010, the IAIC was formed by both MASC and the North American *Arabidopsis* Steering Committee (NAASC) in response to the announcement of the planned termination of federal funding for The Arabidopsis Information Resource (TAIR); TAIR had been the primary publicly-accessible online Arabidopsis database since its inception in 1999 and had received continuous funding by the US National Science Foundation since its founding. The international Arabidopsis community, represented by NAASC and the Multinational Arabidopsis Steering Committee (MASC), convened two workshops to strategize how best to continue the vital services that TAIR had provided, and to ensure continuity and availability of community-generated data and resources (1). IAIC's initial focus was to promote the collaborative development of a new bioinformatics resource, later named 'Araport', which was conceived through a 'Design Workshop' in 2011 (2).

The intent was that Araport would serve as the underlying infrastructure for Arabidopsis informatics resources, not by storing data (as TAIR did/does) but by interacting and linking with resources developed and housed by others, e.g. by linking with data sets generated in individual laboratories located around the world. A key component envisioned for Araport's success was that community-generated resources, tools, and data sets would be linked dynamically to Araport such that the global community could provide, support, update, and access the shared resources. This democratization of workload, expertise, innovation, and financial commitment was intended to enable Araport's sustainability and promote creativity and interaction amongst groups that generate and use tools and datasets.

Concurrent with Araport's design and development, TAIR became sustainable via a not for profit organization, Phoenix Bioinformatics, which allowed the database to continue while TAIR staff refocused on annotation and improvements to the database, all funded through a subscription service (individual, institutional, and even country level, for China and Switzerland). TAIR and Araport have thus co existed in a complementary manner, the former emphasizing functional annotation, the latter on aggregating resources.

Four years after Araport's establishment, the IAIC held another workshop, in May of 2018, entitled "2018 - the Future of Arabidopsis Bioinformatics" to evaluate the current status of Arabidopsis informatics and chart a course for future research and development. In advance of the meeting, organizers solicited input from the broader community via MASC, who distributed an online survey of plant bioinformatic needs (3). The workshop focused on several challenges, including the need for reliable and current annotation, community defined common standards for data and metadata, and accessible and user friendly repositories/tools/methods for data integration and visualization.

Solutions envisioned included (a) a centralized annotation authority to coalesce annotation from new groups, establish a consistent naming scheme, distribute this format regularly and frequently, and encourage and enforce its adoption; (b) community-established guidelines and standards for data and metadata formats; (c) a searchable, central repository for analysis and visualization tools. Improved versioning and user access to make tools more accessible. Finally, workshop participants proposed a "one-stop shop" website, an *Arabidopsis* "Super Portal" to link tools, data resources, programmatic standards, and best practice descriptions for each data type, while emphasizing such a portal must have community buy-in and participation in its establishment and development to encourage adoption.

The 2018 IAIC workshop participants produced a white paper outlining the current state, challenges, and priorities for the future of Arabidopsis bioinformatics resources (4).

(1) https://doi.org/10.1105/tpc.110.078519
(2) https://doi.org/10.1105/tpc.112.100669
(3) http://*Arabidopsis*research.org/images/publications/documents_articles/2018_MASC_BioinfoSurvey.pdf
(4) https://doi.org/10.1002/pld3.109

Planned future activities of your project or resource.

The IAIC's funding is nearly expired and thus its associated activities associated are winding down. IAIC's major focus was on enabling community development of Araport to replace and augment TAIR (as described above). Araport.org was established by PI Chris Town and colleagues and had been funded by NSF since its inception. However, after several recent unsuccessful NSF grant renewal applications, the future of Araport is unclear and the community is at risk of losing access to the valuable bioinformatics resources that were developed with, and linked to, Araport.

The Provart lab at the University of Toronto and TAIR have offered interim hosting assistance, but without additional resources, full upkeep or the addition of new data sets or functionalities will not occur.

Conferences, Workshops and Training events

The IAIC held a workshop in May, 2018 in St. Louis, Missouri, USA, entitled "2018- Future of Arabidopsis Bioinformatics" to evaluate the current status of Arabidopsis informatics and chart a course for future research and development.

The workshop participants produced a white paper outlining the current state, challenges, and priorities for the future of Arabidopsis bioinformatics resources (4). See section (1) above for more details and linked article).

Additional Information

The IAIC, and this material, are based upon work supported by the National Science Foundation under award #1062348. Any opinions, findings, and conclusions or recommendations expressed in this event, or in resulting work, are those of the participants and do not necessarily reflect the views of the National Science Foundation.

Plant Projects and Resources with Strong Participation of Arabidopsis Community

Bio-Analytic Resource for Plant Biology (BAR)

http://bar.utoronto.ca

Nicholas Provart (Director)
nicholas.provart@utoronto.ca

Open Tools and Resources for Arabidopsis Researchers

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

* 150 million gene expression measurements (75 million from A.th.), plus "expressologs" (homologs showing similar patterns of expression in equivalent tissues) for many genes across 10 species. View expression patterns with our popular eFP Browser or newer ePlant tool.
* 70,944 predicted protein-protein interactions plus 62,626 experimentally-determined PPIs (rice interologs also available!) 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, delivered through the MASC Proteomics Subcommittee's site at 1001proteomes.masc-proteomics.org.
* Documented subcellular localizations for 11.7k proteins, predicted localization for most of Arabidopsis proteome, from the SUBA database at the University of Western Australia.

Recent activities of your project or resource.

We worked with collaborators Yuling Jiao and colleagues to incorporate cell-type-specific meristem data from Tian *et al.* (2019) into our Arabidopsis eFP Browser and ePlant tools.

We released a new Arabidopsis Interactions Viewer 2, which accesses our updated database of 91,175 experimentally-document protein-protein interaction entries encompassing 62,626 unique pairs of proteins (through a collaboration with BioGRID, with some interactions being documented by multiple methods and/or groups; see Dong *et al*., 2019). We also predicted 9,065 protein-protein interactions by docking and validating a subset using Y2H. These have added to the existing 70k PPIs predicted using the interolog method in our database (docking results are also described in Dong *et al*., 2019).

For translational researchers, publications came out for a new Wheat eFP Browser (Ramírez-González, 2018), an RNA-seq-based maize developmental atlas for the Maize eFP Browser by Hoopes *et al*. (2018), a new early maize seed development Maize eFP Browser view by Yi *et al*. (2018), and a tomato root Tomato eFP Browser view by Toal *et al*. (2018). We also released 15 ePlants (for maize, poplar, tomato, *Camelina sativa*, soybean, potato, barley, *Medicago truncatula*, eucalyptus, rice, willow, sunflower, Cannabis sativa, wheat and sugarcane), leveraging the Arabidopsis ePlant framework.

BAR Publications

Dong S, Lau V, Song R, Ierullo M, Esteban E, Wu Y, Sivieng T, Nahal H, Gaudinier A, Pasha A, Oughtred R, Dolinski K, Tyers M, Brady SM, Grene R, Usadel B, Provart NJ (2019). Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/New Molecular Interactions Viewer. Plant Physiol. 179:1893-1907. doi: 10.1104/pp.18.01216.

Hoopes GM, Hamilton JP, Wood JC, Esteban E, Pasha A, Vaillancourt B, Provart NJ, Buell CR (2019). An Updated Gene Atlas for Maize Reveals Organ-Specific and Stress-Induced Genes. Plant J. 97:1154-1167. doi: 10.1111/tpj.14184.

International Arabidopsis Informatics Consortium, Doherty C, Friesner J, Gregory B, Loraine A, Megraw M, Provart NJ, Slotkin RK, Town C, Assmann SM, Axtell M, Berardini T, Chen S, Gehan M, Huala E, Jaiswal P, Larson S, Li S, May S, Michael T, Pires C, Topp C, Walley J, Wurtele E (2019). Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. Plant Direct 3: e00109. doi: 10.1002/pld3.109

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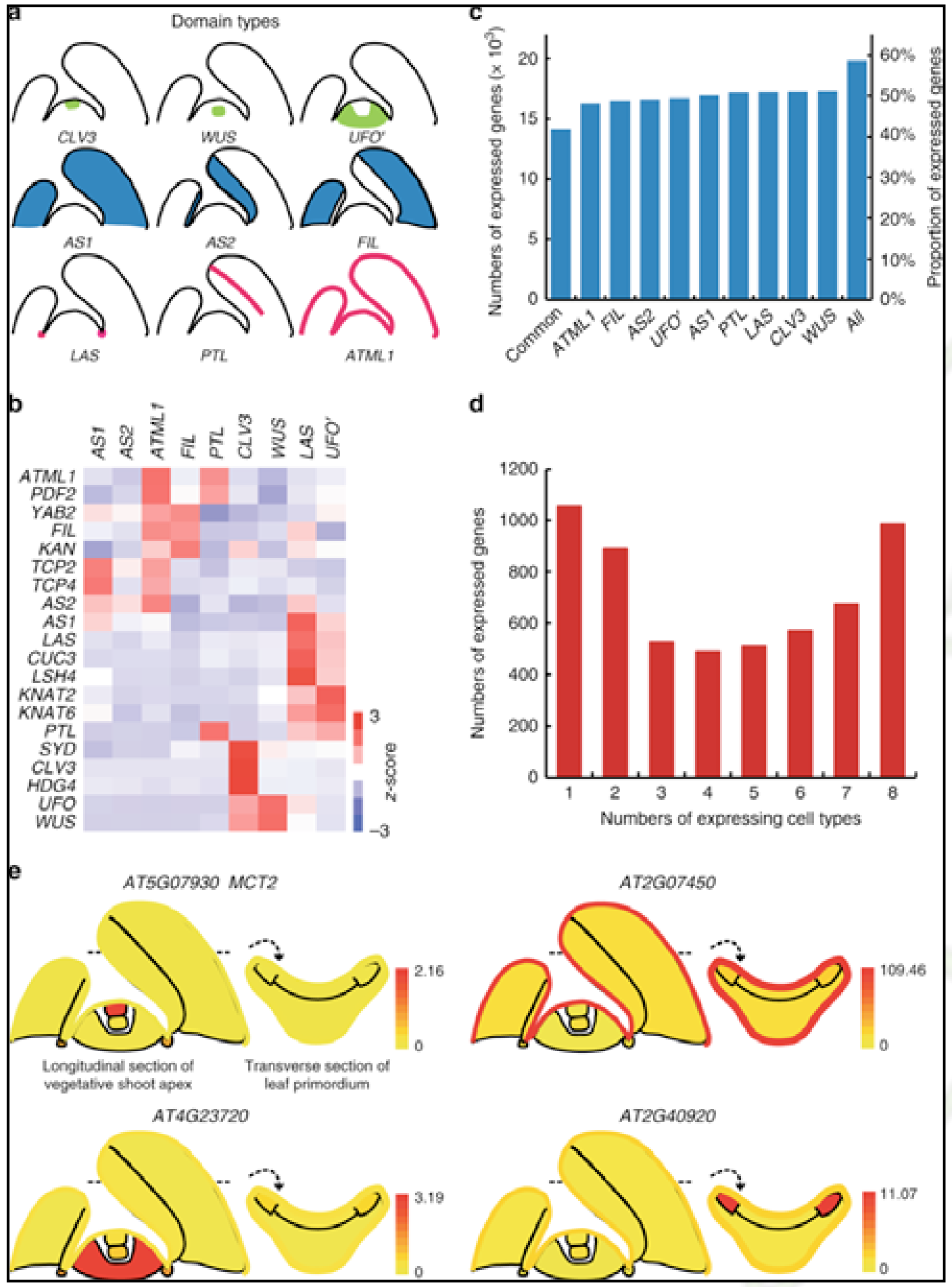

Figure 7. Properties of cellular gene expression. a Diagrams showing different spatial domains being profiled. b Marker gene expression pattern in different cellular transcriptomes. Relative expression (z-score) is displayed in colors, in which red indicates enrichment and blue indicates depletion as shown. Labels on the top show domains. The gene names are shown on the left. c Numbers and proportion of expressed genes in each domain. d Numbers of expressed genes in multiple domain groups. e eFP browser view of expression changes in the shoot apex for selected genes. Whereas MEI2 C-TERMINAL RRM ONLY LIKE 2 (MCT2, AT5G07930) is a previously identified CZ-specific gene21, all others are unknown domain-specific genes. Absolute gene expression values were calculated and shown for each domain

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Planned future activities of your project or resource.

A custom eFP view in ePlant for researcher's own RNA-seq data is in the works, along with an "Intelligent Agent" (kind of like Siri or Alexa, but for Arabidopsis information) as part of a new award from Genome Canada. Several new ePlants are also planned as part of this project, and an ecosystem viewer will also be developed.

Conferences, Workshops and Training events

The BAR participated in the 2018 American Society of Plant Biology (ASPB) Plant Biology conference in Montreal, as part of the Plant AgData Outreach booth and in the Plant Bioinformatics workshop (the BAR also co-organized with Jason Williams of CSHL a workshop on "Data Carpentry/RNA-Seq Analysis/Custom ePlant" held after the main conference); and Plant and Animal Genomes (PAG) XXVII at the start of 2019 in San Diego, California. It also gave a talk in the Gene Regulatory Networks workshop at ICAR 2018 in Turku, Finland.

The BAR principal investigator Nicholas Provart released "Plant Bioinformatics" on Cousera.org at https://www.coursera.org/learn/plant-bioinformatics/, covering 33 tools from genome browsers to transcriptomic data mining to promoter/network analyses and more! The course is free of charge, unless you want a certificate for a small fee. Some of the tools are from the BAR, but many from other labs/sites are covered too.

Additional Information

The BAR principal investigator Nicholas Provart was successful in receiving an award from Genome Canada to integrate ecosystem-level data into its collection of ePlants, build an "Intelligent Agent" for Plant Biology, and a custom eFP view as mentioned above

German Research Priority Program ADAPTOMICS Evolutionary Plant Solutions to Ecological Challenges

– Molecular Mechanisms Underlying Adaptive Traits in the Brassicaceaes.

https://www.ruhr-uni-bochum.de/dfg-spp1529/Seiten/index.html

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https://www.rub.de/mgpp/Seiten_en/index_e.html

The Research Priority Program ADAPTOMICS of the German Research Council (Deutsche Forschungsgemeinschaft, DFG) arose in a competitive bottom-up process designed to identify initiatives that can effectively establish novel original interdisciplinary research fields. ADAPTOMICS provided funding for scientific projects as well as a focused framework for international interaction, scientific exchange and the training of researchers. Under its umbrella, more than 20 projects, many of which were of a collaborative nature, were carried out in parallel over two consecutive funding periods of 3 years at Universities and Research Institutions in Germany (mostly), as well as in Austria and Switzerland, between 2011 and 2018.

The central scientific objective of ADAPTOMICS was to obtain fundamentally novel, comprehensive and increasingly predictive insights into the molecular solutions that plant species develop to match local environmental demands. ADAPTOMICS explicitly focused on Brassicaceae species outside *Arabidopsis thaliana*. Thus, research in this program took advantage of the uniquely advanced molecular understanding of this model Brassicaceae species for studying traits of major ecological and agricultural relevance that cannot be understood in *A. thaliana* alone.

ADAPTOMICS researchers endorsed the program objectives by laying solid ecological and genetic groundwork and by leveraging large-scale genome-wide sequence data in a number of novel model systems. The model systems studied in ADAPTOMICS include altitude adaptation and seed traits in the perennial Arabis alpina, repetitive genome content, endemism, edaphic and drought adaptation in various species of the *Arabidopsis* genus, heavy metal hyperaccumulation in *Arabidopsis halleri*, the evolution and genetic basis of selfing in the *Capsella* genus, apomictic reproduction in *Boechera holboellii*, allotetraploidy in *Arabidopsis suecica*, adaptation to extreme drought in *Biscutella didyma*, leaf shape in *Cardamine hirsuta*, C4 photosynthesis in the *Cleomaceae*, and flooding tolerance in *Rorippa* species. Several projects successfully identified genetic loci contributing to the traits under study.

ADAPTOMICS brought together scientists specialized in different fields, for example ecology, molecular biology, genomics and population genetics, through collaborative research projects, two well-attended International Symposia held in Bad Neuenahr (Germany, 2014) and Berlin (Germany, 2017), as well as a number of specialized workshops.

A joint project used shared data to examine genomic sequence variation across the *Arabidopsis* genus. The "BrassiBase" database is a repository of taxonomy, systematics and evolution of the Brassicaceae, as well as of germplasm resources and specimen collections. Specific methodology was assembled in an "ADAPTOMICS Teaching Module".

Although the full implementation of all ADAPTOMICS objectives will require substantially more time, research in this program has tackled and overcome initial obstacles and has substantially advanced the state of knowledge in each of the model systems. The substantial biological resources built up in ADAPTOMICS, as well as large sets of phenotypic and sequence data, are publicly available.

The work of this priority program is being carried on in a number of follow-up research projects. The program has built a national research community and contributed to the international community in this field.

Further detailed information, all principal investigators, the "ADAPTOMICS Teaching Module" and references to ADAPTOMICS publications are available here:

https://www.ruhr-uni-bochum.de/dfg-spp1529/Seiten/index.html

BrassiBase is available here:
https://brassibase.cos.uni-heidelberg.de/.

International Plant Phenotyping Resources

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International Plant Phenotyping Network

http://www.plant-phenotyping.org/

IPPN is a non-profit association that represents the major plant phenotyping centers worldwide. The association aims to provide all relevant information about plant phenotyping. The goal is to increase the visibility and impact of plant phenotyping and enable cooperation by fostering communication between stakeholders in academia, industry, government, and the public.

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

Within the last year, the IPPN General Assembly has decided to include members from industry and the statutes were modified accordingly. Currently 6 commercial partners joined IPPN resulting in membership form nearly 40 organizations. Additional 10 commercial members are about to join making IPPN an important platform to discuss future development of plant phenotyping that includes academia and industry. Discussion on specific topics in facilitated in eight working groups.

Conferences, Workshops and Training events

The next IPPN Symposium will be held in October 22-26th 2019 in Nanjing China (http://www.ipps2019.plant-phenotyping.com/) offering a platform for interaction for expected over 500 participants

EMPHASIS

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

The European Strategy Forum for Research Infrastructure (ESFRI) has identified “Plant Phenotyping” as a priority for the European research area and the project EMPHASIS has been listed on the ESFRI Roadmap as an infrastructure project to develop and implement a pan-European plant phenotyping infrastructure. The EMPHASIS project (European Infrastructure for Multi-Scale Plant Phenotyping And Simulation for Food Security in a Changing Climate) coordinated by the Institute of Bio- and Ge sciences, IBG-2: Plant Sciences at the Forschungszentrum Jülich.

In 2017 EMPHASIS has started the Preparatory Phase which is a 4 year H2020 funded project (Grant Agreement number: 739514). Within the Preparatory Phase, EMPHASIS will develop a business plan embedded in a sound legal framework for a long tern operation of EMPHASIS.

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

Within the first project phase EMPHASIS-PREP has mapped the plant phenotyping landscape in Europe including available infrastructure, information systems and user demand for phenotyping. Based on this mapping pilot services have been drafted to test services that are required and demanded by the community with the goal to illustrate the potential to generate benefits, the return of investment, feasibility etc. Additionally, close interaction between national plant phenotyping communities was established and extended with 25 national communities having mandated a representative, to form a link to EMPHASIS by contributing to the so-called “Support Group” and shape the development of EMPHASIS.

EMPHASIS has also initiated a close interaction with the ESFRI project ELIXIR (https://emphasis.plant-phenotyping.eu/Collaboration_ELIXIR) which offers access to genetic and genomic data. Finally EMPHASIS is in the process to initiate the Implementation Phase as an essential step sustainable operation by engaging ministries from a number of countries across Europe with the goal to develop legal framework complementing a long term provision of services to divers user groups that can benefit from access to phenotyping facilities, under controlled and field conditions as well as modelling and data management expertise..

Conferences, Workshops and Training events

EMPHASIS aims at organizing annual European plant phenotyping conferences starting in 2020. The first conference is in preparation.

European Plant Phenotyping Network 2020

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

The EPPN2020 is a H2020 funded research infrastructure project (Grant Agreement: 731013) that provides European public and private scientific sectors with access to a wide range of state-of-the-art plant phenotyping facilities, techniques and methods, and help boost the exploitation of genetic and genomic resources available for crop improvement that represents a major scientific challenge for this coming decade. EPPN2020 specifically aims to facilitate the community progressing across the whole phenotyping pipeline, involving sensors and imaging techniques, data analysis in relation to environmental conditions, data organization and storage, data interpretation in a biological context and meta-analyses of experiments carried out on different organs at different scales of plant organization.

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

EPPN2020 has recently finalized a third call for transnational access allowing over 60 experiments in cutting edge plant phenotyping facilities in Europe. A substantial amount of these experiments includes Arabidopsis research and nearly half of the 31 facilities providing access focuses on Arabidopsis research. The experiments include deep phenotyping for high precision screening of specific traits to high throughput screening of large populations.

Planned future activities of your project or resource.

EPPN2020 will announce the fourth call in April/May 2019 that will be followed by additional two calls. In total, we expect to be able to facilitate nearly 200 experiments.

Gramene: A comparative genomics and pathways resource for plants

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Doreen Ware (PI)
http://www.gramene.org

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

Gramene provides open access to comparative plant genomics and pathways data, and analysis tools. Over the past year and in collaboration with Ensembl Plants, we added six new genomes including *Arabidopsis halleri* to our genomics and pathways data collections. We enrich each reference genome with structural and functional gene annotations, genetic and structural variation, gene expression, phylogenetic trees with orthologous and paralogous gene classification, whole-genome alignments and synteny maps, as well as ontology and pathway associations. Our current phylogenetic tree collection was built with the 58 plant genomes in Gramene including three *Arabidopsis* species (*A. thaliana, A. lyrata, and A. halleri*), and it amounts to nearly 93,000 gene families.

Functional and structural information is provided for each family tree in visually informative (e.g., color-coded protein domains and tick marks indicating splice junctions) and interactive ways (e.g., ability to select a specific GO term or InterPro domain) to highlight homologs that share functional features. The homology view of our versatile Gramene search tool also allows the custom pruning of trees to display defined species, and provides the Arabidopsis homolog for any plant gene in the results of a query. *A. thaliana* has been used as the dicot model for pairwise whole-genome alignments collection.

Within the past year, the alignments subset for *A. thaliana* grew from 34 to 57, and now includes alignments between *A. thaliana* and each of *A. lyrata* and *A. halleri*. In addition, *A. lyrata* was aligned to 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 was also updated to include synteny maps for *A. thaliana* and each the following five species: *A. lyrata, Brassica rapa,* Japonica rice, cacao, and grape; and for *A. lyrata* and grapevine. 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. The Arabidopsis

SNP set was combined with phenotypic data for 95 inbred lines described in Atwell *et al* (2010). In our continued collaboration with the Expression Atlas project (EMBL-EBI), we provide baseline expression data for 23 species, including *A. thaliana* and *A. lyrata* through our 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 23 species, including *A. thaliana* and *A. lyrata*. In collaboration with Reactome, Gramene hosts 293 metabolic and regulatory pathways curated in Japonica rice and inferred in 79 additional plant species (including the three Arabidopsis species in Gramene) 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, pathways, and cross-references to other bioinformatics resources, including AraPort, TAIR and NASC for Arabidopsis. Our tools support comparative analyses of our data as well as data brought in by our users, and include a BLAST/BLAT sequence aligner, 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, and multi-species pathway comparisons. Together these comparative data and resources enable powerful cross-species comparisons

Gramene data sets that include Arabidopsis species:

- Structural and functional annotations for 2.2 million gene models in 58 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.
- Nearly 93,000 phylogenetic tree families (built with 58 plant and 5 non-plant species), 268 whole-genome alignments (64 with Arabidopsis species), and 61 synteny maps (6 with Arabidopsis sp.).
- About 224 million genetic and structural variants for 11 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 almost 800 experiments in over 20 plant species, including *A. thaliana* and *A. lyrata*.
- 293 reference metabolic and regulatory pathways curated in rice and inferred in 79 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. Thus, Gramene's genomes portal was developed on the Ensembl infrastructure and in collaboration with the Ensembl Genomes project (EMBL-EBI); the pathways portal of the project is the Plant Reactome (http://plantreactome.gramene.org); and in collaboration with the Expression Atlas project (EMBL-EBI), we provide experimental baseline expression data from both our genomes and pathway browsers. Integrating across these 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 is supported by an NSF grant IOS-1127112, and partially from USDA-ARS (1907-21000-030-00D).

Planned future activities of your project or resource. Please document the planned activities of your project over the next year.

With future support, we will continue to maintain and build the Gramene resource, with aims to: 1) improve and expand our reference data collection of plant genomes and standardized comparative annotations, 2) enrich our Plant Reactome pathways data resource, 3) integrate visualization and analysis tools for exploring emerging genomic and pathway data, and 4) transform the community through communication and training opportunities.

Conferences, Workshops and Training events

In the past year, Gramene participated in nine scientific conferences to present talks, posters, training workshops, and disseminate brochures and other educational materials. We organized community outreach booths for members of the AgBioData Consortium at the Plant & Animal Genomes and Plant Biology conferences. We continued to broadcast live webinars, and made the video-recordings available in Gramene's YouTube channel. As part of our community curation efforts and together with the MaizeCode project, we organized two gene structural annotation jamborees, one for faculty from primarily undergraduate institutions (PUI) and another for maize researchers. Other plant education activities geared to K-12 students and faculty included hands-on activities to celebrate Fascination of Plants Day and a DNA workshop for Science Olympics participants. We plan on continuing our outreach, education and training activities in the next year.

The Global Plant Council

Isabel Mendoza-Poudereux
isabel@globalplantcouncil.org,

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

The Global Plant Council has been developing a set of activities addressed to Early Carrer Researchers (ECR) with the aim to help them in their Job-hunting activities. Among them, the already well stablished monthly #plantscijobs 1-hour long twitterstorm in Twitter (@GlobalPlantGPC), plus the new Global Plant Council #plantscijobs Facebook group. Since this last one was launched in early November, well over 100 job offers have been featured in this platform and almost 600 people have joined the group.

Planned future activities of your project or resource.

In parallel to the GPC website rearrangement, a new section devoted to ECR is in development, with resources specifically address to ECRs in plant science to help them improve their job hunting, grant winning, dissemination and networking skills.

Conferences, Workshops and Training events

Last November the GPC held a workshop at the Annual Meeting of the American Society of Agronomy and the Crop Science Society of America, in Baltimore, USA. The one-day workshop "Enhancing Global Collaborations in Crop Science", brought together over 40 researchers to discuss how best to facilitate international collaboration between researchers, policy and communication experts in crop science. GPC is in the process those discussions into short case studies that would be available in their blog.

For the upcoming ICAR2019 meeting GPC is working on two workshops, on science communication and sustainable agriculture. The proposals are currently in development.

Additional Information

GPC is devoted to free dissemination of research information, specifically plant science events, resources and news from around the world. It is possible to follow the GPC updates by joining their 6500 followers on Twitter (@GlobalPlantGPC) , 2100 followers in Facebook, signing up to the monthly newsletter (http://tinyurl.com/GPCebulletin) or simply visiting their website (www.globalplantcouncil.org) for daily updates on news and

events.

Analysis of Arabidopsis Publications

Outlook for 2018/19

Following a high point in 2014, the annual number of publications in Pubmed journals that include 'Arabidopsis' in the Title or Abstract has since stabilised at approximately 4200 papers. However 2018 sees an important change that may prove informative with regard the future direction of global plant science research. For the first time there are more papers published in PubMed journals that include the words 'rice' or 'oryza' in the Title or Abstract than those that include 'Arabidopsis'. The recent plateau in the number of 'Arabidopsis' papers means that this change has been coming for a while. In addition papers that include either 'maize/corn' or 'wheat/triticum' continue to increase and over the coming years we might expect 'Arabidopsis' papers to slip to fourth in these rankings.

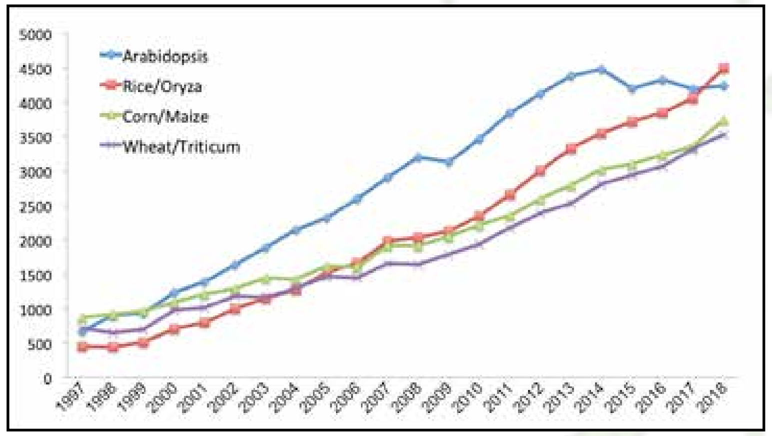

Figure 8. Papers published in Pubmed journals globally with Arabidopsis, rice/oryza, corn/maize or wheat/triticum in the Title/Abstract.

Over the past twenty years, when considering the trend of the lines in Figure 8 it is legitimate to draw a conclusion that the research achievements made using Arabidopsis have enabled subsequent improvements in the amount of publishable research using those other species. However this might not be a direct relationship as the increase in fundamental knowledge gained through use of Arabidopsis has also occurred alongside a myriad of technological improvements. These improvements have allowed more rigorous analysis of plants with larger and complex genomes using experimental techniques that previously might only have been possible in Arabidopsis.

These technical improvements might include but aren't limited to:

1- Improvements in next generation sequencing for genome and/or expression analysis
2- Advances in bioinformatics analysis of big datasets
3- Improved techniques for bulk transformation

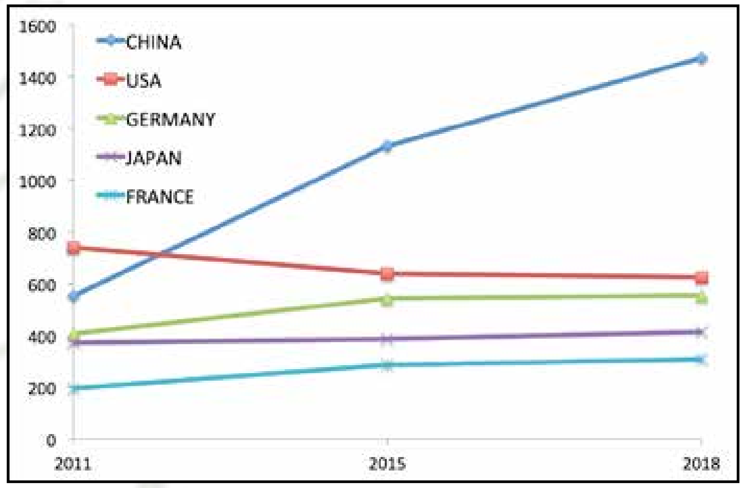

Figure 9. Papers published in Pubmed journals with Arabidopsis in the Title/Abstract since 2011. Globally These countries are have the highest number of publications.

4- Generation of TILLING mutant populations in multiple plant species
5- Improvements in the ability to perform large-scale field-level phenotyping

The pre-eminence of China Plant Research

The overall number of papers shown in Figure 8 is highly dependent on the papers that are published by Chinese researchers. Approximately one-third of all Arabidopsis papers include research from China and over the last four years the number of 'Chinese' Arabidopsis papers continues to increase (figure 9). However in the other four countries with the most Arabidopsis publications (USA, Germany, Japan, France) the number of papers has plateaued (figure 9).

In general, European countries show a small increase in Arabidopsis publications (figure 10) whereas in Oceania and Asia there is a general plateauing, with the exception of India and Singapore that both see an increase (Figure 11). The Americas are a mixed cohort with Canada showing a similar plateau to their neighbours in the USA whilst Mexico, Brazil and Chile show increases, albeit from a lower level (Figure 12).

Although it is outside the scope of this analysis to fully evaluate the myriad reasons behind these trends, they might be broadly attributed to the development of scientific infrastructures in each country. As research infrastructure becomes more developed, such as in China or India, then the number of publications appears to show an equivalent increase. Those countries with already well-developed research infrastructures, such as across Europe or in North America, are now observing a plateau or small decrease in the number of publications that feature Arabidopsis research.

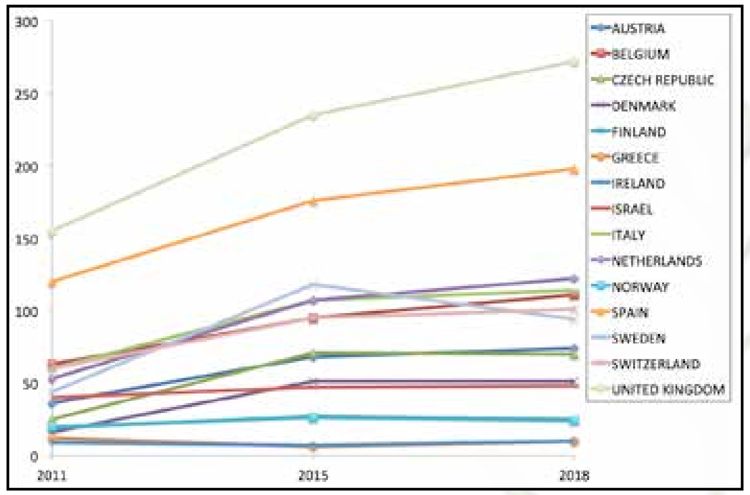

Figure 10. Papers published in Pubmed journals from different European countries with Arabidopsis in the Title/Abstract.

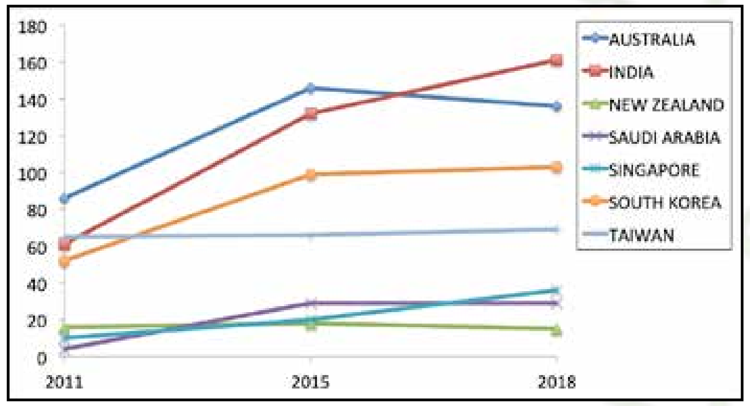

Figure 11 Papers published in Pubmed journals from different Oceania or Asian countries with Arabidopsis in the Title/Abstract.

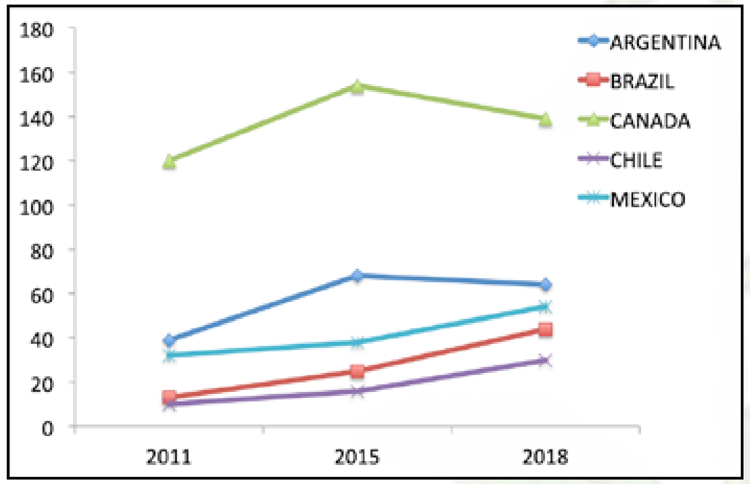

Figure 12 Papers published in Pubmed journals from different American countries with Arabidopsis in the Title/Abstract.

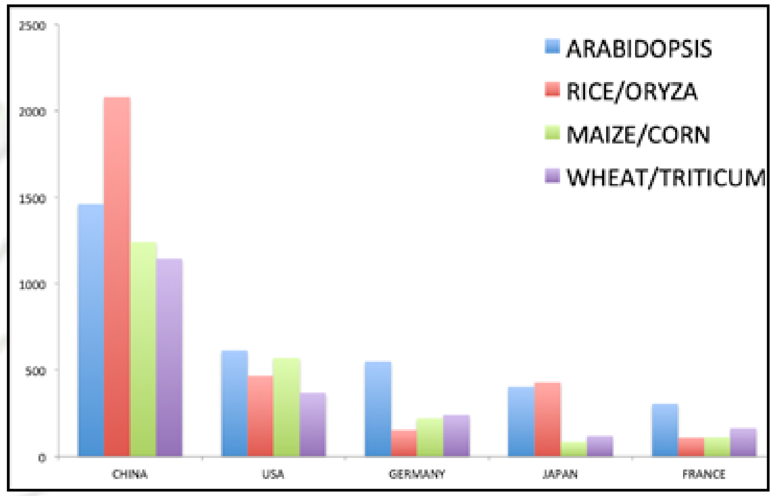

Figure 13 Papers published in Pubmed journals from different countries with *Arabidopsis*, rice/oryza, corn/maize or wheat/triticum in the Title/Abstract. These are the countries with the highest number of *Arabidopsis* publications

In 2018 the number of publications that include research in other plant species is also significantly influenced by Chinese research since a high proportion of overall global publications include research from that country (46% for rice, 33% for maize, 32% for wheat). This reflects anecdotal discussions with Chinese researchers who confirm that the majority of their research funding is for projects that have a more applied focus and are rarely specifically earmarked for Arabidopsis. This information makes the continued production of Chinese Arabidopsis papers all the more remarkable if funding is not largely allocated for that purpose.

From these trends shown in figures 8-13 we can made a strong case that the increase in publications featuring other plants are a result of discoveries made possible by the strength of the knowledge base and research infrastructures that were developed over previous decade(s) of Arabidopsis research. The continued success of this 'discovery pipeline' is surely dependent on maintaining support for Arabidopsis research, which still underpins more applied research. However as outlined within many country submissions in this and in previous MASC annual reports (http://Arabidopsisresearch.org/index.php/en/publications) there is global concern that funding for Arabidopsis and other fundamental plant science research is in decline.

Analysis of Patents.

Accurately determining the importance of Arabidopsis in the development of more applied research in other plant species is extremely challenging. Previous MASC reports have looked at the number of published patents that include keywords from different plant species. In this report we return to this analysis using the European Patent Office Espacenet resource (https://worldwide.espacenet.com/advancedSearch?locale=en_EP) to assess the number of worldwide English-language patents that include the words Arabidopsis, Zea, Oryza, Triticum or Brassica (figure 14).

We have not used the common names of the crop species for a two main reasons: Firstly to remove the chance of including patents that do not have a particularly scientific-based application given the more common general usage of the words rice, maize or wheat. Secondly we think use of the Latin names for crops will more likely apply to a patent that has resulted from a research-derived application.

Therefore we cannot claim that the numbers shown in figure 14 are a true representation of the absolute number of patents but rather it is the trend of the line that is most informative. The 2016 MASC report (Arabidopsisresearch.org/images/publications/mascreports/2016_MASCReport.pdf) showed that there was many more patents that include maize/corn or rice/oryza; numbers that are not reflected in these figures.

The zenith of Arabidopsis-derived patents occurred in the late 1990s and early 2000s and since that time there was initially a steadier increase and more recent decline. This might indicate that the early low-hanging research that focussed on plant processes that could improve crop productivity were initially patented.

More recently the important but arguably more incremental advances in our understanding of plant growth through use of *Arabidopsis* has slowed the pace of patentable research. Since 2012 patents involving all plants show a decline in numbers, which we suspect is linked to global uncertainty regarding the use of genetically modified crops and the risk of investment in these technologies when they might not be economically feasible, particularly in Europe and China.

Intuitively we suspect that the thousands of patents that include work from Arabidopsis importantly underpins those developed in other species. However gaining direct evidence for this relationship is almost impossible without undertaking an extremely rigourous analysis, which is outside the scope of this report.

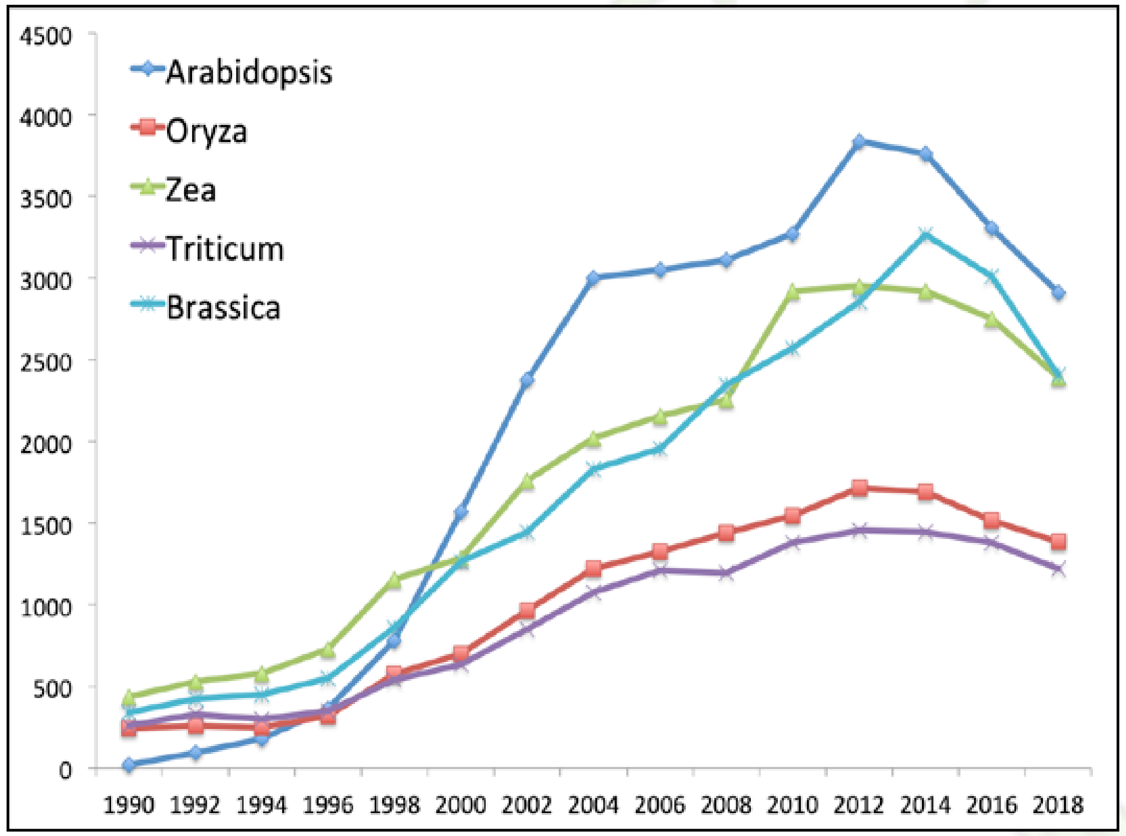

Figure 14 World English-language patents containing keywords *Arabidopsis*, oryza, Zea, triticum or Brassica. Data obtained from https://worldwide.espacenet.com/advancedSearch?locale=en_EP

Country Reports

Over the coming pages MASC country representatives provide details about Arabidopsis activities in each of their nations.

Argentina

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Use of Arabidopsis

There are more than 35 groups conducting varied research with Arabidopsis in Argentina.

They work in different Institutes and Universities scattered throughout the country in cities such as Buenos Aires, Rosario, Mar del Plata, Santa Fe, Córdoba, Mendoza and Bariloche.

Selected Publications

Achkar NP, Cho SK, Poulsen C, Arce AL, Re DA, Giudicatti AJ, Karayekov E, Ryu MY, Choi SW, Harholt J, Casal JJ, Yang SW, Manavella PA (2018) A Quick HYL1-Dependent Reactivation of MicroRNA Production Is Required for a Proper Developmental Response after Extended Periods of Light Deprivation. Dev Cell. 46(2):236-247.e6. doi: 10.1016/j.devcel.2018.06.014.

Bresso EG, Chorostecki U, Rodriguez RE, Palatnik JF, Schommer C (2018) Spatial Control of Gene Expression by miR319-Regulated TCP Transcription Factors in Leaf Development. Plant Physiol. 176(2):1694-1708. doi: 10.1104/pp.17.00823.

Cagnola JI, Cerdán PD, Pacín M, Andrade A, Rodriguez V, Zurbriggen MD, Legris M, Buchovsky S, Carrillo N, Chory J, Blázquez MA, Alabadi D, Casal JJ (2018) Long-Day Photoperiod Enhances Jasmonic Acid-Related Plant Defense. Plant Physiol. 163-173. doi: 10.1104/pp.18.00443.

Crocco CD, Ocampo GG, Ploschuk EL, Mantese A, Botto JF (2018) Heterologous Expression of AtBBX21 Enhances the Rate of Photosynthesis and Alleviates Photoinhibition in Solanumtuberosum. Plant Physiol. 369-380. doi: 10.1104/pp.17.01417.

Dotto M, Gómez MS, Soto MS, Casati P (2018) UV-B radiation delays flowering time through changes in the PRC2 complex activity and miR156 levels in *Arabidopsis thaliana*. Plant Cell Environ. 1394-1406. doi: 10.1111/pce.13166.

Ercoli MF, Ferela A, Debernardi JM, Perrone AP, Rodriguez RE, Palatnik JF (2018) GIF Transcriptional Coregulators Control Root Meristem Homeostasis. Plant Cell. 2018 Feb;30(2):347-359. doi: 10.1105/tpc.17.00856.

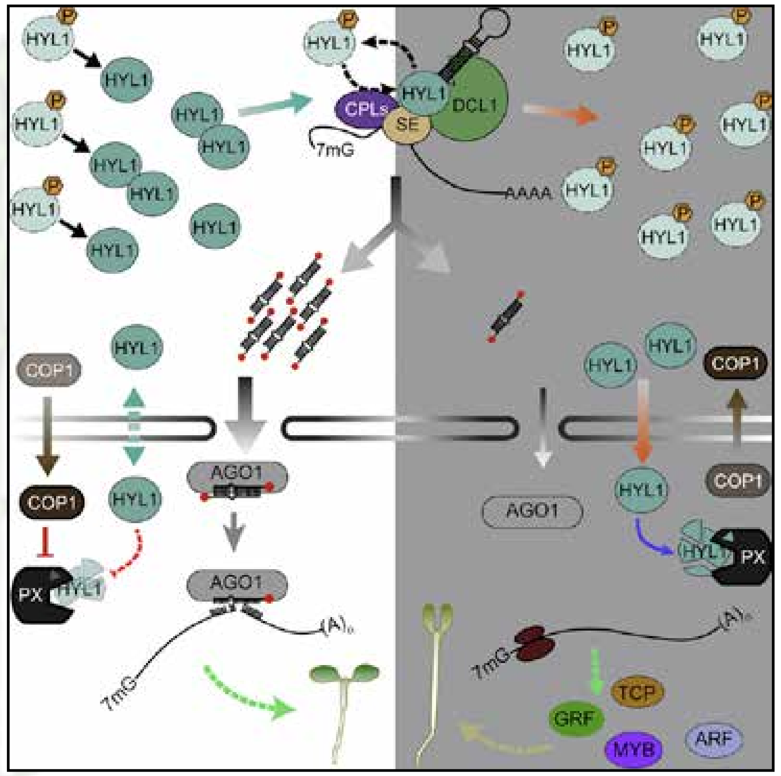

Figure 15. A Quick HYL1-Dependent Reactivation of MicroRNA Production Is Required for a Proper Developmental Response after Extended Periods of Light Deprivation.

Osella AV, Mengarelli DA, Mateos J, Dong S, Yanovsky MJ, Balazadeh S, Valle EM, Zanor MI (2018) FITNESS, a CCT domain-containing protein, deregulates reactive oxygen species levels and leads to fine-tuning trade-offs between reproductive success and defence responses in *Arabidopsis*. Plant Cell Environ. 41(10):2328-2341. doi: 10.1111/pce.13354.

Pucciariello O, Legris M, Costigliolo Rojas C, Iglesias MJ, Hernando CE, Dezar C, Vazquez M, Yanovsky MJ, Finlayson SA, Prat S, Casal JJ (2018) Rewiring of auxin signaling under persistent shade. Proc Natl Acad Sci U S A. 115(21):5612-5617. doi: 10.1073/pnas.1721110115.

Racca S, Welchen E, Gras DE, Tarkowská D, Ture□ková V, Maurino VG, Gonzalez DH (2018) Interplay between cytochrome c and gibberellins during *Arabidopsis* vegetative development. Plant J. 94(1):105-121. doi: 10.1111/tpj.13845.

Scuffi D, Nietzel T, Di Fino LM, Meyer AJ, Lamattina L, Schwarzländer M, Laxalt AM, García-Mata C (2018) Hydrogen Sulfide Increases Production of NADPH Oxidase-Dependent Hydrogen Peroxide and Phospholipase D-Derived Phosphatidic Acid in Guard Cell Signaling. Plant Physiol.):2532-2542. doi: 10.1104/pp.17.01636.

Major Funding Sources

- Argentinean National Reseasrch Council (CONICET)
- Agencia Nacional de Pomoción Científica y Tecnológica (ANPCyT).

Australia

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Australian Research Council Centre of Excellence, Plant Energy Biology, The University of Western Australia.

Use of Arabidopsis

There are over 60 research groups located at most Universities across the country and within Commonwealth Scientific Research Organisation (CSIRO) facilities.

New Resources and Software tools available for Arabidopsis Researchers initiated or funded in 2018 or early 2019

SUBA4: The SubCellular Proteomic Database, housing large scale proteomic, GFP localization data In sillico abundance estimations for Arabidopsis proteins http://suba.live/

Plant stress and root cell methylomes.
http://listerlab.org/browsers.html

Arabidopsis Transposable Element browser.
http://plantenergy.uwa.edu.au/~lister/annoj/browser_te_variants.html

MASCP Gator: a proteomics aggregation utility that displays information from a variety of online Arabidopsis proteomic resources. http://gator.masc-proteomics.org/

1001 Proteomes: Arabidopsis non-synonymous SNP browser created from data made available as part of the 1001 Genomes consortium.
http://1001proteomes.masc-proteomics.org/

Conferences, Workshops and Outreach events

COMBIO 2018, International Convention Centre, Sydney 23-26th September 2018. Annual national conference that includes several symposia dedicated to plant research. This conference incorporated the annual Australian Society of Plant Biologists meeting for 2018 (www.asps.org.au).

Upcoming Events:
Translational Photosynthesis Conference 2019: Innovations in agriculture for food security, Brisbane Convention Centre, Queensland, 30th June 2019

14th International Conference on Tetrapyrrole Photoreceptors in Photosynthetic Organisms, Sydney, July 21 -24 2019

The Australian Society of Plant Scientists conference, ASPS 2019, and Grains Satellite meeting, LaTrobe University, Melbourne, 26 - 29th Nov 2019.

Herbicide Discovery & Development 2020 (HDD2020). The University of Western Australia, Perth, Jan 15th 2020.

The International Congress on Plant Molecular Biology (IPMB), Cairns Convention Centre, Queensland, 24th Oct 2021. http://ipmb2021.org/

Selected Publications

Bhatia N, Åhl H, Jönsson H, Heisler MG (2019) Quantitative analysis of auxin sensing in leaf primordia argues against proposed role in regulating leaf dorsoventrality. Elife. 22;8. pii: e39298.

Eimer H, Sureshkumar S, Singh Yadav A, Kraupner-Taylor C, Bandaranayake C, Seleznev A, Thomason T, Fletcher SJ, Gordon SF, Carroll BJ, Balasubramanian S. (2018) RNA-Dependent Epigenetic Silencing Directs Transcriptional Downregulation Caused by Intronic Repeat Expansions. Cell. 23;174(5):1095-1105

Colas des Francs-Small C, Vincis Pereira Sanglard L, Small I (2018) Targeted cleavage of nad6 mRNA induced by a modified pentatricopeptide repeat protein in plant mitochondria. Commun Biol. 11;1:166

Ebert B, Rautengarten C, McFarlane HE, Rupasinghe T, Zeng W, Ford K, Scheller HV, Bacic A, Roessner U, Persson S, Heazlewood JL (2018) A Golgi UDP-GlcNAc transporter delivers substrates for N-linked glycans and sphingolipids. Nat Plants. 4(10):792-801.

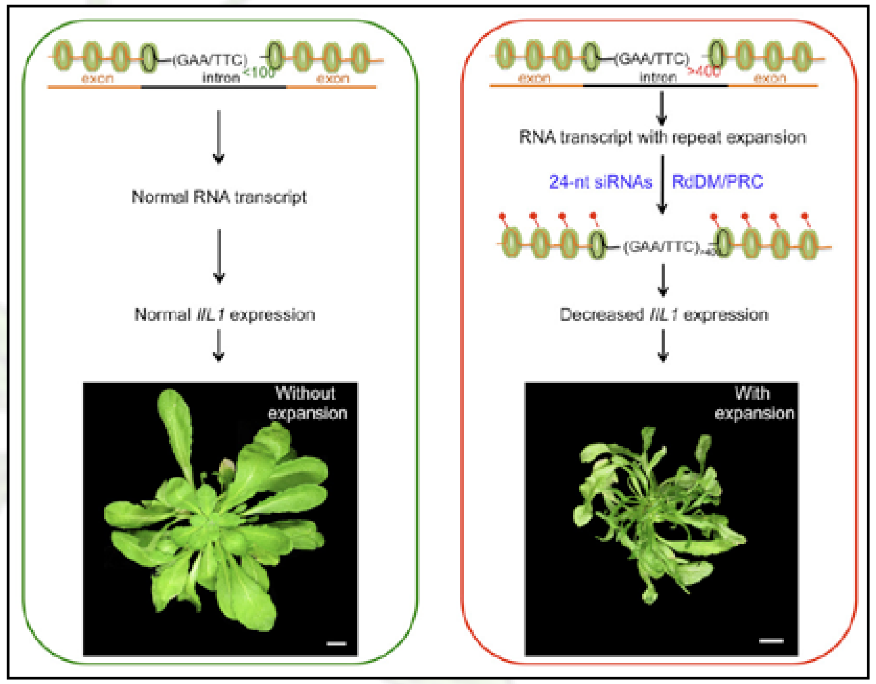


Figure 16. Figure taken from Eimer *et al.*, 2018 who use Arabidopsis as a model to investigate the molecular mechanisms through which intronic repeat expansions lead to transcriptional downregulation.

Sánchez-Rodríguez C, Shi Y, Kesten C, Zhang D, Sancho-Andrés G, Ivakov A, Lampugnani ER, Sklodowski K, Fujimoto M, Nakano A, Bacic A, Wallace IS, Ueda T, Van Damme D, Zhou Y, Persson S (2018) The Cellulose Synthases Are Cargo of the TPLATE Adaptor Complex. Mol Plant. 5;11(2):346-349

Crisp PA, Smith AB, Ganguly DR, Murray KD, Eichten SR, Millar AA, Pogson BJ (2018) RNA Polymerase II Read-Through Promotes Expression of Neighboring Genes in SAL1-PAP-XRN Retrograde Signaling. Plant Physiol. 178(4):1614-1630

Kerbler SM, Taylor NL, Millar AH (2019) Cold sensitivity of mitochondrial ATP synthase restricts oxidative phosphorylation in *Arabidopsis thaliana*. New Phytol. 221(4):1776-1788.

Belt K, Van Aken O, Murcha M, Millar AH, Huang S (2018) An Assembly Factor Promotes Assembly of Flavinated SDH1 into the Succinate Dehydrogenase Complex. Plant Physiol. 177(4):1439-1452.

Wang L, Waters MT, Smith SM (2018) Karrikin-KAI2 signalling provides *Arabidopsis* seeds with tolerance to abiotic stress and inhibits germination under conditions unfavourable to seedling establishment. New Phytol. 219(2):605-618.

Chen W, Salari H, Taylor MC, Jost R, Berkowitz O, Barrow R, Qiu D, Branco R, Masle J (2018) NMT1 and NMT3 N-Methyltransferase Activity Is Critical to Lipid Homeostasis, Morphogenesis, and Reproduction. Plant Physiol. 177(4):1605-1628.

Major Funding Sources

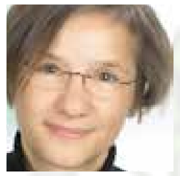
Fundamental and translational research can be funded by the Australian Research Council
www.arc.gov.au

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

http://ipmb2021.org/

Austria



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Use of Arabidopsis

Although Austria is a small European country with around 8.8 mio inhabitants Arabidopsis research is highly active at seven institutions, the University of Natural Resources & Life Science Vienna (BOKU) (www.dagz.boku.ac.at/en/), the Gregor Mendel Institute of Molecular Plant Biology (GMI) (www.gmi.oeaw.ac.at/), the Max F. Perutz Laboratories (MFPL) (https://www.mfpl.ac.at/), the Institute of Science and Technology, Austria (IST Austria) (ist.ac.at/en/), the AIT Austrian Institute of Technology (https://www.ait.ac.at/themen/improvement-of-plant-quality-vigor/), the University of Salzburg, Division of Plant Physiology (https://www.uni-salzburg.at/index.php?id=32790&L=1&MP=205208-207110), the University of Vienna (www.univie.ac.at/mosys) and the University of Graz (https://botanik.uni-graz.at/de/forschung/molecular-plant-physiology/).

The 23 research groups focus on molecular genetics (including population, epi-, and developmental genetics), RNA-, chromosome-, cell-, and glyco-biology as well as stress and hormone signaling. There is a vivid collaboration activity between the research groups sharing experimental tools provided by sequencing, proteomic, genome editing, phenotyping, imaging and computational facilities.
https://www.viennabiocenter.org/facilities/

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018/ early 2019.

Vertical microscope with Airyscan resolution

von Wangenheim D, Hauschild R, Fendrych M, Barone V, Benková E, Friml J. (2017) Live tracking of moving samples in confocal microscopy for vertically grown roots. Elife. 6. pii: e26792. doi: 10.7554/eLife.26792.

Root chip allowing for immediate treatments and simultaneous confocal live imaging

Fendrych M, Akhmanova M, Merrin J, Glanc M, Hagihara S, Takahashi K, Uchida N, Torii KU, Friml J (2018) Rapid and reversible root growth inhibition by TIR1 auxin signalling. Nat Plants. 4:453-459. doi: 10.1038/s41477-018-0190-1.

Nanopore

Schon MA, Kellner MJ, Plotnikova A, Hofmann F, Nodine MD (2018) NanoPARE: parallel analysis of RNA 5′ ends from low-input RNA. Genome Res 28:1931-42. doi: 10.1101/gr.239202

Arabidopsis Embryo Transcriptome

Hofmann F, Schon MA, Nodine MD (2018) The embryonic transcriptome of *Arabidopsis thaliana*. Plant Reprod. [epub] preprint: bioRxiv:479584. doi: 10.1007/s00497-018-00357-2

Root Development Methods and Protocols Part of the Methods in Molecular Biology book series
DOI https://doi.org/10.1007/978-1-4939-7747-5

Conferences, Workshops and Outreach events

21st European Network on Plant Endomembrane Research, ENPR 2018; 4.-7. September 2018 (Main organisers Yasin Dagdas and Jürgen Kleine-Vehn)

Selected Publications

Adamowski M, Narasimhan M, Kania U, Glanc M, De Jaeger G, Friml J (2018) A Functional Study of AUXILIN-LIKE1 and 2, Two Putative Clathrin Uncoating Factors in *Arabidopsis*. Plant Cell. 30:700-716. doi: 10.1105/tpc.17.00785

Capitao C, Shukla N, Wandrolova A, Mittelsten Scheid O, Riha K. (2018) Functional Characterization of SMG7 Paralogs in Arabidopsis thaliana. Front Plant Sci. 9:1602.

Glanc M, Fendrych M, Friml J. (2018) Mechanistic framework for cell-intrinsic re-establishment of PIN2 polarity after cell division. Nat Plants 4:1082-1088 doi: 10.1038/s41477-018-0318-3

Herrmann A, Livanos P, Lipka E, Gadeyne A, Hauser MT, Van Damme D, Müller S (2018) Dual localized kinesin-12 POK2 plays multiple roles during cell division and interacts with MAP65-3. EMBO Rep. 19: pii: e46085. doi: 10.15252/embr.201846085.

Higo A, Kawashima T, Borg M, Zhao M, López-Vidriero I, Sakayama H, Montgomery SA, Sekimoto H, Hackenberg D, Shimamura M, Nishiyama T, Sakakibara K, Tomita Y, Togawa T, Kunimoto K, Osakabe A, Suzuki Y, Yamato KT, Ishizaki K, Nishihama R, Kohchi T, Franco-Zorrilla JM, Twell D, Berger F, Araki T. (2018) Transcription factor DUO1 generated by neo-functionalization is associated with evolution of sperm differentiation in plants. Nat Commun 9:5283. doi: 10.1038/s41467-018-07728-3

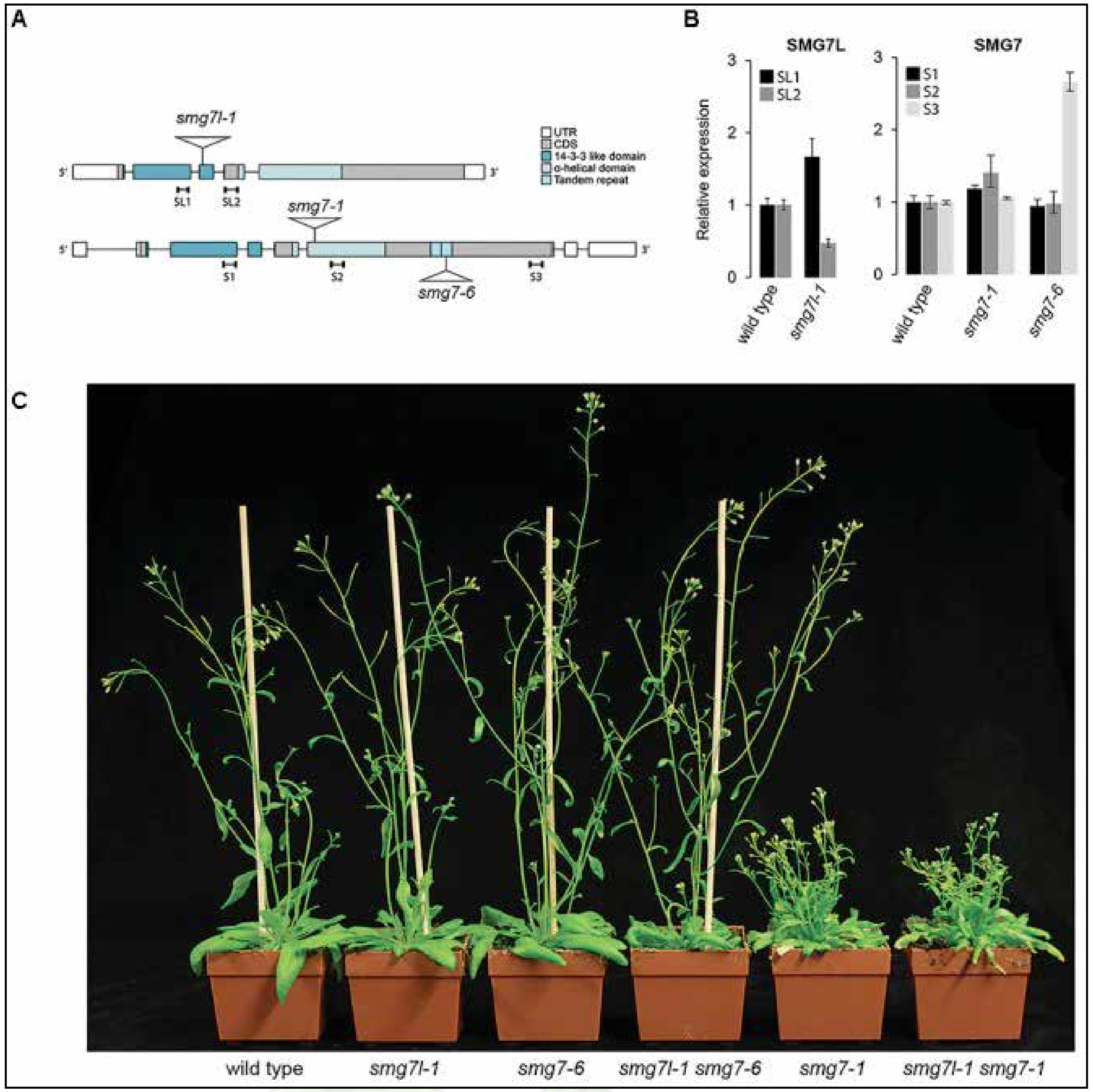

Figure 17 SMG7 proteins are evolutionary conserved across eukaryotes and primarily known for their function in nonsense mediated RNA decay (NMD). In contrast to other NMD factors, SMG7 proteins underwent independent expansions during evolution indicating their propensity to adopt novel functions. (A) Diagram of SMG7 and SMG7L genes with positions of T-DNA insertions and functional domains. (B) qRT-PCR analysis of SMG7L and SMG7 transcripts. Positions of the regions amplified by PCR are indicated in (A). Error bars represent SEM of three biological replicas. (C) Five week-old wild type and mutant plants. Taken from Capitao *et al.*, 2018, doi: 10.3389/fpls.2018.01602.

Kania U, Nodzynski T, Lu Q, Hicks GR, Nerinckx W, Mishev K, Peurois F, Cherfils J, De Rycke RM, Grones P, Robert S, Russinova E, Friml J (2018) Endosidin 4 inhibitor targets the SEC7 domain-type ARF-GEFs and interferes with subcellular trafficking in eukaryotes. Plant Cell. 30:2553-2572. doi: 10.1105/tpc.18.00127

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Pedrotti L, Weiste C, Nägele T, Wolf E, Lorenzin F, Dietrich K, Mair A, Weckwerth W, Teige M, Baena-González E, Dröge-Laser W (2018) Snf1-RELATED KINASE1-Controlled C/S1-bZIP Signaling Activates Alternative Mitochondrial Metabolic Pathways to Ensure Plant Survival in Extended Darkness. Plant Cell. 30:495-509. doi: 10.1105/tpc.17.00414.

Salanenka Y, Verstraeten I, Löfke C, Tabata K, Naramoto S, Glanc M, Friml J (2018) Gibberellin DELLA signaling targets the retromer complex to redirect protein trafficking to the plasma membrane. Proc Natl Acad Sci U S A 115:3716-3721. doi: 10.1073/pnas.1721760115

Shin YJ, Vavra U, Veit C, Strasser R (2018) The glycan-dependent ERAD machinery degrades topologically diverse misfolded proteins. Plant J. 94:246-259. doi: 10.1111/tpj.13851.

Smakowska-Luzan E, Mott GA, Parys K, Stegmann M, Howton TC, Layeghifard M, Neuhold J, Lehner A, Kong J, Grünwald K, Weinberger N, Satbhai SB, Mayer D, Busch W, Madalinski M, Stolt-Bergner P, Provart NJ, Mukhtar MS, Zipfel C, Desveaux D, Guttman DS, Belkhadir Y (2018) An extracellular network of *Arabidopsis* leucine-rich repeat receptor kinases. Nature 553:342-6. doi: 10.1038/nature25184

Wang H, Jiang D, Axelsson E, Lorkovic ZJ, Montgomery S, Holec S, Pieters BJGE, Al Temimi AHK, Mecinovic J, Berger F (2018) LHP1 Interacts with ATRX through Plant-Specific Domains at Specific Loci Targeted by PRC2. Mol Plant.11:1038-1052. doi: 10.1016/j.molp.2018.05.004

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Major Funding Sources

European Research Council (ERC) Advanced grant EPICLINES "Elucidating the causes and consequences of the global pattern of epigenetic variation in *Arabidopsis thaliana*" Magnus Nordborg, Gregor Mendel Institute of Molecular Plant Biology

ETAP "Tracing Evolution of Auxin Transport and Polarity in Plants" Jiri Friml, Institute of Science and Technology Austria

European Research Council (ERC) Starting grant AuxinER "Project Mechanisms of Auxin-dependent Signaling in the Endoplasmic Reticulum" to Jürgen Kleine-Vehn, University of Natural Resources and Life Sciences, Vienna

FEAR-SAP "Project Function and Evolution of Attack and Response Strategies during Allelopathy in Plants" Claude Becker, Gregor Mendel Institute of Molecular Plant Biology

sRNA-EMB "Small RNA regulation of the body plan and epigenome in *Arabidopsis* embryos" Michael Nodine, Gregor Mendel Institute of Molecular Plant Biology

Further funding Sources

FWF https://www.fwf.ac.at/

OeAD (https://oead.at/en/to-austria/grants-and-scholarships/)

Austrian Academy of Sciences (ÖAW) (www.oeaw.ac.at/stipendien-foerderungen/stipendien-preise/nachwuchsfoerderung/)

Vienna Science and Technology Fund (WWTF) (wwtf.at/index.php?lang=EN)

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

Further funding sources at the European level

ERA-CAPS http://www.eracaps.org/

ITN-EU MEICOM https://cordis.europa.eu/project/rcn/211682/factsheet/en

ITN-EU EPIDIVERSE https://cordis.europa.eu/project/rcn/211879/factsheet/en

Marie Skłodowska-Curie actions (http://ec.europa.eu/research/mariecurieactions/)

EMBO Long-Term Fellowships (www.embo.org/funding-awards/fellowships)

Belgium

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Use of Arabidopsis

Research Facilities

Arabidopsis Research Centers in Belgium:

VIB-UGent Center for Plant Systems Biology, https://www.psb.ugent.be/
University of Ghent https://www.ugent.be/en
University of Leuven https://www.kuleuven.be/english
University of Antwerpen https://www.uantwerpen.be/en/
University of Hasselt http://www.uhasselt.be/en
Universite catholique de Louvain https://uclouvain.be/fr/index.html
University of Liege https://www.ulg.ac.be/cms/c_5000/en/home

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

TF2Network, a tool for predicting transcription factor regulators and gene regulatory networks in *Arabidopsis* using publicly available binding site information https://www.ncbi.nlm.nih.gov/pubmed/29272447

Curse, an online curation tool for building expression atlases and co-expression networks from public RNA-Seq data (https://www.ncbi.nlm.nih.gov/pubmed/30590391)

Conferences, Workshops and Outreach events

Conferences and Workshops:
- Regulatory Oxylipins | VIB Conference series
https://vibconferences.be/event/regulatory-oxylipins

International Conference on Polyploidy | VIB Conference series
https://vibconferences.be/event/international-conference-on-polyploidy

ABPP 2019 Target discovery and visualization using chemical probes
https://agenda.kuleuven.be/en/content/abpp-2019-target-discovery-and-visualization-using-chemical-probes

Selected Publications

Bhosale R, Boudolf V, Cuevas F, Lu R, Eekhout T, Hu Z, Van Isterdael G, Lambert GM, Xu F, Nowack MK, Smith RS, Vercauteren I, De Rycke R, Storme V, Beeckman T, Larkin JC, Kremer A, Höfte H, Galbraith DW, Kumpf RP, Maere S, De Veylder L (2018) A Spatiotemporal DNA Endoploidy Map of the Arabidopsis Root Reveals Roles for the Endocycle in Root Development and Stress Adaptation. Plant Cell. 30(10):2330-2351. doi: 10.1105/tpc.17.00983. Epub 2018 Aug 16. PMID: 30115738

Corso M, Doccula FG, de Melo JRF, Costa A, Verbruggen N (2018) Endoplasmic reticulum-localized CCX2 is required for osmotolerance by regulating ER and cytosolic Ca2+ dynamics in Arabidopsis. Proc Natl Acad Sci U S A. 10;115(15):3966-3971. doi: 10.1073/pnas.1720422115. PMID: 29581277

Gao Z, Daneva A, Salanenka Y, Van Durme M, Huysmans M, Lin Z, De Winter F, Vanneste S, Karimi M, Van de Velde J, Vandepoele K, Van de Walle D, Dewettinck K, Lambrecht BN, Nowack MK (2018) KIRA1 and ORESARA1 terminate flower receptivity by promoting cell death in the stigma of Arabidopsis. Nat Plants. 4(6):365-375. doi: 10.1038/s41477-018-0160-7 PMID: 29808023

Houbaert A, Zhang C, Tiwari M, Wang K, de Marcos Serrano A, Savatin DV, Urs MJ, Zhiponova MK, Gudesblat GE, Vanhoutte I, Eeckhout D, Boeren S, Karimi M, Betti C, Jacobs T, Fenoll C, Mena M, de Vries S, De Jaeger G, Russinova E (2018) POLAR-guided signalling complex assembly and localization drive asymmetric cell division. Nature. 563(7732):574-578. doi: 10.1038/s41586-018-0714-x. PMID: 30429609

Miyashima S, Roszak P, Sevilem I, Toyokura K, Blob B, Heo JO, Mellor N, Help-Rinta-Rahko H, Otero S, Smet W, Boekschoten M, Hooiveld G, Hashimoto K, Smetana O, Siligato R, Wallner ES, Mähönen AP, Kondo Y, Melnyk CW, Greb T, Nakajima K, Sozzani R, Bishopp A, De Rybel B, Helariutta Y (2019) Mobile PEAR transcription factors integrate positional cues to prime cambial growth. Nature. 565(7740):490-494. doi: 10.1038/s41586-018-0839-y. PMID: 30626969

Orman-Ligeza B, Morris EC, Parizot B, Lavigne T, Babé A, Ligeza A, Klein S, Sturrock C, Xuan W, Novák O, Ljung K, Fernandez MA, Rodriguez PL, Dodd IC, De Smet I, Chaumont F, Batoko H, Périlleux C, Lynch JP, Bennett MJ, Beeckman T, Draye X (2018) The Xerobranching Response Represses Lateral Root Formation When Roots Are Not in Contact with Water. Curr Biol.28(19):3165-3173.e5. doi: 10.1016/j.cub.2018.07.074. PMID: 30270188

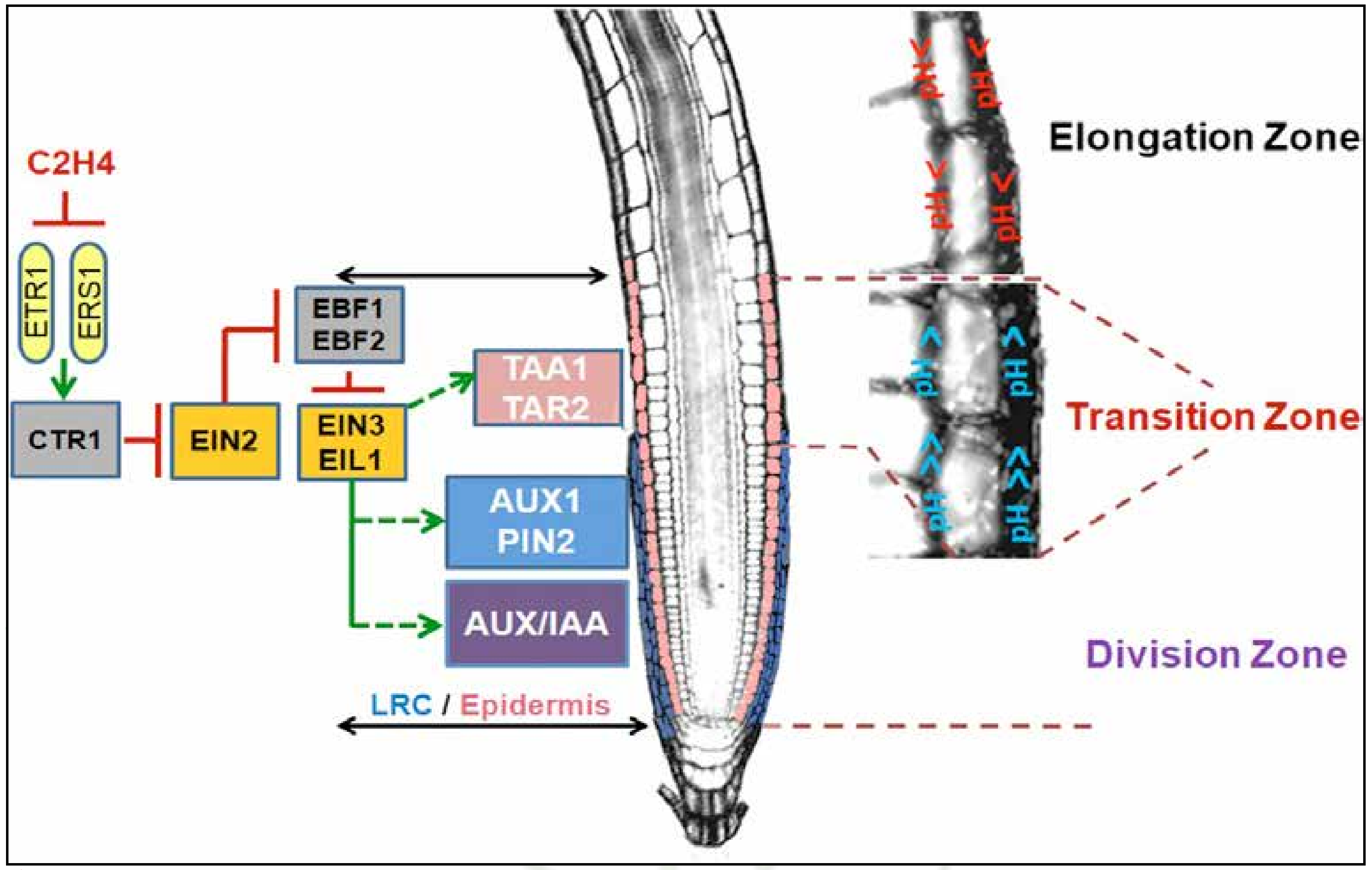

Figure 18. Integrative model of ethylene feedback on auxin homeostasis in the root tip. Ethylene perceived in the LRC and epidermis of the cell division zone regulates root growth by positive control on auxin transport and local auxin biosynthesis in the TZ. Ethylene signals perceived in the root tip relieve the suppression of CTR1 on EIN2 and EIN3/EIL1. AUX, PIN2, AUX/IAA, and TAA1 in the LRC and epidermis are indirect targets for positive regulation by EIN3/EIL1. Surface pH drops from the meristem/TZ boundary toward the zone of fast elongation (57). Low auxin concentrations stimulate and high auxin concentrations inhibit root growth, corresponding to apoplastic acidification and transient alkalinization, respectively (51), while ethylene causes growth inhibition concomitant with apoplastic alkalinization. Hence, through its control over auxin levels, ethylene restricts elongation growth. The symbols > and < indicate relatively higher and lower pH values compared with the adjacent zones.

Oyarce P, De Meester B, Fonseca F, de Vries L, Goeminne G, Pallidis A, De Rycke R, Tsuji Y, Li Y, Van den Bosch S, Sels B, Ralph J, Vanholme R, Boerjan W (2019) Introducing curcumin biosynthesis in Arabidopsis enhances lignocellulosic biomass processing. Nat Plants. 5(2):225-237. doi: 10.1038/s41477-018-0350-3. PMID: 30692678

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Vaseva II, Qudeimat E, Potuschak T, Du Y, Genschik P, Vandenbussche F, Van Der Straeten D (2018) The plant hormone ethylene restricts *Arabidopsis* growth via the epidermis. Proc Natl Acad Sci U S A. 24;115(17):E4130-E4139. doi: 10.1073/pnas.1717649115. PMID: 29643073

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Major Funding Sources

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

Brazil

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Use of Arabidopsis

In Brazil the number of institutions using Arabidopsis in their research is growing each year. At the moment, at least ten different institutions are using it as a model plant. Although research with Arabidopsis in Brazil range from developmental and hormone biology to abiotic and biotic stress, only a relatively small number of these labs is solely dedicated to Arabidopsis research or using Arabidopsis as the main model plant.

Hence, other species are usually employed, particularly crop species, given that dedicated grants programs are usually able to fund research projects in sugarcane, tomato, maize, rice, coffee, but virtually there is no such funding programs towards Arabidopsis.

It is important to mention that research in Brazil is only starting to use Arabidopsis and there is a gradual increase in the usage of Arabidopis as a model plant to molecular and genetic studies due to its power as an easily manipulated model system to test crop gene functions.

Conferences, Workshops and Outreach events

XXII International Congress of Genetics, Foz de Iguaçu, Rio Grande do Sul, Brazil. The Congress occured from September 10 to 14, 2018 and it had the overarching theme of "Genetics for a World in Evolution".

47th Annual Meeting of the Brazilian Society for Biochemistry and Molecular Biology (SBBq), Joinville, Santa Catarina, Brazil, May 26th to 29th, 2018
VI Simpósio Brasileiro de Genética Molecular de Plantas, Campos do Jordao, Sao Paulo Brazil, from April 29 to May 03, 2019.

XVII Brazilian Congress of Plant Physiology, which will be held in Cuiabá, Mato Grosso Brazil, from June 9 to 12, 2019.

65th Brazilian Congress of Genetics, Águas de Lindóia, SP, from September 17th to 20th. The central theme of this event will be "Edition of Genes and Genome"

Selected Publications

Antunes D, Jorge NAN, Garcia de Souza Costa M, Passetti F, Caffarena ER (2019) Unraveling RNA dynamical behavior of TPP riboswitches: a comparison between Escherichia coli and *Arabidopsis thaliana*. Sci Rep. 12;9(1):4197. doi: 10.1038/s41598-019-40875-1.

Calil IP, Quadros IPS, Araújo TC, Duarte CEM, Gouveia-Mageste BC, Silva JCF Brustolini OJB, Teixeira RM, Oliveira CN, Milagres RWMM, Martins GS, Chory J, Reis PAB, Machado JPB, Fontes EPB (2018) A WW domain-containing protein forms immune nuclear bodies against begomoviruses. Mol. Plant 11, 1449–1465. doi: 10.1016/j.molp.2018.09.009

Campos WF, Dressano K, Ceciliato PHO, Guerrero-Abad JC, Silva AL,Fiori CS, Morato do Canto A, Bergonci T, Claus LAN, Silva-Filho MC, Moura DS (2018) *Arabidopsis thaliana* rapid alkalinization factor 1-mediated root growth inhibition is dependent on calmodulin-like protein 38. J Biol Chem. 293(6):2159-2171. doi: 10.1074/jbc.M117.808881.

Cavalcanti JHF, Kirma M, Barros JAS, Quinhones CGS, Pereira-Lima ÍA, Obata T, Nunes-Nesi A, Galili G, Fernie AR, Avin-Wittenberg T, Araújo WL (2018) An L,L-diaminopimelate aminotransferase mutation leads to metabolic shifts and growth inhibition in Arabidopsis. J Exp Bot. 69(22):5489-5506. doi: 10.1093/jxb/ery325.

da Fonseca-Pereira P, Daloso DM, Gago J, de Oliveira Silva FM, Condori-Apfata JA, Florez-Sarasa I, Tohge T, Reichheld JP, Nunes-Nesi A, Fernie AR, Araújo WL (2019) The Mitochondrial Thioredoxin System Contributes to the Metabolic Responses Under Drought Episodes in Arabidopsis. Plant Cell Physiol. 60(1):213-229. doi: 10.1093/pcp/pcy194.

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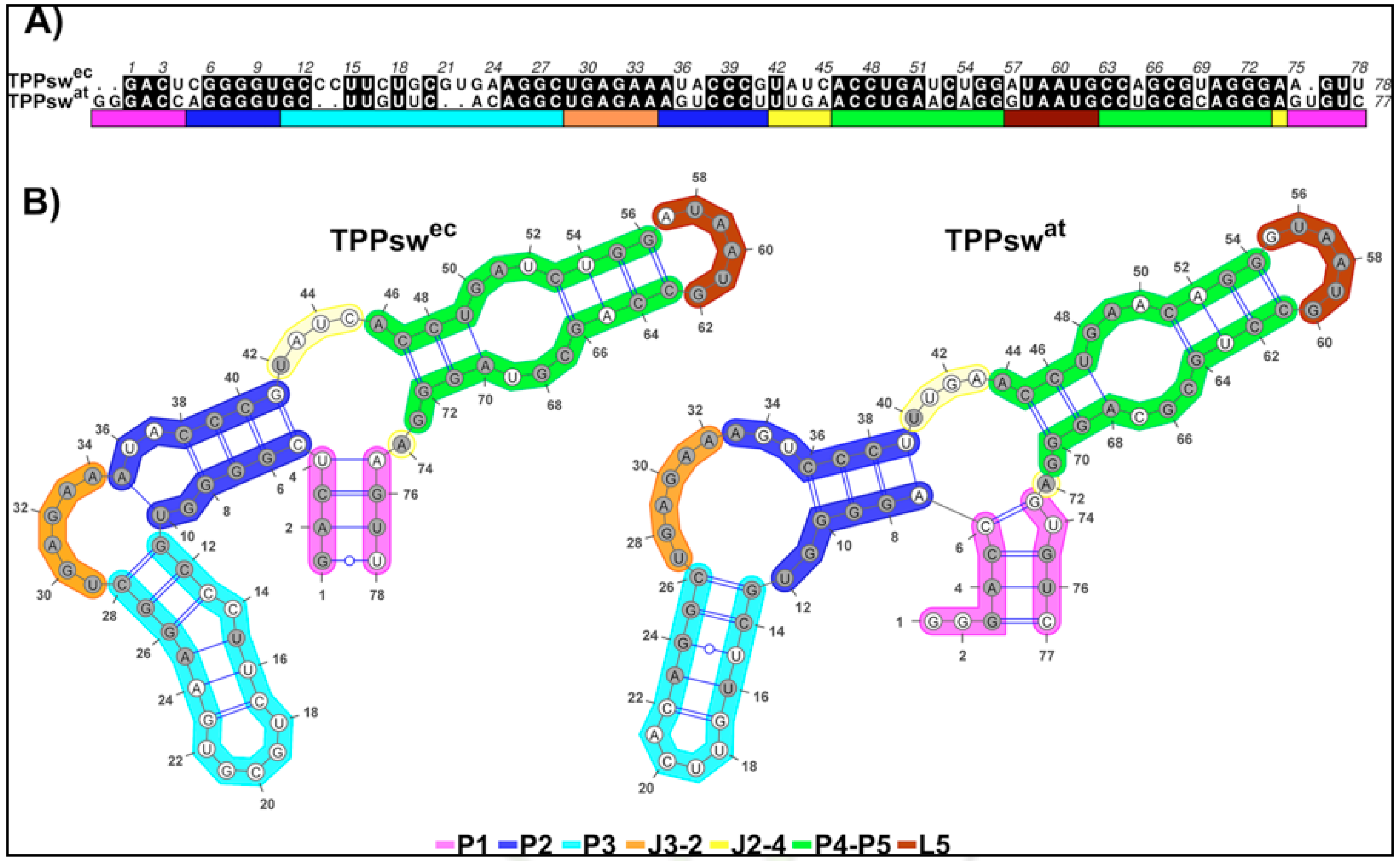

Figure 19. Sequence alignment and secondary structures of TPPswec and TPPswat. (A) Sequence alignment between TPPswec and TPPswat. Black filled positions of the alignment represent conserved residues. (B) Secondary structure of TPPswec and TPPswat. Conserved nucleotides were colored in grey. Stems, loops, and junctions were identified according to the figure legend caption.

Pereira WEL, Ferreira CB, Caserta R, Melotto M, de Souza AA (2019) *Xylella fastidiosa subsp. pauca and fastidiosa* Colonize Arabidopsis Systemically and Induce Anthocyanin Accumulation in Infected Leaves. Phytopathology.109(2):225-232. doi: 10.1094/PHYTO-05-18-0155-FI.

Silva, G. F., Silva, E. M., Correa, J. P., Vicente, M. H., Jiang, N. , Notini, M. M., Junior, A. C., De Jesus, F. A., Castilho, P. , Carrera, E. , López-Díaz, I. , Grotewold, E. , Peres, L. E. and Nogueira, F. T. (2019), Tomato floral induction and flower development are orchestrated by the interplay between gibberellin and two unrelated microRNA controlled modules. New Phytol, 221: 1328-1344. doi:10.1111/nph.15492

Thiers KLL, da Silva JHM, Sartori GR, Dos Santos CP, Saraiva KDDC, Roque ALM, Arnholdt-Schmitt B, Costa JH (2019) Polymorphisms in plastoquinol oxidase (PTOX) from Arabidopsis accessions indicate SNP-induced structural variants associated with altitude and rainfall. J Bioenerg Biomembr. 51(2):151-164. doi: 10.1007/s10863-018-9784-6

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Major Funding Sources

- National Council for Scientific and Technological Development (CNPq-Brazil)
- Brazilian Federal Agency for Support and Evaluation of Graduate Education (CAPES-Brazil)
- Foundation for Research Assistance of the Sao Paulo (FAPESP-Brazil)
- Foundation for Research Assistance of the Rio de Janeiro State (FAPERJ-Brazil)
- Foundation for Research Assistance of the Rio Grande do Sul State (FAPERGS-Brazil)
- Foundation for Research Assistance of the Minas Gerais State (FAPEMIG-Brazil)

Although funding in Brazil is available through several calls, it is becoming increasingly difficult to obtain funding for basic research, particularly to finance Arabidopsis research, given that the general trend is a more supportive program for applied research.

Canada

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Use of Arabidopsis

Approximately 55 groups conduct varied research with Arabidopsis in Canada.

Unfortunately, the U.S. National Science Foundation did not provide renewed funding for Araport.org, leaving its future uncertain. At a meeting Maryland in March 2019, curators and informaticians from several resources, including TAIR and the BAR met to decide a path forward.

It was decided that the Thalemine functionality of Araport.org would move to the BAR, while its JBrowse instance would be moved to TAIR – stay tuned for an update to this seemingly never-ending saga.

The BAR (Bio-Analytic Resource) received new funding from Genome Canada to expand the popular ePlant tool to incorporate ecosystem-level data.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

A new Arabidopsis Interactions Viewer (AIV2) was released by the Provart Lab (Dong et al., 2019). The authors also predicted almost 10,000 protein-protein interactions (PPIs) using a docking algorithm, and have worked with BioGRID to incorporate 42,605 experimentally-determined PPIs into the new interface, along with 2.8M protein-DNA interactions.
The new AIV2 is available at:
http://bar.utoronto.ca/interactions2.

Youssef Belhkadir's group at GMI in Austria together with a number of colleagues published a leucine-rich repeat receptor kinase cell surface interaction network (CSILRR) of 567 interactions between the extracellular domains of 225 LRR-RKs (Smakowska-Luzan et al., 2018). These data are available in the AIV2 mentioned earlier.

Conferences, Workshops and Outreach events

The BAR participated in the 2017 American Society of Plant Biology (ASPB) Plant Biology conference in Hawaii, as part of the Plant AgData Outreach booth; and Plant and Animal Genomes (PAG) XXVI at the start of 2018 in San Diego, California. It also gave a talk in the Arabidopsis Informatics workshop at ICAR2017 in St. Louis, Missouri.

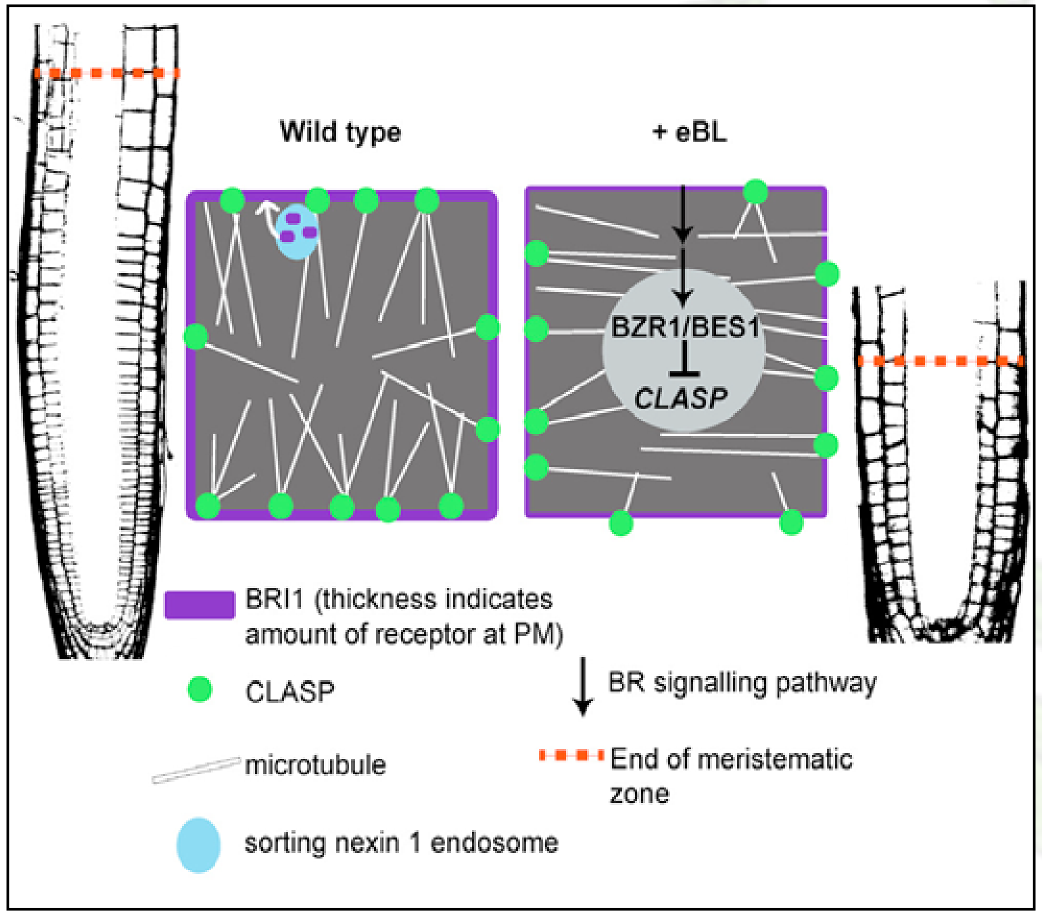

Figure 20. Taken from Ruan Y et al, Current Biology 8(17):2718-2729.e5

Selected Publications

Ahmed MB, Santos KCGD, Sanchez IB, Petre B, Lorrain C, Plourde MB, Duplessis S, Desgagné-Penix I, Germain H (2018) A rust fungal effector binds plant DNA and modulates transcription. Sci Rep. 8(1):14718.

Cabanillas DG, Jiang J, Movahed N, Germain H, Yamaji Y, Zheng H, Laliberté JF (2018) Turnip Mosaic Virus Uses the SNARE Protein VTI11 in an Unconventional Route for Replication Vesicle Trafficking. Plant Cell. 30(10):2594-2615.

Connell MB, Lee MJY, Li J, Plaxton WC, Jia Z (2018) Structural and biochemical characterization of citrate binding to AtPPC3, a plant-type phosphoenolpyruvatecarboxylase from *Arabidopsis thaliana*. J Struct Biol. 204(3):507-512.

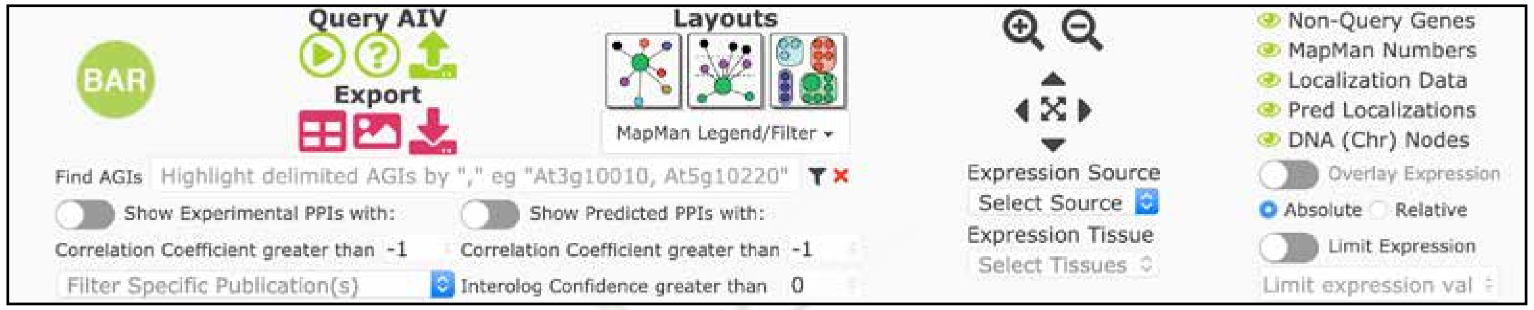

Figure 21. Interface of the Arabidopsis Interactions Viewer (AIV2): http://bar.utoronto.ca/interactions2

Ding Y, Sun T, Ao K, Peng Y, Zhang Y, Li X, Zhang Y (2018) Opposite Roles of Salicylic Acid Receptors NPR1 and NPR3/NPR4 in Transcriptional Regulation of Plant Immunity. Cell. 173(6):1454-1467.e15.

Dong OX, Ao K, Xu F, Johnson KCM, Wu Y, Li L, Xia S, Liu Y, Huang Y, Rodriguez E, Chen X, Chen S, Zhang Y, Petersen M, Li X (2018) Individual components of paired typical NLR immune receptors are regulated by distinct E3 ligases. Nat Plants. 4(9):699-710

Labandera AM, Uhrig RG, Colville K, Moorhead GB, Ng KKS (2018) Structural basis for the preference of the *Arabidopsis thaliana* phosphatase RLPH2 for tyrosine-phosphorylated substrates. Sci Signal. 11(524).

Ruan Y, Halat LS, Khan D, Jancowski S, Ambrose C, Belmonte MF, Wasteneys GO (2018) The Microtubule-Associated Protein CLASP Sustains Cell Proliferation through a Brassinosteroid Signaling Negative Feedback Loop. Curr Biol. 28(17):2718-2729.e5.

Smakowska-Luzan E, Mott GA, Parys K, Stegmann M, Howton TC, Layeghifard M, Neuhold J, Lehner A, Kong J, Grünwald K, Weinberger N, Satbhai SB, Mayer D, Busch W, Madalinski M, Stolt-Bergner P, Provart NJ, Mukhtar MS, Zipfel C, Desveaux D, Guttman DS, Belkhadir Y (2018) An extracellular network of *Arabidopsis* leucine-rich repeat receptor kinases. Nature. 553(7688):342-346.

Thulasi Devendrakumar K, Li X, Zhang Y (2018) MAP kinase signalling: interplays between plant PAMP- and effector-triggered immunity. Cell Mol Life Sci. 75(16):2981-2989.

Wang L, Wen R, Wang J, Xiang D, Wang Q, Zang Y, Wang Z, Huang S, Li X, Datla R, Fobert PR, Wang H, Wei Y, Xiao W (2019) *Arabidopsis* UBC13 differentially regulates two programmed cell death pathways in responses to pathogen and low-temperature stress. New Phytol. 221(2):919-934.

Major Funding Sources

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

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

Chile

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Universidad Andres Bello, Chile.

Use of Arabidopsis

1. Centro de Biotecnologia Vegetal- UNAB (http://cbv.unab.cl/)
2. Centro de Biotecnologia Vegetal- Universidad de Chile
3. Centro de Ciencia y Biotecnología Vegetal PUC – (http://agronomia.uc.cl/centros-unidades-y-laboratorios/cecibuc). P. Universidad Católica de Chile. Santiago, Chile
4. Millennium Nucleus in Plant Systems and Synthetic Biology (http://www.genomicavegetal.cl/). P. Universidad Católica de Chile. Santiago, Chile
5. Department of Molecular Genetics and Microbiology. P. Universidad Católica de Chile. Santiago, Chile
6. Laboratorio de Bioingeniería, Facultad de Ingeniería y Ciencias, Universidad Adolfo Ibáñez, Santiago, Chile Center for Applied Ecology and Sustainability, Santiago, Chile
7. Instituto de Ciencias Biológicas. Universidad de Talca (http://biologia.utalca.cl/index.html)
8. Instituto de Bioquímica y Microbiología. Universidad Austral de Chile. Valdivia, Chile
9. Centro de Genómica y Bioinformática, Facultad de Ciencias, Universidad Mayor. Santiago, Chile.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

Contreras-López O, Moyano TC, Soto DC, Gutiérrez RA (2018) Step-by-Step Construction of Gene Co-expression Networks from High-Throughput Arabidopsis RNA Sequencing Data. Methods Mol Biol. 1761:275-301. doi: 10.1007/978-1-4939-7747-5_21.

The authors provide step-by-step instructions using published RNA-seq experimental data obtained from a public database. This guide includes basic instructions for the operation of widely used open source platforms such as Bio-Linux, R, and Cytoscape. Even though the data we used in this example was obtained from *Arabidopsis thaliana*, the workflow developed in this guide can be easily adapted to work with RNA-seq data from any organism.

Conferences, Workshops and Outreach events

January 9th - 18th, 2018
COURSE: "GENETICAL IMPROVEMENT IN PSEUDOCEREALS AND THE SOCIO-CULTURAL IMPLICANCES."
This course was held at Universidad de Chile, Santiago - Chile.
The Ph.D. program "Ciencias Silvoagropecuarias y Veterinarias" offered the course entitled "Genetical improvement in Pseudocereals and the socio-cultural implications" to students.
Organizer: Escuela de Postgrado, Facultad de Ciencias Agronomicas, Universidad de Chile.

July 23th - 24th, 2018
2ND SCIENTIFIC MEETING ON VEGETAL BIOLOGY AND BIOTECHNOLOGY
The meeting was held in Salón Bicentenario de la U. de Talca, Campus Lircay, Talca – Chile.
The meeting was organized including three thematical areas: Biotic and abiotic stress, phytogenetics resources, and molecular and functional ecology.
Organizer: Ph.D. program on Sciences, mention plant genetics on Instituto de Ciencias Biológicas of Universidad de Talca – Chile.

August 21th, 2018.
SEMINAR WAYNE PARROTT. PLANT BREEDING AND CRISPR
Seminar presented by Wayne Parrot Ph.D., an international expert on the research of new techniques of genetical improvement of agronomical species from the University of Georgia.
Organizer: American Academy of Science and Technology, UCDavis Chile, Universidad Andrés Bello and Universidad de Talca.

October 2nd – 3rd, 2018
WORKSHOP ON PLANT CELL WALL
This workshop was held at Plant Biotechnology Center at Universidad Andres Bello, Santiago – Chile.
Organizers: Plant Biotechnology Center, Universidad Andrés Bello and Chilean Society of Plant Biologists.

November 29th, 2018
WORKSHOP "APPLIED PLANT BIOLOGY III"
This workshop was held at Auditorio Instituto de Ciencias Biológicas, Talca – Chile.
Organized by The Functional Genomics, Biochemistry & plant physiology group, ICB – Universidad de Talca.
Guests:
Dr. Jorge Paiva
Dr. Hannetz Roschttardtz
Dr. Ross Atkinson

December 3rd – 6th, 2018
XIII CHILEAN PLANT BIOLOGY MEETING
The last meeting was held at Enjoy Hotel in Puerto Varas – Chile. It included several symposiums for instance Plant Biotic Interactions, Natural Variation & Plant Breeding, Ecophysiology and Plant-Water Relationship, Iron Homeostasis and Plant Nutrition, Plant Biotechnology for Agriculture Development, Postharvest. Nearly 250 abstracts were submitted, including works from national and international research centers, presented by undergrad and graduated students, young scientist, and faculty from the major plant research centers in the country.
Organizer: Chilean Society of Plant Biologists

January 14th - 20th, 2019
INTERNATIONAL GRADUATE COURSE ON ECOPHYSIOLOGY OF THE RHIZOSPHERE
This workshop was held at Parque Katalapi, Región de Los Lagos, Chile
Main topics of the course: Soil properties, Plant nutrition, Rhizosphere components, Mycorrhizae diversity, Nitrogen fixation, Salt tolerance, Cluster roots functioning, Rhizodeposition, organic matter and soil microorganisms, Plant growth promoting rhizobacteria (PGPR), Endophyte, Phytoremediation, Molecular plant microbe-interaction.
Organizers: Luisa Bascuñán, Universidad de Concepción; Alex Valentine, Stellenbosch University; Alejandra Zúñiga Feest, Universidad Austral de Chile.

January 9th, 2019
SEMINAR: ORANGE ON TOP: IS THERE MUTUAL EXCLUSION BETWEEN ANTHOCYANIN AND CAROTENOIDS BIOSYNTHESIS IN PETUNIA FLOWERS?
This seminar was held at Facultad de Ciencias of Universidad de Chile (Santiago – Chile)
Organizers: Universidad de Chile – Santiago, Chile.
Guest:
Dr. Julian Verdonk, Wageningen University. The Netherlands

Selected Publications

Arraño-Salinas P, Domínguez-Figueroa J, Herrera-Vásquez A, Zavala D, Medina J, Vicente-Carbajosa J, Meneses C, Canessa P, Moreno AA, Blanco-Herrera F (2018) WRKY7, -11 and -17 transcription factors are modulators of the bZIP28 branch of the unfolded protein response during PAMP-triggered immunity in *Arabidopsis thaliana*. Plant Sci. 277:242-250. doi: 10.1016/j.plantsci.2018.09.019.

Duran C, Arce-Johnson P, Aquea F (2018) Methylboronic acid fertilization alleviates boron deficiency symptoms in *Arabidopsis thaliana*. Planta. 248(1):221-229. doi: 10.1007/s00425-018-2903-0.

Fredes I, Moreno S, Díaz FP, Gutiérrez RA (2018) Nitrate signaling and the control of *Arabidopsis* growth and development. Curr Opin Plant Biol.47:112-118. doi: 10.1016/j.pbi.2018.10.004. Review.

Gras DE, Vidal EA, Undurraga SF, Riveras E, Moreno S, Dominguez-Figueroa J, Alabadi D, Blázquez MA, Medina J, Gutiérrez RA (2018) SMZ/SNZ and gibberellin signaling are required for nitrate-elicited delay of flowering time in *Arabidopsis thaliana*. J Exp Bot. 23;69(3):619-631. doi: 10.1093/jxb/erx423.

Henríquez-Valencia C, Arenas-M A, Medina J, Canales J (2018) Integrative Transcriptomic Analysis Uncovers Novel Gene Modules That Underlie the Sulfate Response in *Arabidopsis thaliana*. Front Plant Sci. 2018 Apr 10;9:470. doi: 10.3389/fpls.2018.00470.

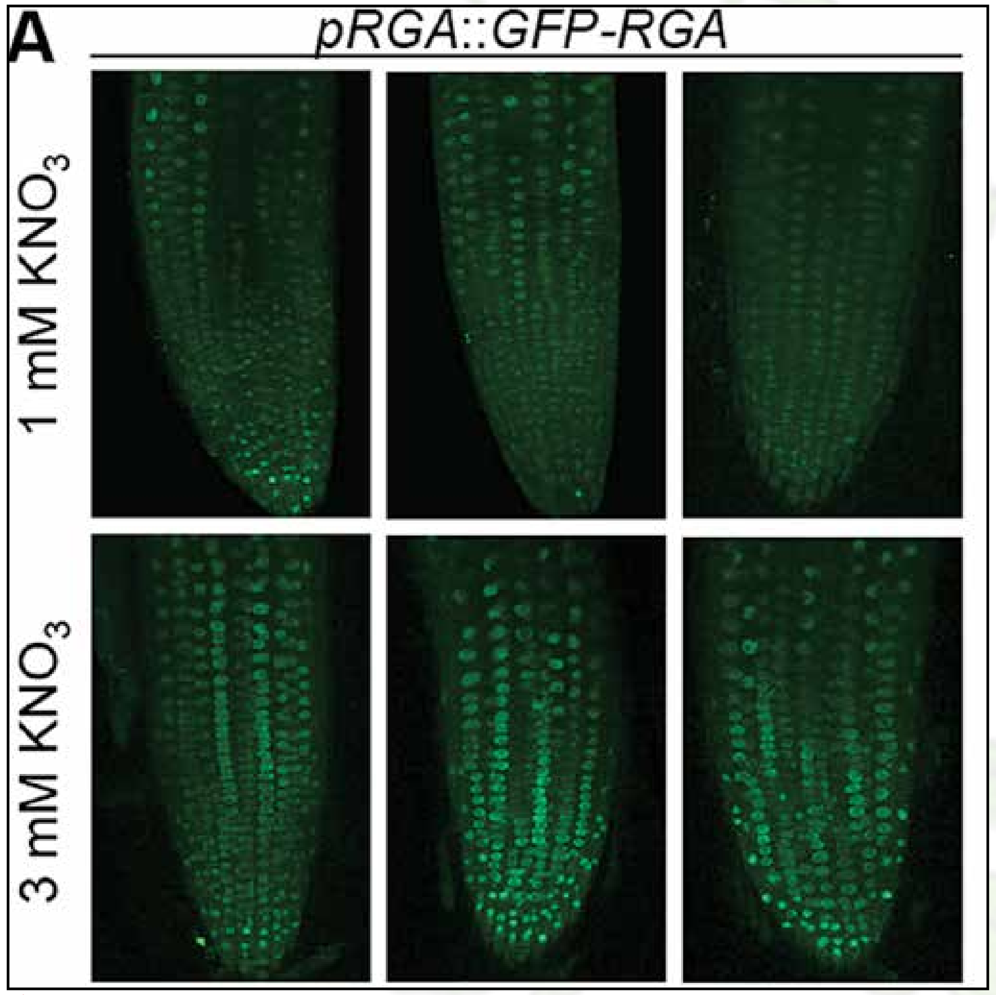


Figure 22. High nitrate availability promotes the accumulation of DELLA proteins and the induction of the downstream targets GNC and CGA1/GNL, triggering the up-regulation of SMZ and SNZ transcript levels. Representative confocal images showing roots of 7-d-old Arabidopsis RGA::GFP-RGA seedlings grown on agar plates in N-free nutrient medium supplemented with either 1 mM or 3 mM KNO3 (A)

Ibeas MA, Grant-Grant S, Coronas MF, Vargas-Pérez JI, Navarro N, Abreu I, Castillo-Michel H, Avalos-Cembrano N, Paez Valencia J, Perez F, González-Guerrero M, Roschzttardtz H (2019) The Diverse Iron Distribution in Eudicotyledoneae Seeds: From Arabidopsis to Quinoa. Front Plant Sci. 2019 Jan 15;9:1985. doi: 10.3389/fpls.2018.01985.

Salinas-Grenet H, Herrera-Vásquez A, Parra S, Cortez A, Gutiérrez L, Pollmann S, León G, Blanco-Herrera F (2018) Modulation of Auxin Levels in Pollen Grains Affects Stamen Development and Anther Dehiscence in Arabidopsis. Int J Mol Sci. 19(9). pii: E2480. doi: 10.3390/ijms19092480.

Rodriguez-Furlán C, Rubilar-Hernández C, Norambuena L (2018) Chemical Genomics Translatability from Unicellular to Multicellular Models.
Methods Mol Biol. 1795:189-201. doi: 10.1007/978-1-4939-7874-8_16.

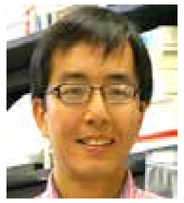
Romero-Romero JL, Inostroza-Blancheteau C, Orellana D, Aquea F, Reyes-Díaz M, Gil PM, Matte JP, Arce-Johnson P (2018) Stomata regulation by tissue-specific expression of the Citrus sinensis MYB61 transcription factor improves water-use efficiency in Arabidopsis. Plant Physiol Biochem. 130:54-60. doi: 10.1016/j.plaphy.2018.06.034.

Zúñiga A, Fuente F, Federici F, Lionne C, Bônnet J, de Lorenzo V, González B (2018) An Engineered Device for Indoleacetic Acid Production under Quorum Sensing Signals Enables Cupriavidus pinatubonensis JMP134 To Stimulate Plant Growth. ACS Synth Biol. 15;7(6):1519-1527. doi: 10.1021/acssynbio.8b00002.

Major Funding Sources

Fondecyt- Fondo Nacional de Desarrollo Científico y Tecnológico **(http://www.conicyt.cl/fondecyt/)**
FONDAP- Fondo de Financiamiento de Centros de Investigación en Áreas Prioritarias
(http://www.conicyt.cl/fondap/)
PIA- Programa de Investigación Asociativa
(http://www.conicyt.cl/pia/)
Iniciativa Científica Milenio
(http://www.iniciativamilenio.cl/)
FONDEF (Fondo de Fomento al Desarrollo Científico y Tecnológico)
(http://www.conicyt.cl/fondef/)
CORFO- Corporación de Fomento de la Producción
(https://www.corfo.cl/sites/cpp/home)

China



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Use of Arabidopsis

There are a large number of Chinese research institutions that conduct Arabidopsis research. Because of the large size of the country, it is difficult to precisely estimate the exact number of research labs using Arabidopsis, although the number must be over 500. This can in part be reflected by the large number of Arabidopsis related posters and talks at each annual National Congress of Plant Biology.

Not surprisingly, research topics range from developmental and hormone biology to abiotic and biotic stress, and to evolution. Hence, Arabidopsis is the model plant of choice to many groups. However, only a small portion of these labs is solely dedicated to Arabidopsis research or using Arabidopsis as the main model plant, which may be very different from many other countries. A major reason behind would be the current funding priority.

Whereas there are dedicated grants to basic and applied research in maize, rice, wheat, and virtually each minor crop, there is no such funding programs towards Arabidopsis. As a result, Arabidopsis is often used as an easily manipulated model system to test crop gene functions.

Most Arabidopsis research occurs in research universities, Chinese Academy of Sciences (CAS) institutes, and Chinese Academy of Agricultural Sciences institutes. In addition, most provinces have one or more agricultural universities, where you can find at least some Arabidopsis research.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

Transcription factor library
A Gateway-compatible Gal4-AD-TF library of ~1600 Arabidopsis transcription factors, which can be easily screened by mating-based yeast-one-hybrid (Y1H) and yeast-two-hybrid (Y2H) methods, have been developed in Dr. Li-Jia Qu's group. The efficiency of the system has been validated by a number of large-scale Y1H and Y2H studies. This system will be available for other *Arabidopsis* researchers.

Shoot cell type-specific transcriptome profiling lines
A collection of Arabidopsis transgenic lines expressing His6-FLAG tagged RPL18 under the shoot apical meristem and leaf primordium cell type-specific promoter has been developed in Dr. Yuling Jiao's group. This set of cell type marker lines allows other researchers to perform in-house cell type-specific gene expression analysis without the need of specialized equipment. By contrast, previous analysis based on laser microdissection or fluorescence-activated cell sorting cannot be easily adopted by others. An eFP browser of the gene expression data in wild-type vegetative plants is available at http://jiaolab.genetics.ac.cn/sa.

New Software Tools

- Arabidopsis Root Cell Atlas
http://wanglab.sippe.ac.cn/rootatlas/

- AHD2.0: Arabidopsis hormone database 2.0
http://ahd.cbi.pku.edu.cn/

- PlantGSEA: a gene set enrichment analysis toolkit for plant community
http://structuralbiology.cau.edu.cn/PlantGSEA/

- PlantTFDB: Plant transcription factor database
http://planttfdb.cbi.pku.edu.cn/link.php

- PsRobot: Plant small RNA analysis toolbox
http://omicslab.genetics.ac.cn/psRobot/

- Shoot cell type-specific expression ebrowser
http://bar.utoronto.ca/efp_*Arabidopsis*/cgi-bin/efpWeb.cgi?dataSource=Shoot_Apex

Conferences, Workshops and Outreach events

Major conferences held in 2018
- 2nd International Conference on Plant Meristem Biology (Meristem 2018), June 9-10, 2018, Hefei, Anhui (www.meristem2018.com)
- 3rd Molecular Plant International Symposium: Plant-Environment Interactions, June 12-15, 2018, Xi'an, Shaanxi (http://www.mplant.org/2018symposium/)
- Agricultural Bioscience International Conference 2018 (ABIC 2018), September 15-18, 2018, Weifang, Shandong
- 2018 National Congress of Plant Biology, October 18-22, 2018 Tai'an, Shandong (http://www.ncpb.net/2018/)

Highlights on upcoming international events
- 30th International Conference on *Arabidopsis* Research (ICAR2019), June 16-21, 2019, Wuhan, Hubei
http://icar2019.*Arabidopsis*research.org/

- International Symposium on Plant Receptor Kinases and Cell Signaling, June 21-23, 2019, Beijing

- 21st International Conference on Nitrogen Fixation (ICNF 2019), October 10-15, 2019 Wuhan, Hubei

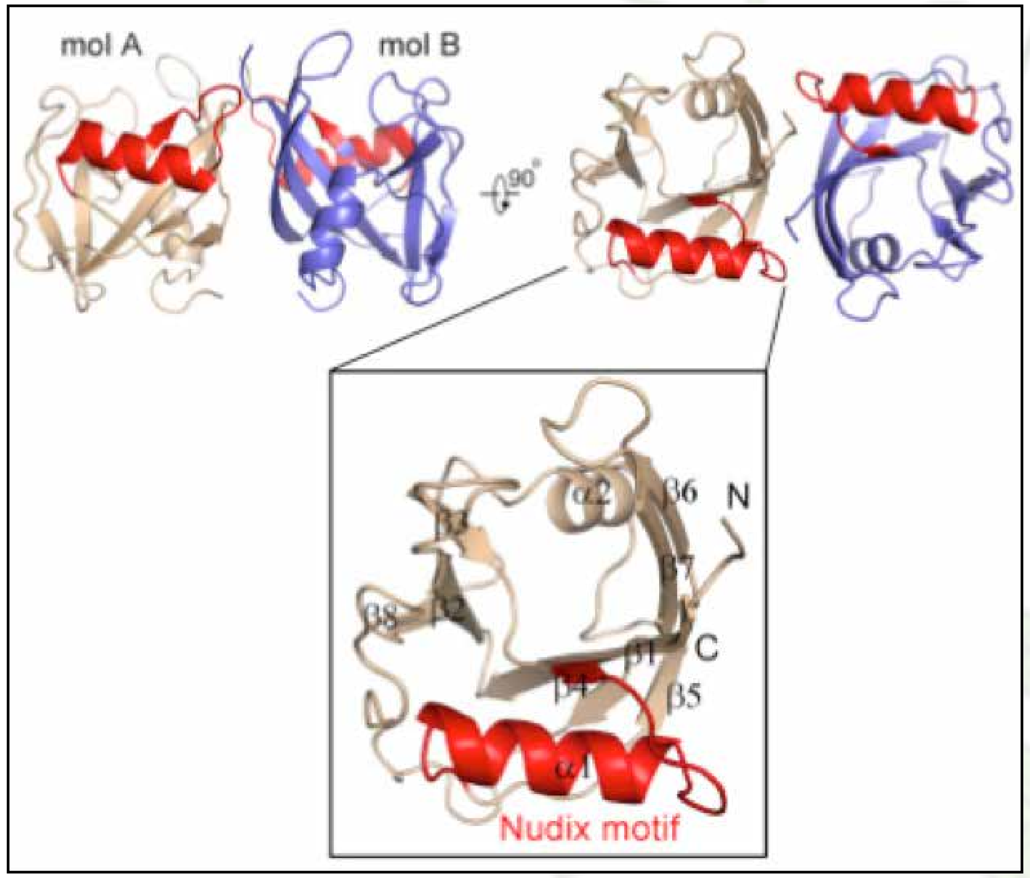

Figure 23. Dimeric structure of cytosolic hydrolase AtNUDX1, which is responsible for noncanonical monoterpene biosynthesis. Molecule A is in brown, molecule B is in blue, and the Nudix motif is highlighted in red. Figure from Liu *et al.*, 2018 Mol. Plant 11(1): 218-221. https://doi.org/10.1016/j.molp.2017.10.006

Selected Publications

Ding Y, Jia Y, Shi Y, Zhang X, Song C, Gong Z, Yang S. (2018) OST1-mediated BTF3L phosphorylation positively regulates CBFs during plant cold responses. EMBO J. 37(8): e98228.

Liu J, Guan Z, Liu H, Qi L, Zhang D, Zou T, Yin P (2018) Structural Insights into the Substrate Recognition Mechanism of *Arabidopsis* GPP-Bound NUDX1 for Noncanonical Monoterpene Biosynthesis. Mol Plant. 11(1):218-221. doi: 10.1016/j.molp.2017.10.006

Liang T, Mei S, Shi C, Yang Y, Peng Y, Ma L, Wang F, Li X, Huang X, Yin Y, Liu H. (2018) UVR8 interacts with BES1 and BIM1 to regulate transcription and photomorphogenesis in Arabidopsis. Dev. Cell 44(4): 512-523.

Peng Y, Chen L, Li S, Zhang Y, Xu R, Liu Z, Liu W, Kong J, Huang X, Wang Y, Cheng B, Zheng L, Li Y. (2018) BRI1 and BAK1 interact with G proteins and regulate sugar-responsive growth and development in Arabidopsis. Nat. Commun. 9(1):1522.

Shi B, Guo X, Wang Y, Xiong Y, Wang J, Hayashi KI, Lei J, Zhang L, Jiao Y. (2018) Feedback from lateral organs controls shoot apical meristem growth by modulating auxin transport. Dev Cell 44(2): 204-216.

Wang G, Wang C, Liu W, Ma Y, Dong L, Tian J, Yu Y, Kong Z. (2018) Augmin antagonizes katanin at microtubule crossovers to control the dynamic organization of plant cortical arrays. Curr. Biol. 28(8): 1311-1317.

Wang J, Grubb LE, Wang J, Liang X, Li L, Gao C, Ma M, Feng F, Li M, Li L, Zhang X, Yu F, Xie Q, Chen S, Zipfel C, Monaghan J, Zhou J-M. (2018) A regulatory module controlling homeostasis of a plant immune kinase. Mol. Cell 69(3): 493-504.

Xing L, Liu Y, Xu S, Xiao J, Wang B, Deng H, Lu Z, Xu Y, Chong K. (2018) Arabidopsis O-GlcNAc transferase SEC activates histone methyltransferase ATX1 to regulate flowering. EMBO J. 37(19): e98115

Yang L, Wang H-N, Hou X-H, Zou Y-P, Han T-S, Niu X-M, Zhang J, Zhao Z, Todesco M, Balasubramanian S, Guo Y-L. (2018) Parallel evolution of common allelic variants confers flowering diversity in Capsella rubella. Plant Cell 30(6): 1322-1336.

Yang Y, Liang T, Zhang L, Shao K, Gu X, Shang R, Shi N, Li X, Zhang P, Liu H. (2018) UVR8 interacts with WRKY36 to regulate HY5 transcription and hypocotyl elongation in Arabidopsis. Nat. Plants 4(2): 98-107.

Zhang TQ, Xu ZG, Shang GD, Wang JW (2019) A Single-Cell RNA Sequencing Profiles the Developmental Landscape of Arabidopsis Root. Mol Plant. pii: S1674-2052(19)30133-9. doi: 10.1016/j.molp.2019.04.004

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, Department of Exp. Plant Biol. and Inst. of Exp. Bot. Acad. Sci. of the Czech Rep. Prague

Use of Arabidopsis

There are 10 institutions (five universities, two centers and three institutes of the Academy of Sciences of the Czech Rep.) and about 30 labs within these institutions using Arabidopsis as a model plant for the research.

Conferences, Workshops and Outreach events

- 43rd FEBS Congress 7.-12. July, 2018 Prague, Czech Republic
- ACPD2018 - "Auxins and Cytokinins in Plant Development", July 1–5, 2018, Prague
- Plant Biology CS 2019, University of South Bohemia and Biology Centre CAS, Ceske Budejovice, Czech Republic 25th-30th 2019 www.plantbiologycs.cz

Selected Publications

Aleš Pencík, Rubén Casanova-Sáez, Veronika Pilarová, Asta Žukauskaite, Rui Pinto, José Luis Micol, Karin Ljung, Ondrej Novák (2018) Ultra-rapid auxin metabolite profiling for high-throughput mutant screening in Arabidopsis, Journal of Experimental Botany,69: 2569–2579, https://doi.org/10.1093/jxb/ery084

Ferretti, U., Ciura, J. , Ksas, B. , Rác, M. , Sedlárová, M. , Kruk, J. , Havaux, M. and Pospíšil, P. (2018), Chemical quenching of singlet oxygen by plastoquinols and their oxidation products in Arabidopsis. Plant J, 95: 848-861. doi:10.1111/tpj.13993

Ivan Kulich, Zdenka Vojtíková, Peter Sabol, Jitka Ortmannová, Vilém Nedela, Eva Tihlaríková, Viktor Žárský (2018) Exocyst Subunit EXO70H4 Has a Specific Role in Callose Synthase Secretion and Silica Accumulation. Plant Physiology 176 (3) 2040-2051; DOI: 10.1104/pp.17.01693

Janecková, H, Husicková, A, Ferretti, U, et al (2018) The interplay between cytokinins and light during senescence in detached Arabidopsis leaves. Plant Cell Environ. 41: 1870– 1885. https://doi.org/10.1111/pce.13329

Ilík, P., Špundová, M. , Šicner, M. , Melkovicová, H. , Kucerová, Z. , Krchnák, P. , Fürst, T. , Vecerová, K. , Panzarová, K. , Benediktyová, Z. and Trtílek, M. (2018), Estimating heat tolerance of plants by ion leakage: a new method based on gradual heating. New Phytol, 218: 1278-1287. doi:10.1111/nph.15097

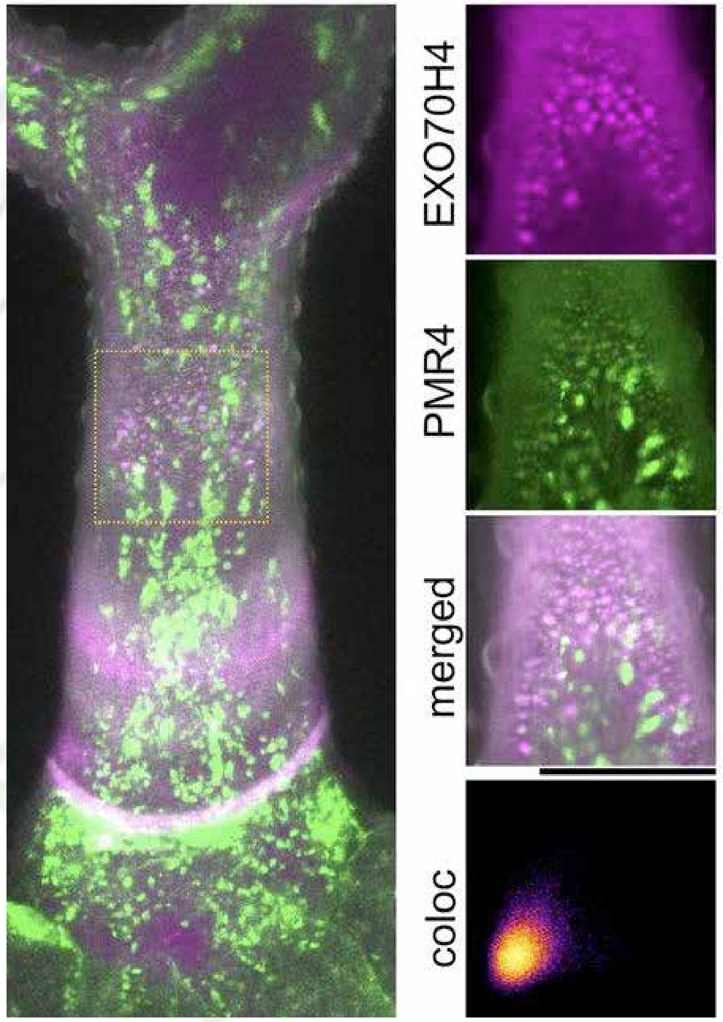

Figure 24. EXO70H4 recruits PMR4 to the ingrowths of the trichome cell wall. A, Left, Overall view of the trichome expressing mCH-EXO70H4 (magenta) and GFP-PMR4 (green). Projection of 14 sections. Yellow dotted square depicts detailed view on the right. Right, Detailed view of a single section with cell wall ingrowths decorated by EXO70H4 and PMR4 with a 2D histogram for the colocalization (Pearson's R value, 0.35; Li's ICQ value, 0,127).

Miroslav Ovecka, Daniel von Wangenheim, Pavel Tomancák, Olga Šamajová, George Komis & Jozef Šamaj (2018) Multiscale imaging of plant development by light-sheet fluorescence microscopy. Nature Plants, vol. 4, pages639–650

Major Funding Sources

1. Czech Science Foundation/GACR, Prague
http://www.gacr.cz
2. Ministry of Education, Youth and Sports of Czech Republic, Prague
http://www.msmt.cz/research-and-development-1
3. Technology Agency of the Czech Republic
http://www.tacr.cz/english/
4.Ministry of Agriculture, National Agency for Agricultural
https://goo.gl/JPGv1O

Denmark

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Use of Arabidopsis

Arabidopsis research in Denmark primarily takes place at University of Copenhagen. Arabidopsis research is also carried out at University of Aarhus. Copenhagen Plant Science Centre (CPSC) at the Department of Plant and Environmental Sciences, University of Copenhagen, includes up-to-date facilities for Arabidopsis research.

Conferences, Workshops and Outreach events

The biannual Plant Biology Europe conference, the biggest of its kind in Europe and jointly organized by Federation of European Societies of Plant Biology (FESPB) and European Plant Science Organization (EPSO), took place June 18-21, 2018, in Copenhagen, Denmark.

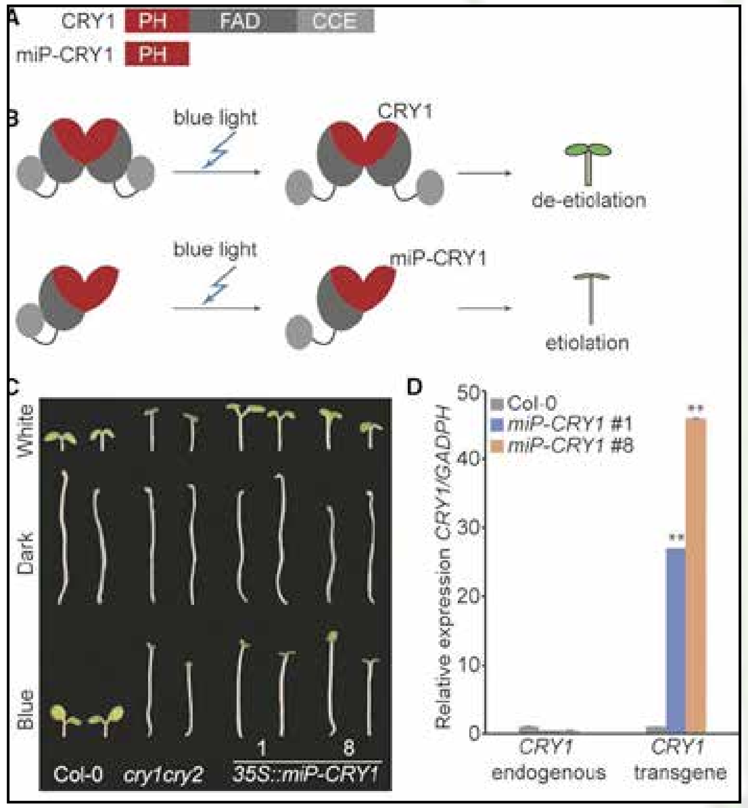


Figure 25. Inhibition of CRY1 by the synthetic microProtein miP-CRY1. A, Domain structures of CRY1 and miP-CRY1. B, Model depicting CRY1 function and miP-CRY1 inhibition. The CRY1 homodimer is activated by a blue light signal. Activated CRY1 regulates de-etiolation of the plant. MiP-CRY1 forms a nonfunctional heterodimer with CRY1 that leads to hypocotyl elongation under blue light. C, Image of representative Col-0, cry1cry2, and two independent 35S::miP-CRY1 lines grown under white light, dark, or blue light conditions. D, RT-qPCR showing expression of endogenous CRY1 and transgene miP-CRY1 in 35S::miP-CRY1 lines compared with Col-0. Experimental replicates were statistically tested using a Student's t test (**P < 0.01).

Selected Publications

Barghetti A, Sjögren L, Floris M, Paredes EB, Wenkel S, Arribas-Hernández L, Bressendorff S, Hansen MH, Poulsen C, Erdmann S, Brodersen P (2018) An m6A-YTH module controls developmental timing and morphogenesis in Arabidopsis. Plant Cell 30: 952-967.

Dolde U, Rodrigues V, Straub D, Bhati KK, Choi S, Yang SW, Wenkel S (2018) Synthetic microProteins: Versatile tools for posttranslational regulation of target proteins. Plant Physiol. 176: 3136-3145.

Kindgren P, Ard R, Ivanov M, Marquardt S (2018) Transcriptional read-through of the long non-coding RNA SVALKA governs plant cold acclimation. Nat Commun. 9: 4561.

Schultz-Larsen T, Lenk A, Kalinowska K, Vestergaard LK, Pedersen C, Isono E, Thordal-Christensen H (2018) The AMSH3 ESCRT-III-associated deubiquitinase is essential for plant immunity. Cell Rep. 25: 2329-2338.e5.

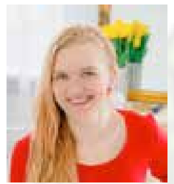
Stranne M, Ren Y, Fimognari L, Birdseye D, Yan J, Bardor M, Mollet JC, Komatsu T, Kikuchi J, Scheller HV, Sakuragi Y (2018) TBL10 is required for O-acetylation of pectic rhamnogalacturonan-I in *Arabidopsis thaliana*. Plant J. 96: 772-785.

van Wonterghem M, Thieffry A, Boyd M, Bornholdt J, Brodersen P (2018) A new class of genic nuclear RNA species in Arabidopsis. FEBS Lett. 592: 631-643.

Major Funding Sources

In Denmark it is becoming increasingly difficult to obtain funding for basic research on Arabidopsis as the general trend is shifting towards supporting applied research.

Estonia



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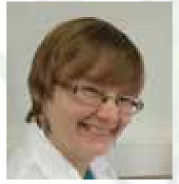

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Estonian University of Life Sciences

The research of Estonian Arabidopsis community is mainly focused on stomatal regulation in response to abiotic stressors, myosin functions in plant development and plant-pathogen interactions.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018/ early 2019.

Gas exchange analysis equipment, new improved and much faster version #3, which enables real-time gas exchange measurements such as stomatal conductance, transpiration, photosynthesis etc of single intact Arabidopsis plants in controlled and adjustable conditions. Air temperature, air composition (humidity, CO_2, O_3 etc) and light conditions can be manipulated throughout the experiment.

Selected Publications

Hannes Kollist, Sara I.Zandalinas, Soham Sengupta, Maris Nuhkat, Jaakko Kangasjärvi, Ron Mittler (2019). Rapid Responses to Abiotic Stress: Priming the Landscape for the Signal Transduction Network. Trends in Plant Science, 24 (1), 25–37.10.1016/j.tplants.2018.10.003.

Jalakas, Pirko; Tulva, Ingmar; Kangor, Tiia; Sooväli, Pille; Rasulov, Bakhtier; Tamm, Ülle; Koppel, Mati; Kollist, Hannes; Merilo, Ebe; (2018). Gas exchange-yield relationships of malting barley genotypes treated with fungicides and biostimulants. European Journal of Agronomy, 99, 129–137.10.1016/j.eja.2018.07.001.

Merilo, Ebe; Yarmolinsky, Dmitry; Jalakas, Pirko; Parik, Helen; Tulva, Ingmar; Rasulov, Bakhtier; Kilk, Kalle; Kollist, Hannes (2018). Stomatal VPD Response: There Is More to the Story Than ABA. Plant Physiology, 176 (1), 851–864.10.1104/pp.17.00912.

Ojangu, E.-L.; Ilau, B.; Tanner, K.; Talts, K.; Ihoma, E.; Dolja, V. V.; Paves, H.; Truve, E. (2018). Class XI Myosins Contribute to Auxin Response and Senescence-Induced Cell Death in Arabidopsis. Frontiers in Plant Science, 9.10.3389/fpls.2018.01570.

Tõldsepp, K; Zhang, J; Takahashi, Y; Sindarovska, Y; Hõrak, H; Ceciliato, PH. O.; Koolmeister, K; Wang, YS; Vaahtera, L; Jakobson, L; Yeh, CY; Park, J; Brosche, M; Kollist, H; Schroeder, JI. (2018). Mitogen-activated protein kinases MPK4 and MPK12 are key components mediating CO2-induced stomatal movements. The Plant Journal, 96 (5), 1018–1035.10.1111/tpj.14087.

Major Funding Sources

Estonian Research Council
www.etag.ee

Centre of Excellences funded by European Regional Development Fund, coordinated in Estonia by Archimedes Foundation. www.archimedes.ee

Figure 26. Gas exchange analysis for phenotyping *Arabidopsis* in a multi-cuvette system since 2006 (University of Tartu, prof Hannes Kollist). Photo by Kaspar Koolmeister.

Finland

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Use of Arabidopsis

Largest users of Arabidopsis in research: University of Helsinki, University of Turku, University of Oulu
The number of labs depends on definition and many plant labs even focusing on other plant species will use Arabidopsis as a tool.

Arabidopsis continues to be the primary model plant species in Finnish molecular plant science and also helps to drive research on other models and agronomically important species (for example trees). The majority of plant science using Arabidopsis as a model organism is combined in the Academy of Finland Centre of Excellence “Molecular Biology of Primary Producers” (2014-2019). This Centre of Excellence, led by Prof. Eva-Mari Aro (University of Turku, Finland) and Prof. Jaakko Kangasjärvi brings together the research areas of photosynthesis, plant development and responses to environmental stimuli. The Centre of Excellence will host a conference on this topic “Plants in a changing climate” in November 2019 in Helsinki, Finland.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

National Plant Phenotyping Infrastructure https://www.helsinki.fi/en/infrastructures/national-plant-phenotyping

PhenomatoR: An R Package for the Analysis of Large-Scale Phenomics Data https://github.com/jsalojar/PhenomatoR

Conferences, Workshops and Outreach events

- International Conference on Arabidopsis Research, Turku, Finland, June 25 to 29, 2018

- Plants in a Changing Climate “Integration of Photosynthesis, Adaptation and Development”, Helsinki Finland, November 6-8, 2019

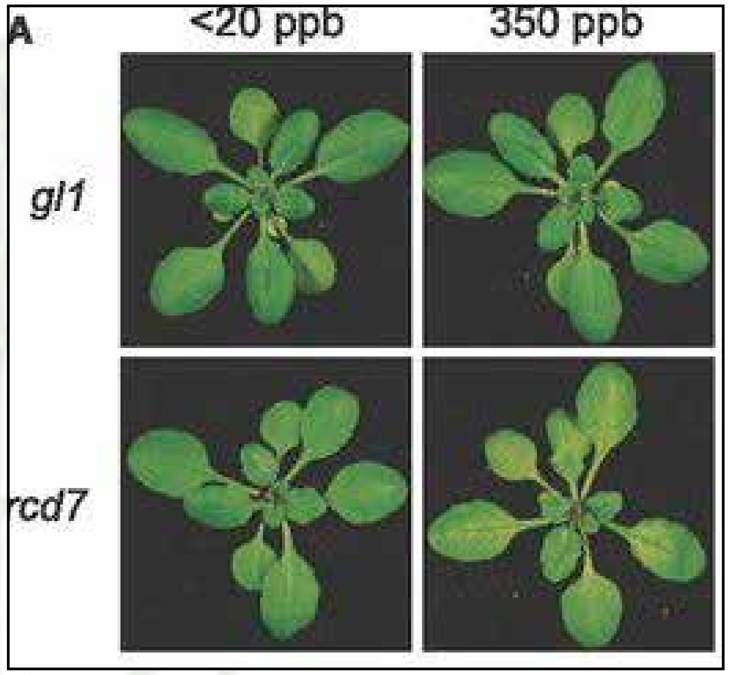

Figure 27. Phenotypes of the rcd7 Mutant and Candidate Insertion Mutants and Allelism Tests. (A) Representative photographs of 3-week-old O3-treated (350 ppb) and clean air (CA) control (<20 ppb) Col-0 gl1 and rcd7 plants taken 18 h after the end of a 6 h exposure to O3.

Selected Publications

Abou-Saleh RH, Hernandez-Gomez MC, Amsbury S, Paniaqua C, Bourdon M, Miyashima S, Helariutta Y, Fuller M, Budtova T, Connell SD, Ries ME, Benitez-Alfonso Y (2018) Interactions between callose and cellulose revealed through the analysis of biopolymer mixtures. Nature Communications 9(1):4538

Koskela MM, Brünje A, Ivanauskaite A, Grabsztunowicz M, Lassowskat I, Neumann U, Dinh TV, Sindlinger J, Schwarzer D, Wirtz M, Tyystjarvi E, Finkemeier I, Mulo P (2018) Chloroplast acetyltransferase NSI is required for state transitions in *Arabidopsis thaliana*. Plant Cell 30: 1695–1709

Nikkanen L, Toivola J, Trotta A, Guinea Diaz M, Tikkanen M, Aro EM, Rintamäki E. (2018) Regulation of cyclic electron flow by chloroplast NADPH-dependent thioredoxin system. Plant Direct 2(11):e00098

Sierla M, Hõrak H, Overmyer K, Waszczak C, Yarmolinsky D, Maierhofer T, Vainonen JP, Salojärvi J, Denessiouk K, Laanemets K, Tõldsepp K, Vahisalu T, Gauthier A, Puukko T, Paulin L, Auvinen P, Geiger D, Hedrich R, Kollist H, Kangasjärvi J (2018) The Receptor-like Pseudokinase GHR1 Is Required for Stomatal Closure. Plant Cell 30 (11):2813-2837

Shapiguzov A, Vainonen J, Hunter K, Tossavainen H, Tiwari A, Järvi S, Hellman M, Aarabi F, Alseekh S, Wybouw B, Van Der Kelen K, Nikkanen L, Krasensky-Wrzaczek J, Sipari N, Keinänen M, Tyystjärvi E, Rintamäki E, De Rybel B, Salojärvi J, Van Breusegem F, Fernie AR, Brosché M, Permi P, Aro EM, Wrzaczek M, Kangasjärvi J. 2019. Arabidopsis RCD1 coordinates chloroplast and mitochondrial functions through interaction with ANAC transcription factors. eLife 8: e43284

Smetana O, Mäkilä R, Lyu M, Amiryousefi A, Sánchez Rodríguez F, Wu MF, Solé-Gil A, Leal Gavarrón M, Siligato R, Miyashima S, Roszak P, Blomster T, Reed JW, Broholm S, Mähönen AP (2019) High levels of auxin signalling define the stem-cell organizer of the vascular cambium. Nature 565: 485–489.

Vaattovaara A, Brandt B, Sitaram R, Safronov O, Veidenberg A, Luklová M, Kangasjärvi J, Löytynoja A, Hothorn M, Salojärvi J, Wrzaczek M. 2019. Mechanistic insights into the evolution of DUF26-containing proteins in land plants. Communications Biology 2: 56.

Wirthmueller L, Asai S, Rallapalli G, Sklenar J, Fabro G, Kim DS, Lintermann R, Jaspers P, Wrzaczek M, Kangasjärvi J, MacLean D, Menke FLH, Banfield MJ, Jones JDG (2018) Arabidopsis downy mildew effector HaRxL106 suppresses plant immunity by binding to RADICAL-INDUCED CELL DEATH1. New Phytologist 220(1):232-248

Major Funding Sources

The major funding source for plant research in Finland is the Academy of Finland (http://www.aka.fi).
Additional funding sources are the Finnish Cultural Foundation (http://www.skr.fi) and Kone Foundation (https://koneensaatio.fi/en/).
TEKES funds applied and translational research (https://www.businessfinland.fi/en/).

France

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Institut Jean-Pierre Bourgin (INRA-AgroParisTech-CNRS), Université Paris-Saclay.

Use of Arabidopsis

- About twenty research institutes

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

- *Arabidopsis* stock center
http://publiclines.versailles.inra.fr

Plant Genomic Center
https://cnrgv.toulouse.inra.fr/Library/*Arabidopsis*

- IPS2: FlagDB++ v6.3 : Integrative database around plant genomes
http://tools.ips2.u-psud.fr/projects/FLAGdb++/HTML/index.shtml

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

-LPCV, Grenoble:
ChloroKb: decoding the chloroplast, http://big.cea.fr/drf/big/english/Pages/News/Scientific-results/L56_GCurien.aspx, for direct access http://chlorokb.fr/

Conferences, Workshops and Outreach events

-Plant Organ Growth Symposium 2019 , Bordeaux, France, April 24 - 26, 2019, https://symposium.inra.fr/pogs2019

- 23rd International Conference on Plant Growth Substances, Universite Paris-Descartes, Paris, France, June 25 - 29, 2019, https://www.ipgsa2019.com/

- SPS Summer School 2019, Specialized plant metabolites: from analysis to engineering
June 30 – July 4, 2019 – Versailles and Orsay, France, https://www6.inra.fr/saclay-plant-sciences_eng/Teaching-and-training/Summer-schools/Summer-School-2019

- Doctoral Training: Biology at Different Scales: Interplay between Physics and Integrative Biology, from May 27, 2019 to Jun 7, 2019 – Les Houches, France

Selected Publications

Castrec B, Dian C, Ciccone S, Ebert CL, Bienvenut WV, Le Caer JP, Steyaert JM, Giglione C, Meinnel T (2018) Structural and genomic decoding of human and plant myristoylomes reveals a definitive recognition pattern. Nat Chem Biol. 14(7):671-679

Derrien B, Clavel M, Baumberger N, Iki T, Sarazin A, Hacquard T, Ponce MR, Ziegler-Graff V, Vaucheret H, Micol JL, Voinnet O, Genschik P (2018) A Suppressor Screen for AGO1 Degradation by the Viral F-Box P0 Protein Uncovers a Role for AGO DUF1785 in sRNA Duplex Unwinding. Plant Cell. 30(6):1353-1374

Gonneau M, Desprez T, Martin M, Doblas VG, Bacete L, Miart F, Sormani R, Hématy K, Renou J, Landrein B, Murphy E, Van De Cotte B, Vernhettes S, De Smet I, Höfte H (2018) Receptor Kinase THESEUS1 Is a Rapid Alkalinization Factor 34 Receptor in *Arabidopsis*. Curr Biol. 28(15):2452-2458.

Hugouvieux V, Silva CS, Jourdain A, Stigliani A, Charras Q, Conn V, Conn SJ, Carles CC, Parcy F, Zubieta C (2018) Tetramerization of MADS family transcription factors SEPALLATA3 and AGAMOUS is required for floral meristem determinacy in *Arabidopsis*. Nucleic Acids Res. 46(10):4966-4977

Morel P, Heijmans K, Ament K, Chopy M, Trehin C, Chambrier P, Rodrigues Bento S, Bimbo A, Vandenbussche M (2018) The Floral C-Lineage Genes Trigger Nectary Development in Petunia and *Arabidopsis*. Plant Cell. 30(9):2020-2037.

Nassrallah A, Rougée M, Bourbousse C, Drevensek S, Fonseca S, Iniesto E, Ait-Mohamed O, Deton-Cabanillas AF, Zabulon G, Ahmed I, Stroebel D, Masson V, Lombard B, Eeckhout D, Gevaert K, Loew D, Genovesio A, Breyton C, De Jaeger G, Bowler C, Rubio V, Barneche F (2018) DET1-mediated degradation of a SAGA-like deubiquitination module controls H2Bub homeostasis. Elife. 7. pii: e37892.

Perraki A, Gronnier J, Gouguet P, Boudsocq M, Deroubaix AF, Simon V, German-Retana S, Legrand A, Habenstein B, Zipfel C, Bayer E, Mongrand S, Germain V (2018) REM1.3's phospho-status defines its plasma membrane nanodomain organization and activity in restricting PVX cell-to-cell movement. PLoS Pathog.14(11):e1007378

Platre MP, Noack LC, Doumane M, Bayle V, Simon MLA, Maneta-Peyret L, Fouillen L, Stanislas T, Armengot L, Pejchar P, Caillaud MC, Potocký M, Copic A, Moreau P, Jaillais Y (2018) A Combinatorial Lipid Code Shapes the Electrostatic Landscape of Plant Endomembranes. Dev Cell. 45(4):465-480

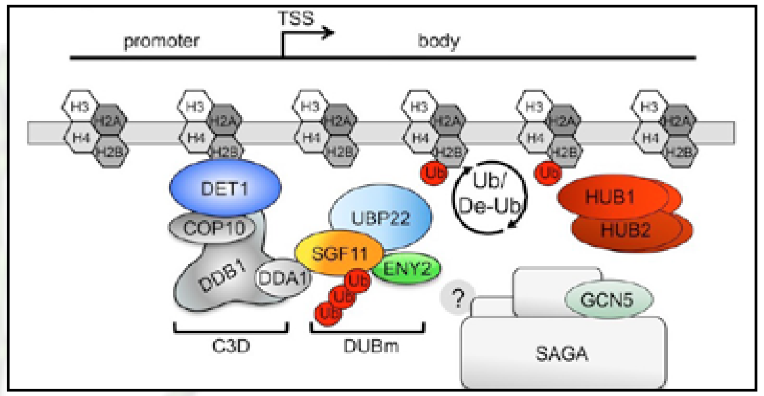

Figure 28 DET1 controls histone H2B monoubiquitination levels by opposing DUBm activity. Proposed model depicting the C3D complex activity in regulating histone H2Bub homeostasis through ubiquitin-mediated control of the DUBm stability. UBP22 is a Ubp8 homolog acting with SGF11 and ENY2 in H2Bub deubiquitination, possibly promoting transcription under optimal growth conditions. The C3D complex DDA1 subunit targets SGF11 for degradation, favoring degradation of the DUBm. DET1 affinity for non-acetylated histone H2B (Benvenuto *et al.*, 2002) may favor this degradation nearby H2Bub-rich regions. DET1 may further influence histone H2B acetylation status via an unknown mechanism, possibly involving the DUBm/SAGA activities or independent pathways. In the absence of Sgf73 homolog in plants, the DUBm may act independently from SAGA.

Tang N, Shahzad Z, Lonjon F, Loudet O, Vailleau F, Maurel C (2018) Natural variation at XND1 impacts root hydraulics and trade-off for stress responses in *Arabidopsis*. Nat Commun. 9(1):3884

Zervudacki J, Yu A, Amesefe D, Wang J, Drouaud J, Navarro L, Deleris A (2018) Transcriptional control and exploitation of an immune-responsive family of plant retrotransposons. EMBO J. 37(14).

Major Funding Sources

- Research organizations such as CNRS, INRA, CEA or Universities provide recurrent funding to their laboratories in addition to payment of salaries of permanent researchers and technicians.

- The French national research agency, ANR (http://www.agence-nationale-recherche.fr/en/about-anr/about-the-french-national-research-agency/), provides funding for project-based research. The main calls deal with societal issues that do not very well support fundamental research in general, including in plant biology. Funding on Arabidopsis projects is decreasing, although since 2017 ANR calls include again calls dedicated to fundamental mechanisms.

European funding:
ERC
http://erc.europa.eu/funding- and-grants
Marie-Curie research programmes
http:// ec.europa.eu/research/mariecurieactions/
EMBO
http://www.embo.org/funding-awards)

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University of Tübingen, Tübingen

Use of Arabidopsis

Arabidopsis research in Germany is performed in all corners of the country and this wide distribution also reflects the high diversity of topics explored by German scientists. The major sites hosting Arabidopsis researchers are Universities, Max Planck Institutes, Helmholtz Centers and Leibniz Institutes.

Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

- 1001 Genomes Project
http://1001genomes.org/

- German Plant Phenotyping Network
http://www.dppn.de/dppn/EN/Home/home_node.html

- The Arabidopsis Protein Phosphorylation Site Database http://phosphat.uni-hohenheim.de/index.html: in addition to the database, the PhosPhAt offers a plant-specific phosphorylation site predictor

- GABI Primary Database
http://www.gabipd.org/

- Plant Genome and Systems Biology Databases
http://pgsb.helmholtz-muenchen.de/plant/plantsdb.jsp

- Plant Transcription Factor Database
http://plntfdb.bio.uni-potsdam.de/v3.0/

- The AraGWAS Catalog: a curated and standardized *Arabidopsis thaliana* GWAS catalog
https://aragwas.1001genomes.org

qPortal: A large set of software tools and portlets are accessible via the recently established web-based science portal of the Quantitative Biology Center (QBiC) of the University of Tübingen (https://portal.qbic.uni-tuebingen.de/portal/web/qbic/software).

nQuire: a statistical framework for ploidy estimation using next generation sequencing. nQuire is implemented as a stand-alone Linux command line tool in the C programming language and is available at https://github.com/clwgg/nQuire.

findGSE: estimating genome size variation within human and Arabidopsis using k-mer frequencies. The R package of findGSE is freely available at https://github.com/schneebergerlab/findGSE and supported on linux and Mac systems

myTAI: evolutionary transcriptomics with R. The myTAI package is available at https://github.com/HajkD/myTAI and https://cran.r-project.org/web/packages/myTAI/index.html

Conferences, Workshops and Outreach events

Conferences

- 11th Tri-National Arabidopsis Meeting, 10. – 12. April 2019, Zürich, Switzerland

- International Plant Science Conference (Botanikertagung), 15. – 19. September 2019, Rostock, Germany

- Conference on Climate Change-Linked Stress Tolerance in Plants,13. – 16. May 2019, Hannover, Germany (http://www.keystonesymposia.org/index.cfm?e=Web.Meeting.Program&meetingid=1655&subTab=program)

- EMBL Conference: CO2 Fixation Summit, 03. – 04. June 2019, Heidelberg, Germany (https://www.embl.de/training/events/2019/COS19-01/index.html)

- 15th International Rapeseed Congress, 16. – 19. June 2019, Berlin, Germany (https://www.irc2019-berlin.com/)

- 5th Plants and People (P&P) Conference, 03. – 04.09.2019, Potsdam, Germany (https://plants-and-people.mpg.de/)

- 16th Horizons in Molecular Biology Symposium, 09. – 12.09.2019, Göttingen, Germany (https://www.horizons-molbio.de/)

- International Plant Science Conference (Botanikertagung), 15. – 19.09.2019, Rostock, Germany (https://www.botanikertagung2019.de/)

- 24th EUCARPIA Maize and Sorghum Conference, 07. – 09.10.2019, Weihenstephan/Freising, Germany (https://www.events.tum.de/frontend/index.php?sub=120)

- 9th International Conference on Functional-Structural Plant Models (FSPM2020), 05. – 09. October 2020, Hannover, Germany (https://www.fspm2020.net/).

Workshops

4th Summer Academy on Plant Molecular Biology, 23. – 25. September 2019, Heiligkreuztal, Germany (https://www.summer-academy-2019.info/)

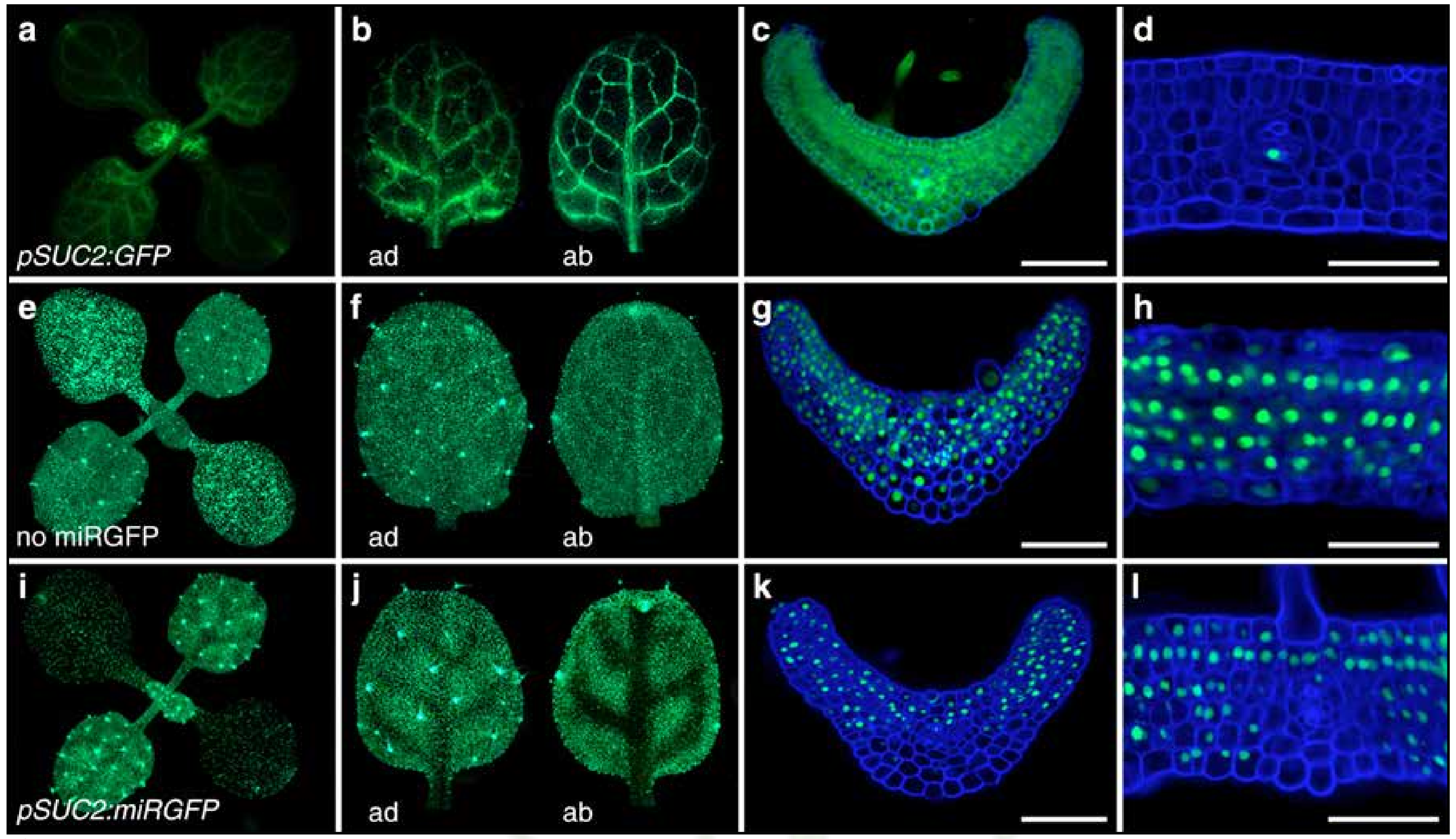

Figure 29. miRNA mobility is regulated independently from small protein movement. a–d Free GFP expressed in phloem companion cells (pSUC2:GFP) diffuses throughout a, c young sink leaves, but behaves cell autonomously in b, d mature source leaves. e–h In p35S:3xNLS-GFP seedlings not expressing miRGFP (no miRGFP), GFP is ubiquitously expressed. i–l miRGFP expressed in phloem companion cells (pSUC2:miRGFP) results in a non-cell autonomous pattern of GFP silencing that extends over 4–6 cells and appears more extensive on the abaxial (ab) side of k young as well as j, l mature leaves. ad, adaxial; ab, abaxial. Scale bars, 50 μm

7th European Workshop on Plant Peptides & Receptors, 11. – 13. September 2019, Freudenstadt, Germany (http://www.plant-peptides-and-receptors2019.uni-tuebingen.de/)

TUM Summer School on „Selection and Breeding“, 25. June to – 02. July 2019, Herrsching am Ammersee, Germany (http://www.plantbreeding.wzw.tum.de/index.php?id=133)

Outreach Events

The PLANT2030 is an initiative from the German Federal Ministry of Education and Research (BMBF) that fosters research projects within public-private partnerships (http://www.pflanzenforschung.de/de/plant-2030/uberblick).

German institutions are very active in communicating plant science to the general public. Max Planck Institutes, for instance, offer guided tours, events and informative booklets for people of all ages. Some examples are listed below.

- Wissenschaftsscheune, “The Science Barn” (http://www.wissenschaftsscheune.de/)
- Open House of the Tübingen MPI (http://www.eb.tuebingen.mpg.de/institute/information-for-the-public.html)
- Frag die Erbse, “Ask the Pea” booklet series (http://www.mpimp-golm.mpg.de/22409/Frag_die_Erbse_Booklet)

- 5th International Fascination of Plant Day, 18. May 2019, (https://www.pflanzenforschung.de/de/plant-2030/termine/2019-05-18-5th-international-fascination-plants-day-2019).

- 5th Plants and People (P&P) Conference, 03. – 04.09.2019, Potsdam, Germany (https://plants-and-people.mpg.de/)

Selected Publications

Brackmann K, Qi J, Gebert M, Jouannet V, Schlamp T, Grünwald K, Wallner ES, Novikova DD, Levitsky VG, Agustí J, Sanchez P, Lohmann JU, Greb T (2018). Spatial specificity of auxin responses coordinates wood formation. Nat Commun 9:875. doi: 10.1038/s41467-018-03256-2.

Capovilla G, Delhomme N, Collani S, Shutava I, Bezrukov I, Symeonidi E, de Francisco Amorim M, Laubinger S, Schmid M (2018).PORCUPINE regulates development in response to temperature through alternative splicing. Nat Plants, doi: 10.1038/s41477-018-0176-z.

Damianos S. Skopelitis, Kristine Hill, Simon Klesen, Cristina F. Marco, Patrick von Born,Daniel H. Chitwood & Marja C.P. Timmermans (2018). Gating of miRNA movement at defined cell-cell interfaces governs their impact as positional signals. Nature Comm. 9:3107, doi: 10.1038/s41467-018-05571-0.

Durán P, Thiergart T, Garrido-Oter R, Agler M, Kemen E, Schulze-Lefert P, Hacquard S (2018).Microbial Interkingdom Interactions in Roots Promote *Arabidopsis* Survival. Cell 175:973-983.e14. doi: 10.1016/j.cell.2018.10.020.

Förster S, Schmidt LK, Kopic E, Anschütz U, Huang S, Schlücking K, Köster P, Waadt R, Larrieu A, Batistia O, Rodriguez PL, Grill E, Kudla J, Becker D (2019).Wounding-Induced Stomatal Closure Requires Jasmonate-Mediated Activation of GORK K+ Channels by a Ca2+ Sensor-Kinase CBL1-CIPK5 Complex. Dev Cell 48:87-99, doi: 10.1016/j.devcel.2018.11.014.

Holzwart E, Huerta AI, Glöckner N, Garnelo Gómez B, Wanke F, Augustin S, Askani JC, Schürholz AK, Harter K, Wolf S (2018). BRI1 controls vascular cell fate in the *Arabidopsis* root through RLP44 and phytosulfokine signaling. Proc Natl Acad Sci USA 30: 201814434, doi: 10.1073/pnas.1814434115.

Hoppen C, Müller L, Albrecht AC, Groth G (2019).The NOP-1 peptide derived from the central regulator of ethylene signaling EIN2 delays floral senescence in cut flowers. Sci Rep. 9:1287, doi: 10.1038/s41598-018-37571-x.

Hyun, Y., Vincent, C., Tilmes, V., Bergonzi, S., Kiefer, C., Richter, R., Martinez-Gallegos, R., Severing, E., Coupland, G. (2019) A regulatory circuit conferring varied flowering response to cold in annual and perennial plants. Science 363: 409-412, doi: 10.1126/science.aau8197.

Neu A, Eilbert E, Asseck LY, Slane D, Henschen A, Wang K, Bürgel P, Hildebrandt M, Musielak TJ, Kolb M, Lukowitz W, Grefen C, Bayer M (2019). Constitutive signaling activity of a receptor-associated protein links fertilization with embryonic patterning in *Arabidopsis thaliana*. Proc Natl Acad Sci USA 116:5795-5804, doi: 10.1073/pnas.1815866116.

Speth C, Szabo EX, Martinho C, Collani S, Zur Oven-Krockhaus S, Richter S, Droste-Borel I, Macek B, Stierhof YD, Schmid M, Liu C, Laubinger S (2018). *Arabidopsis* RNA processing factor SERRATE regulates the transcription of intronless genes. Elife 7: e37078, doi: 10.7554/eLife.37078.

Major Funding Sources

The German Science Foundation (DFG) is the major source financing *Arabidopsis* research in Germany http://www.dfg.de/en/index.jsp

Contact: Catherine Kistner: catherine.kistner@dfg.de

DFG Deutsche Forschungsgemeinschaft

Greece

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Use of Arabidopsis

These instiutions conduct some research with Arabidopsis:

- Agricultural University of Athens, Athens, Greece
- Aristotle University of Thessaloniki, Thessaloniki, Greece
- National and Kapodistrian University of Athens, Athens, Greece
- University of Crete, Crete, Greece
- Mediterannean Agronomic Institute of Chania, Chania, Crete, Greece

Selected Publications

Kotak J, Saisana M, Gegas V, Pechlivani N, Kaldis A, Papoutsoglou P, Makris A, Burns J, Kendig AL, Sheikh M, Kuschner CE, Whitney G, Caiola H, Doonan JH, Vlachonasios KE, McCain ER, Hark AT. (2018). The Histone Acetyltransferase GCN5 and the Transcriptional Coactivator ADA2b Affect Leaf Development and Trichome Morphogenesis in Arabidopsis. Planta 248: 613-628

Panteris E, Diannelidis BE, Adamakis ID. (2018) Cortical microtubule orientation in *Arabidopsis thaliana* root meristematic zone depends on cell division and requires severing by katanin. Journal of Biological Research-Thessaloniki 25: 12

Podia V, Milioni D, Katsareli E, Valassakis C, Roussis A, Haralampidis K. (2018) Molecular and functional characterization of *Arabidopsis thaliana* VPNB1 gene involved in plant vascular development. Plant Science 277: 11–19

Podia V, Milioni D, Martzikou M, Haralampidis K. (2018) The role of *Arabidopsis thaliana* RASD1 gene in ABA-dependent abiotic stress response. Plant Biology 20: 307-317

Poulios S, Vlachonasios KE. (2018) Synergistic action of GCN5 and CLAVATA1 in the regulation of gynoecium development in *Arabidopsis thaliana*. New Phytologist 220: 593-608

Tsitsekian D, Daras G, Alatzas A, Templalexis D, Hatzopoulos P, Rigas S. (2018) Comprehensive analysis of Lon proteases in plants highlights independent gene duplication events. Journal of Experimental Botany doi: 10.1093/jxb/ery440

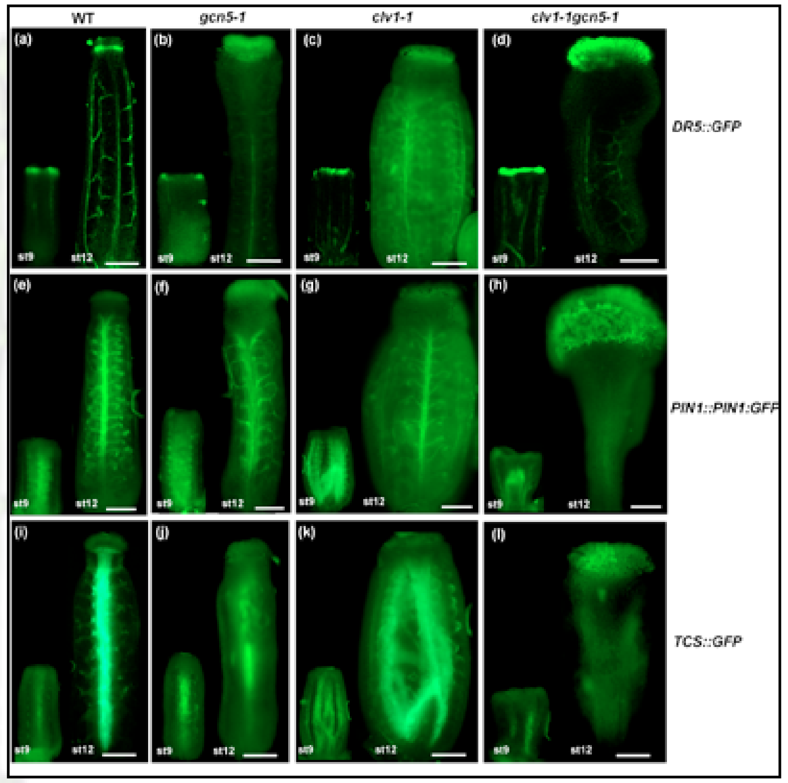


Figure 30 Auxin signaling and transport and cytokinin signaling, as detected by the DR5::GFP, PIN1::PIN1:GFP and TCS::GFP reporter genes respectively, in *Arabidopsis thaliana* flower stage 9 and 12 gynoecia. (a–d) DR5::GFP expression in (a) wild-type (WT), (b) gcn5-1, (c) clv1-1 and (d) clv1-1gcn5-1 gynoecia. (e–h) PIN1::PIN1:GFP expression in (e) WT, (f) gcn5-1, (g) clv1-1 and (h) clv1-1gcn5-1 gynoecia. (i–l) TCS::GFP expression in (i) WT, (j) gcn5-1, (k) clv1-1 and (l) clv1-1gcn5-1 gynoecia. Bars, 250 lm. GCN5, GENERAL CONTROL NON DEREPRESSIBLE 5; CLV1, CLAVATA. doi: 10.1111/nph.15303

Tornkvist A, Liu C, Moschou P. (2019) Proteolysis and Nitrogen: emerging insights. Journal of Experimental Botany doi: 10.1093/jxb/erz024

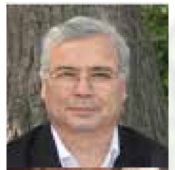
Major Funding Sources

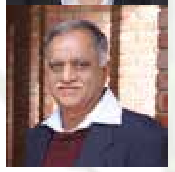
State Scholarships Foundation (IKY) www.iky.gr/en/

General Secretariat for Research and Technology (GSRT) www.gsrt.gr/central.aspx?sId=119I428I1089I323I488743&JScript=1

Hellenic Foundation for Research and Innovation (HFRI) www.elidek.gr/en/homepage/

India





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Use of Arabidopsis

The research activitiesin India continue to be centered around understanding molecular mechanisms involved in plant development, light, hormone and sugar signalling, plant-pathogen interaction and abiotic stress tolerance.

Ashis Kumar Nandi's group established that polycomb-group repressor protein MEDEA attenuates plant defense to maintain the balance between growth and development. The group identified *Arabidopsis thaliana*OXIDATION-RELATED ZINC FINGER 1 (AtOZF1) protein and showed that it promotes NPR1-independent SA signalling in *Arabidopsis*. This group has also established the role of the AP2-family protein APD1 in systemic acquired resistance.

Girdhar Pandey's group is working on the relationship of mineral nutrient deficiency and abiotic stress signaling pathways, especially Ca2+ mediated signaling under stress condition and the involvement of CBL-CIPK components.

Dr Laxmi's group has functionally characterized members of a glucose-regulated FLZ (FCS-Like Zinc Finger gene family (FLZ6 and FLZ10) and shown that the regulation is mediated through SnRK1 and TOR kinases in plants, which are ancient master regulators of energy signaling, growth and resilience.

Majee's group using ASK13 overexpression and knockdown lines have shown that ASK13 positively influences seed germination and seedling growth, particularly under abiotic stress.

Dr Utpal Nath's group has elucidated the redundnat role of two phytochrome 'B' (PHYB) interacting transcription factors, VOZ1 and VOZ2 (VASCULAR PLANT ONE-ZINC FINGER), in promoting flowering by modulating CONSTANS (CO) function(Figure), and that too independent of FLC (Flowering Locus C), the well worked out floral repressor.In addition, this group has also defined a role of class II TCP genes in regulating trichome differentiation, establishing a link between organ morphogenesis and cellular differentiation.

Sribash Roy's group has been involved in collection of Indian populations of *Arabidopsis thaliana*, collected from different altitudes of Western Himalaya and have shown that these accessions genetically distinct from the other world population. Further studies are likely to provide insight into the evolution and adaptation mechanisms of the Himalayan populations of *A. thaliana*.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

A database containing 636 gene entries related to 44 types of different stress factors with their related information related to *Arabidopsis thaliana*, has been created by Borkotoky *et al.* (2018). Details are as follows:

Borkotoky *et al.* (2018) The Arabidopsis Stress Responsive Gene DatabaseInternational Journal of Plant Genomics Volume 2013, http://dx.doi.org/10.1155/2013/949564

Conferences, Workshops and Outreach events

Indian Society for Plant Physiology (ISPP) organized an International Conference of Plant Physiology-2018 (IPCC-2018) at NBRI Lucknow during 2-5th December, 2018, where several articles on Arabidopsis were presented and discussed.

Selected Publications

- Jamsheer KM, Shukla BN, Jindal S, Gopan N, Mannully CT and Laxmi A (2018) The FCS-like zinc finger scaffold of the kinase SnRK1 is formed by the coordinated actions of the FLZ domain and intrinsically disordered regions. J. Biol. Chem. 293(34):13134-13150

- Kumar S, Choudhary P, Gupta M, Nath U (2018) VASCULAR PLANT ONE-ZINC-FINGER1 (VOZ1) and VOZ2 interact with CONSTANS and promote photoperiodic flowering transition. Plant Physiol. 176: 2917-2930

- Rao V, Petla BP, Verma P, Salvi P, Kamble NU, Ghosh S, Kaur H, Saxena SC, Majee M (2018) *Arabidopsis* SKP1-like protein13 (ASK13) positively regulates seed germination and seedling growth under abiotic stress. J Exp Bot. 69:3899-3915

- Roy S (2018) *Arabidopsis* natural variants and the Indian scenario. Current Science, 114, 263-265.

- Roy S, Gupta P, Rajabhoj MP, Maruthachalam R, Nandi AK (2018) The polycomb-group repressor MEDEA attenuates pathogen defense. Plant Physiology 177:1728-1742,

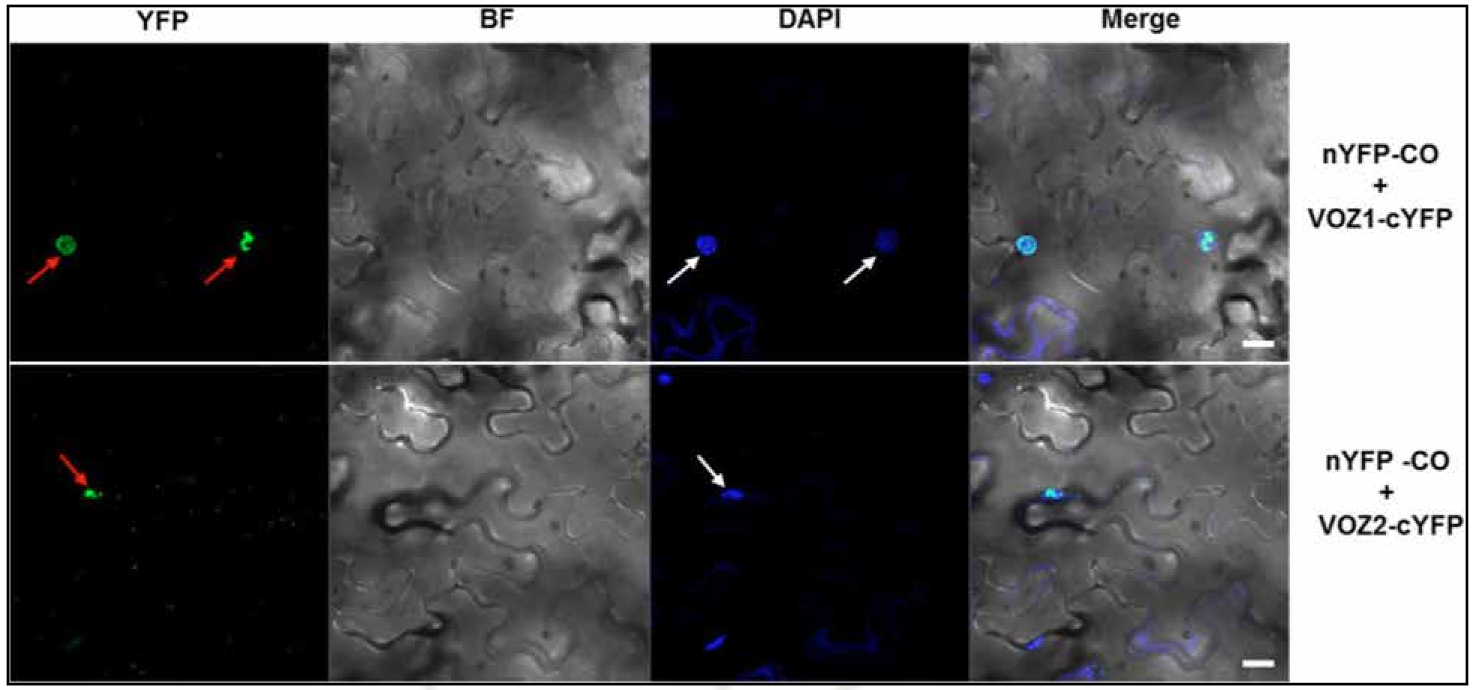

Figure 31. BiFC analysis indicates thatthe two phytochrome B-interacting transcription factors, VASCULAR PLANT ONE-ZINC FINGER1 (VOZ1) (top) and VOZ2, (bottom) proteins interact with CO in N. benthamiana epidermal cells. www.plantphysiol.org/cgi/doi/10.1104/pp.17.01562

- Sarkar, S., Das, A., Khandagale, P., Maiti, IB., Chattopadhyay, S. and Dey, N. (2018). Interaction of Arabidopsis TGA3 and WRKY53 transcription factors on Cestrum yellow leaf curling virus (CmYLCV) promoter mediates salicylic acid-dependent gene expression in planta. Planta247:181–199.

- Singh A, Yadav AK, Kaur K, Sanyal SK, Jha SK, Fernandes JL, Sharma P, Tokas I, Pandey A, Luan S, Pandey GK (2018) Protein Phosphatase 2C, AP2C1 Interacts with and Negatively Regulates the Function of CIPK9 under Potassium Deficient Conditions in *Arabidopsis*. Journal of Experimental Botany. 69(16): 4003-4015.

- Singh N, Swain S, Singh A, Nandi AK (2018) AtOZF1 positively regulates defense against bacterial pathogens and NPR1- independent salicylic acid signaling. Mol Plant Microbe Interact 2018 31:323-333

- Vadde BVL, Challa KR, Nath U (2018) The TCP4 transcription factor regulates trichome cell differentiation by directly activating GLABROUS INFLORESCENCE STEMS in *Arabidopsis thaliana*. Plant J. 93: 259-269

- Yadav AK, Jha SK, Sanyal SK, Luan S, Pandey GK. (2018) *Arabidopsis* Calcineurin B-like proteins differentially regulate phosphorylation activity of CBL-interacting protein kinase 9. Biochemical Journal. 475(16): 2621-2636.

Major Funding Sources

Department of Biotechnology (DBT), Government of India http://dbtindia.nic.in/

Department of Science & Technology (DST), Government of India http://www.dst.gov.in/

Science and Engineering Research Board (SERB), Government of India http://www.serbonline.in/

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/

Ireland

Prof. Charles Spillane
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Use of Arabidopsis

Ireland (population > 4.6 million) has a relatively small and diverse plant research community (approx 30-40 research groups). There are currently no private sector institutions working with *Arabidopsis thaliana* in Ireland.

The following research groups in Ireland are conducting research using the model plant *Arabidopsis thaliana*:

1. Prof Charles Spillane, Genetics and Biotechnology Lab, Plant and AgriBiosciences Research Centre (PABC), Ryan Institute, National University of Ireland Galway (NUI Galway), Ireland.
2. Dr. Ronan Sulpice, Plant Systems Biology Lab, Plant and AgriBiosciences Research Centre (PABC), Ryan Institute, National University of Ireland Galway (NUI Galway), Ireland.
3. Dr. Sara Farrona, Plant Developmental Epigenetics Lab, Plant and AgriBiosciences Research Centre (PABC), Ryan Institute, National University of Ireland Galway (NUI Galway), Ireland.
4. Dr. Zoe Popper, Plant Cell Wall Lab, Plant and AgriBiosciences Research Centre (PABC), Ryan Institute, National University of Ireland Galway (NUI Galway), Ireland.
5. Dr. Frank Wellmer, Plant Developmental Genetics, Smurfit Institute of Genetics, Trinity College Dublin.
6. Dr. Paul McCabe, School of Biology & Environmental Science, University College Dublin, Dublin, Ireland.
7. Dr. Carl Ng, School of Biology & Environmental Science, University College Dublin, Dublin, Ireland.
8. Dr. Fiona Doohan, School of Biology & Environmental Science, University College Dublin, Dublin, Ireland.
9. Dr. Rainer Melter, School of Biology and Environmental Science, University College Dublin (UCD), Dublin, Ireland.
10. Dr. Marcel Jansen, Zoology, Ecology & Plant Science (ZEPs), University College Cork, Ireland.
11. Prof. Astrid Wingler, Zoology, Ecology & Plant Science (ZEPs), University College Cork, Ireland.
12. Dr. Fuquan Liu, School of Biological Sciences, Queens University Belfast, Northern Ireland.
13. Dr. Emmanualle Graciet, School of Biology, National University of Ireland Maynooth, Ireland.
14. Dr. Mario Fares, Smurfit Institute of Genetics, Trinity College Dublin. RIP.

Conferences, Workshops and Outreach events

There is an annual Irish Arabidopsis Meeting which aims to bring together the Arabidopsis researcher community in Ireland.

Selected Publications

Alvarez-Ponce, D., Ruiz-González, M., Vera-Sirera, F., Feyertag, F., Perez-Amador, M. and Fares, M (2018) Arabidopsis Heat Stress-Induced Proteins Are Enriched in Electrostatically Charged Amino Acids and Intrinsically Disordered Regions. International journal of molecular sciences, 19(8), p.2276.

Coffey, A. and Jansen, M.A (2019) Effects of natural solar UV-B radiation on three Arabidopsis accessions are strongly affected by seasonal weather conditions. Plant physiology and biochemistry, 134, pp.64-72.

Duszynska, D., Vilhjalmsson, B., Bravo, R.C., Swamidatta, S., Juenger, T.E., Donoghue, M.T., Comte, A., Nordborg, M., Sharbel, T.F., Brychkova, G. and McKeown, P.C (2019) Transgenerational effects of inter-ploidy cross direction on reproduction and F2 seed development of *Arabidopsis thaliana* F1 hybrid triploids. Plant Reproduction, pp.1-15.

Engelhorn, J., Wellmer, F. and Carles, C.C (2018). Profiling Histone Modifications in Synchronized Floral Tissues for Quantitative Resolution of Chromatin and Transcriptome Dynamics. In Plant Chromatin Dynamics (pp. 271-296). Humana Press, New York, NY.

Hohenstatt, M.L., Mikulski, P., Komarynets, O., Klose, C., Kycia, I., Jeltsch, A., Farrona, S. and Schubert, D., 2018. PWWP-DOMAIN INTERACTOR OF POLYCOMBS1 interacts with Polycomb-group proteins and histones and regulates Arabidopsis flowering and development. The Plant Cell, 30(1), pp.117-133

Käppel, S., Melzer, R., Rümpler, F., Gafert, C. and Theißen, G (2018) The floral homeotic protein SEPALLATA 3 recognizes target DNA sequences by shape readout involving a conserved arginine residue in the MADS domain. The Plant Journal, 95(2), pp.341-357.

Mermaz, B., Liu, F. and Song, J (2018) RNA Immunoprecipitation Protocol to Identify Protein–RNA Interactions in *Arabidopsis thaliana*. In Plant Chromatin Dynamics (pp. 331-343). Humana Press, New York, NY.

Mikulski, P., Hohenstatt, M.L., Farrona, S., Smaczniak, C., Stahl, Y., Kalyanikrishna, K., Kaufmann, K., Angenent, G.C. and Schubert, D (2019) The chromatin-associated protein PWO1 interacts with plant nuclear lamin-like components to regulate nuclear size. The Plant Cell, Jan 1

Ó'Maoiléidigh, D.S., Stewart, D., Zheng, B., Coupland, G. and Wellmer, F (2018) Floral homeotic proteins modulate the genetic program for leaf development to suppress trichome formation in flowers. Development, 145(3), p.dev157784.

Rümpler, F., Theißen, G. and Melzer, R (2018). A conserved leucine zipper-like motif accounts for strong tetramerization capabilities of SEPALLATA-like MADS-domain transcription factors. Journal of experimental botany, 69(8), pp.1943-1954.

Tuteja, R., McKeown, P.C., Ryan, P., Morgan, C.C., Donoghue, M.T., Downing, T., O'Connell, M.J. and Spillane, C (2019) Paternally expressed imprinted genes under positive Darwinian selection in *Arabidopsis thaliana*. Molecular Biology and Evolution Mar 26

Xu, Y., Prunet, N., Gan, E.S., Wang, Y., Stewart, D., Wellmer, F., Huang, J., Yamaguchi, N., Tatsumi, Y., Kojima, M. and Kiba, T (2018) SUPERMAN regulates floral whorl boundaries through control of auxin biosynthesis. The EMBO journal, 37(11), p.e97499.

Zheng, B., Thomson, B. and Wellmer, F (2018) A Specific Knockdown of Transcription Factor Activities in Arabidopsis. In Plant Transcription Factors (pp. 81-92). Humana Press, New York, NY.

Major Funding Sources

Funding sources for Arabidopsis research in Ireland have to date included Science Foundation Ireland (SFI); Department of Agriculture, Fisheries and Food; Irish Research Council for Science, Engineering and Technology; and the European Union.

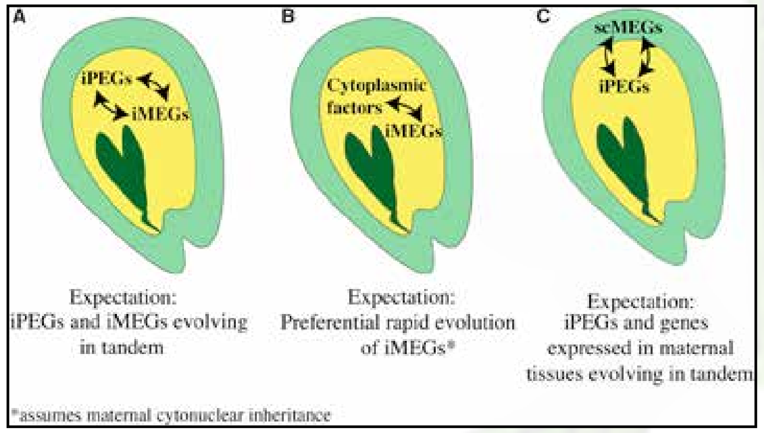

Figure 32. Summary of scenarios for selection on imprinted plant genes. Schematic of *Arabidopsis thaliana* seed summarizing the impacts of genomic imprinting on genetic selection as predicted by major hypotheses for genomic imprinting. In each case, the diploid F1 embryo is shown in dark green, surrounded by the triploid F1 endosperm, shown in yellow) in which imprinting occurs, and the diploid seed coat (SC) which is part of the maternal sporophyte, shown in light green.

Israel

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Technion - Israel Institute of Technology,
Haifa, Israel

Use of Arabidopsis

Arabidopsis research is conducted in different labs located in seven major research centers and universities: The Hebrew University of Jerusalem, Tel Aviv University, the Weizmann Institute of Science, Ben Gurion University of the Negev, Bar Ilan University, Agriculture Research Organization/Volcani Center and the Technion - Israel Institute of Technology.

Areas of research include plant physiology, biochemistry, metabolomics, development and genomics.

Conferences, Workshops and Outreach events

- 10th Symposium of the International Society of Root Research (ISRR10) 8-12 July, 2018, Yearim Hotel, Israel
- International Conference of Plant Mitochondrial Biology, 10-15.3.2019, Ein-Gedi, Israel
- The Israeli Society of Plant Sciences Conference, February 13th, 2019, Sde-Boker, Israel

Publications

Abu-Abied M, Belausov E, Hagay S, Peremyslov V, Dolja V, Sadot E (2018) Myosin XI-K is involved in root organogenesis, polar auxin transport, and cell division J Exp Bot. 69(12), 2869-2881.

Battat M, Eitan A, Rogachev I, Hanhineva K, Fernie AR, Tohge T, Beekwilder J, Aharoni A. (2019) A MYB Triad Controls Primary and Phenylpropanoid Metabolites for Pollen Coat Patterning. Plant Physiol. doi: 10.1104/pp.19.00009.

Butenko Y, Lin A, Naveh L, Kupervaser M, Levin Y, Reich Z, Adam Z (2018) Differential Roles of the Thylakoid Lumenal Deg Protease Homologs in Chloroplast Proteostasis. Plant Physiol. 178(3), 1065-1080.

Chen T, Fluhr R (2018) Singlet Oxygen Plays an Essential Role in the Root's Response to Osmotic Stress Plant Physiol. 177(4),1717-1727.

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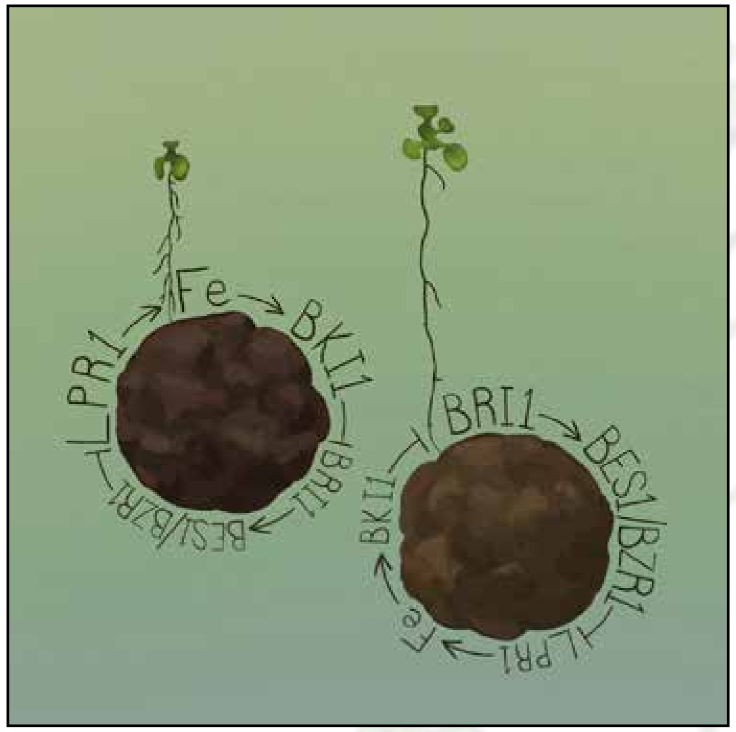

Figure 33. Interdependent Nutrient Availability and Steroid Hormone Signals Facilitate Root Growth Plasticity.

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Zhang Y, Nasser V1, Pisanty O, Omary M, Wulff N, Di Donato M, Tal I, Hauser F, Hao P, Roth O, Fromm H, Schroeder JI, Geisler M, Nour-Eldin HH, Shani E. (2018). A transportome-scale amiRNA-based screen identifies redundant roles of *Arabidopsis* ABCB6 and ABCB20 in auxin transport. Nature comm., 9(1), 4204.

Major Funding Sources

- ISF
- BSF
- NSF-BSF

Italy

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IBPM-National Research Council (CNR),
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Use of Arabidopsis

A few groups mainly in the Universities and in the CNR (National Research Council) laboratories continue to utilize *Arabidopsis* as a model organism for plant biology research and their results are published in high impact journals. Research is mainly focused on root and flower development, seed germination, xylem differentiation, ion transport in plant vacuoles, plant defense responses and plant responses to environment.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

Single and multiple *Arabidopsis* T-DNA insertion lines, as well as overexpressing lines, GUS- YFP- and GFP-tagged lines, RNA-seq data described in publications are available.

Conferences, Workshops and Outreach events

Advances in Plant Reproduction – from gametes to seeds- SEB conference Florence 30 June - 1 July 2018

Selected Publications

Benedetti M, Verrascina I, Pontiggia D, Locci F, Mattei B, De Lorenzo G, Cervone F. (2018) Four Arabidopsis berberine bridge enzyme-like proteins are specific oxidases that inactivate the elicitor-active oligogalacturonides. PLANT JOURNAL. Apr; 94(2):260-273.

Carabelli M, Possenti M, Sessa G, Ruzza V, Morelli G, Ruberti I. (2018) Arabidopsis HD-Zip II proteins regulate the exit from proliferation during leaf development in canopy shade. JOURNAL OF EXPERIMENTAL BOTANY 69: 5419-5431

Cucinotta M, Manrique S, Cuesta C, Benkova E, Novak O, and Colombo L. (2018) CUP-SHAPED COTYLEDON1 (CUC1) and CUC2 regulate cytokinin homeostasis to determine ovule number in Arabidopsis. JOURNAL OF EXPERIMENTAL BOTANY, 69 (21): 5169–5176

Di Ruocco G, Bertolotti G, Pacifici E, Polverari L, Tsiantis M, Sabatini S, Costantino P, Dello Ioio R. (2018) Differential spatial distribution of miR165/6 determines variability in plant root anatomy. DEVELOPMENT Jan 9;145(1). pii: dev153858

Ghelli R, Brunetti P, Napoli N, De Paolis A, Cecchetti V, Tsuge T, Serino G, Matsui M, Mele G, Rinaldi G, Palumbo A, Costantino P and Cardarelli M (2018) A newly identified flower-specific splice variant of AUXIN RESPONSE FACTOR 8 Regulates Stamen Elongation and Endothecium Lignification in *Arabidopsis*. PLANT CELL, 30: 620-637

Lorrai R, Gandolfi F, Boccaccini A, Ruta V, Possenti M, Tramontano A, Costantino P, Lepore R, Vittorioso P. (2018)Genome-wide RNA-seq analysis indicates that the DAG1 transcription factor promotes hypocotyl elongation acting on ABA, ethylene and auxin signaling SCIENTIFIC REPORT; 8:1-13

Mainieri D, Marrano CA, Prinsi B, Maffi D, Tschofen M, Espen L, Stöger E, Faoro F, Pedrazzini E, Vitale A. (2018) Maize 16-kD g-zein forms very unusual disulfide-bonded polymers in the end oplasmic reticulum: implications for prolamin evolution. JOURNAL OF EXPERIMENTAL BOTANY 69:5013-5027.

Mattioli R, Biancucci M, El Shall A, Costantino P, Mosca L, Funck D, and Trovato M. (2018). Proline synthesis in developing microspores is required for full pollen development and fertility. BMC PLANT BIOLOGY. 18:356

Mizzotti C, Rotasperti L, Moretto M, Tadini L, Resentini F, Galliani B M., Galbiati M, Engelen K, Pesaresi P and Masiero S (2018). Arabidopsis silique transcriptome discloses essential genes in fruit development and maturation. PLANT PHYSIOLOGY, 178(3):1249-1268.

Pacifici E, Di Mambro R, Dello Ioio R, Costantino P, Sabatini S. (2018) Acidic cell elongation drives cell differentiation in the Arabidopsis root. EMBO JOURNAL. Aug 15;37(16).

Punzo P, Ruggiero A, Possenti M, Nurcato R, Costa A, Morelli G, Grillo S, Batelli G. (2018) The PP2A-interactor TIP41 modulates ABA responses in *Arabidopsis thaliana*. PLANT JOURNAL. 94 (6): 991-1009

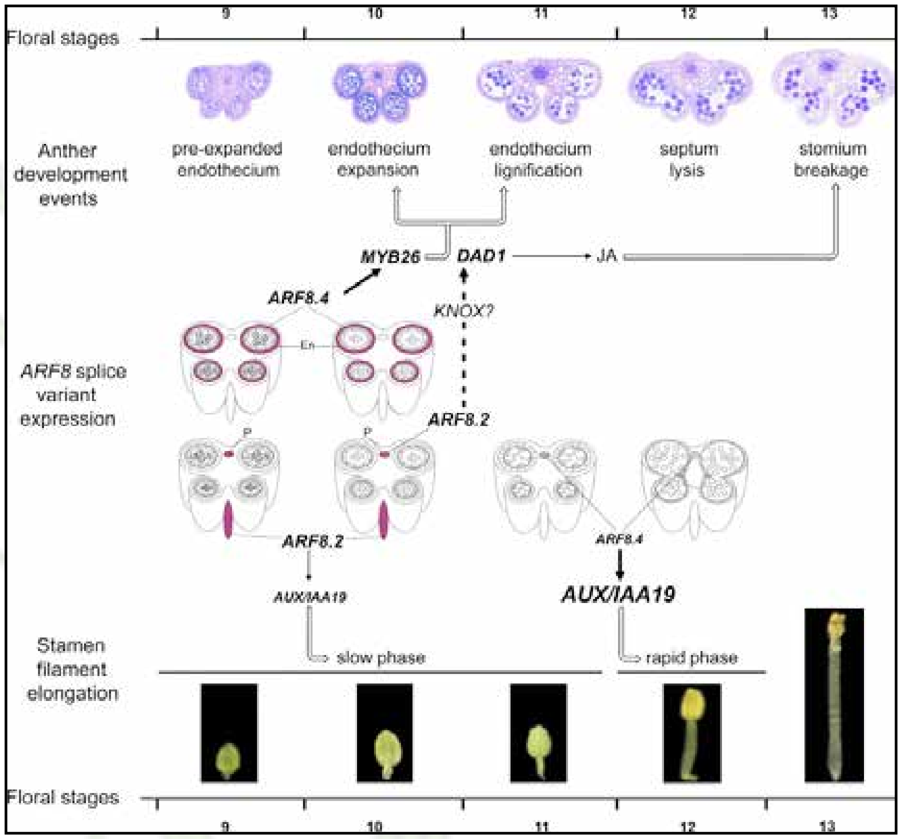

Figure 34 Model Showing the Role of the Splice Variants ARF8.4 and ARF8.2 in Stamen Elongation and Anther Dehiscence during Late *Arabidopsis* Development. Anther developmental events, stamen filament elongation phases, and relevant gene functions (MYB26, DAD1, and AUX/IAA19) from stages 9 to 13 (Bowman, 1994). ARF8.4 and ARF8.2 expression, as inferred from our in situ hybridization data, was simplified, only showing transcript localization in the endothecium and in the anther or stamen filament procambium. En, endothecium; P, procambium.

Major Funding Sources

The Italian Ministry of Education, University and Research funded:

- Project SIR(2015-2018) for independence of young researcher, on 'MADS box transcription factor SHORT VEGETATIVE PHASE, understanding the molecular mechanism and involvement in sense and antisense transcript regulation. RBSI14BTZR. Coordinator Veronica Gregis;

- Local funding from: Sapienza University of Rome, Roma Tre University of Rome and University of Milan

Other funding:

- Project Horizon 2020 EU RISE project "EXPOSEED" Exploring the molecular control of seed yield in crops (https://ec.europa.eu/research/mariecurieactions/about/research-innovation-staff-exchange_en)

- Project Promotion of consumer health of the National technological cluster Agrifood. Participant Ida Ruberti.

Japan

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Use of Arabidopsis

Approximately 350 labs in Japan use Arabidopsis in their research.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

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)
- PASMet - Prediction, Analysis and Simulation of Metabolic Reaction Networks (http://pasmet.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) (http://bit.ly/1sObBEE)

Plant and Cell Physiology, Volume 59, Issue 10, 1 October 2018, Pages 2030–2038,
https://doi.org/10.1093/pcp/pcy122
- The Chloroplast Function Database (http://rarge-v2.psc.riken.jp/chloroplast/)
- RIKEN *Arabidopsis* Phenome Information Database (http://rarge.psc.riken.jp/phenome/)
- HanaDB
- PASMet - Prediction, Analysis and Simulation of Metabolic Reaction Networks (http://pasmet.riken.jp/)
- 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)
- PGDBj Plant Genome DataBase Japan (http://pgdbj.jp/?ln=en)
- KaPPA-View4 for integration of transcriptome and metabolome data on metabolic maps (http://kpv.kazusa.or.jp/)
- MFSearcher molecular formula searcher (http://bit.ly/1RN2BFp)

Conferences, Workshops and Outreach events

- Mar. 13-15, 2019: 60th Annual Meeting of Japanese Society of Plant Physiologists. Nagoya Univ. (https://jspp.org/annualmeeting/60/E-index.html)
- Mar. 14-16, 2019: Japan-Taiwan Plant Biology 2019 (JTPB2019): Nagoya Univ. (https://jspp.org/annualmeeting/JTPB2019/)
- Mar. 18-30, 2019: Post-Transcriptional Gene Regulation in Plants (PGRP) 2019 NARA (https://pgrp2019.jimdofree.com/)

Selected Publications

Kurihara, Y., Makita, Y., Kawashima, M., Fujita, T., Iwasaki, S. and Minami, M. (2018) Transcripts from downstream alternative transcription start sites evade uORF-mediated inhibition of gene expression in Arabidopsis. Proc Natl Acad Sci U S A. 115:7831-7836. doi: 10.1073/pnas.1804971115.

Kuroha, T., Nagai, K., Gamuyao, R., Wang, D.R., Furuta, T., Nakamori, M., Kitaoka, T., Adachi, K., Minami, A., Mori, Y., Mashiguchi, K., Seto, Y., Yamaguchi, S., Kojima, M., Sakakibara, H., Wu, J., Ebana, K., and Ashikari, M. (2018) Ethylene-Gibberellin Signaling Underlies Adaptation of Rice to Periodic Flooding. Science, 361, 6398, 181-186. doi: 10.1126/science.aat1577.

Nakaminami, K., Okamoto, M., Higuchi-Takeuchi, M., Yoshizumi, T., Yamaguchi, Y., Fukao, Y., Shimizu, M., Ohashi, C., Tanaka, M., Matsui, M., Shinozaki, K., Seki, M. and Hanada, K. (2018) AtPep3 is a hormone-like peptide that plays a role in the salinity stress tolerance of plants. Proc Natl Acad Sci U S A. 115:5810-5815. doi:10.1073/pnas.1719491115.

Sakamoto, T., Tsujimoto-Inui, Y.,Sotta, N., Hirakawa, T., M. Matsunaga, T., Fukao, F., Matsunaga, S. and Fujiwara, T. (2018) Proteasomal degradation of BRAHMA promotes Boron tolerance in Arabidopsis. Nature Communications 9: 5285. doi: 10.1038/s41467-018-0739.

Takahashi, F., Suzuki, T., Osakabe, Y., Betsuyaku, S., Kondo, Y., Dohmae, N., Fukuda, H., Yamaguchi-Shinozaki, K. and Shinozaki, K. (2018) A small peptide modulates stomatal control via abscisic acid in long-distance signalling. Nature 556:235-238. doi: 10.1038/s41586-018-0009-2.

Toyota, M., Spencer, D., Sawai-Toyota, S., Jiaqi, W., Zhang, T., Koo, A.J., Howe, G.A. and Gilroy, S. (2018) Glutamate triggers long-distance, calcium-based plant defense signaling. Science 361:1112-1115. doi:10.1126/science.aat7744.

Uchida, N., Takahashi, K., Iwasaki, R., Yamada, R., Yoshimura, M., Endo, T.A., Kimura, S., Zhang, H., Nomoto, M., Tada, Y., Kinoshita, T., Itami, K., Hagihara, S., and Torii, K.U. (2018) Chemical hijacking of auxin signaling with an engineered auxin-TIR1 pair. Nature Chem. Biol. 14:299-305. doi: 10.1038/nchembio.2555.

Uraguchi, D., Kuwata, K., Hijikata, Y., Yamaguchi, R., Imaizumi, H., Sathiyanarayanan, A.M., Rakers, D., Mori, N., Akiyama, K., Irle, S., McCourt, P., Kinoshita, T., Ooi, T. and Tsuchiya, Y. (2018) A femto-molar range suicide germination stimulant for the parasitic plant Striga hermonthica. Science, 362, 1301-1305. doi: 10.1126/science.aau5445.

Yamaguchi, N., Huang, J., Tatsumi, Y., Abe, M., Sugano, S.S., Kojima, M., Takebayashi, Y., Kiba, T. Yokoyama, R., Nishitani, K., Sakakibara, H. and Ito, T. (2018) Chromatin-mediated feed-forward auxin biosynthesis in floral meristem determinacy. Nature Commun. 9:5290. doi: 10.1038/s41467-018-07763-0.

Figure 35 Dose–response test of the AtPep3/AT13 peptide affected in salinity stress tolerance. (Left) Representative images of plants from the AT13-5 dose–response test. https://doi.org/10.1073/pnas.1719491115

Yu, L.J., Suga, M., Wang-Otomo, Z.Y. and Shen, J.R. (2018) Structure of photosynthetic LH1-RC super-complex at 1.9 Å resolution. Nature 556:209-213. doi: 10.1038/s41586-018-0002-9.

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)

New Zealand

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Use of Arabidopsis

Arabidopsis is used as a research tool in approximately eight institutions in New Zealand (University of Auckland, University of Otago, Massey University, University of Canterbury, Lincoln University and Victoria University, AgResearch Ltd, Plant and Food Research Ltd.)

Conferences, Workshops and Outreach events

AustralAsia Genetics Society Meeting, July 3-6, 2017, Queenstown Reaserch Week: Plant Biology Satellite. Queenstown, New Zealand. 30-31 August 2018

Plant Science Central. Palmerston North, New Zealand. 2-4 July 2019

International Congress on Photosynthesis. Rotorua, New Zealand. 2-7 August 2020

Selected Publications

BBulman S, Richter F, Marschollek S, Benade F, Julke S and Ludwig-Müller (2018) *Arabidopsis thaliana* expressing PbBSMT, a gene encoding a SABATH-type methyltransferase from the plant pathogenic protist Plasmodiophora brassicae, show leaf chlorosis and altered host susceptibility. Plant Biology 21 Suppl 1:120-130 doi: 10.1111/plb.12728

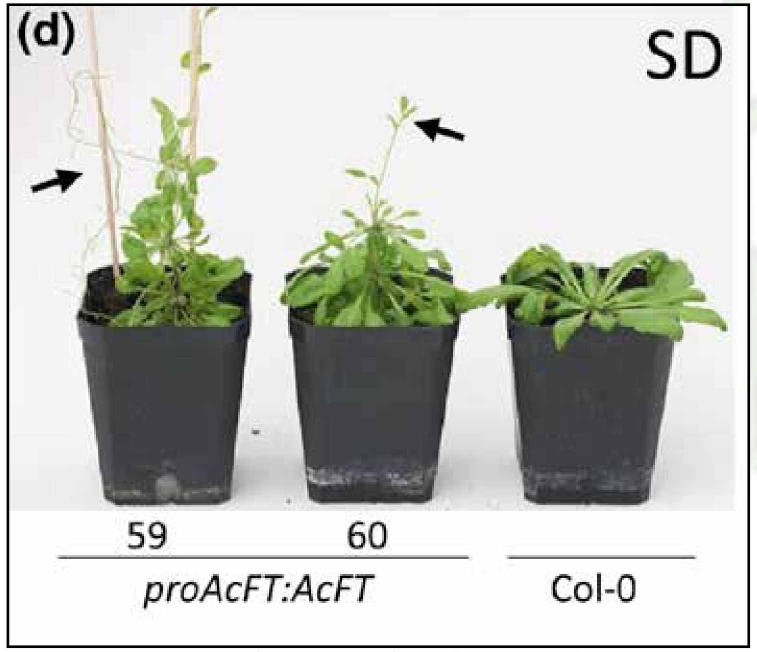

Figure 36: Expression of an FT gene from the AcFT and AcFT1 promoters is sufficient for flowering in noninductive conditions in transgenic *Arabidopsis*. Early bolting and growth of aerial rosettes in transgenic proAcFT:AcFT Arabidopsis in SD.

Choi S, Jayaraman J and Sohn KH (2018) *Arabidopsis thaliana* SOBER1 (SUPPRESSOR OF AVRBST-ELICITED RESISTANCE 1) suppresses plant immunity triggered by multiple bacterial acetyltransferase effectors. New Phytologist 219:324-335 doi: 10.1111/nph.15125

Gould KS, Jay-Allemand C, Logan BA, Baissac Y and Bidel LPR (2018) When are foliar anthocyanins useful to plants? Re-evaluation of the photoprotection hypothesis using *Arabidopsis thaliana* mutants that differ in anthocyanin accumulation. Environmental and Experimental Botany 154:11-22 doi: 10.1016/j.envexpbot.2018.02.006

Moss, SMA, Wang T, Voogd C, Brian LA, Wu R, Hellens RP, Allan AC, Putterill J and Varkonyi-Gasic E (2018) AcFT promotes kiwifruit in vitro flowering when overexpressed and *Arabidopsis* flowering when expressed in the vasculature under its own promoter. Plant Direct 2: e00068 doi: 10.1002/pld3.68

Newman TE, Lee J, Williams SJ, Chio S, Halane MK, Zhou J, Solomon P, Kobe B, Jones JDG, Segonzac C and Sohn KH (2018) Autoimmunity and effector recognition in *Arabidopsis thaliana* can be uncoupled by mutations in the RRS1-R immune receptor. New Phytologist doi: 10.1111/nph.15617

Raad M, Glare TR, Brochero HL, Muller C and Rostás M (2019) Transcriptional reprogramming of *Arabidopsis thaliana* defence pathways by the entomopathogen Beauveria bassiana correlates with resistance against a fungal pathogen but not against insects. Frontiers in Microbiology. Doi: 10.3389/fmicb.2019.00615

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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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Conferences, Workshops and Outreach events

The national plant biology conference in Bergen had a strong Arabidopsis element.
https://norplantbio2018.w.uib.no/
The next one will be in November 2019 in Oslo

Selected Publications

Engelsdorf T, Gigli-Bisceglia N, Veerabagu M, McKenna JF, Vaahtera L, Augstein F, Van der Does D, Zipfel C, Hamann T (2018) The plant cell wall integrity maintenance and immune signaling systems cooperate to control stress responses in *Arabidopsis thaliana*. Sci Signal. 11(536). pii: eaao3070. doi: 10.1126/scisignal.aao3070.

Gigli-Bisceglia N, Engelsdorf T, Strnad M, Vaahtera L, Khan GA, Yamoune A, Alipanah L, Novák O, Persson S, Hejatko J, Hamann T (2018) Cell wall integrity modulates *Arabidopsis thaliana* cell cycle gene expression in a cytokinin- and nitrate reductase-dependent manner. Development. 145(19). pii: dev166678. doi: 10.1242/dev.166678.

Shi CL, von Wangenheim D, Herrmann U, Wildhagen M, Kulik I, Kopf A, Ishida T, Olsson V, Anker MK, Albert M, Butenko MA, Felix G, Sawa S, Claassen M, Friml J, Aalen RB (2018) The dynamics of root cap sloughing in Arabidopsis is regulated by peptide signalling. Nat Plants. (8):596-604. doi: 10.1038/s41477-018-0212-z.

Urbancsok J, Bones AM, Kissen R (2018) Benzyl Cyanide Leads to Auxin-Like Effects Through the Action of Nitrilases in *Arabidopsis thaliana*.Front Plant Sci. 2018 Aug 24;9:1240. doi: 10.3389/fpls.2018.01240. eCollection 2018.

Major Funding Sources

Norwegian Research Council

https://www.forskningsradet.no/en/Home_page/1177315753906

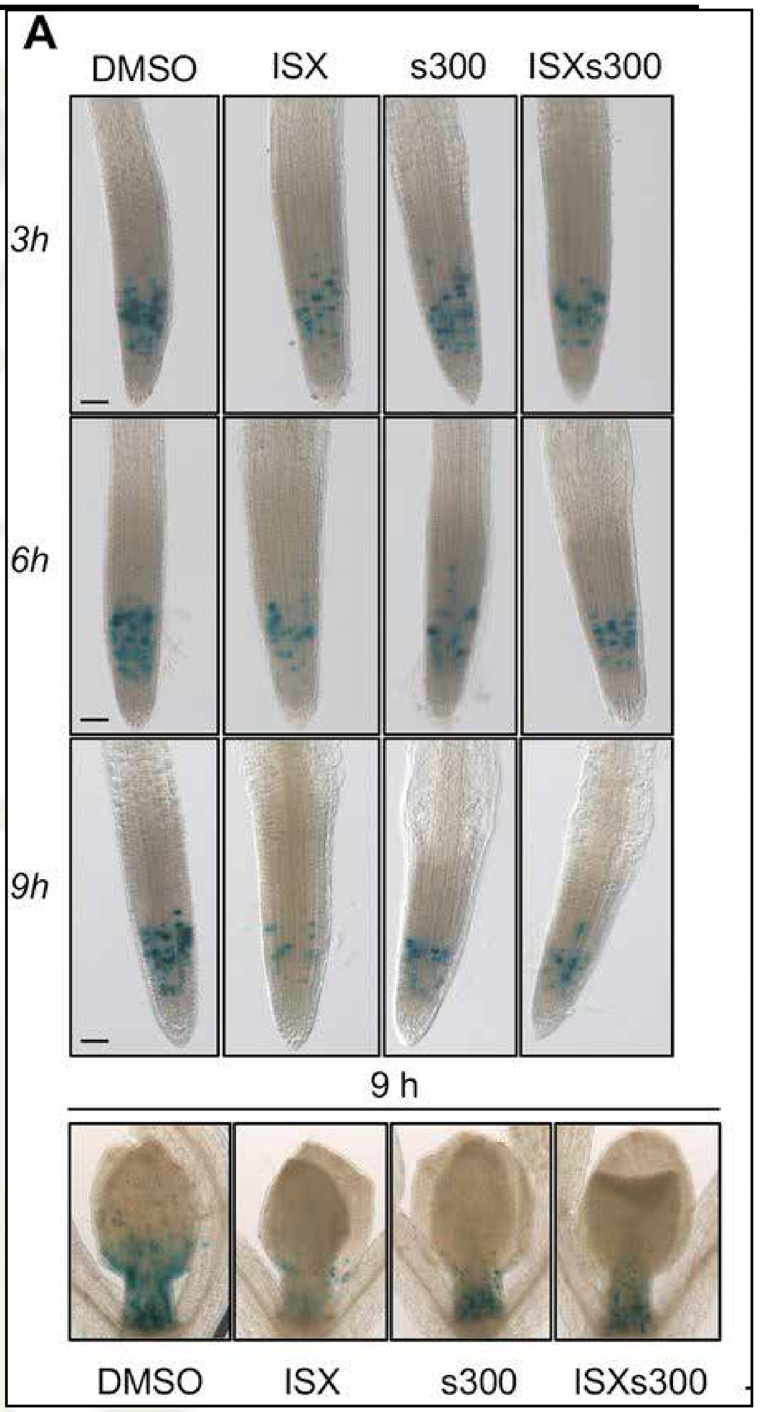

Figure 37. ISX-induced reduction of CYCB1;1 and CYCD3;1 transcript levels is attenuated by sorbitol co-treatment. (A) Representative images of pCYCB1;1::CYCB1;1:GUS seedlings treated with DMSO, ISX, s300 or ISXs300 for different periods and stained for GUS activity (n=15).

Poland

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Use of Arabidopsis

Arabidopsis thaliana has turned out to be a very successful model to study different aspects of Plant Sciences. At present numerous research groups in Poland use this plant as a major research object. This is reflected by growing population of research grants and publications of Polish scientists.

The main granting institution – National Science Center Poland (https://www.ncn.gov.pl), creates positive environment for basic research in Poland. Most successful Arabidopsis research topics are related to RNA molecular biology and molecular aspects of transcriptional and posttranscriptional regulation. Recently we can also see more independent groups working on physiological aspects of plant adaptation to adverse environmental conditions as well as successful research groups whose work aims at understanding of various plant-pathogen interactions. It is also remarkable that more frequently our researchers explore genetic diversity in Arabidopsis to address fundamental biological questions or to support research on crop plants.

Similarly to other European countries we are also facing the fact that GMO plants cannot be commercially used. This fact has downgrading impact on translational applied plant research where findings on Arabidopsis can be transferred to important crop plants. Never the less we can observe slow but significant development of initiatives where Arabidopsis brings solutions for plant breeding and other sectors of agriculture.

It is our mission as Arabidopsis community to explain the system and its usefulness to crop researchers and industrial entities. The future work in Poland is to highlight the importance of research conducted on this plant and to prevent the situation where strict division between basic and applied research occurs. In particular we need to support further development of "proof of concept" projects since this aspect has not been properly addressed in Poland.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

The mirEX - Arabidopsis pri-miRNA Expression Atlas
http://www.combio.pl/mirex1/

tRex –Database of tRNA-derived short fragments (tRFs) and tRNAs in *Arabidopsis thaliana*
http://combio.pl/trex

Conferences, Workshops and Outreach events

- Congres BIO2018, Gdansk 18-21 September 2018

- IPG PAS Integrative Plant Biology Conference, Poznan 7-9 November 2018

- The 44th FEBS Congress, Krakow 6-11 July 2019

- 9th Conference of the Polish Society of Experimental Plant Biology, Torun 9-12 September 2019

- 7th Central European Congress of Life Sciences EUROBIOTECH 2019, Kraków 23-25 September 2019

Selected Publications

Knop, K., Stepien, A., Barciszewska-Pacak, M., Taube, M., Bielewicz, D., Michalak, M., Borst, J.W., Jarmolowski, A., and Szweykowska-Kulinska, Z. (2016). Active 5' splice sites regulate the biogenesis efficiency of Arabidopsis microRNAs derived from intron-containing genes. Nucleic Acids Research 45, 2757-2775.

Pislewska-Bednarek, M., Nakano, R.T., Hiruma, K., Pastorczyk, M., Sanchez-Vallet, A., Singkaravanit-Ogawa, S., Ciesiołka, D., Takano, Y., Molina, A., Schulze-Lefert, P., and Bednarek, P. (2018). Glutathione Transferase U13 Functions in Pathogen-Triggered Glucosinolate Metabolism. Plant physiology 176, 538-551.

Rozpadek, P., Nosek, M., Domka, A., Wazny, R., Jedrzejczyk, R., Tokarz, K., Pilarska, M., Niewiadomska, E., and Turnau, K. (2019). Acclimation of the photosynthetic apparatus and alterations in sugar metabolism in response to inoculation with endophytic fungi. Plant, Cell & Environment 42, 1408-1423.

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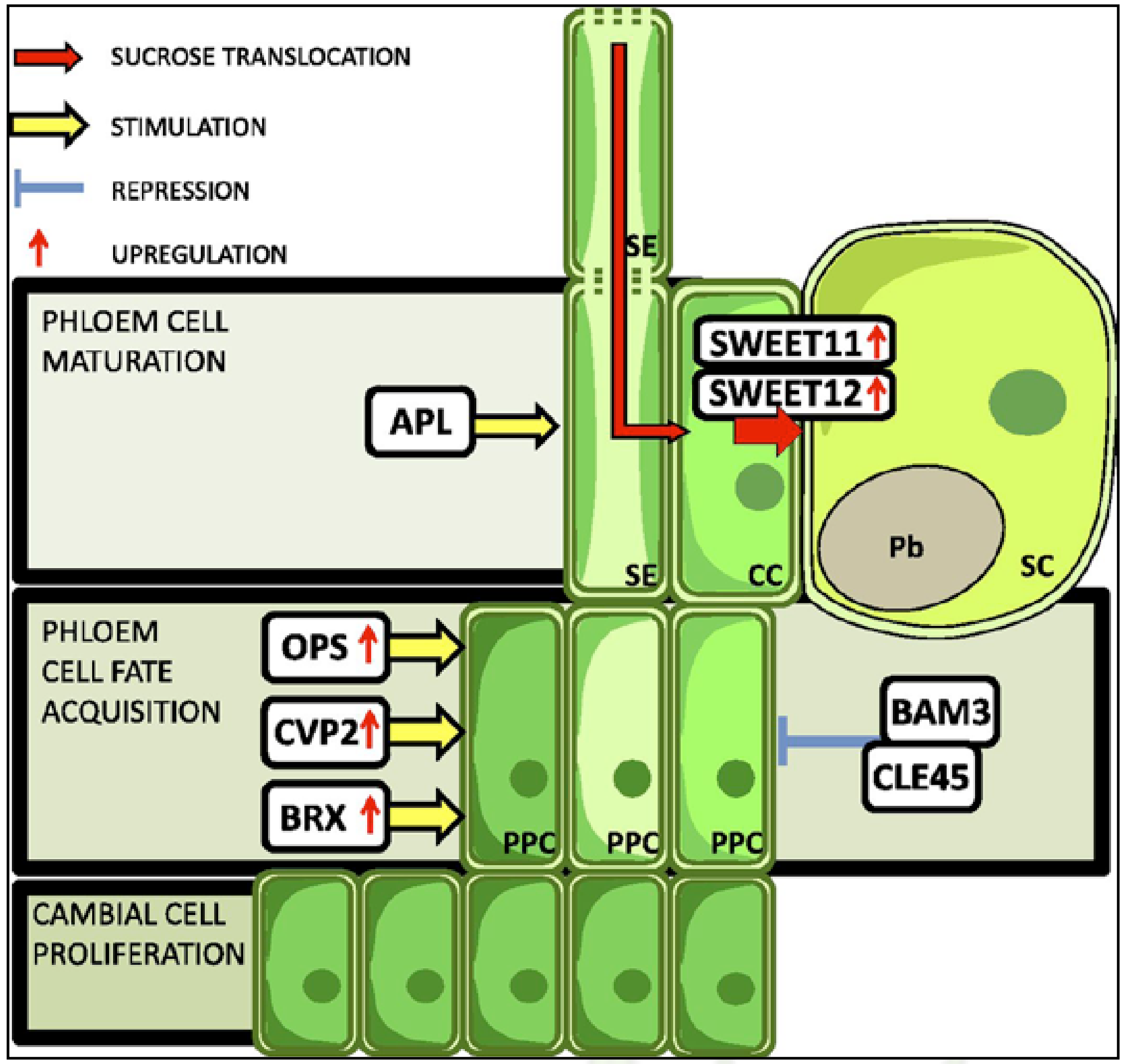


Figure 38. Schematic Representation of the P. brassicae-Driven Developmental Phloem Reprogramming and Stimulation of Sucrose Transport to Pathogen-Colonized Cells.

Szechynska-Hebda, M., Kruk, J., Górecka, M., Karpinska, B., and Karpinski, S. (2010). Evidence for Light Wavelength-Specific Photoelectrophysiological Signaling and Memory of Excess Light Episodes in Arabidopsis The Plant Cell 22, 2201

Walerowski, P., Gündel, A., Yahaya, N., Truman, W., Sobczak, M., Olszak, M., Rolfe, S., Borisjuk, L., and Malinowski, R. (2018). Clubroot Disease Stimulates Early Steps of Phloem Differentiation and Recruits SWEET Sucrose Transporters within Developing Galls. The Plant Cell 30, 3058-3073.

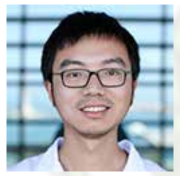
Zmienko, A., Samelak-Czajka, A., Kozlowski, P., Szymanska, M., and Figlerowicz, M. (2016). Arabidopsis thaliana population analysis reveals high plasticity of the genomic region spanning MSH2, AT3G18530 and AT3G18535 genes and provides evidence for NAHR-driven recurrent CNV events occurring in this location. BMC Genomics 17, 893.

Major Funding Sources

National Science Center Poland
https://www.ncn.gov.pl

Foundation for Polish Science
https://www.fnp.org.pl

Saudi Arabia



Yunhe Jiang
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King Abdullah University of Science and Technology (KAUST)

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018/ early 2019.

MVApp, Multivariate analysis application for streamlined data analysis and curation
http://mvapp.kaust.edu.sa/MVApp/

Julkowska, M.M., Saade, S., Gao, G., Morton, M.J.L., Awlia, M., Tester, M.A., MVApp.pre-release_v2.0 mmjulkowska/MVApp: MVApp.pre-release_v2.0, https://zenodo.org/record/1067974#.XMcDWaZ7mfU

Conferences, Workshops and Outreach events

Plant Science workshop, Thuwal, Saudi Arabia, April 14-25, 2019
https://psws.kaust.edu.sa/

Selected Publications

Abuauf, H., Haider, I., Jia, K.-P., Ablazov, A., Mi, J., Blilou, I., and Al-Babili, S. (2018). The *Arabidopsis* DWARF27 gene encodes an all-trans-/9-cis-B-carotene isomerase and is induced by auxin, abscisic acid and phosphate deficiency. Plant Science 277, 33-42.

Al-Younis, I., Wong, A., Lemtiri-Chlieh, F., Schmöckel, S., Tester, M., Gehring, C., and Donaldson, L. (2018). The *Arabidopsis thaliana* K+-Uptake Permease 5 (AtKUP5) Contains a Functional Cytosolic Adenylate Cyclase Essential for K+ Transport. Frontiers in Plant Science 9.

Aman, R., Mahas, A., Butt, H., Aljedaani, F., and Mahfouz, M. (2018). Engineering RNA Virus Interference via the CRISPR/Cas13 Machinery in *Arabidopsis*. Viruses 10.

de Zélicourt, A., Synek, L., Saad, M.M., Alzubaidy, H., Jalal, R., Xie, Y., Andrés-Barrao, C., Rolli, E., Guerard, F., Mariappan, K.G., Daur, I., Colcombet, J., Benhamed, M., Depaepe, T., Van Der Straeten, D., and Hirt, H. (2018). Ethylene induced plant stress tolerance by Enterobacter sp. SA187 is mediated by 2keto4methylthiobutyric acid production. PLoS genetics 14, e1007273.

Eida, A.A., Ziegler, M., Lafi, F.F., Michell, C.T., Voolstra, C.R., Hirt, H., and Saad, M.M. (2018). Desert plant bacteria reveal host influence and beneficial plant growth properties. PLOS ONE 13, e0208223.

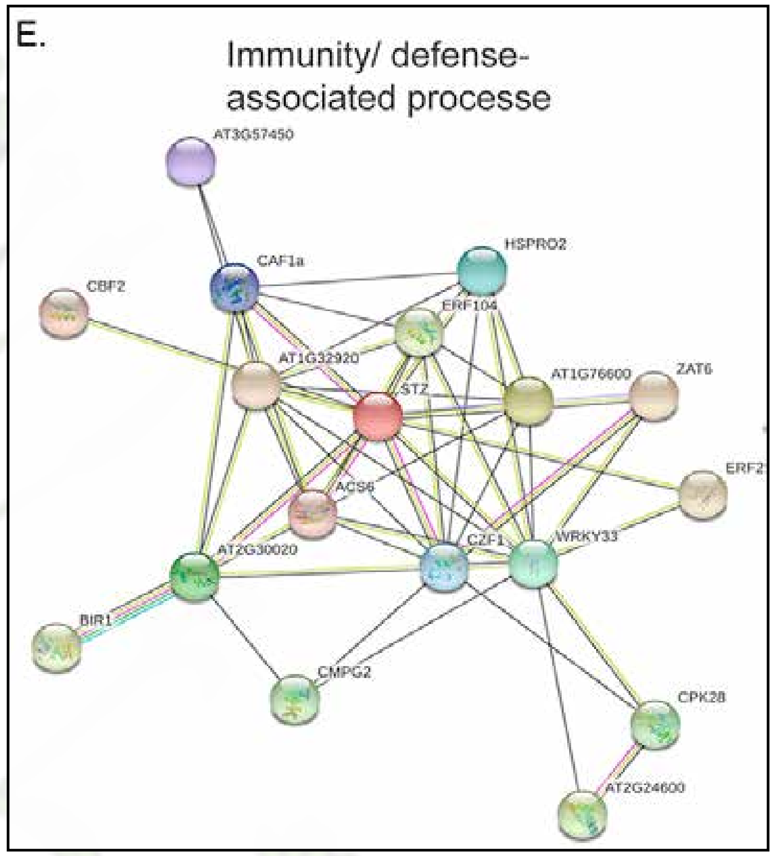

Figure 39. Genome-wide identification of IDD4 chromatin-bound regions and functional categorization of primary target genes. Protein interaction networks derived from the IDD4 ChIP-SEQ targets. All significant IDD4 ChIP-SEQ targets were pooled and used to generate a network using STRING (version 10.0). Minimum required interaction score defined as high confidence 0.700, Meaning of network edges "evidence".

Serrano, N., Ling, Y., Mahfouz, M.M., Veluchamy, A., Gehring, C., Gao, G., Benhamed, M., Woo, Y.H., Atia, M., Mokhtar, M., Bazin, J., Crespi, M., and Reddy, A.S.N. (2018). Thermopriming triggers splicing memory in *Arabidopsis*. Journal of Experimental Botany 69, 2659-2675.

Völz, R., Kim, S.-K., Mi, J., Rawat, A.A., Veluchamy, A., Mariappan, K.G., Rayapuram, N., Daviere, J.-M., Achard, P., Blilou, I., Al-Babili, S., Benhamed, M., and Hirt, H. (2019). INDETERMINATE-DOMAIN 4 (IDD4) coordinates immune responses with plant-growth in *Arabidopsis thaliana*. PLOS Pathogens 15, e1007499.

Major Funding Sources

King Abdullah University of Science and Technology.

Singapore

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Use of Arabidopsis

Arabidopsis research in Singapore is mainly led by PIs at the National University of Singapore (NUS), Temasek Life Sciences Laboratory (TLL) and Nanyang Technological University (NTU).

Plant research community in Singapore also includes researchers working on rice and leafy vegetables to which knowledges gained in Arabidopsis research is actively being transferred and vice versa. Despite being small in an urban setting, research community in Singapore embraces big challenges in environmental sustainability and food security by advancing our basic understanding on plants using Arabidopsis as a major model system.

Our areas of research is diverse with complementary strengths, ranging from developmental biology, plant immunity, stress biology, evolutionary genetics, and stem cell biology.

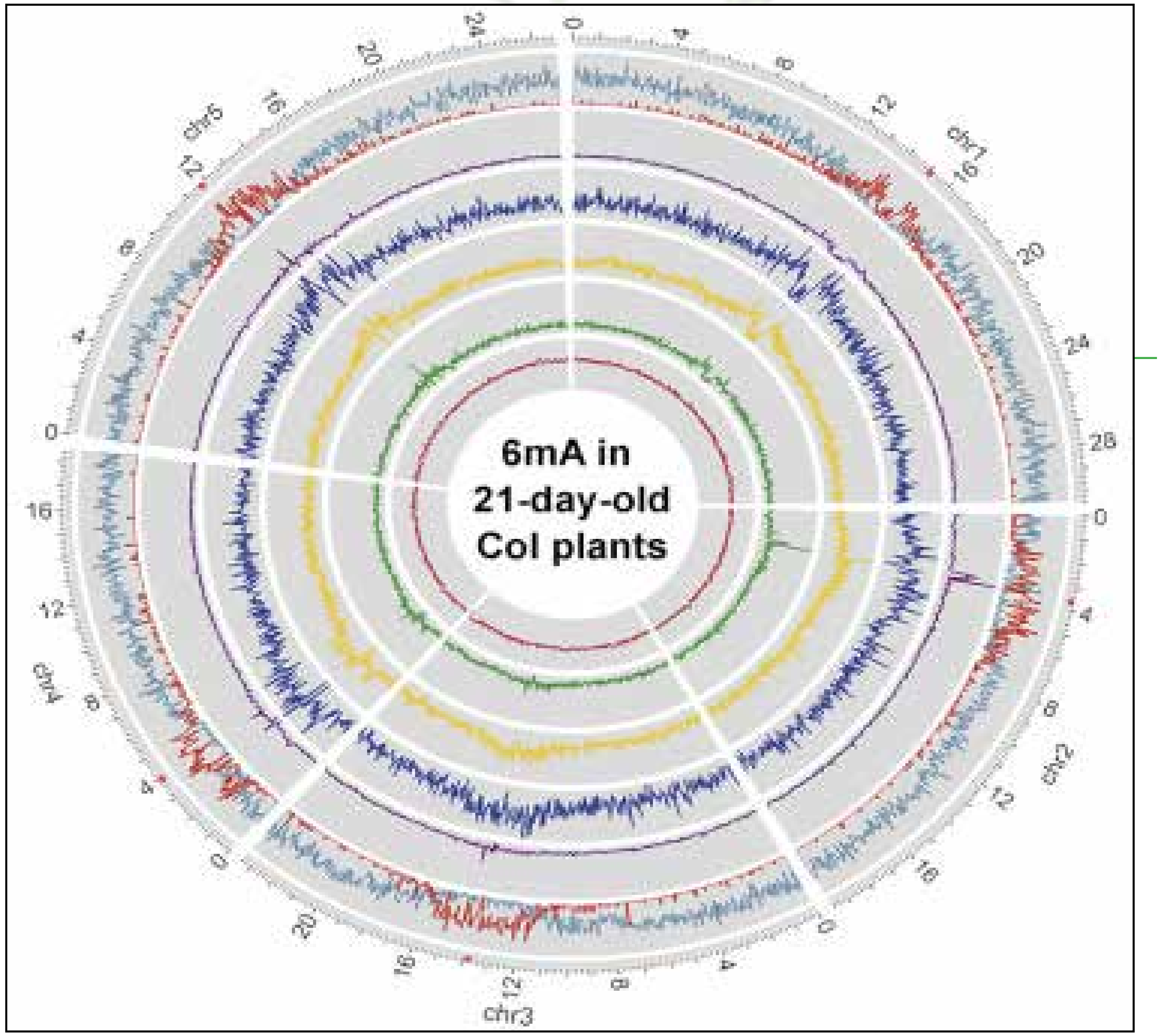

Figure 40: DNA N6-Adenine Methylation in *Arabidopsis thaliana*

Conferences, Workshops and Outreach events

18th International Congress of Developmental Biology (June 18-22, 2017)
http://isdb2017.com/

RNA Biology Symposium (September 13-14, 2018)
https://www.csi.nus.edu.sg/ws/rna-biology-symposium

10th Anniversary Conference, Mechanobiology Institute, National University of Singapore (November 7-10, 2018)
https://mbi.nus.edu.sg/mbi-10th-anniversary-conference/

Molecular mechanisms of developmental and regenerative biology (November 11-13, 2018)
http://meetings.embo.org/event/18-devandregeneration

Selected Publications

Hong JH, Savina M, Du J, Devendran A, Kannivadi Ramakanth K, Tian X, Sim WS, Mironova VV, Xu J (2017) A Sacrifice-for-Survival Mechanism Protects Root Stem Cell Niche from Chilling Stress. Cell. 170(1):102-113.e14. doi: 10.1016/j.cell.2017.06.002.

Lau OS, Song Z, Zhou Z, Davies KA, Chang J, Yang X, Wang S, Lucyshyn D, Tay IHZ, Wigge PA, Bergmann DC (2018) Direct Control of SPEECHLESS by PIF4 in the High-Temperature Response of Stomatal Development. Curr Biol. Apr 23;28(8):1273-1280.e3. doi: 10.1016/j.cub.2018.02.054.

Li C, Zhang B, Chen B, Ji L, Yu H (2018) Site-specific phosphorylation of TRANSPARENT TESTA GLABRA1 mediates carbon partitioning in Arabidopsis seeds. Nat Commun. 9(1):571. doi: 10.1038/s41467-018-03013-5.

Li X, Tu H, Pan SQ (2018) Agrobacterium Delivers Anchorage Protein VirE3 for Companion VirE2 to Aggregate at Host Entry Sites for T-DNA Protection. Cell Rep. 25(2):302-311.e6. doi: 10.1016/j.celrep.2018.09.023.

Liang Z, Shen L, Cui X, Bao S, Geng Y, Yu G, Liang F, Xie S, Lu T, Gu X, Yu H (2018) DNA N6-Adenine Methylation in *Arabidopsis thaliana*. Dev Cell. 45(3):406-416.e3. doi: 10.1016/j.devcel.2018.03.012.

Park BS, Yao T, Seo JS, Wong ECC, Mitsuda N, Huang CH, Chua NH (2018) Arabidopsis NITROGEN LIMITATION ADAPTATION regulates ORE1 homeostasis during senescence induced by nitrogen deficiency. Nat Plants. 4(11):898-903. doi: 10.1038/s41477-018-0269-8.

Ravindran P, Kumar PP (2019) Regulation of Seed Germination: The Involvement of Multiple Forces Exerted via Gibberellic Acid Signaling. Mol Plant. 12(1):24-26. doi: 10.1016/j.molp.2018.12.013.

Ravindran P, Verma V, Stamm P, Kumar PP (2017) A Novel RGL2-DOF6 Complex Contributes to Primary Seed Dormancy in *Arabidopsis thaliana* by Regulating a GATA Transcription Factor. Mol Plant. 10(10):1307-1320. doi: 10.1016/j.molp.2017.09.004.

Seo JS, Sun HX, Park BS, Huang CH, Yeh SD, Jung C, Chua NH (2018) ELF18-INDUCED LONG-NONCODING RNA Associates with Mediator to Enhance Expression of Innate Immune Response Genes in Arabidopsis. Plant Cell. 29(5):1024-1038. doi: 10.1105/tpc.16.00886

Sun H, Qiao Z, Chua KP, Tursic A, Liu X, Gao YG, Mu Y, Hou X, Miao Y (2018) Profilin Negatively Regulates Formin-Mediated Actin Assembly to Modulate PAMP-Triggered Plant Immunity. Curr Biol. 28(12):1882-1895.e7. doi: 10.1016/j.cub.2018.04.045.

Tao Z, Shen L, Gu X, Wang Y, Yu H, He Y (2017) Embryonic epigenetic reprogramming by a pioneer transcription factor in plants.Nature. 2;551(7678):124-128. doi: 10.1038/nature24300

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/

Agri-Food and Veterinary Authority of Singapore (AVA)
https://www.ava.gov.sg/

Temasek Foundation Innovates
http://www.temasekfoundation-innovates.org.sg/

South Korea

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Pohang University of Science and Technology

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018/ early 2019.

- Next generation breeding program, will be starting in the second half of 2019 focusing on genome editing, approximately 7M USD/yr for 7 years.

Conferences, Workshops and Outreach events

- In year 2019, Cold Spring Harbor Asia conference on plant cell and development

Selected Publications

- Han S, Cho H, Noh J, Qi J, Jung HJ, Nam H, Lee S, Hwang D, Greb T, Hwang I (2018) BIL1-mediated MP phosphorylation integrates PXY and cytokinin signaling in secondary growth. Nat Plants. 4:605-614.

- Kang BC, Yun JY, Kim ST, Shin Y, Ryu J, Choi M, Woo JW, Kim JS. (2018) Precision genome engineering through adenine base editing in plants. Nat Plants. 4:427-431.

- Kim H, Kim HJ, Vu QT, Jung S, McClung CR, Hong S, Nam HG. (2018) Circadian control of ORE1 by PRR9 positively regulates leaf senescence in *Arabidopsis*. Proc Natl Acad Sci U S A. 115:8448-8453.

- Kim JY, Yang W, Forner J, Lohmann JU, Noh B, Noh YS. (2018) Epigenetic reprogramming by histone acetyltransferase HAG1/AtGCN5 is required for pluripotency acquisition in *Arabidopsis*. EMBO J. 37. pii: e98726.

- Kim TW, Youn JH, Park TK, Kim EJ, Park CH, Wang ZY, Kim SK, Kim TW. (2018) OST1 Activation by the Brassinosteroid-Regulated Kinase CDG1-LIKE1 in Stomatal Closure. Plant Cell. 30:1848-1863.

- Kwon Y, Shen J, Lee MH, Geem KR, Jiang L, Hwang I. (2018) AtCAP2 is crucial for lytic vacuole biogenesis during germination by positively regulating vacuolar protein trafficking. Proc Natl Acad Sci U S A. 115:E1675-E1683.

- Lee HG, Seo PJ. (2019) MYB96 recruits the HDA15 protein to suppress negative regulators of ABA signaling in *Arabidopsis*. Nat Commun. 10:1713.

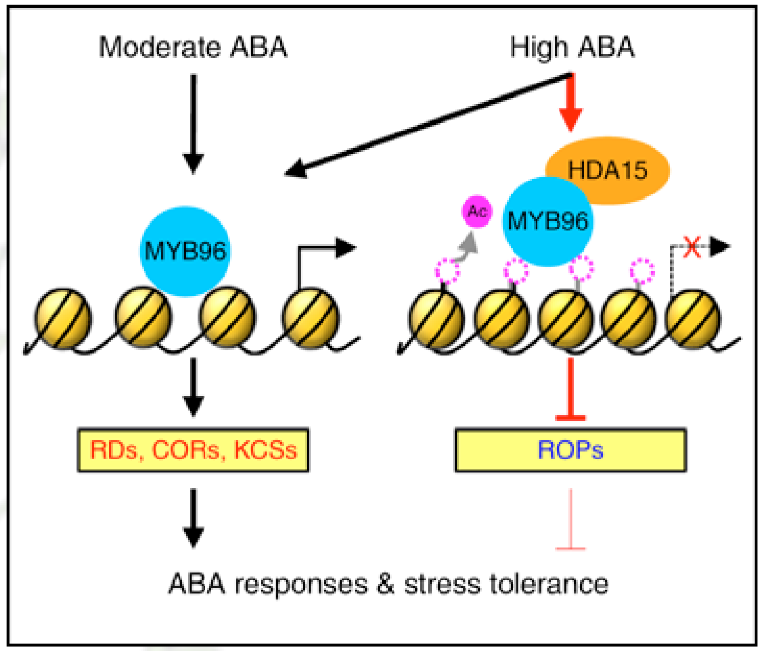

Figure 41. Proposed working model. In the presence of abscisic acid (ABA), MYB96 alone is sufficient to promote expression of ABA-induced genes, including KCS genes. However, MYB96 requires HDA15 to repress the ABA-repressed genes ROP6, ROP10, and ROP11. MYB96 interacts with HDA15 especially at high concentrations of ABA. MYB96 and HDA15 bind to the ROP promoters and repress expression by promoting H3 and H4 deacetylation. MYB96 confers strong ABA responses by simultaneously activating positive regulators and suppressing negative regulators of ABA signaling

- Lee Y, Yoon TH, Lee J, Jeon SY, Lee JH, Lee MK, Chen H, Yun J, Oh SY, Wen X, Cho HK, Mang H, Kwak JM. (2018) A Lignin Molecular Brace Controls Precision Processing of Cell Walls Critical for Surface Integrity in *Arabidopsis*. Cell. 173:1468-1480.e9.

- Nguyen HH, Lee MH, Song K, Ahn G, Lee J, Hwang I. (2018) The A/ENTH Domain-Containing Protein AtECA4 Is an Adaptor Protein Involved in Cargo Recycling from the trans-Golgi Network/Early Endosome to the Plasma Membrane. Mol Plant. 11:568-583.

- Park HJ, Baek D, Cha JY, Liao X, Kang SH, McClung CR, Lee SY, Yun DJ, Kim WY. (2019) HOS15 Interacts with the Histone Deacetylase HDA9 and the Evening Complex to Epigenetically Regulate the Floral Activator GIGANTEA. Plant Cell. 31:37-51.

Major Funding Sources

- National Research Funding (Korea)
https://www.nrf.re.kr/

- Rural Development Agency (Korea)
https://www.rda.go.kr/

Spain

José Luis Micol
jlmicol@umh.es
Universidad Miguel Hernández,
Elche, Spain

Use of Arabidopsis

About 100 laboratories.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

Some software packages were made available to the community, including:

“Easymap: a program that eases mapping-by-sequencing of large insertions and point mutations.”, developed by D. Wilson-Sánchez, S.D. Lup, S. Andreu-Sánchez and J.L. Micol. Available at http://genetics.edu.umh.es/resources/easymap/

“MyROOT: a method and software for the semiautomatic measurement of primary root length in Arabidopsis seedlings”, developed by I. Betegón, Putze, A. González, X. Sevillano, D. Blasco-Escámez, A.I. Caño-Delgado. Available at https://www.cragenomica.es/research-groups/brassinosteroid-signaling-in-plant-development

Conferences, Workshops and Outreach events

- The “XIV Meeting on Plant Molecular Biology” was organized by plant biologists lead by Prof. Óscar Lorenzo in Salamanca (July 4-6, 2018).

- The “III Workshop on New Frontiers in Plant Biology” was organized by members of the Center of Plant Biotechnology and Genomics lead by Prof Antonio Molina in Madrid (May 30-June 1, 2018).

- The “At the Forefront of Plant Research 2019” workshop was organized by members of the Centre for Research in Agricultural Genomics lead by Prof José Luis Riechmann in Barcelona (May 6-8, 2019).

- SEB Annual Meeting: July 2nd-5th, Sevilla:
http://www.sebiology.org/events/event/seb-seville-2019

- SEB Plant and Cell Symposium on Impact of chromatin domains on plant phenotypes: December 9th-11th, El Escorial, near Madrid Spain.
https://www.sebiology.org/events/event/impact-of-chromatin-domains-on-plant-phenotypes

Selected Publications

Abbas M, Hernández-García J, Pollmann S, Samodelov SL, Kolb M, Friml J, Hammes UZ, Zurbriggen MD, Blázquez MA and Alabadí D (2018) Auxin methylation is required for differential growth in Arabidopsis. PNAS 115: 6864-6869.

Figure 42. Discovered a novel regulatory mechanism for acclimation of plants to cold
http://cib.csic.es/news/research/discovered-novel-regulatory-mechanism-acclimation-plants-cold

Fábregas N, Lozano-Elena F, Blasco-Escámez D, Tohge T, Martínez-Andújar C, Albacete A, Osorio S, Bustamante M, Riechmann JL, Nomura T, Yokota T, Conesa A, Alfocea FP, Fernie AR and Caño-Delgado AI (2018) Overexpression of the vascular brassinosteroid receptor BRL3 confers drought resistance without penalizing plant growth. Nature Communications 9: 4680.

Gómez-Zambrano A, Crevillén P, Franco-Zorrilla JM, López JA, Moreno-Romero J, Roszak P, Santos-González J, Jurado S, Vázquez J, Kohler C, Solano R, Piñeiro M and Jarillo JA (2018) *Arabidopsis* SWC4 binds DNA and recruits the SWR1 Complex to modulate histone H2A.Z deposition at key regulatory genes. Molecular Plant 11: 815-832.

Huertas R, Catalá R, Jiménez-Gómez JM, Castellano MM, Crevillén P, Piñeiro M, Jarillo JA and Salinas J (2019) Arabidopsis SME1 regulates plant development and response to abiotic stress by determining spliceosome activity specificity. Plant Cell 31: 537-554.

Martínez C, Espinosa-Ruíz A, de Lucas M, Bernardo-García S, Franco-Zorrilla JM and Prat S (2018) PIF4-induced BR synthesis is critical to diurnal and thermomorphogenic growth. EMBO Journal 37: e99552.

Mateo-Bonmatí E, Esteve-Bruna D, Juan-Vicente L, Nadi R, Candela H, Lozano FM, Ponce MR, Pérez-Pérez JM and Micol JL (2018) INCURVATA11 and CUPULIFORMIS2 are redundant genes that encode epigenetic machinery components in Arabidopsis. Plant Cell 30: 1596-1616.

Ojeda V, Pérez-Ruiz JM and Cejudo FJ (2018) 2-cys peroxiredoxins participate in the oxidation of chloroplast enzymes in the dark. Molecular Plant 11: 1377-1388.

Olate E, Jiménez-Gómez JM, Holuigue L and Salinas J (2018) NPR1 mediates a novel regulatory pathway in cold acclimation by interacting with HSFA1 factors. Nature Plants 4: 811-823.

Ortiz-Alcaide M, Llamas E, Gómez-Cadenas A, Nagatani A, Martínez-García JF and Rodríguez-Concepción M (2019) Chloroplasts modulate elongation responses to canopy shade by retrograde pathways Involving HY5 and Abscisic Acid. Plant Cell 31: 384-398.

Sánchez-Montesino R, Bouza-Morcillo L, Márquez J, Ghita M, Durán-Nebreda S, Gómez L, Holdsworth MJ, Bassel G and Oñate-Sánchez L (2019) A regulatory module controlling GA-mediated endosperm cell expansion is critical for seed germination in Arabidopsis. Molecular Plant 12: 71-85.

Major Funding Sources

About 80 grants from the State Research Agency of Spain (Ministry of Science, Innovation and Universities) fund *Arabidopsis* research projects at individual laboratories.

Additional Information

Authors from laboratories studying *Arabidopsis* in Spain published about 400 papers in the last year. Prof. Crisanto Gutiérrez was awarded a European Research Council Advanced Grant ("Exploiting genome replication to design improved plant growth strategies").

Prof. José Luis Micol was elected President of the Genetics Society of Spain.

Sweden

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Umeå University, Umeå Plant Science Centre, Umeå

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

National resources available to the Arabidopsis community

- 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/

New Software Tools

The PlantGenIE platform; web portals for enabling in-depth exploration of poplar, Norway spruce, and *Arabidopsis* http://plantgenie.org/

Computational Genetics Division Uppsala University, Carlborg Lab
http://www.computationalgenetics.se/

Conferences, Workshops and Outreach events

15-16 March, 2018, Lund 'Promoting Plant Research'. The meeting was organized
by PlantLink in collaboration with Umeå Plant Science Center and the Linnaean Center for Plant Biology focusing on Swedish plant research.

18 May, 2019 'Fascination of Plants Day' is celebrated at most major plant science centres across Sweden

27 August, 2019, Stockholm, Symposium of the Royal Swedish Academy of Sciences (KVA), 'How can basic plant science contribute to feeding the world?'

28-30 August, 2019, Umeå. SPPS2019 Scandinavian Plant Physiology Society's Congress

Selected Publications

Chahtane, H; Zhang, B; Norberg, M.; *et al* (2018) LEAFY activity is post-transcriptionally regulated by BLADE ON PETIOLE2 and CULLIN3 in *Arabidopsis* New Phytologist 220, 579-592

Edwards, KD; Takata, N; Johansson, M.; *et al* (2018) Circadian clock components control daily growth activities by modulating cytokinin levels and cell division-associated gene expression in Populus trees Plant Cell and Environment 41, 1468-1482

Kumar, KRR; Blomberg J; Bjorklund, S (2018) The MED7 subunit paralogs of Mediator function redundantly in development of etiolated seedlings in *Arabidopsis* Plant Journal 96, 578-594

Moreno-Romero, J; Del Toro-De Leon, G; Yadav, VK.; *et al* (2019) Epigenetic signatures associated with imprinted paternally expressed genes in the *Arabidopsis* endosperm Genome Biology 20, 41

Mozgova, I; Wildhaber, T; Trejo-Arellano, MS.; *et al* (2018) Transgenerational phenotype aggravation in CAF-1 mutants reveals parent-of-origin specific epigenetic inheritance New Phytologist 220, 908-921

Singh, RK; Maurya, JP; Azeez, A *et al* (2018) A genetic network mediating the control of bud break in hybrid aspen Nature Communications 9, 4173

Singh, RK; Miskolczi, P; Maurya, JP.; *et al* (2019) A Tree Ortholog of SHORT VEGETATIVE PHASE Floral Repressor Mediates Photoperiodic Control of Bud Dormancy Current Biology 29, 128-133

Tylewicz, S; Petterle, A; Marttila, S.; *et al* (2018) Photoperiodic control of seasonal growth is mediated by ABA acting on cell-cell communication. (2018) Science 360, 212-214

Wang, J; Ding, J; Tan, B.; *et al* (2018) A major locus controls local adaptation and adaptive life history variation in a perennial plant Genome Biology 19; 72

Zan, Y; Carlborg, Ö (2019) A Polygenic Genetic Architecture of Flowering Time in the Worldwide *Arabidopsis thaliana* Population Molecular Biology and Evolution 36, 141-154

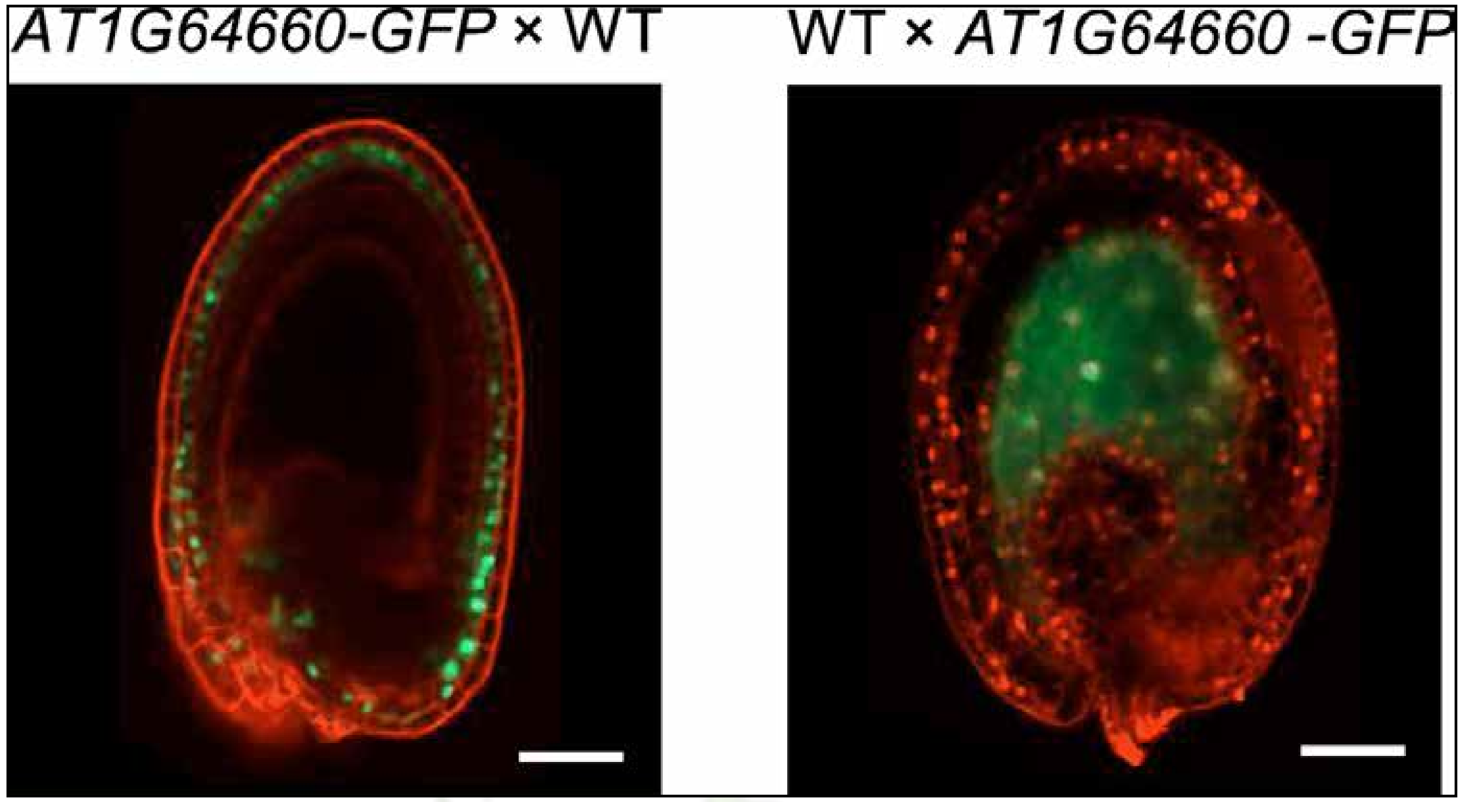


Figure 43. Reporter lines for AT1G64660 confirm imprinted expression. Representative images of seeds derived after reciprocal crosses of the AT1G64660 reporter line (fusion with green fluorescent protein (GFP)) with wild-type (WT) plants. GFP fluorescence was detected in the seed coat when the AT1G64660 reporter was maternally inherited, but endosperm-specific expression was only detected when the AT1G64660 reporter was paternally inherited. Seeds at 2 DAP were used for imaging. Red stain is propidium iodide. Scale bars correspond to 50 µm

Major Funding Sources

- The Swedish Research Council (VR; http://www.vr.se) a core funder of researcher-initiated basic research.

- The Swedish Foundation for Strategic Research (http://www.stratresearch.se) supports strategic research in natural science, engineering and medicine.

- The Swedish Agency for Innovation Systems (VINNOVA; http://www.vinnova.se) promotes sustainable growth by funding needs-driven research and the development of effective innovation systems.

- The Royal Academy of Science/ (http://www.kva.se) Agriculture and Forestry (http://www.ksla.se)

- The Swedish Research Council Formas (http://www.formas.se) supports basic research and need-driven research in the areas Environment, Agricultural Sciences and Spatial Planning.

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

- Carl Tryggers Foundation for Scientific Research (http://www.carltryggersstiftelse.se/) is a private foundation supporting research within the areas of agriculture, forestry, biology, chemistry and physics.

- The Kempe Foundations (http://www.kempe.com) private foundations devoted to support scientific research in Northern Sweden

- Stiftelsen Olle Engkvist Byggmästare (http://engkviststiftelserna.se/)

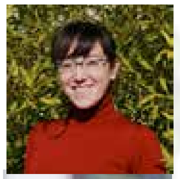
- Sven and Lily Lawski's foundation for research in Natural Sciences (Biochemistry and Genetics); http://www.lawskistiftelsen.se/ A private foundation supporting basic science

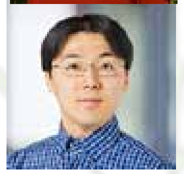
Two plant scientists have been selected to be 'Wallenberg Scholars' and will receive 18 million Swedish krona each from the Wallenberg Foundations in the form of a five-year grant for free research:

Claudia Köhler, Professor of Molecular Plant Cell Biology, Swedish University of Agricultural Sciences, Uppsala

Markus Schmid, Professor in Plant Physiology, Umeå University, Umeå

Switzerland





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Swiss Plant Science Web
coordination-spsw@unibas.ch

Use of Arabidopsis

c.a. 12 institutions and c.a 100 labs.

2019 Highlights
- Trinational Arabidopsis meeting will be held in Zurich in April 2019.

Switzerland has had regularly a high-quality publications (e.g. Paape T *et al*., Nat Commun. 2018, Schumacher P *et al*., Nat Commun. 2018, Schmid MW *et al*., Nat Commun. 2018, Hohmann U *et al*., Nat Plants. 2018, Song YH *et al*.,Nat Plants. 2018).

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

- Software tools
- Homeolog expression quantification methods for allopolyploids

Kuo TCY, Hatakeyama M, Tameshige T, Shimizu KK, Sese J. Brief Bioinform. 2018 Dec 27.
doi: 10.1093/bib/bby121.

- Resources

Rapid extraction of living primary veins from the leaves of *Arabidopsis thaliana*.
Kurenda A, Farmer EE.
Protocol Exchange (2018)
doi:10.1038/protex.2018.119

Conferences, Workshops and Outreach events

Conferences
- PSC Summer school 2018, Responsible Research and Innovation in Plant Sciences, 10 – 14 Sep 2018, Einsiedeln
https://www.plantsciences.uzh.ch/dam/jcr:e9880fdf-8519-4805-b551-29705dbbea29/Flyer_PSC_Summer_School_2018_final%5B2%5D.pdf

- Plant Receptor Kinases and Related Pathways, 30 Oct 2018, Zurich
https://www.botinst.uzh.ch/dam/jcr:c8706be2-9920-45f9-a570-e8692a2cbd60/Programm_RLK-Symposium.pdf

- PSC Symposium 2018, Breakthroughs in Plant Sciences, 5 Dec 2018, Zurich
https://www.plantsciences.uzh.ch/en/outreach/conferences/breakthroughs-in-plant-sciences.html

- SwissPLANT symposium 2019, 30 Jan - 1 Feb 2019, Meiringen
https://swissplantscienceweb.unibas.ch/fileadmin/user_upload/swissplantscienceweb/Event/Swissplant/swissplant2019_program_v2.pdf

- Lausanne Genomics Days 2019, 7 – 8 Feb 2019, Lausanne http://www.genomyx.ch/thur-feb-7-fri-feb-8-2019-lausanne-genomics-days-2019/

- Biology19, 7 – 8 Feb 2019, Zurich
https://www.biology19.ch/

- 11th TNAM (Tri-National *Arabidopsis* Meeting), 10-12 Apr 2019, Zurich
https://www.tnam2019.ethz.ch/

- SwissPLANT symposium 2020, 29 – 31 Jan 2020, Ovronnaz
https://swissplantscienceweb.unibas.ch/en/events/swissplant/

Workshops
Outreach Activities
- Plant Science at School

Continuing 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.html
http://www.snf.ch/en/funding/science-communication/agora/Pages/default.aspx

Selected Publications

Arongaus AB, Chen S, Pireyre M, Glöckner N, Galvão VC, Albert A, Winkler JB, Fankhauser C, Harter K, Ulm R (2018) Arabidopsis RUP2 represses UVR8-mediated flowering in noninductive photoperiods Genes Dev. 2018 Oct 1;32(19-20):1332-1343. doi: 10.1101/gad.318592.118.

de Wit M, George GM, Ince YÇ, Dankwa-Egli B, Hersch M, Zeeman SC, Fankhauser C (2018) Changes in resource partitioning between and within organs support growth adjustment to neighbor proximity in *Brassicaceae* seedlings. Proc Natl Acad Sci U S A. 115(42):E9953-E9961. doi: 10.1073/pnas.1806084115.

Hohmann U, Nicolet J, Moretti A, Hothorn LA, Hothorn M (2018) The SERK3 elongated allele defines a role for BIR ectodomains in brassinosteroid signalling. Nat Plants 4(6):345-351. doi: 10.1038/s41477-018-0150-9.

Nguyen CT, Kurenda A, Stolz S, Chételat A, Farmer EE (2018) Identification of cell populations necessary for leaf-to-leaf electrical signaling in a wounded plant Proc Natl Acad Sci U S A. 115(40):10178-10183. doi: 10.1073/pnas.1807049115.

Paape T, Briskine RV, Halstead-Nussloch G, Lischer HEL, Shimizu-Inatsugi R, Hatakeyama M, Tanaka K, Nishiyama T, Sabirov R, Sese J, Shimizu KK (2018) - Patterns of polymorphism and selection in the subgenomes of the allopolyploid *Arabidopsis* kamchatica. Nat Commun. 9(1):3909. doi: 10.1038/s41467-018-06108-1.

Schmid MW, Heichinger C, Coman Schmid D, Guthörl D, Gagliardini V, Bruggmann R, Aluri S, Aquino C, Schmid B, Turnbull LA, Grossniklaus U (2018) Contribution of epigenetic variation to adaptation in *Arabidopsis* Nat Commun. 9(1):4446. doi: 10.1038/s41467-018-06932-5

Schreier TB, Cléry A, Schläfli M, Galbier F, Stadler M, Demarsy E, Albertini D, Maier BA, Kessler F, Hörtensteiner S, Zeeman SC, Kötting O (2018) Plastidial NAD-Dependent Malate Dehydrogenase: A Moonlighting Protein Involved in Early Chloroplast Development through Its Interaction with an FtsH12-FtsHi Protease Complex Plant Cell 1745-1769. doi: 10.1105/tpc.18.00121.

Schumacher P, Demarsy E, Waridel P, Petrolati LA, Trevisan M, Fankhauser C (2018) A phosphorylation switch turns a positive regulator of phototropism into an inhibitor of the process Nat Commun. 9(1):2403. doi: 10.1038/s41467-018-04752-1.

Song YH, Kubota A, Kwon MS, Covington MF, Lee N, Taagen ER, Laboy Cintrón D, Hwang DY, Akiyama R, Hodge SK, Huang H, Nguyen NH, Nusinow DA, Millar AJ, Shimizu KK, Imaizumi T (2018) Molecular basis of flowering under natural long-day conditions in *Arabidopsis* Nat Plants. 4(10):824-835. doi: 10.1038/s41477-018-0253-3.

Major Funding Sources

1. Swiss National Science Foundation (SNSF) http://www.snf.ch/en/Pages/default.aspx
2. European Research Council (ERC), https://erc.europa.eu/
3. SystemsX.ch, http://www.systemsx.ch/
4. Syngenta (Plant Science Center - Syngenta Fellowship), https://www.plantsciences.uzh.ch/en/research/fellowships/syngenta.html
5. Research and Innovation Staff Exchange (RISE) of European Commission http://ec.europa.eu/research/mariecurieactions/about/research-innovation-staff-exchange_en
6. State Secretariat for Education, Research, and Innovation (SERI), https://www.sbfi.admin.ch/sbfi/en/home.html
7. University Research Priority Program of Evolution in Action: From Genomes to Ecosystems (directors: Beat Keller, Ueli Grossniklaus, University of Zurich) http://www.evolution.uzh.ch/en.html
8. Japan Science and Technology Agency (JST), Core Research for Evolutional Science and Technology (CREST), https://www.jst.go.jp/kisoken/crest/en/

Figure 44: Measuring wound-induced electrical signals in a 5 week-old *Arabidopsis* rosette. (By courtesy of Prof. Edward Elliston Farmer, University of Lausanne.)

Taiwan

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New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

Please provide a list of all resources based in your country that are accessible for use both by Arabidopsis researchers in your country and by the global community.

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 http://trim.sinica.edu.tw/

Conferences, Workshops and Outreach events

1. TAIWAN Prostate Cancer Consortium Mini-symposium.

2. Taiwan Protein Project (TPP) Symposium

3. EMBO Workshop- Neural Development

4. 2018 IPMB Scientific Advisory Board Meeting

5. 2018 NTU- CUHKPlant Biology Symposium

6. 19th International Symposium on Iron Nutrition and Interactions in Plants (ISINIP)

7. Global Leadership Summit Taiwan

8. NPAS Seminar: 2019 ASIA-PACIFIC DROSOPHILA NEUROBIOLOGY CONFERENCE

9. AS-NIH-TMU Joint Neuroscience Symposium

10. The 17th International Symposium on Rice Functional Genomics (ISRFG2019)

11. SFEM 2018/IUFRO 4.02.02

12. The 6th Taiwan–Japan Ecology Workshop

13. 7th ASIAN SYMPOSIUM OF FERNS & LYCOPHYTES

14. Frontiers in BioAgricultural Research: The 20th Anniversary of the Agricultural Biotechnology Research Center, Academia Sinica

15. 2019 Symposium on Biotechnology Development in Taiwan – Medical Structural Biology and Cryo-EM Technology

16. International Membrane Conference in Taiwan (IMCT2019)

17. International Conference on Planarization / CMP Technology (ICPT 2019)

18. The 2nd International Conference on Nanomaterials and Advanced Composites

Selected Publications

- Chao, Y.C., Fleischer, J., and Yang, R.B. (2018). Guanylyl cyclase-G is an alarm pheromone receptor in mice. EMBO J 37, 39-49.

- Chen, H.F., Hsu, C.M., and Huang, Y.S. (2018). CPEB2-dependent translation of long 3’-UTR Ucp1 mRNA promotes thermogenesis in brown adipose tissue. EMBO J 37.

- Chen, Y.L., Chen, L.J., Chu, C.C., Huang, P.K., Wen, J.R., and Li, H.M. (2018). TIC236 links the outer and inner membrane translocons of the chloroplast. Nature 564, 125-129.

- Grillet, L., Lan, P., Li, W., Mokkapati, G., and Schmidt, W. (2018). IRON MAN is a ubiquitous family of peptides that control iron transport in plants. Nat Plants 4, 953-963. 5.

- Li, F.W., Brouwer, P., Carretero-Paulet, L., Cheng, S., de Vries, J., Delaux, P.M., Eily, A., Koppers, N., Kuo, L.Y., Li, Z., *et al.* (2018). Fern genomes elucidate land plant evolution and cyanobacterial symbioses. Nat Plants 4, 460-472.

- Lin, P.P., Jaeger, A.J., Wu, T.Y., Xu, S.C., Lee, A.S., Gao, F., Chen, P.W., and Liao, J.C. (2018). Construction and evolution of an Escherichia coli strain relying on nonoxidative glycolysis for sugar catabolism. Proc Natl Acad Sci U S A 115, 3538-3546.

- Liu, C.P., Tsai, T.I., Cheng, T., Shivatare, V.S., Wu, C.Y., Wu, C.Y., and Wong, C.H. (2018). Glycoengineering of antibody (Herceptin) through yeast expression and in vitro enzymatic glycosylation. Proc Natl Acad Sci U S A 115, 720-725.

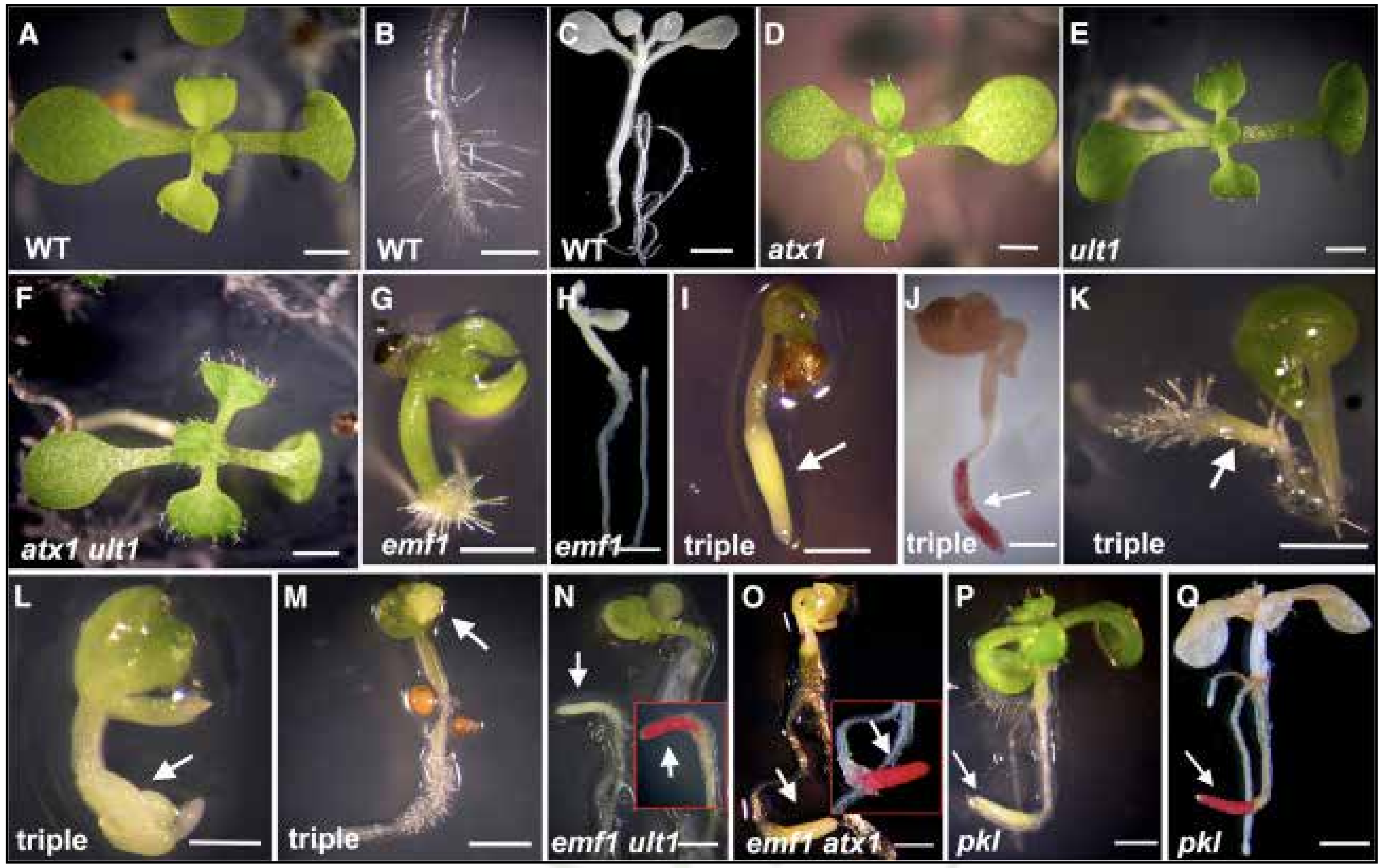

Figure 45 EMF1, ATX1, and ULT1 Together Prevent Excessive Seed Storage Reserve Accumulation Following Germination. (A and B) Wild-type (WT) seedling (A) and root (B). Scale bar, 1 mm.(C) Fat red-stained WT seedlings. Scale bar, 0.5 mm. (D–F) atx1 (D), ult1 (E), and atx1 ult1 (F) seedlings. Scale bars, 1 mm.(G) emf1 mutant seedling. Scale bar, 0.5 mm. (H) Fat red-stained emf1 seedling. Scale bar, 0.5 mm.(I) emf1 atx1 ult1 triple mutant (triple) with emf1-like shoot and swollen primary root tip (arrow). Scale bar, 0.5 mm.(J) Fat red-stained emf1 atx1 ult1 seedlings. Arrow indicates a Fat red-positive swollen root. Scale bar, 0.5 mm.(K–M) emf1 atx1 ult1 triple mutants. Arrows indicate the swollen primary root (K), embryo-like structures arising from hypocotyl (L), and callus-like tissues arising from cotyledon (M). Scale bar, 0.5 mm. (N) emf1 ult1 double mutant with swollen primary root tip (arrow). The inset shows Fat red-stained emf1 ult1 root. (O) emf1 atx1 double mutant with swollen primary root tip (arrow). The inset shows Fat red-stained emf1 atx1 root. Scale bar, 0.5mm. (P and Q) pkl mutant (P) and Fat red-stained pkl mutant (Q). Arrows indicate the pkl root tip. Scale bar, 1mm.

- Liu, W., Duttke, S.H., Hetzel, J., Groth, M., Feng, S., Gallego-Bartolome, J., Zhong, Z., Kuo, H.Y., Wang, Z., Zhai, J., *et al*. (2018). RNA-directed DNA methylation involves co-transcriptional small-RNA-guided slicing of polymerase V transcripts in Arabidopsis. Nat Plants 4, 181-188.

- Ren, R., Wang, H., Guo, C., Zhang, N., Zeng, L., Chen, Y., Ma, H., and Qi, J. (2018). Widespread Whole Genome Duplications Contribute to Genome Complexity and Species Diversity in Angiosperms. Mol Plant 11, 414-428

- Xu, F., Kuo, T., Rosli, Y., Liu, M.S., Wu, L., Chen, L.O., Fletcher, J.C., Sung, Z.R., and Pu, L. (2018). Trithorax Group Proteins Act Together with a Polycomb Group Protein to Maintain Chromatin Integrity for Epigenetic Silencing during Seed Germination in *Arabidopsis*. Mol Plant 11, 659-677.

Major Funding Sources

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

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

United Kingdom

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GARNet, Cardiff University, UK

Use of Arabidopsis

The United Kingdom has approximately 45 academic departments and research institutes that are actively conducting *Arabidopsis* research.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

- The Eurasian Arabidopsis Stock Centre (uNASC) is based at the University of Nottingham.
http://*Arabidopsis*.info/

- The PhenomUK: The UK Plant Phenomics Network is a Technology Touching Life network grant that provides phenotyping opportunities for UK researchers to use the core facilities situated around the country.
https://www.phenomuk.net/

- Ara-BOX-cis database allows interrogation on how bHLHs and bZIPs (which are expressed in seedlings) regulate genes downstream of perfect G-boxes (CACGTG).
http://araboxcis.org/

- The DNA BioFoundry at the Earlham Institute. This synthetic biology hub allows facile preparation of golden gate clones for use by plant scientists.
http://www.earlham.ac.uk/earlham-dna-foundry

- Community Wheat Transformation resource allows UK Arabidopsis researchers to propose for their gene of interest to be introduced into wheat.
https://www.niab.com/transgenic

- Visit the GARNet Resources Page for a categorised list of software tools available for plant scientists. These have been curated from the pages of previous MASC Annual reports so are up to date with new resources.
https://www.garnetcommunity.org.uk/resources

- The Computer Vision Lab at the University of Nottingham is developing a range of software tools for plant phenotyping in which Arabidopsis is used as a test organism.
https://www.nottingham.ac.uk/research/groups/cvl/projects/the4dplant.aspx

- Advice for Gene Editing in Arabidopsis from Jonathan Jones' lab at The Sainsbury Lab, Norwich.
Castel B, Tomlinson L, Locci F, Yang Y, Jones JDG (2019) Optimization of T-DNA architecture for Cas9-mediated mutagenesis in *Arabidopsis*. PLoS One https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0204778

- The Hidden Half at the University of Nottingham is an outstanding scientific and science communication project that uses X-ray computed tomography to visualise plant roots.
https://www.nottingham.ac.uk/hiddenhalf/home.aspx

Conferences, Workshops and Outreach events

- GARNet2018: University of York. September 18th-19th 2018. GARNet welcomed 80 delegates to its biennial meeting in which researchers learnt about cutting edge areas of plant biology.
http://garnet2018.weebly.com/
- GARNet-New Phytologist CRISPR Workshop: University of Bristol. March 23rd-24th 2018. Over 100 delegates learnt about the technical and regulatory issues surrounding the use of gene editing technology.
https://garnet-ge-workshop.weebly.com/
- GARNet-CyverseUK RNAseq Analysis Workshop. December 10th-12th 2018. This event held at the Earlham institute provides software tools available for the analysis of this widely used source of data.
http://www.earlham.ac.uk/cyverse-uk-rnaseq-workshop-2018
- Plant Preview 2018: Lancaster University. September 3-4th 2018 http://wp.lancs.ac.uk/plastidpreview2018/
- BSPP Imaging Plant-Microbe Interactions. University of Warwick. December 10th-11th 2018
http://www.bspp.org.uk/meetings/bspppres2018.php
- RMS Botanical Microscopy 2019: University of Oxford. April 14th-18th 2019.
https://www.rms.org.uk/discover-engage/event-calendar/botanical-microscopy-2019.html
- European Plant Science Retreat: University of Nottingham. July 8th-10th 2019.
https://epsr2019.wordpress.com/about/
- IS-MPMI University of Glasgow: July 14th-18th 2019.
https://www.ismpmi.org/Congress/2019/Pages/default.aspx
- CellWall2019: University of Cambridge. July 7th-12th 2019. http://cellwall2019.org/
- GARNet workshop on Advances in Plant Imaging. University of Warwick. September 9th-10th 2019. https://garnetimaging19.weebly.com/
- Plants Planet People Symposium: Kew Gardens. September 4th-5th 2019
https://www.newphytologist.org/symposia/ppp2019
- ICAR2021 will return to the UK for the first time since 2009. The meeting will take place at the ICC Belfast in Northern Ireland between **June 21st-25th 2021.**
http://icar2021.Arabidopsisresearch.org

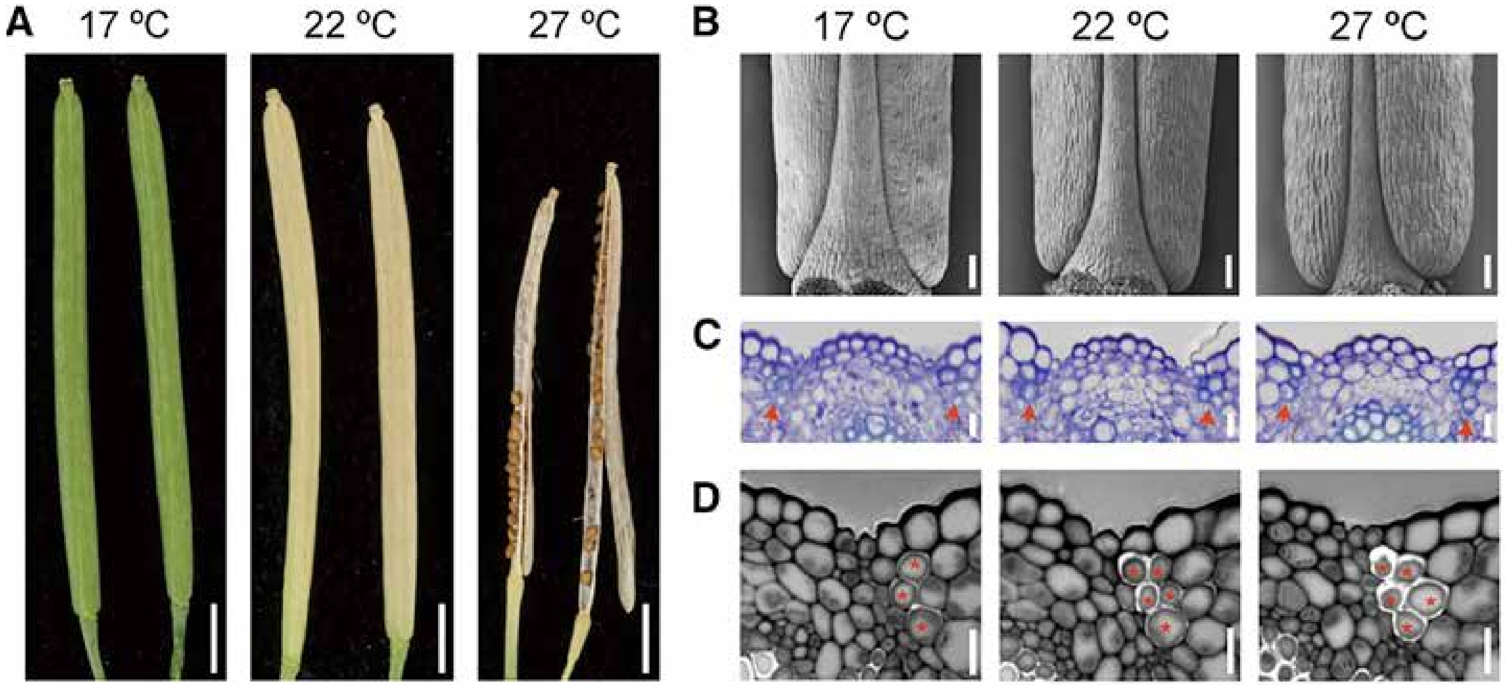

Figure 46. Higher Temperature Accelerates Fruit Dehiscence in Brassicaceae. (A) Fruit dehiscence of wild-type Col-0 siliques at 14 days after flowering (DAF) developed at 17°C, 22°C, and 27°C. Scale bars, 2 mm.(B) Scanning electron microscopy images showing the bases of Col-0 fruits at stage 17b developed at different temperatures. Scale bars, 100 μm.(C) Transverse sections of stage-17b fruits in Col-0 plants grown at 17°C, 22°C, and 27°C, stained with toluidine blue O. Red arrows indicate lignified valve-margin cells. Scale bars, 10 μm.(D) Cross-sections of stage-17b Col-0 fruits at different temperatures, stained with crystal violet. The lignified cells in the valve margin are marked by red stars. Scale bars, 10 μm.

Selected Publications

The majority set of UK publications that feature *Arabidopsis* are documented on the GARNet blog. http://blog.garnetcommunity.org.uk/*Arabidopsis*-research-roundups/

Calixto CPG, Guo W, James AB, Tzioutziou NA, Entizne JC, Panter PE, Knight H, Nimmo HG, Zhang R, Brown JWS (2018) Rapid and Dynamic Alternative Splicing Impacts the Arabidopsis Cold Response Transcriptome. Plant Cell. doi: 10.1105/tpc.18.00177

Choi K, Zhao X, Tock AJ, Lambing C, Underwood CJ, Hardcastle TJ, Serra H, Kim J, Cho HS, Kim J, Ziolkowski PA, Yelina NE, Hwang I, Martienssen RA, Henderson IR (2018) Nucleosomes and DNA methylation shape meiotic DSB frequency in *Arabidopsis thaliana* transposons and gene regulatory regions. Genome Res. doi: 10.1101/gr.225599.117

Frank A, Matiolli CC, Viana AJC, Hearn TJ, Kusakina J, Belbin FE, Wells Newman D, Yochikawa A, Cano-Ramirez DL, Chembath A, Cragg-Barber K, Haydon MJ, Hotta CT, Vincentz M, Webb AAR, Dodd AN (2018) Circadian Entrainment in Arabidopsis by the Sugar-Responsive Transcription Factor bZIP63. Curr Biol. doi: 10.1016/j.cub.2018.05.092

Gould PD, Domijan M, Greenwood M, Tokuda IT, Rees H, Kozma-Bognar L, Hall AJ, Locke JC (2018) Coordination of robust single cell rhythms in the Arabidopsis circadian clock via spatial waves of gene expression. Elife. doi: 10.7554/eLife.31700

Li XR, Deb J, Kumar SV, Østergaard L (2018) Temperature Modulates Tissue-Specification Program to Control Fruit Dehiscence in Brassicaceae. Mol Plant. doi: 10.1016/j.molp.2018.01.003

Srivastava AK, Orosa B, Singh P, Cummins I, Walsh C, Zhang C, Grant M, Roberts MR, Anand GS, Fitches E, Sadanandom A (2018) SUMO Suppresses the Activity of the Jasmonic Acid Receptor CORONATINE INSENSITIVE1. Plant Cell. doi: 10.1105/tpc.18.00036

Walker J, Gao H, Zhang J, Aldridge B, Vickers M, Higgins JD, Feng X (2018) Sexual-lineage-specific DNA methylation regulates meiosis in Arabidopsis. Nat Genet. doi: 10.1038/s41588-017-0008-5

Williams A, Pétriacq P, Schwarzenbacher RE, Beerling DJ, Ton J (2018) Mechanisms of glacial-to-future atmospheric CO(2) effects on plant immunity. New Phytol. doi: 10.1111/nph.15018

Whitewoods CD, Cammarata J, Nemec Venza Z, Sang S, Crook AD, Aoyama T, Wang XY, Waller M, Kamisugi Y, Cuming AC, Szövényi P, Nimchuk ZL, Roeder AHK, Scanlon MJ, Harrison CJ (2018) CLAVATA Was a Genetic Novelty for the Morphological Innovation of 3D Growth in Land Plants. Curr Biol. doi: 10.1016/j.cub.2018.05.068

Wibowo A, Becker C, Durr J, Price J, Spaepen S, Hilton S, Putra H, Papareddy R, Saintain Q, Harvey S, Bending GD, Schulze-Lefert P, Weigel D, Gutierrez-Marcos J (2018) Partial maintenance of organ-specific epigenetic marks during plant asexual reproduction leads to heritable phenotypic variation. Proc Natl Acad Sci U S A. doi: 10.1073/pnas.1805371115

Major Funding Sources

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

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

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

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

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

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

The Newton Fund
https://www.newtonfund.ac.uk/

United States of America

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University of California, Davis, with input from the North American *Arabidopsis* Steering Committee (NAASC)
https://www.araport.org/community/group/naasc

Use of Arabidopsis

It's not straightforward to get accurate numbers of Arabidopsis users in the United States. However, according to two major resources, The Arabidopsis Information Resource (TAIR) and the Arabidopsis Biological Resource Center (ABRC), estimates are that there are approximately 4,700 labs that use Arabidopsis resources registered in the US, and 12,500 people.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 2018 or early 2019

1. DiversifyPlantSci Resource: NAASC is committed to promoting a global plant sciences community that reflects the true diversity of all its members. To further this mission the NAASC Diversity and Inclusion Task Force have created the DiversifyPlantSci online resource, a list of plant biologists from under-represented groups* to reference for consideration when inviting speakers, reviewers, and participants for career or mentorship opportunities. This list is intended to highlight the diversity within the global plant science community. We hope to increase diversity and inclusion by making it easy to expand invitations past one's personal networks. *List includes plant scientists who identify in 1 or more of these under-represented categories as defined by NSF: Women; persons with disabilities; and three racial and ethnic groups—blacks, Hispanics, and American Indians or Alaska Natives—are underrepresented in US STEM; we also include Filipino. www.nsf.gov/statistics/2017/nsf17310/digest/introduction/

a. You may add your name (or forward to others to add themselves) at this google form URL: https://goo.gl/forms/s461eDrbKzoK1JzD2
b. Public list: https://tinyurl.com/DiversifyPlantSci; Twitter: @DiversifyPlants
2. ViVa: Visualizing Variation in the *Arabidopsis thaliana* 1001 genomes project
a. tool website: plantsynbiolab.bse.vt.edu/ViVa
b. tool description: https://www.biorxiv.org/content/10.1101/488395v1?rss=1

Conferences, Workshops and Outreach events

1. 6-10 July, 2020: ICAR 2020: Novel Approaches and Planning Underway for the 31st International Conference on Arabidopsis Research: Seattle, Washington, USA, at the University of Washington, Seattle. The next ICAR (http://icar2020.Arabidopsisresearch.org) will be organized by NAASC in Seattle for the first time. Notably, NAASC is undertaking new approaches to develop an exciting and diverse program. We will achieve this in four ways:
a. We will invite session proposals from the community via an online interface (preliminary submission deadline: 31 July 2019. This new approach will enable platform concurrent sessions to be proposed and organized by the community and will include some funds to cover registration costs for organizers and speakers in the selected sessions. Covering registration will enable session leaders to recruit speakers and simultaneously enable new, creative topics to be put forth by the plant science community.
b. We will solicit new session topics and invited speaker nominations from the community via the online interface*. This approach will expand the conference's diversity of themes and speakers.
c. NAASC recently developed the DiversifyPlantSci online resource to promote diversity, inclusion and equity (https://tinyurl.com/DiversifyPlantSci); "DiversifyPlantSci" is a list of self-identified plant scientists from under-represented groups to reference when inviting speakers and participants for ICAR sessions. This list is intended to highlight the diversity within the global plant science community. NAASC will strongly encourage diversity within community session proposals and invited speaker lists and will monitor submissions to ensure they reflect geographic and institutional diversity as well as diversity in career stage, gender, topic, etc. We are also setting aside several platform sessions to be organized by students and postdocs to promote career development.
d. An international external advisory board (EAB) was convened for ICAR 2020, an effort led by Jose Dinneny of NAASC, and chaired by past NAASC member, Blake Meyers (Danforth Center). The EAB met several times in late 2017/early 2018 and provided numerous recommendations to NAASC with respect to ICAR 2020. The ICAR 2020 EAB members are listed at the NAASC site: www.araport.org/community/group/naasc

These new approaches will contribute to a new and creative ICAR program, enable us to get beyond the 'usual networks', and develop an engaging plant science conference that is inclusive and welcoming to all.
*The online interface for submissions and input can be found via the survey linked at the ICAR 2020 homepage; the site also contains the preliminary deadline for community submissions for propsals (31 July 2019): http://icar2020.Arabidopsisresearch.org

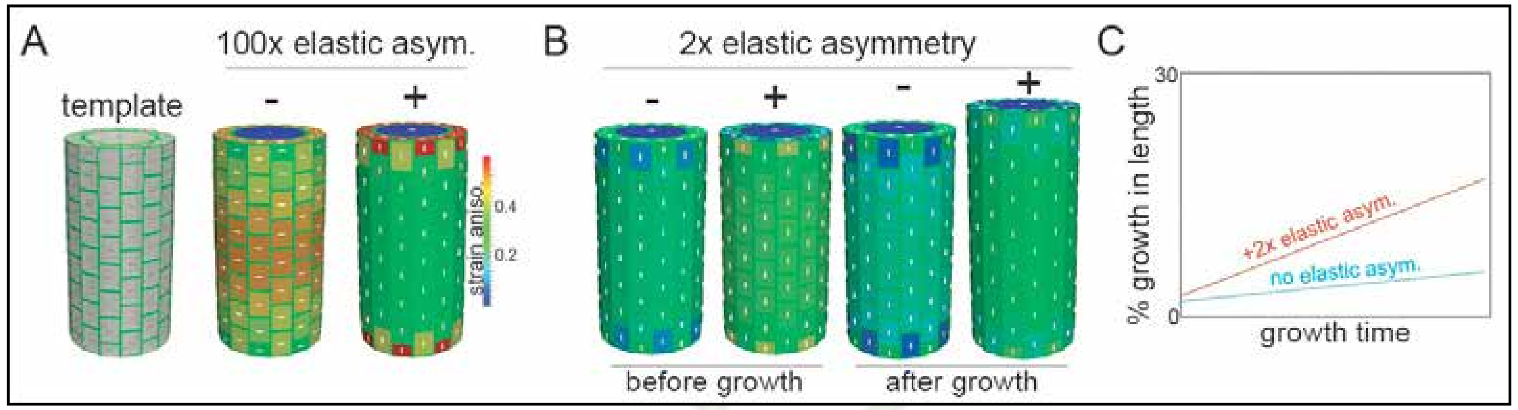

Figure 47. Microtubule alignment and cell elastic asymmetry additively regulate anisotropic growth *in silico*. (A) Template for finite element method simulation of a growing hypocotyl epidermis, alongside predicted strain anisotropy (growth) with no anisotropic information and with or without 100x elastic asymmetry added. White lines indicate the maximal stress direction. (B) Pre-growth and after-growth simulation results for a case with material anisotropy information provided by the internal epidermal face. The magnitude of anisotropy is enhanced by the addition of 2-fold elastic asymmetry, resulting in increased growth of the template. (C) Simulation output as percent growth in time from the simulation in (B) showing the increased relative growth achieved by addition of 2-fold elastic asymmetry https://elifesciences.org/articles/38161

2. November, 2018: "Broadening the Impact of Plant Science Through Community-Based Innovation, Evaluation and Sharing of Outreach Programs" Workshop*: José Dinneny, Liz Haswell, Roger Innes and Joanna Friesner of NAASC led the workshop at UC Davis (Davis, CA, USA); the workshop's overarching objective was to "re-envision how plant science outreach programs are funded, evaluated, acknowledged and shared within the plant science community" with specific focus on being more Innovative, Inclusive, and Integrative in how plant scientists engage with students, the broader public, and leverage the power of plants to improve our world now and in the future. A white paper generated by workshop participants is in development.

3. November 2018: "Seeds of Change: Using Plants to Broaden the Impact of Science in Society" Minisymposium*- Videos of talks are posted at https://www.araport.org/community/group/naasc. The symposium featured these 7 speakers with titles: "Overview on Science Outreach Approaches, J. Dinneny", "Developing the next generation of diverse scientists: Be A Scientist program as a model for University-public school partnerships, M. Wildermuth"; "Rapid-cycling Brassica rapa as an educational a model plant, R. Amasino"; "Let the real you shine: programs to enhance diversity and inclusion in graduate education, Y. Sun"; "Democratizing science education, A. Schnoes"; "Improving science literacy through art, R. Hangarter"; "Podcasting for community-building and community-broadening, L. Haswell".

a. Videos at: https://www.araport.org/community/group/naasc

4. June 2018: " Communicating Science in the Age of Fake News: Broadening Your Impact" Workshop*: Roger Innes (moderator) and Liz Haswell, of NAASC, organized this community workshop which focused on effectively communicating science with the general public, during the 2018 ICAR in Finland. Presentation slides and summary are posted at https://community.plantae.org/article/5053302916895475351/communicating-science-in-the-age-of-fake-news-broadening-your-impact. The workshop's main objectives were to share effective public science engagement activities and to enable conversations amongst participants that can lead to future discussions and implementation of novel ideas and approaches.
The presenters cover a diverse set of public engagement activities (e.g. hands-on activities at public gatherings, YouTube videos, educational modules for schools, social media, etc.) followed by Q&A and small group breakout discussions of success stories and challenges that were overcome during public engagement. Speakers presented on: "Overview/Objectives, R. Innes"; "The public engagement imperative, O. Leyser"; "Reaching out to K-12, A. N. Stepanova", "Overcoming the language barrier with fascinating plants, K. Sims-Huopaniemi; and "The 2Blades Foundation, H. P. van Esse".

a. Presentation slides and workshop findings summary at: https://community.plantae.org/article/5053302916895475351/communicating-science-in-the-age-of-fake-news-broadening-your-impact
* These workshops were based upon work supported by the National Science Foundation under Grant No. #1518280. Any opinions, findings, and conclusions or recommendations expressed in this event, or in resulting work, are those of the participants and do not necessarily reflect the views of the NSF.

5. May 2018: "The Future of Arabidopsis Bioinformatics" Workshop: The International Arabidopsis Informatics Consortium (IAIC), initiated in 2010 by NAASC and led by former NAASC member Blake Meyers (Danforth Center) held this NSF-supported workshop in St. Louis, Missouri, USA, to evaluate the current status of Arabidopsis informatics and chart a course for future research and development (for more details please see the IAIC report in this MASC report's section on Community resources). The workshop participants published a white paper outlining the current state, challenges, and priorities

for the future of Arabidopsis bioinformatics resources (https://doi.org/10.1002/pld3.109). This workshop was based upon work supported by the National Science Foundation under Grant No. #11062348. Any opinions, findings, and conclusions or recommendations expressed in this event, or in resulting work, are those of the participants and do not necessarily reflect the views of the NSF.

Selected Publications

- Hadia Ahmed, T. C. Howton, Yali Sun, Natascha Weinberger, Youssef Belkhadir & M. Shahid Mukhtar (2018) Network biology discovers pathogen contact points in host protein-protein interactomes. Nature Communications; https://www.nature.com/articles/s41467-018-04632-8

- *Arabidopsis* bioinformatics resources (2019) The current state, challenges, and priorities for the future. International *Arabidopsis* Informatics Consortium. Plant Direct. 3:1–7. https://doi.org/10.1002/pld3.109

- Bou Daher F, Chen Y, Bozorg B, Clough J, Jönsson H, Braybrook SA (2018) Anisotropic growth is achieved through the additive mechanical effect of material anisotropy and elastic asymmetry. Elife. doi: 10.7554/eLife.38161

- Javier Brumos, Linda M. Robles, Jeonga Yun, Savannah Jackson, Jose M. Alonso, Anna N. Stepanova (2018) Local Auxin Biosynthesis Is a Key Regulator of Plant Development. Developmental Cell. 2018; https://doi.org/10.1016/j.devcel.2018.09.022

- de Luis Balaguer MA, Fisher AP, Clark NM, Fernandez-Espinosa MG, Möller BK, Weijers D, Lohmann JU, Williams C, Lorenzo O, Sozzani R (2017). Predicting gene regulatory networks by combining spatial and temporal gene expression data in *Arabidopsis* root stem cells. Proc Natl Acad Sci; doi: 10.1073/pnas.1707566114

- Joanna Friesner, et. al. Siobhan M. Brady (2017) The Next Generation of Training for *Arabidopsis* Researchers: Bioinformatics and Quantitative Biology. Plant Phys; https://doi.org/10.1104/pp.17.01490

- Gaudinier A, Rodriguez-Medina J, Zhang L, Olson A, Liseron-Monfils C, Bågman AM, Foret J, Abbitt S, Tang M, Li B, Runcie DE, Kliebenstein DJ, Shen B, Frank MJ, Ware D, Brady SM (2018) Transcriptional regulation of nitrogen-associated metabolism and growth. Nature; doi: 10.1038/s41586-018-0656-3

- Hongqing Guo, Trevor M. Nolan, Gaoyuan Song, Sanzhen Liu, Zhouli Xie, Jiani Chen, Patrick S. Schnable, Justin W. Walley, Yanhai Yin (2018) FERONIA Receptor Kinase Contributes to Plant Immunity by Suppressing Jasmonic Acid Signaling in *Arabidopsis thaliana*. Current Biology; https://doi.org/10.1016/j.cub.2018.07.078

- Jakub Rajniak, Ricardo F. H. Giehl, Evelyn Chang, Irene Murgia, Nicolaus von Wirén & Elizabeth S. Sattely (2018) Biosynthesis of redox-active metabolites in response to iron deficiency in plants. Nature Chem Biology. 2018; https://www.nature.com/articles/s41589-018-0019-2

- Masatsugu Toyota, Dirk Spencer, Satoe Sawai-Toyota, Wang Jiaqi, Tong Zhang, Abraham J. Koo, Gregg A. Howe, Simon Gilroy (2018) Glutamate triggers long-distance, calcium-based plant defense signaling. Science. 2018; http://science.sciencemag.org/content/361/6407/1112

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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; e.g. Siobhan Brady, Jose Dinneny, Elizabeth Haswell, Jennifer Nemhauser, Elizabeth Sattely
(2) HHMI Investigators; Phil Benfey, Dominique Bergmann, Xuemei Chen, Joanne Chory, Jeff Dangl, Xinnian Dong, Joe Ecker, Mark Estelle, Sheng Yang He, Steve Jacobsen, Zach Lippmann, Rob Martienssen, Elliot Meyerowitz, Craig Pikaard, Elizabeth Sattely, Keiko Torii and Ning Zheng (the next anticipated competition opens in 2020!)

Additional Information

1. In fall 2018, Federica Brandizzi (MSU-DOE Plant Research Laboratory, Michigan State University) and Anna Stepanova (North Carolina State University) were elected by the North American Arabidopsis community to serve a five-year term. They replaced Sally Assmann (Penn State University) and Erich Grotewold (Michigan State University) who had concluded their five-year term of service.

a. Federica and Anna join these NAASC members, in order of longest to shortest elected service on NAASC: Elizabeth Haswell (Washington University in St. Louis), José R. Dinneny (Stanford University), Peter McCourt (University of Toronto), Roger Innes (Indiana University), Sean Cutler (UC Riverside), and Jennifer Nemhauser (University of Washington- Seattle).
b. Current and former NAASC members, and NAASC information, can be found at:
https://www.araport.org/community/group/naasc

2. US researchers that use *Arabidopsis* and were elected as fellows of the National Academy of Science in 2018 include (1) Joy M. Bergelson; Professor and Chair, Department of Ecology and Evolution, The University of Chicago, Chicago; (2) Sean Cutler; Professor (current NAASC member), Department of Botany and Plant Sciences, University of California, Riverside, and (3) Richard D. Vierstra; George and Charmaine Mallinckrodt Professor of Biology (recent NASAC member), Department of Biology, Washington University, St. Louis.

3.TapRoot Podcast (https://plantae.org/podcasts/the-taproot/) by Elizabeth Haswell, NAASC member: One challenge with outreach and retention activities is reaching geographically, ideologically, or intellectually isolated individuals. Podcasting provides an alternative source of support and community for plant science trainees, with low barriers to access, production, and distribution, and a highly diverse audience. While podcasts are rapidly growing in popularity they are underutilized as a mechanism for science outreach. Of the over half a million active podcasts, less than 1000 are related to science.

In 2017, Ivan Baxter and I started The Taproot Podcast (tagline: “We tell the story behind the science”) with support from ASPB and Plantae. In each episode, we discuss the publication of a plant biology paper with one of its authors, addressing the narratives that aren’t represented in a final manuscript—such as technology development, work-life balance, career gaps, gender discrimination, and student mental health. About half of our podcast guests work on Arabidopsis specifically.

TapRoot
A Plantae
Podcast

We also maintain an active @taprootpodcast Twitter account (>1200 followers) to foster discussion and solicit feedback, and to reach as broad an audience as possible. Ultimately, we aim to foster a sense of belonging, agency and community among plant biology trainees, thereby improving diversity and inclusion. We have released 17 episodes over two seasons with over 34,000 downloads to date.

According to a survey in the summer of 2018, 46% of our listeners identify as female, over 50% are PhD students and postdocs, and 85% are in North America or Europe. Future efforts will aim to continue to seek guests with diverse ethnicity, career level, geographical location, and research area, in part by crowdsourcing suggestions via Twitter. In addition, we will engage with a more global audience and have identified several young plant biology leaders in South America and Africa to serve as ambassadors for the podcast in their countries.

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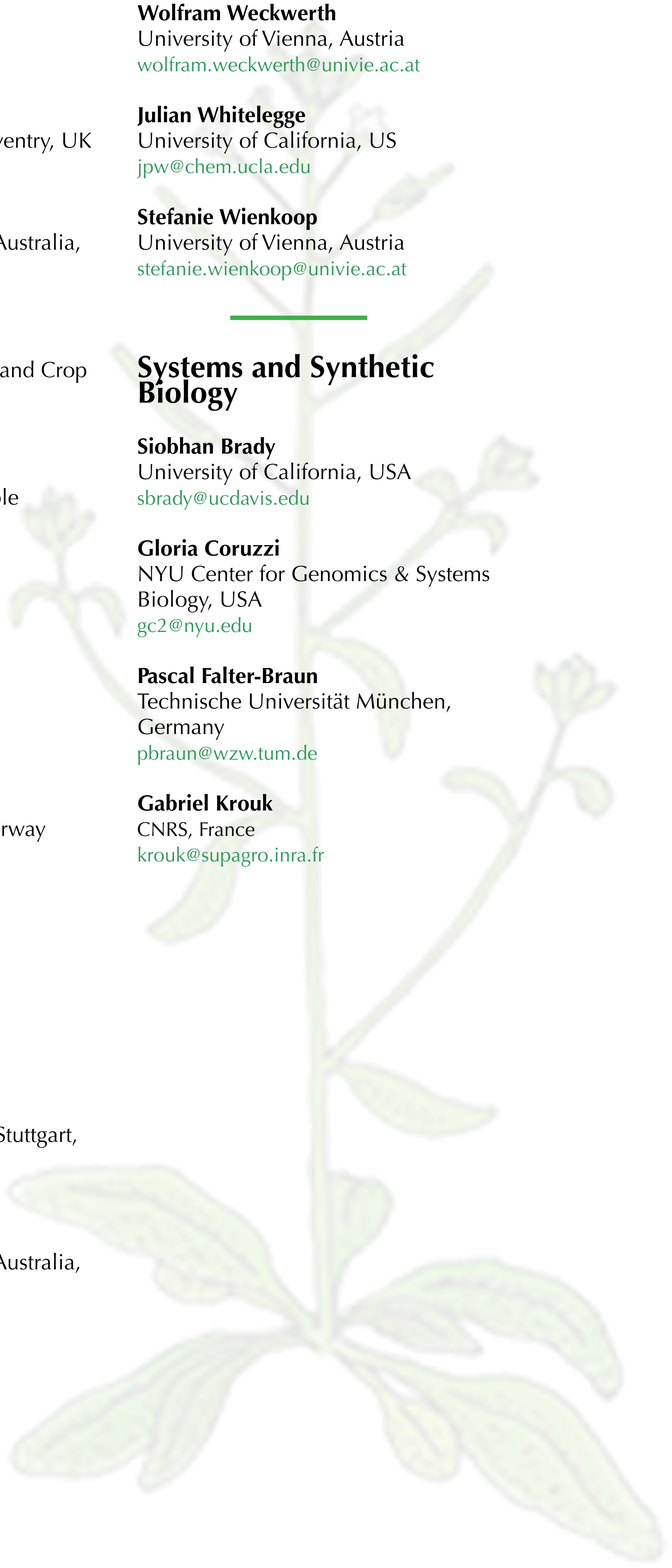

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