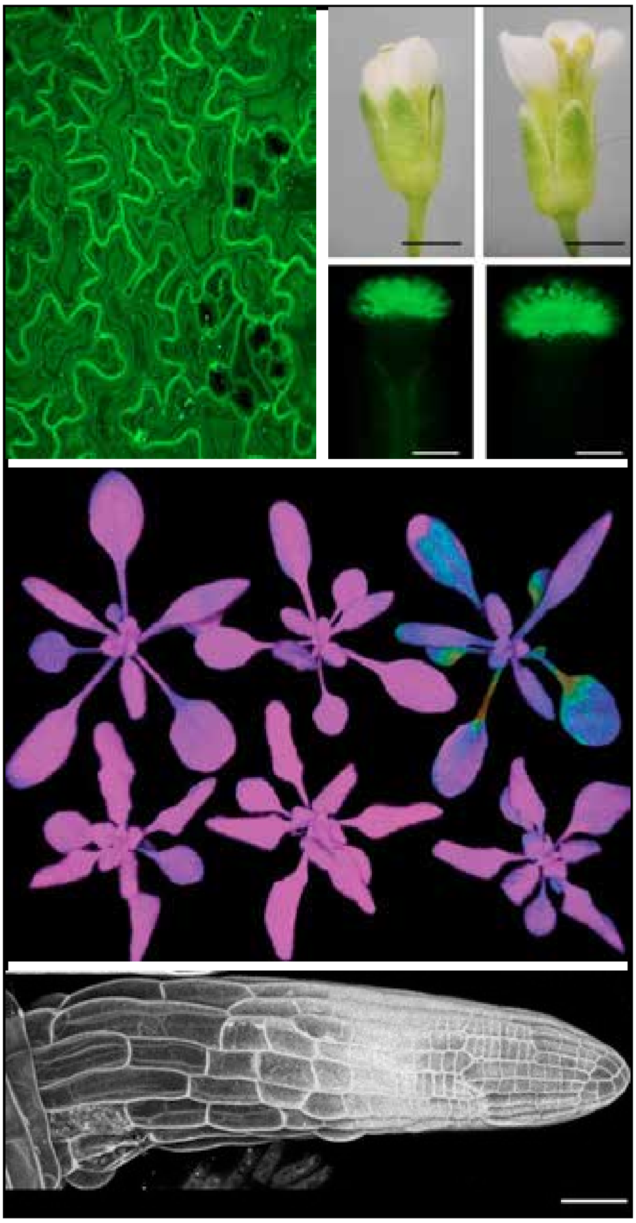
From Bench to Bountiful Harvests

Multinational Arabidopsis Steering Committee (MASC)

Annual Report 2019/2020



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

The MASC report 2019/20 and previous reports are available online at:

- > MASC, The Multinational Arabidopsis Steering Committee:
  http://*Arabidopsis*research.org/index.php/publications/masc-reports
- > uNASC, The Nottingham Arabidopsis Stock Centre:
  http://*Arabidopsis*.info/progreports.html
- > TAIR, The Arabidopsis Information Resource:
  http://www.*Arabidopsis*.org/portals/masc/masc_docs/masc_reports.jsp
- > GARNet
  http://garnetcommunity.org.uk/reports

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

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Annual Report 2019/2020

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Activities of MASC

MASC web page: www.Arabidopsisresearch.org

MASC Inc has now been incorporated as a not-for-profit in Canada for the past two years. 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)

In late 2020 two new directors will be elected for a four-year term. In that election we hope 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. We will circulate details of the MASC election procedure later in 2020.

From August 2020 Dr Geraint Parry will be paid by MASC Inc to oversee its activities, which remain at the minimum level to maintain the activity of the organisation. However 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. 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. For the first time from 2020 MASC will directly pay to support coordinator activities, albeit for these limited roles.

- Serving as executive secretary of MASC
- Collating, writing and editing of the annual MASC progress report with input from MASC members
- Maintaining and updating the MASC web pages to inform the global research community about various opportunities, collaborations, large-scale activities and research progress
- Organising the MASC annual meeting during ICAR meetings

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 subcommittees: Bioinformatics, Epigenetics and Epigenomes, ORFeomics, Metabolomics, Natural Variation and Comparative Genomics, Proteomics, Plant Immunity and Systems and Synthetic Biology. The activities of the Phenomics subcommittee have been captured within the report from International Plant Phenotyping projects.

We are delighted to include the inaugural submission from the **Plant Immunity Subcommittee** and are very grateful to Dr Shadid Muktar for leading this activity.

Subcommittees have certain loose guidelines for their activities:
- Subcommittee chairs are usually required for a 3-year minimum term to provide continuity
- Chair/co-chair should confirm and represent the interests of subcommittee members
- Submission of an annual report
- Input at MASC annual meetings

MASC

www.arabidopsisresearch.org

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

One strength of the global Arabidopsis research community comes in the form of the genomic resources and seed stocks that are available for use. Each of the major international stock centres (ABRC, NASC, RIKEN) report that the distribution of Arabidopsis seed stocks remain strong. In addition this document includes reports from the major international phenotyping projects, the International Arabidopsis Informatics Consortium, Gramene and the Global Plant Council. Finally the report includes submissions from TAIR and the BAR project, which now include extra activities that had previously been run through Araport.

Country reports provide the bulk of the MASC report and highlight the new resources and publications that have been generated from different parts of the world. After the addition of five new countries in 2019 (Estonia, Poland, Saudi Arabia, Singapore, Taiwan) to an all-time high of 32 and we are grateful to the 30 country representatives that submitted for this report. We are delighted to include an inaugural report from Turkey, in which there is an interesting analysis of the distribution of available Arabidopsis ecotypes.

We are extremely grateful to all representative of subcommittees, projects or countries as they voluntarily give their time toward MASC activities. All MASC contributors are invited to attend the remote MASC annual meeting that will take place on July 21st 8pm GMT. This is in place of the usual meeting that occurs during ICAR meetings but of course has been cancelled due to the COVID-19 pandemic. We are happy to invite interested observers to this remote 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. If this is of interest to you then please contact Geraint Parry.

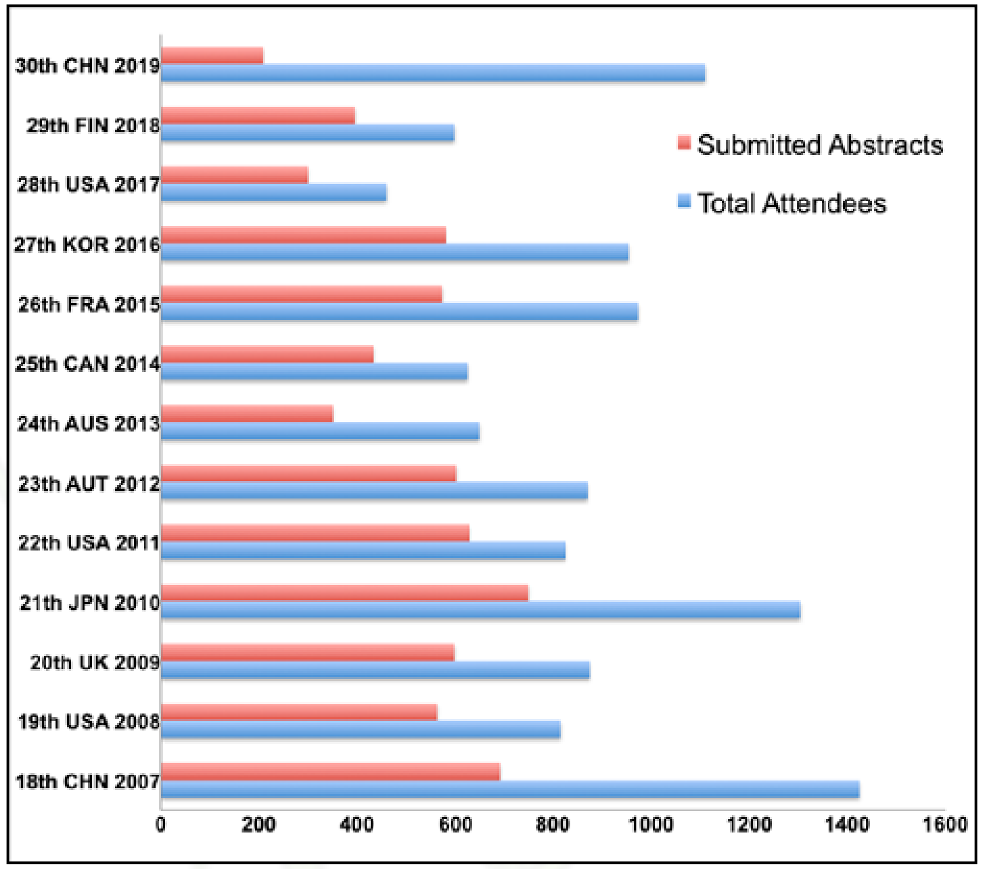


Figure 1. Number of attendees (blue) and number of posters presented (red) at the International Conference on Arabidopsis Research since 2007, when information about posters became available.

International Conference on Arabidopsis Research (ICAR)

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

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

Unfortunately the COVID-19 pandemic meant that the ICAR2020 meeting in Seattle was postponed until 2021. However the community came together to make the best of this situation. A full description of this process is explained within the country report from the USA.

Therefore these are the locations for upcoming ICAR meetings:

-- 31st ICAR, Seattle, USA June 21st-25th 2021: http://icar2020.Arabidopsisresearch.org/

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

- 33rd ICAR, Organised by RIKEN in Toyko, Japan 2023

- 34th ICAR, The Americas. 2024

- 35th ICAR, Europe. 2025

The 30th International Conference on *Arabidopsis* Research (ICAR) was held in Wuhan, China between June 16th-21th 2019 where the organising committee was led by MASC director Xuelu Wang. The total number of attendees was 1110, which was the highest number since ICAR2010 in Japan. 208 delegates submitted abstracts, which was significantly below the previous ICAR average of a 63% abstract submission rate. The reasons for this is not clear but perhaps is linked to the requirement for submission of English-language abstracts, which might have been more challenging for the majority Chinese delegation.

ICAR2019 highlighted the global strength of Chinese plant science research as there were many outstanding talks both by Chinese scientists who have remained in China and those who are now working internationally. There were 20 concurrent sessions but only six workshops, one of which was a Science Communication session organised by MASC contributor The Global Plant Council. The GARNet blog includes a brief meeting reports from Gatsby Foundation supported PhD student Gina Garzón Martínez from Aberystwyth University: http://blog.garnetcommunity.org.uk/meeting-report-from-icar2019/

The North American Arabidopsis Steering Committee (NAASC) are the organisers of ICAR2020 -now-ICAR2021 and committed to extending the opportunities for delegates to contribute to the meeting program. They received over 80 proposals to organise mini-symposiums, which is an outstanding community response. Detlef Weigel and Joanne Chory will provide Keynote talks at ICAR2021.

The MASC Code of Conduct

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

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

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

The MASC website

http://Arabidopsisresearch.org/

The MASC website is hosted in Canada by Hostpapa, maintained by Geraint Parry and Nick Provart and has two main 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 the latest tools and publications from each of those subcommittees, resources or countries.

These resources can be found here:

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

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

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

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

Executive Summary and Analysis

Thanks for being interested in the latest activities of the Multinational Arabidopsis Steering Committee (MASC). The first task is to thank the many contributors who have submitted pieces for this annual report. Without their input then MASC would be unable to prepare this document, which aims to track of the progress and challenges of the global Arabidopsis community. In 2020 MASC are delighted to include a new Country report from Turkey.

This summary provides an update from the MASC Subcommittees, MASC-associated Projects and MASC Country reports.

Update from MASC Subcommittees

The MASC subcommittees were established in 2002 at the beginning of the second MASC decadal roadmap bring together an international group of researchers who work in the same area in order to report on advances in that particular area. Over the past 18 years these subcommittees, have fed into the MASC Annual report as well as leading concurrent or workshop sessions at ICAR meetings and engaged with the wider community by organising external meetings.

Over the past year a significant development in Arabidopsis research has come from within the proteomics community with a study from Mergner *et al* that explored the total number of Arabidopsis proteins (18K+), their dynamic expression range (six-fold changes) and their phosphorylation state (43K sites across the proteome)(Mergner, J., *et al*. (2020) Mass-spectrometry-based draft of the Arabidopsis proteome. Nature 579, 409–414 doi: 10.1038/s41586-020-2094-2). In addition McWhite *et al* generated a complimentary database of stable protein complex organisation from across 13 plant species, which included Arabidopsis (McWhite CD *et al*, (2020) A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. Cell. doi: 10.1016/j.cell.2020.02.049). These datasets are exciting resources that are available for independent analysis and are being integrated into existing community databases.

The Mergner *et al* manuscript includes transcriptome information for each protein product yet it does not represent the entirety of the predicted 29K open reading frames (ORFome). The MASC ORFeomics subcommittee continues to monitor the resources that provide access to different sets of Arabidopsis clones, each of which are outlined in the MASC annual report. They propose an international project that would catalogue the ORF clones that correspond to the remaining uncharacterised 6K protein-coding genes. It appears that these gene products were not identified in the Mergner *et al* manuscript so it remains to be discovered if and where the proteins coded by these remaining ORFs reside.

Epigenetics and Epigenomes research in Arabidopsis is an area of great interest as it has remains the workhorse for elucidating mechanistic underpinnings of numerous epigenetic phenomena. These studies have both discovered and reinforced the importance of small RNAs, histone modifications, and DNA methylation during epigenome reinforcement, in detection of self from non-self, and in responding to versatile environmental challenges. This research is aided by the community-facing Arabidopsis RNA-seq Database, which contains gene expression data from 20K+ publically available RNA-Seq databases (http://ipf.sustc.edu.cn/pub/athrna/). This resource will dovetail with a soon-to-be released resource of whole genome bisulfite sequencing datasets.

The Bioinformatics subcommittee highlights that the exploration of RNA-seq data is further enhanced through a newly released eFP-Seq Browser that visualises read map profiles and summarized gene expression levels across two large compendia (Sullivan A *et al* (2019) An 'eFP-Seq Browser' for visualizing and exploring RNA sequencing data. Plant J. doi: 10.1111/tpj.14468).

The Plant Cell Atlas is a US National Science Foundation-funded research coordination network based at the Carnegie Institute in Stanford and aims to generate data sets and develop tools to integrate these often times large yet disparate 'omic data sets in order to generate testable models of plant cell function (www.plantcellatlas.org). This project kicked off with a virtual workshop in May 2020. Arabidopsis is almost certain to be one of the focus plants.

Over the past year the Arabidopsis bioinformatics community had to overcome the unfortunate loss of funding for the Araport resource. Fortunately other community projects have stepped up to take on some of its important features. This includes the hosting of the JBrowse tool at TAIR (The Arabidopsis Information resource, (https://bit.ly/2Qhb5xC) and the Thalemine resource by the BAR (https://bar.utoronto.ca/thalemine/). The third component of the revamped Araport is hosted by the Genome Context Viewer (https://gcv-arabidopsis.ncgr.org), which enables the dynamic comparison of multiple genomes on the basis of their shared functional elements.

The Arabidopsis metabolome is the best studied in any plant species and is used as an exemplar for investigations that are focused on crop species. The MASC metabolomics subcommittee continues to support the integration of genomic data taken from natural populations with ecologically relevant metabolomic data that can reveal how a plant has ultimately adapted to environmental stresses. The subcommittee made the case that as metabolomic platforms are more cost-effective than NGS platforms it is important that metabolomics is considered an equal partner to sister techniques as we develop a full picture of a plant. This will be an important consideration during the preparation of the upcoming fourth dedacal roadmap.

The interrogation of Arabidopsis natural variation has been an area of clear success during the period of the current decadal roadmap. The 1001 genomes project has been hugely successful and has led to the development of software tools for further analysis of these publically available databases. These including the ViVa: Visualizing Variation (Hamm, MO *et al* (2019) Accelerating structure-function mapping using the ViVa webtool to mine natural variation. Plant Direct. doi: 10.1002/pld3.147) and the AraPheno/AraGWAS tools (Togninalli M *et al* (2019) AraPheno and the AraGWAS Catalog 2020: a major database update including RNA-Seq and knockout mutation data for Arabidopsis thaliana, Nucleic Acids Research, doi: 10.1093/nar/gkz925). However there remains plenty of Arabidopsis geographic variation that has not yet been analysed. This is highlighted in the MASC country report from Turkey that looks at the distribution of the available ecotypes in the Nottingham Arabidopsis Stock Centre (NASC)(Figure 43). This demonstrates that many ecotypes growing across diverse geographic locations (including Turkey) are underrepresented in the available germplasm.

During 2019 there has been significant activity in the research area of the MASC Systems and Synthetic Biology subcommittee, particularly with the development of BAR-integrated software to analyse protein-protein interaction networks (http://bar.utoronto.ca/interactions2/) and in the TuxNet software that analyses RNA-seq data to infers gene regulatory networks (https://omictools.com/tuxnet-tool). The subcommittee has been active in the organisation of external meetings with the inaugural International Plant Systems Biology Meeting taking place in France in September 2018, with the follow-up second event in Venice postponed until 2021 (https://meetings.embo.org/event/20-plant-systems).

Shahid Mukhtar from University of Alabama at Birmingham is the inaugural chair of the Plant Immunity subcommittee, a necessary initiative that expands MASC activities into an area in which Arabidopsis research has led our current understanding on the molecular mechanisms of pathogen resistance. Over the past year this research area has seen exciting developments that are highlighted within the subcommittee report. These include the first solving of the structure of a plant NLR (Wang J, *et al* (2019) Reconstitution and structure of a plant NLR resistosome conferring immunity. Science. doi: 10.1126/science.aav5870), a full characterisation of the Arabidopsis NLRome (Van de Weyer AL *et al* (2019) A Species-Wide Inventory of NLR Genes and Alleles in Arabidopsis thaliana. Cell. doi: 10.1016/j.cell.2019.07.038). It is encouraging that members of the subcommittee are active within meeting organisations, outreach and generation of analysis tools.

Update on International Projects with an Arabidopsis Focus.

The success of the international Arabidopsis stock centres (NASC, The Arabidopsis Biological Research Centre (ABRC) and the RIKEN Bioresource Centre) are perhaps the primary example of the collaborative nature of this global community. Annually ABRC distributes almost twice as many seed stocks as NASC (190K versus 100K) despite reporting a downward trend over the past decade. NASC has seen increases over the past few years that undoubtedly reflects that it is the go-to stock-centre for orders from China. The continued success of the stock centres relies on donations from the community and NASC reports that over the past few years German scientists have provided their largest number of donations.

Despite losing centralised funding over five years ago TAIR continues its excellent biocuration services via an innovative and successful subscription service (Reiser L *et al* (2016) Sustainable funding for biocuration: The Arabidopsis Information Resource (TAIR) as a case study of a subscription-based funding model, Database, doi: 10.1093/database/baw018). Each week TAIR loads 50 - 90 papers with the term 'Arabidopsis' in the title or abstract into their curation queue. This includes a steady number of papers that report on functions for previously characterized genes and an increase in the number of papers that describe high throughput experiments and contain large datasets. For a variety of reasons, curating from some papers can be challenging so TAIR have produced a document to advise researchers how to make the details of their research more 'findable' (https://conf.arabidopsis.org/pages/viewpage.action?pageId=22807345).

The BAR resource continues to be a central hub for researchers who want to interrogate and visualise their expression data. Although its ePlant Browsers have expanded to include many other plant species, its core activities are focused on Arabidopsis. The new eFP-Seq Browser allows researchers to explore RNA-seq-based gene expression levels for a gene of interest using their unique visual output of developmental stages (Sullivan A *et al* (2019) An 'eFP-Seq Browser' for visualizing and exploring RNA sequencing data. Plant J. doi: 10.1111/tpj.14468). However BAR is far more than eFP browsers and the website includes access to a broad set of genomic tools and widgets than have a focus on analysis of Arabidopsis datasets. BAR has obtained funding from Genome Canada that will allow the development of a custom eFP view in ePlant for a researcher's own RNA-seq data as well as the initiation of several new ePlant browsers.

Oversight of the wider Arabidopsis informatics strategy has largely fallen to the International Arabidopsis Informatics Consortium (IAIC), which has been funded by the NSF until 2020. In 2018 IAIC hosted a workshop in St Louis and the take home recommendation in a resulting publication was the establishment of a centralized 'annotation authority' to advise on submissions from new groups, establish a consistent naming scheme, distribute this format regularly and frequently, and encourage and enforce its adoption. In addition the article recommends that there should be community-established guidelines and standards for data and metadata formats alongside a searchable, central repository for analysis and visualization tools (International Arabidopsis Informatics Consortium. Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. Plant Direct. doi: 10.1002/pld3.109). Fortunately the implementation of these recommendations would be facilitated by a closely-linked international community and will undoubtedly made a significant portion of the next decadal Roadmap.

The International Plant Phenotyping community provides excellent links between Arabidopsis research and that conducted in other plant species. The MASC report includes updates from three international phenotyping networks. A general feature of these networks is in their provision of access to phenotyping infrastructures to researchers who do not have them available at their home institutions, serving to widen participation. The European Infrastructure for Plant Phenotyping (EMPHASIS) project is arguably the most interesting development in this area. When it becomes fully operational in 2022 EMPHASIS will place plant phenotyping in a position to obtain centralised European funding through similar mechanisms to those which support other large European infrastructure projects http://roadmap2018.esfri.eu/.

MASC Country Reports

The MASC Country Reports provide an overview on the progress of Arabidopsis research on a national scale; cataloguing important publications, new software tools and community resources.

Figure 11 shows a plateau in the number of global Arabidopsis publications over the past five years yet it does not reveal that this is not an even trend in all countries. The plateau is maintained by a continued rise in publications coming from Chinese researchers, which shows little slowing in the increases that began a decade ago (Figure 11). This also shows that the other countries with the highest annual number of publications showed increases in the 2000s but now a plateau or slight decline.

China is an interesting case as the country report states that '*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 [it] as the main model plant…. 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 are no such funding programs towards Arabidopsis research*'. This suggests that Chinese researchers are showing great ingenuity to maintain such a high level of productivity despite a lack of dedicated funding for Arabidopsis research.

MASC representatives provide an opinion on the current status of Arabidopsis research in their countries. It is challenging to obtain a consistent metric for these evaluations as different countries will view their situation from a different starting position. The United Kingdom publishes around 200 'Arabidopsis papers' per year and there is ~£8M in annual funding for 'Arabidopsis research' yet this represents a reduction in funding so the situation is not as healthy as in previous years. Similarly in Italy where 'Unfortunately, as in previous years, the Italian Ministry of Education, University and Research, has continued to decrease funding for basic research thus causing a reduction in the amount of work produced on Arabidopsis'.

In contrast, Brazilian researchers generate relatively few Arabidopsis publications each year (52 in 2019) but their country representatives, have a positive opinion towards Arabidopsis research; 'In Brazil even though there is virtually no such funding programs towards Arabidopsis, the number of institutions using Arabidopsis in their research is growing each year. We are seeing 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 investigate gene functions'. Similarly José Pío Beltrán from IBMCP-CSIC in Valencia, Spain reports that '….there is not a localized decrease in Arabidopsis research. Therefore, in Spain, Arabidopsis still is predominant among the financed lines of plant science research'.

It is pleasing that the majority of country representatives are positive about the status of their Arabidopsis research despite there being a general admission that there is movement toward more applied research.

This is exemplified by a response from Belgium; '*….plant scientists feel an increasing pressure from funding agencies, universities, and research institutes to focus on more applied research aspects. This being said, it is likely that Arabidopsis will remain a major tool to generate and test hypothesis even in applied research projects*'. Globally Arabidopsis clearly remains a critical experimental model for understanding 'how plants work', which will lead to technological advances and knowledge increases that feed into applied projects across a variety of crop plants.

Moving toward the Fourth Roadmap

Over the past 30 years MASC has led in the preparation of the series of decadal Roadmap documents that have advised on the future activities of the community. These Roadmaps were published in 1990 as 'A Long range plan for the Genome Research project'; in 2002 as 'Beyond the Whole genome Sequence' and in 2012 as 'From Bench to Bountiful Harvests'. The lead up toward preparation of the fourth decadal Roadmap has now begun, a document that will look toward 2030 and the future of the Arabidopsis research community.

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

1. Build a Predictive Model of an Arabidopsis Plant from its Molecular Parts

2. Build the International Arabidopsis Informatics Consortium, an International Informatics and Data Infrastructure

3. Exploit the Wealth of Natural Variation That Exists in Arabidopsis to Further Our Understanding of Adaptation and Evolution

4. Establish an Effective Knowledge Exchange Pipeline from the Laboratory to the Field and Vice Versa

5. Deepen International Cooperation and Coordination.

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

The loss of funding for Araport was disappointing for the community and highlights that there is work to do to integrate international infrastructures, particularly between Western and Eastern hemispheres. In some areas international cooperation is excellent, such as in the coordination of conference planning, yet elsewhere it can be improved. These challenges include but aren't limited to implementation of effective mechanisms of data sharing, cultural and language differences and availability of global funding initiatives.

At this time MASC calls on all Arabidopsis researchers to consider topics for inclusion in the next decadal Roadmap. We expect strong participation from long-time community leaders, such as the North American Arabidopsis Steering Committee (NAASC), and collaborators from the UK, Germany, and Japan. We strongly hope that there will be contributions toward decadal priorities from a broader group of MASC members, especially those representing countries with significant Arabidopsis research. The positive sense of East-West collaboration that was felt by those who attended ICAR2019 in Wuhan was a promising beginning to these discussions.

Possible Areas for Inclusion in the Next Decadal Roadmap

- What are the strategies that might be used to build globally sustainable digital infrastructures to support the integration of multi-omic data sets?
- How can both the data and metadata from complex multi-omic experiments be collated and shared for the benefit of the wider community in order to feed into translational pipelines?
- How can we integrate mechanistic and quantitative genetic insights to enable plant acclimation to vastly different climates, within a very short time period?
- How can the community build internationally cohesive and diverse collaborative teams of scientists to answer important questions in plant science?

Over the next year these ideas will be developed and will coalesce during discussions at a MASC-supported discussion session at ICAR2021 in Seattle. The Roadmap will be launched and published prior to ICAR2022 in Belfast and will hopefully lead in the planning of community-driven projects over the coming decade.

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.

Arabidopsis Informatics – TAIR, BAR and the National Center for Genome Resources (NCGR) in New Mexico collaborated to ensure that the data and tools formerly provided by Araport remain available to the community. Araport's JBrowse instance migrated to TAIR, Thalemine was redeployed with updated data at the BAR, and a new tool for exploring micro- and macrosynteny in Arabidopsis thaliana ecotypes was released by the NCGR.

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

TAIR: With help from members of the Araport and GMOD projects, TAIR installed the latest version of JBrowse at TAIR (see an example region here: https://bit.ly/2Qhb5xC) starting with the tracks that were available at Araport, fixing ones that had become non-functional and adding to these with new community tracks, e.g. TRAP-seq data under hypoxia from Lee and Bailey-Serres (2019). TAIR staff also performed software updates and technical improvements, updating TAIR's BLAST service (https://www.arabidopsis.org/Blast/index.jsp) to the latest version of NCBI BLAST (2.9.0) and providing a graphical display of alignments.

TAIR curators continued to extract experimental gene function data from the current literature and codify the data in the form of annotations to Gene Ontology and Plant Ontology terms as well as curated gene summaries, alleles and phenotypes, and gene symbols. In 2019 TAIR started an initiative to add GO terms for sets of genes for which there were no GO annotations at all, by reviewing linked literature, and adding annotations where possible. TAIR continues to produce quarterly updates of current data for subscribers (https://www.arabidopsis.org/download/index-auto.jsp?dir=/download_files/Subscriber_Data_Releases), and year old data for use by all (https://www.arabidopsis.org/download/index-auto.jsp?dir=/download_files/Public_Data_Releases).

Bio-Analytic Resource (BAR): BAR rolled out a revived and updated version of Araport's Thalemine at https://bar.utoronto.ca/thalemine/ as part of the aforementioned multi-lab effort to resuscitate Araport.

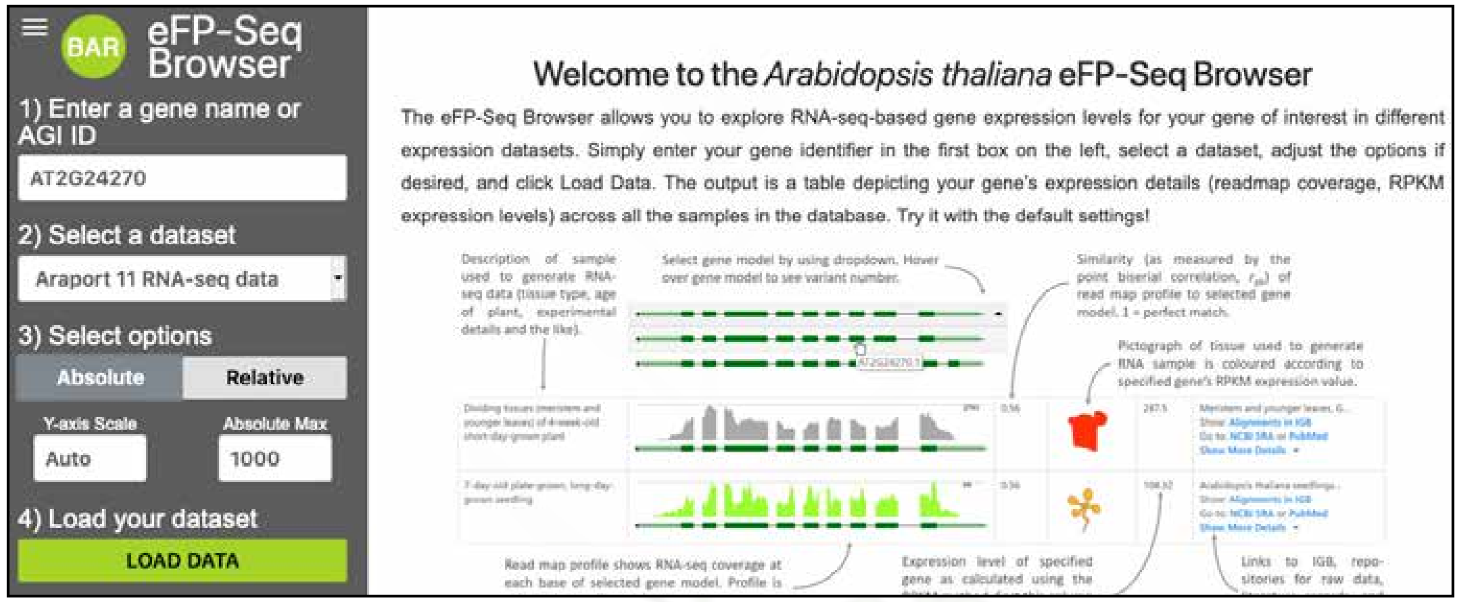
The BAR also published its eFP-Seq Browser at https://bar.utoronto.ca/eFP-Seq_Browser/ for exploring RNA-seq data as both read map profiles and summarized gene expression levels across two large compendia, in order to be able to quickly identify samples with the highest level of expression or where alternative splicing might be occurring (Sullivan *et al.*, 2019).

NCGR: Andrew Farmer and Alan Cleary developed their Genome Context Viewer (GCV) to enable the dynamic comparison of multiple genomes on the basis of their shared functional elements such as genes (Cleary and Farmer, 2017). An instance of the GCV is now running at https://gcv-arabidopsis.ncgr.org as the third component of the revamped Araport. The reference Arabidopsis thaliana Col-0 genome (TAIR10/Araport11) and genomes from several other data sources, including two sets of newly assembled A. thaliana genomes of various ecotypes from Jiao and Schneeberger (2020) and from the 1001 Genomes project from the Weigel lab (Bemm, Kubica, and Weigel, unpublished), as well as a number of Brassicaceae genomes from Phytozome and the BMAP project are available. Check it out!

Large-scale Data Sets of Note

Edward Marcotte's group used co-fractionation mass spectrometry to identify protein complexes in 13 plant species, including Arabidopsis. An astonishing 3,076,999 pairwise interactions were elucidated in this amazing study, which permits the identification of conserved and rewired protein complexes in plants (McWhite *et al.*, 2020). The data set is searchable at http://plants.proteincomplexes.org/search.

The Gazzarrini and Lumba Labs (Carianopol *et al.* 2019, https://doi.org/10.1038/s42003-020-0866-8) identified 125 SnRK1 complex interacting proteins using a meso-scale Y2H screening approach against ABA-regulated gene products. The Desveaux Lab (Cao *et al.* 2019, https://doi.org/10.1111/tpj.14425) generated an ABA-T3SE interactome network (ATIN) between P. syringae Type 3 Secreted Effectors (T3SEs) and Arabidopsis proteins encoded by ABA-regulated genes in order to further understand how plant pathogens can manipulate endogenous hormone signaling pathways. ATIN consists of 476 PPIs between 97 Arabidopsis ABA-regulated gene products and 56 T3SEs from four pathovars of *P. syringae*, as determined using Y2H.



1) Enter a gene name or AGI ID

AT2G24270

2) Select a dataset

Araport 11 RNA-seq data

3) Select options

Y-axis Scale: Auto

Absolute Max: 1000

4) Load your dataset

Welcome to the *Arabidopsis thaliana* eFP-Seq Browser

The eFP-Seq Browser allows you to explore RNA-seq-based gene expression levels for your gene of interest in different expression datasets. Simply enter your gene identifier in the first box on the left, select a dataset, adjust the options if desired, and click Load Data. The output is a table depicting your gene's expression details (readmap coverage, RPKM expression levels) across all the samples in the database. Try it with the default settings!

Description of sample used to generate RNA-seq data (tissue type, age of plant, experimental details and the like).

Select gene model by using dropdown. Hover over gene model to see variant number.

Similarity (as measured by the point biserial correlation, r_{pb}) of read map profile to selected gene model. 1 = perfect match.

Pictograph of tissue used to generate RNA sample is coloured according to specified gene's RPKM expression value.

Read map profile shows RNA-seq coverage at each base of selected gene model. Profile is

Expression level of specified gene as calculated using the

Links to IGB, repositories for raw data,

Figure 2. https://bar.utoronto.ca/eFP-Seq_Browser/

Also in terms of plant-pathogen interactions, The Guttman and Desveaux Labs (Laflamme *et al.*, 2020) published an analysis of the plant pan-genome immunity landscape using their PsyTEC compendium, which consisted of 529 representative P. syringae T3SEs screened against Arabidopsis to identify those which trigger an immune response. The results showed that relatively few genes (including two novel ones) in Arabidopsis recognize the majority of P. syringae effectors.

An interesting large-scale data set for Arabidopsis and 12 other species was generated by a "meltome" analysis, using a mass-spec-based proteomics approach for 48,000 proteins across 13 species covering melting temperatures of 30–90 °C (Jarzab *et al.*, 2020).

scRNA-Seq Search Tools. While several scRNA-seq data sets were published in the past year, two useful tools are now available to query some of these data sets. The Wang Lab developed its Root Cell Atlas search tool at http://wanglab.sippe.ac.cn/rootatlas/ based on scRNA-seq data they generated (Zhang *et al.*, 2019) and the BAR's eFP Browser (http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi?dataSource=Single_Cell) provides the ability to query scRNA-seq data from Ryu *et al.* (2019).

A Plant Cell Atlas project kicked-off in 2019 (Rhee *et al.*, 2019), which will provide unprecedented cell-level resolution of many different 'omes in plants, along with models to describe cell growth and behaviour. Keep an eye on http://www.plantcellatlas.org/ for updates!

Pedagogy, Policy and Outreach: Nicholas Provart released a Plant Bioinformatic Methods Specialization encompassing 4 courses on Coursera.org: Bioinformatic Methods I, Bioinformatic Methods II, Plant Bioinformatics, and a Plant Bioinformatics Capstone. See https://www.coursera.org/specializations/plant-bioinformatic-methods. You can audit the courses for free, or obtain certificates for a small fee.

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Cao, F.Y., Khan, M., Taniguchi, M., Mirmiran, A., Moeder, W., Lumba, S., Yoshioka, K., and Desveaux, D. (2019). A host–pathogen interactome uncovers phytopathogenic strategies to manipulate plant ABA responses. Plant J. 100: 187–198.

Carianopol, C.S., Chan, A.L., Dong, S., Provart, N.J., Lumba, S., and Gazzarrini, S. (2020). An abscisic acid-responsive protein interaction network for sucrose non-fermenting related kinase1 in abiotic stress response. Commun. Biol. 3: 145.

Cleary, A. and Farmer, A. (2017). Genome Context Viewer: visual exploration of multiple annotated genomes using microsynteny. Bioinformatics 34: 1562–1564.

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Jiao, W.-B. and Schneeberger, K. (2020). Chromosome-level assemblies of multiple Arabidopsis genomes reveal hotspots of rearrangements with altered evolutionary dynamics. Nat. Commun. 11: 989.

Laflamme, B., Dillon, M.M., Martel, A., Almeida, R.N.D., Desveaux, D., and Guttman, D.S. (2020). The pan-genome effector-triggered immunity landscape of a host-pathogen interaction. Science 367: 763.

Lee, T.A. and Bailey-Serres, J. (2019). Integrative Analysis from the Epigenome to Translatome Uncovers Patterns of Dominant Nuclear Regulation during Transient Stress. Plant Cell 31: 2573–2595.

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

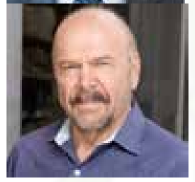
Rhee, S.Y., Birnbaum, K.D., and Ehrhardt, D.W. (2019). Towards Building a Plant Cell Atlas. Trends Plant Sci. 24: 303–310.

Ryu, K.H., Huang, L., Kang, H.M., and Schiefelbein, J. (2019). Single-Cell RNA Sequencing Resolves Molecular Relationships Among Individual Plant Cells. Plant Physiol. 179: 1444.

Sullivan, A. *et al*. (2019). An 'eFP-Seq Browser' for visualizing and exploring RNA sequencing data. Plant J. 100: 641–654.

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

Clone-Based Functional Genomics Resources (ORFeomics)



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ORFeomics subcommittee has tracked the progress made towards the production of full-length cDNAs and open reading frame (ORF) clones for all annotated Arabidopsis protein-coding genes. 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 6,000 protein-coding genes. After that, only the non-coding genes remain to be isolated.

With the completion of isolating all 29,000 Arabidopsis protein-coding genes, comprehensive analysis of plant gene function will become possible by various functional analyses using transgenic and protein expression approaches.

Recently developed 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 the attachment table).

Recent or Future activities of Subcommittee members..

Subcommittee goals:

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

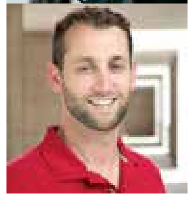
ORFeomics subcommittee would like to propose a new project to collect all ORF (full-length cDNA) clones from every Arabidopsis protein-coding gene so as to test protein-protein, protein-DNA and protein-RNA interactions.

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

Ali, M.R.M., Uemura, T., Ramadan, A., Adachi, K., Nemoto, K., Nozawa, A., Hoshino, R., Abe, H., Sawasaki, T. and Arimura, G.I. (2019) The Ring-Type E3 Ubiquitin Ligase JUL1 Targets the VQ-Motif Protein JAV1 to Coordinate Jasmonate Signaling. Plant Physiol. 179:1273-1284.

Epigenetics and Epigenomics



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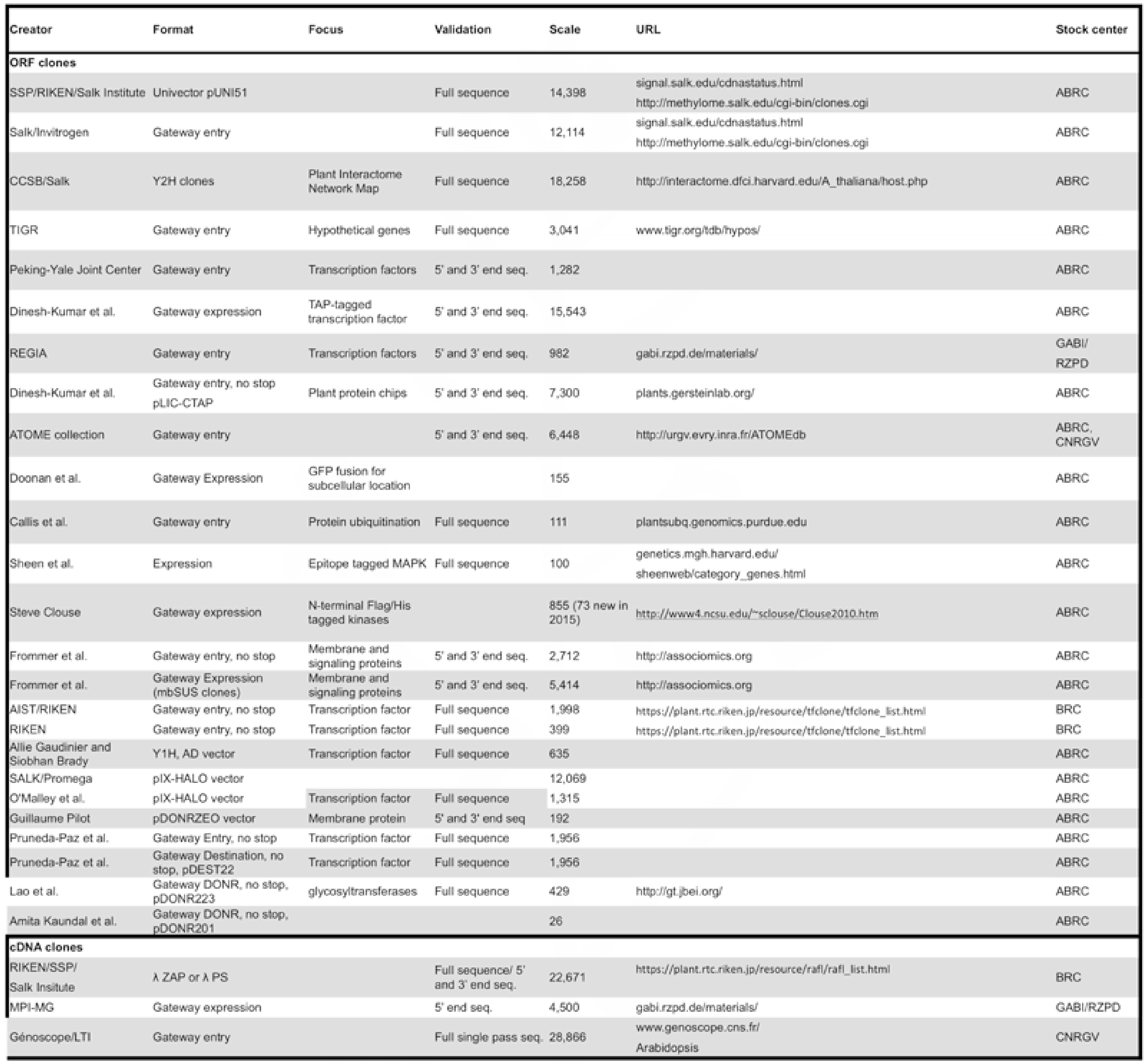
Please describe the current state of your subcommittee's research area.

Arabidopsis thaliana has proven to be the workhorse for elucidating mechanistic underpinnings of numerous epigenetic phenomena. Recent emphasis by the research community has been on studying the interaction between parental epigenomes throughout sexual reproduction and epigenetic regulation of environmental adaptation.

These studies are revealing the importance of small RNAs, histone modifications, and DNA methylation in epigenome reinforcement, in detection of self from non-self, and in responding to versatile environmental challenges. While genetic and genomic studies continue to provide important insights, recent biochemical efforts have reconstructed the core and regulatory components of key epigenetic complexes and has linked them to various signaling pathways. Several epigenome editing approaches have also been developed to target specific DNA methylation pathways to selected regions of the genome to initiate silencing.

While the field continues to work on the basic epigenetic mechanisms in genome function and development, a new focus on linking signaling pathways to chromatin dynamics has emerged. Another major focus of the field is exploring how epigenetic mechanisms are conserved and/or vary in plant species, particularly crop plants. Even though many chromatin/DNA methylation pathways are conserved, there is a surprising amount of variation in certain enzymatic components and how they are utilized by host genomes for gene regulation, transposon silencing, and genome stability.



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.

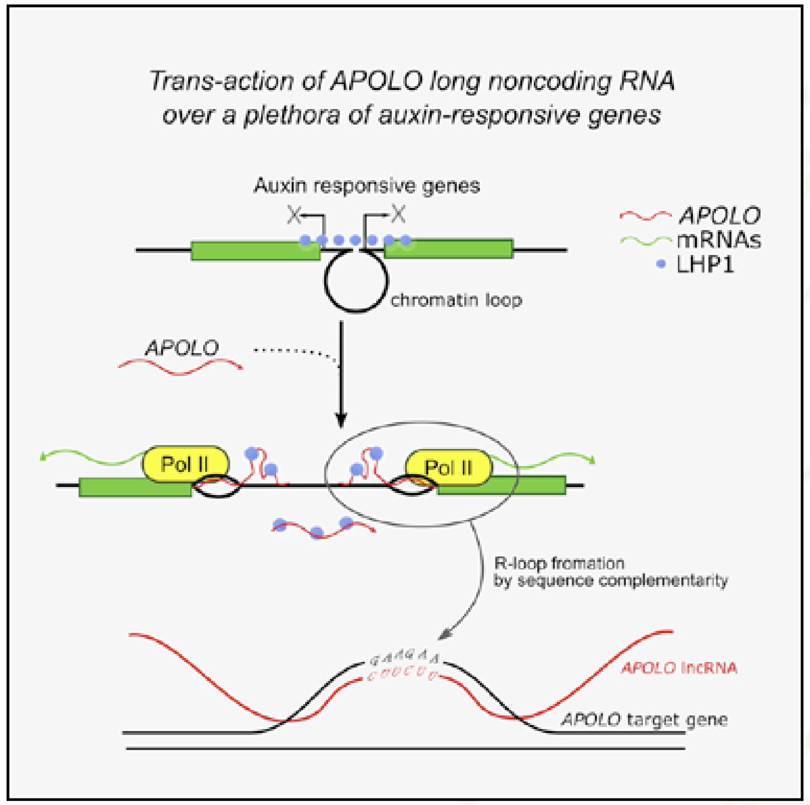


Figure 3: R-Loop Mediated trans Action of the APOLO Long Noncoding RNA

Recently developed Open Tools and Resources for Arabidopsis Researchers

Developed a website for a collection of ~20,000 Arabidopsis RNA-seq datasets http://ipf.sustc.edu.cn/pub/athrna/ This is an important community resource containing ~20,000 Arabidopsis RNA-seq datasets of various genetics mutants, developmental stages, biotic and abiotic stress treatments, etc. More importantly, it contains many wild-type Col-0 samples from different labs worldwide as a further reference for any Col-0 samples from individual lab. This resource is particularly useful to search for potential new regulators (both genetic and environmental factors) of given genes and pathways.

A similar website containing large collection of whole genome bisulfite sequencing datasets is currently under construction and will be available to the global community upon completion

Recent or Future activities of Subcommittee members

The Epigenetics and Epigenomics Subcommittee members organized and participated several epigenetic sections associated with various international conferences in 2019. These were held at Plant Genomes Conference and Gordon Research Conference in USA, Japanese Society of Plant Physiologists 60th Annual Meeting, 30th ICAR and plant epigenetics symposium in China, European workshop on plant chromatin in Germany, Mini-symposium on Epigenetic stress memory in Michigan State University and Wisconsin, and Symposium on Impact of Nuclear Domains on Plant Phenotypes in Spain. 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. This research topic has also attracted a large amount of interest from the media and the general public.

Conferences and Workshops

2019

- 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)

- Epigenetic workshop, Nanjing Agricultural University, Nanjing, China, June 2019
European workshop on plant chromatin, MPI Cologne, June 2019

- CSHL Frontiers and Techniques in Plant Science, CSHL, NY, June 2019

- SEB-INDEPTH Symposium on Impact of Nuclear Domains on Plant Phenotypes, Madrid, Spain, December 2019. https://www.brookes.ac.uk/indepth/

2020
- Cold Spring Harbor-Asia Conference: Integrative Epigenetics in Plants, Awaji, Japan December, 2020

Selected Publications

Ariel F, Lucero L, Christ A, *et al*. R-Loop Mediated trans Action of the APOLO Long Noncoding RNA. Mol Cell. 2020;77(5):1055□1065.e4. doi:10.1016/j.molcel.2019.12.015

Fang, X., Wang, L., Ishikawa, R., Li, Y., Fiedler, M., Liu, F., Calder, G., Rowan, B., Weigel, D., Li, P., & Dean, C. (2019). Arabidopsis FLL2 promotes liquid-liquid phase separation of polyadenylation complexes. Nature, 569(7755), 265–269. doi:10.1038/s41586-019-1165-8

Gallego-Bartolomé J, Liu W, Kuo PH, *et al*. Co-targeting RNA Polymerases IV and V Promotes Efficient De Novo DNA Methylation in Arabidopsis. Cell. 2019;176(5):1068-1082.e19. doi:10.1016/j.cell.2019.01.029

He S, Vickers M, Zhang J, Feng X. Natural depletion of histone H1 in sex cells causes DNA demethylation, heterochromatin decondensation and transposon activation. Elife. 2019;8:e42530. doi:10.7554/eLife.42530

Kirkbride RC, Lu J, Zhang C, Mosher RA, Baulcombe DC, Chen ZJ. Maternal small RNAs mediate spatial-temporal regulation of gene expression, imprinting, and seed development in Arabidopsis Proc Natl Acad Sci U S A. 2019;116(7):2761-2766. doi:10.1073/pnas.1807621116

Metabolomics

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Please describe the current state of your subcommittee's research area

The Arabidopsis metabolomics platform mostly represented by the activities of the members of the Multinational Arabidopsis Steering Committee is a strong pillar for functional analysis not only in this model plant. Many tools have been developed in this model system that are trend-setting for the application in crop plant research. What is a clear future trajectory of research is the systematic metabolomic analysis of germplasm collections of *Arabidopsis thaliana* and the linkage to genome wide association studies and genomic prediction.

Arabidopsis also serves as a model system for translational research for crop plants as more and more large germplasm collections with whole genome sequences are available (Weckwerth *et al*. 2020).

At the moment there is no better curated database available for any plant system than the 1001 genome collection of natural Arabidopsis accessions (Alonso-Blance *et al*. 2016). Another research area is ecological metabolomics with natural Arabidopsis populations (Nagler *et al*. 2018). The combination of metabolomics and whole-genome data of large collections of accessions in their native habitats as well as in common garden experiments enables the analysis of evolutionary adaptation processes from genome to metabolic plasticity.

Alonso-Blanco *et al*. (2016) 1,135 genomes reveal the global pattern of polymorphism in *Arabidopsis thaliana*. Cell 166: 481-491

Nagler *et al*. (2018) Eco-Metabolomics and Metabolic Modeling: Making the Leap From Model Systems in the Lab to Native Populations in the Field. Front Plant Sci 9: 1556

Weckwerth *et al*. (2020) PANOMICS meets Germplasm. Plant Biotechnol J. doi: 10.1111/pbi.13372.

Recently developed Open Tools and Resources for Arabidopsis Researchers

Databases
http://plasma.riken.jp/
A cheminformatics approach to characterize metabolomes in stable-isotope-labeled organisms.
Tsugawa *et al* (2019) Nat Methods. 16: 295-298.
doi: 10.1038/s41592-019-0358-2

Sample preparation for metabolomics
Metabolomics in the Context of Plant Natural Products Research: From Sample Preparation to Metabolite Analysis.
Salem *et al* (2020) Metabolites. 10: E37
doi: 10.3390/metabo10010037

Pathway analysis for model organisms
PathBank: a comprehensive pathway database for model organisms.
Wishart *et al* (2020) Nucleic Acids Res. 48: D470-D478
doi: 10.1093/nar/gkz861

Method of GCMS for volatile apocarotenoid in Arabiodpsis
Volatile apocarotenoid discovery and quantification in Arabidopsis thaliana: optimized sensitive analysis via HS-SPME-GC/MS.
Rivers *et al* (2019) Metabolomics 15: 79
doi: 10.1007/s11306-019-1529-y

Rapid protocol for subcellular plant metabolism analysis
Resolving subcellular plant metabolism.
Fürtauer *et al* (2019) Plant J 100: 438-455
doi: 10.1111/tpj.14472

Recent or Future 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.

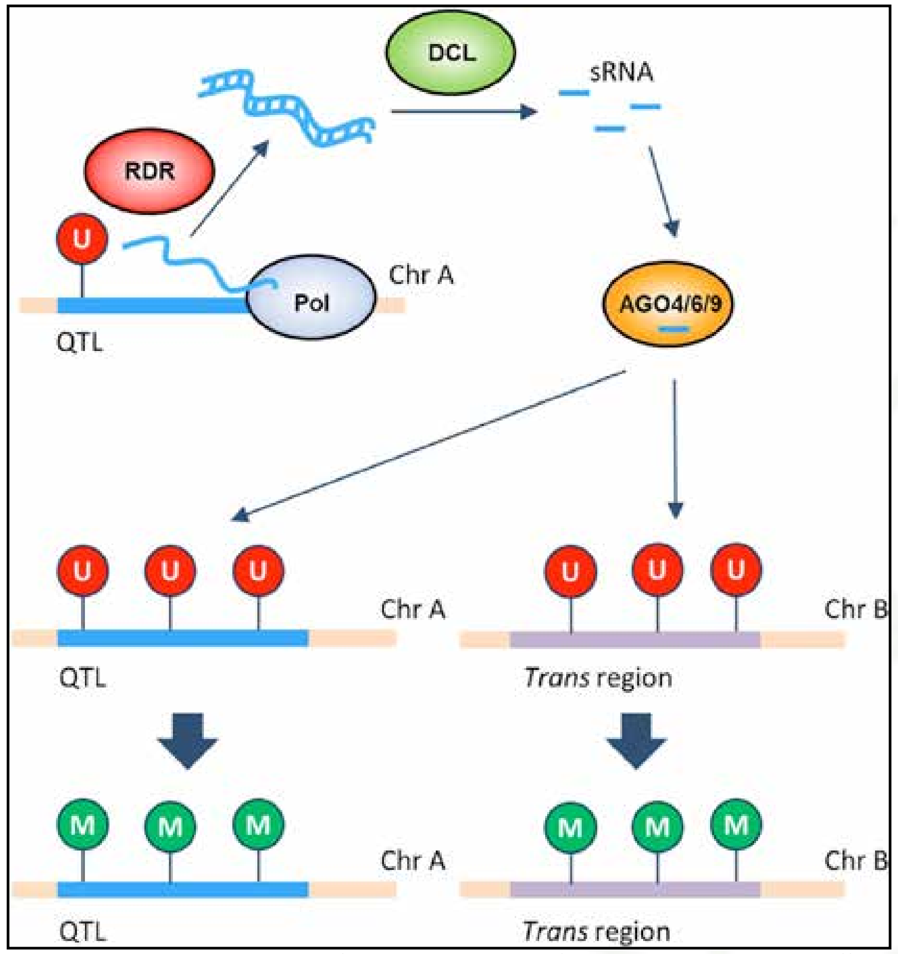

Figure 4: Theoretical model for the regulation of DNA methylation by differential targeting of sRNA to loci in trans. Changes in DNA methylation can be induced directly by differential recruitment of components of the RdDM pathway, or indirectly by post-transcriptional silencing of genes. (DCL) Dicer, (M) methylated, (Pol) RNA polymerase, (RDR) RNA-dependent RNA polymerase, (U) unmethylated.

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. A specific webpage for these MASC metabolomics subcommittee activities will be discussed.

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

2020/6/21-24 Phytochemical Society of North America, Kelowna, Canada. Now in 2021.
https://psna2020.ca/

2020/7/6-10 Metabolomics 2020, Shanghai, China
http://metabolomics2020.org/

Selected Publications

Kooke R, Morgado L, Becker F, van Eekelen H, Hazarika R, Zheng Q, de Vos RCH, Johannes F and Keurentjes JJB (2019) Epigenetic mapping of the Arabidopsis metabolome reveals mediators of the epigenotype-phenotype map. Genome Res 29: 96-106

Kozuka T, Sawada Y, Imai H, Kana, M, Hirai MY, Mano S, Uemura M, Nishimura M, Kusaba M and Nagatani A. (2020) Regulation of Sugar and Storage Oil Metabolism by Phytochrome during De-etiolation. Plant Physiol 182: 1114-1129

Perez de Souza L, Garbowicz K, Brotman Y, Tohge T and Fernie AR. (2020) The Acetate Pathway Supports Flavonoid and Lipid Biosynthesis in Arabidopsis. Plant Physiol 182: 857-869

Mangel N, Fudge JB, Li KT, Wu TY, Tohge T, Fernie AR, Szurek B, Fitzpatrick TB, Gruissem W, Vanderschuren H (2019) Enhancement of vitamin B6 levels in rice expressing Arabidopsis vitamin B6 biosynthesis de novo genes. Plant J 99: 1047-1065

Shimizu Y, Rai A, Okawa Y, Tomatsu H, Sato M, Kera K, Suzuki H, Saito K, Yamazaki M (2019) Metabolic diversification of nitrogen-containing metabolites by the expression of a heterologous lysine decarboxylase gene in Arabidopsis. Plant J 100: 505-521

Natural Variation and Comparative Genomics

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Recently developed Open Tools and Resources for Arabidopsis Researchers

- AraPheno: AraPheno is a public database collection of Arabidopsis thaliana phenotypes. This Database allows to search and filter for public phenotypes and to obtain additional meta-information.
https://arapheno.1001genomes.org/

- JBrowse at TAIR: The current NV/GV tracks of interest are the 1001 Genomes track.
We have additional Phytozome13 tracks for orthologous genes in 61 other plant species that are in testing on our dev server that should go live within the next month.
https://www.arabidopsis.org/servlets/jbrowse/arabidopsis?default=true

- Thalemine/Araport now includes several complete A. thaliana genomes now from the Schneeberger lab and the 1001 Genomes Project (Zmienko *et al*, 2020)
https://bar.utoronto.ca/thalemine/begin.do

- Andrew Farmer's Genome Context Viewer (GCV) loaded 14 Arabidopsis thaliana assembled genomes. This links to new Araport: GCV, TAIR's resuscitation of the Araport JBrowse tracks, and the Provart lab's reinstatiating of Thalemine at the BAR. An instance of this viewer has been set up and is now running from NCGR (https://gcv-arabidopsis.ncgr.org) as the third component of the "second generation" Araport. The viewer provides convenient links to related resources for genes and genomic regions, thereby facilitating traversal into the other components of the reconfigured Araport project as well as other relevant tools. The gene family classifications utilized by the current instance are based on PANTHER 14.1 (Mi *et al*., 2013, doi: 10.1093/nar/gks1118) and links are provided to the trees developed for these families by the PhyloGenes project (phylogenes.org).

Recent or Future activities of Subcommittee members.

This is an exciting time for the Comparative Genomics community as there is movement to establish the plant order Brassicales as a model clade and a large proposal is being assembled for that research. This is enhanced by the discovery of a new family of Brassicales that will feed into this new classification (Swanepoel *et al*, 2020).

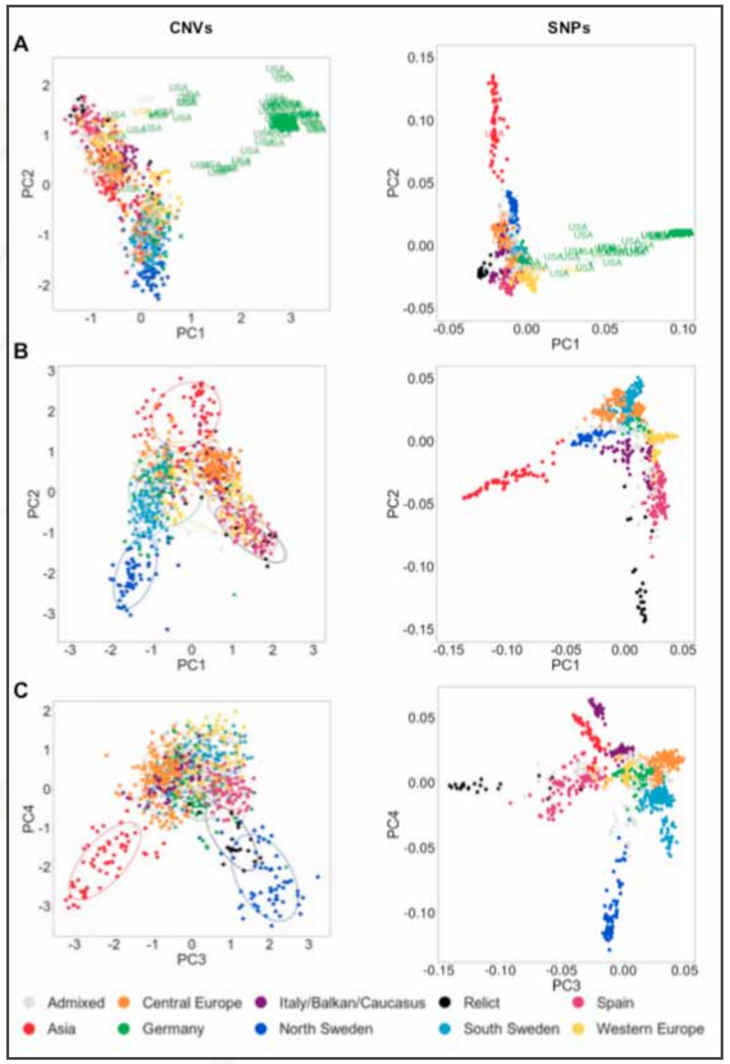

Figure 5: *A. thaliana* population structure based on the analysis of CNV genotypes. Principal component analysis (PCA) was performed on 1,060 accessions and on genotyping data from 1,050 CNV-PCGs (left). For comparison, another PCA was performed on the same set of accessions and 117,232 SNPs from the 1001 Genomes Project (right). A, PC1 and PC2 components; all accessions were included. USA accessions assigned to the Germany subgroup were distinguished from the other samples. B, PC1 and PC2 components; USA accessions from the Germany subgroup were excluded from the analysis. C, PC3 and PC4 components; all accessions were included. The accessions in PCA plots are colored based on their 1001 Genomes Project grouping.

Selected Publications

de Jong M, Tavares H, Pasam RK, Butler R, Ward S, George G, Melnyk C, challis R, Kover PX, Leyser O (2019) Natural variation in Arabidopsis shoot branching plasticity in response to nitrate supply affects fitness. PLOS Genetics 15(9): e1008366. doi:10.1371/journal.pgen.1008366

Niu XM, Xu YC, Li ZW, Bian YT, Hou XH, Chen JF, Zou YP, Jiang J, Wu Q, Ge S, Balasubramanian S, Guo YL (2019) Transposable elements drive rapid phenotypic variation in Capsella rubella. Proc Natl Acad Sci U S A 116: 6908-6913.

Seung D, Echevarría-Poza A, Steuernagel B, Smith AM. (2020) Natural Polymorphisms in Arabidopsis Result in Wide Variation or Loss of the Amylose Component of Starch. Plant Physiol. 182: 870-881. doi: 10.1104/pp.19.01062

Swanepoel W, Chase MW, Christenhusz MJM, Maurin O, Forest F, van Wyk AE. (2020). From the frying pan: an unusual dwarf shrub from Namibia turns out to be a new brassicalean family. Phytotaxa. 439 (3): 171–185. doi:10.11646/phytotaxa.439.3.1

Togninalli M, Seren Ü, Freudenthal J, Monroe JG, Meng D, Nordborg M, Weigel D, Borgwardt K, Korte A, Grimm DG (2020) AraPheno and the AraGWAS Catalog 2020: a major database update including RNA-Seq and knockout mutation data for Arabidopsis thaliana. Nucleic Acids Research 48 Issue D1, https://doi.org/10.1093/nar/gkz925

Zmienko A, Marszalek-Zenczak M, Wojciechowski P, Samelak-Czajka A, Luczak M, Kozlowski P, Karlowski WM, Figlerowicz M (2020) AthCNV: A map of DNA copy number variations in the Arabidopsis thaliana genome. The Plant Cell Apr 2020, tpc.00640.2019; DOI: 10.1105/tpc.19.00640

Plant Immunity

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Please describe the current state of your subcommittee's research area.

The concept of growth to defense tradeoffs in plants has been known for over three decades (Coley *et al*., 1985). Upon activation of antimicrobial or anti-herbivore defenses, plants redirect their limited resources to invest in the immune response at the cost of growth, development, reproduction, and overall yield. However, the molecular mechanisms governing this balancing act have only recently begun to be elucidated.

Upon infection with the bacterial pathogen *Pseudomonas syringae*, a massive reprogramming of transcriptional and translational activities occurs to boost the immune response while hampering growth and development. It is now well established that a small subset of mRNAs that possess upstream Open Reading Frames (uORFs) in their 5′ UTRs are selectively translated in response to immune stimulation, while general translational activities are attenuated. This process is dependent on a phosphorylation of eukaryotic Initiation Factor 2B (eIF2B) by GCN2 (General Control Nonderepressible 2), a sensor kinase conserved in all eukaryotes. While the molecular mechanisms underlying growth to defense tradeoffs are complex and multifaceted, hormone crosstalk has emerged as a major player in regulating tradeoffs needed to achieve a balance.

Recently, it was shown that Arabidopsis GCN2 differentially contributes to pre- and post-invasive immunity against *P. syringae* through abscisic acid biosynthesis and signaling (Liu *et al*., 2019, doi:10.1038/s42003-019-0544-x). Moreover, the construction of large scale protein-protein interaction networks not only illuminated the first layer of plant immunity but also highlighted the molecular circuitry of how plant extracellular receptors perceive growth signals vs. immune signals. These interaction patterns help to mechanically understand how an immune signal in PTI (Pattern-Triggered Immunity) can override basic developmental and growth programs, and relay downstream messages to promote defense responses (Ahmed *et al*., 2018, doi:10.1038/s41467-018-04632-8 ; Smakowska-Luzan *et al*., 2018, doi:10.1038/nature25184).

Another topic that is currently gaining a lot of momentum is how the plant hosts differentiate friends from foes – specifically, how the roots and leaves discriminate between signals of beneficial vs. pathogenic microbes. This process is in a large part accomplished by the identification of receptors for microbe/pathogens-associated molecular patterns (PAMPs/MAMPs) and damage-associated molecular patterns (DAMPs) (Zhou *et al*., 2020, doi:10.1016/j.cell.2020.01.013).

The recent advances in sequencing technology allow us to gain deeper insights into the community of leaf and root microbiota and their influence on plant growth. In parallel, Arabidopsis genetics provides means to identify the important components for the host interaction with beneficial/commensal microbes (Teixeira *et al*., 2019, doi: 10.1016/j.mib.2019.08.003). The ultimate goal of this research is to apply the resulting knowledge for agriculture to contribute food security worldwide.

In the second layer of defense, pathogen molecules or effectors are recognized by R (resistance) proteins, where NLRs (NOD-like receptors) play prominent roles. NLR biology is another fast growing field of molecular plant-microbe interactions. Both plant as well as animal NLR research was substantially boosted within the past year, and major steps were taken that will enable the community to discover new mechanisms, develop new cutting-edge technologies and to dive deeper into the fascinating world of plant immunity and plant-microbe interactions.

The solving of the first plant NLR full length protein structure by cryo-electron microscopy and the discovery of an enzymatic (NADase) activity of plant-, animal- and bacterial TIR domains are only two major discoveries of the recent year (Burdett *et al*., 2019, doi:10.1016/j.chom.2019.07.020; Wan *et al*., 2019, doi:: 10.1126/science.aax1771; Wang *et al*., 2019, doi: 10.1126/science.aav5870; Wang *et al*., 2019, doi: 10.1126/science.aav5868) . The primary goal of a virulent pathogen is not to interfere or suppress immune response, but to acquire nutrients, which will allow its survival, growth and multiplication, and in the long term – its evolutionary success. During effector-triggered susceptibility (ETS), pathogens utilize a suite of effectors to evade receptor-mediated recognition, suppress immune responses and acquire nutrients.

Another emerging frontier in plant immunity, namely the nutrient war between the host and pathogen has been in the limelight. Specifically, the research programs aiming to understand how pathogens can hijack the host transcriptional machinery by directly or indirectly altering the host signaling and/or biosynthetic pathways to siphon sugars and amino acids. Other very exciting developments were achieved in the field of small RNAs and their role in plant-microbe (pathogenic as well as symbiotic) interactions and their potential cross-kingdom trafficking via so called exosomes or exosomal membranes/vesicles (Vincent *et al*., 2019, doi:10.3389/fpls.2019.01626).

Finally, new biochemical (Bio-ID labelling) and genetic/genome-editing (optimized CRSIPR/CAS) tools have been developed and optimized for plant research (Khan *et al*., 2018, doi:10.1038/s41598-018-27500-3; Cui *et al*., 2019, doi:10.1186/s13007-019-0500-2; Ahmad *et al*., 2020, doi:10.1002/jcp.29052).

Recently developed Open Tools and Resources for Arabidopsis Researchers

- ProteomicsDB and ATHENA databases (Mass-spectrometry-based draft of the Arabidopsis proteome – Mergner *et al*., 2020 Nature, 579: 409-414)

- EffectorK (www.effectork.org) – (EffectorK, a comprehensive resource to mine for pathogen effector targets in the Arabidopsis proteome – Gonzalez-Fuente *et al*., 2020 bioRxiv)

- *P. syringae* Type III Effector Compendium (PsyTEC) – (The pan-genome effector-triggered immunity landscape of a host-pathogen interaction – Laflamme *et al*., 2020 Science)

- Prime genome editing in rice and wheat – Lin *et al*., 2020 Nature Biotechnology

- Super-Agrobacterium ver. 4: Improving the Transformation Frequencies and Genetic Engineering Possibilities for Crop Plants doi:10.3389/fpls.2019.01204

- New biosensor for detection of ethylene gas in fruits and leaves doi:10.1038/s41467-019-13758-2

Recent or Future activities of Subcommittee members.

The members of plant immunity subcommittee organized workshop/conference sessions, and presented talks and posters at various international conferences in 2019. These include 2019 IS-MPMI XVIII Congress, in Glasgow, Scotland, International workshop of plants and nematodes interaction" at the RIKEN Yokohama, Japan institute, Systems Biology and machine learning workshop at PAG, San Diego, "Plant Signaling in Abiotic and Biotic Stress", Columbia, MO (May 2019), Southern Section of American Society of Plant Biologists (SS-ASPB) in March 2019 (Clemson University, SC, USA), and NSF-sponsored workshop "Reintegrating Biology Jumpstart" (Atlanta, December 2019).

A subcommittee member in collaboration with other scientists from the community developed valuable tools. This includes (1) a new biosensor for ethylene gas and successfully detected ethylene production in fruits and also in Arabidopsis leaves during PAMP-triggered immunity and effector-triggered immunity (Nat Commun. doi: 10:5746, 2019); and (2) Super-Agrobacterium that gives higher transformation efficiency in plants by introducing both the ACC deaminase (acdS) and GABA transaminase (gabT) genes, whose resultant enzymes degrade ACC, the ethylene precursor, and GABA, respectively (Front Plant Sci. doi: 10:1204, 2019). The subcommittee members have also organized laboratory workshops on training of high school teachers in plant biology and plant blindness as well as hands on training to minority students in plant pathology.

In summary, the combined efforts of subcommittee members have contributed tremendously in the field of plant immunity, enhanced national and international

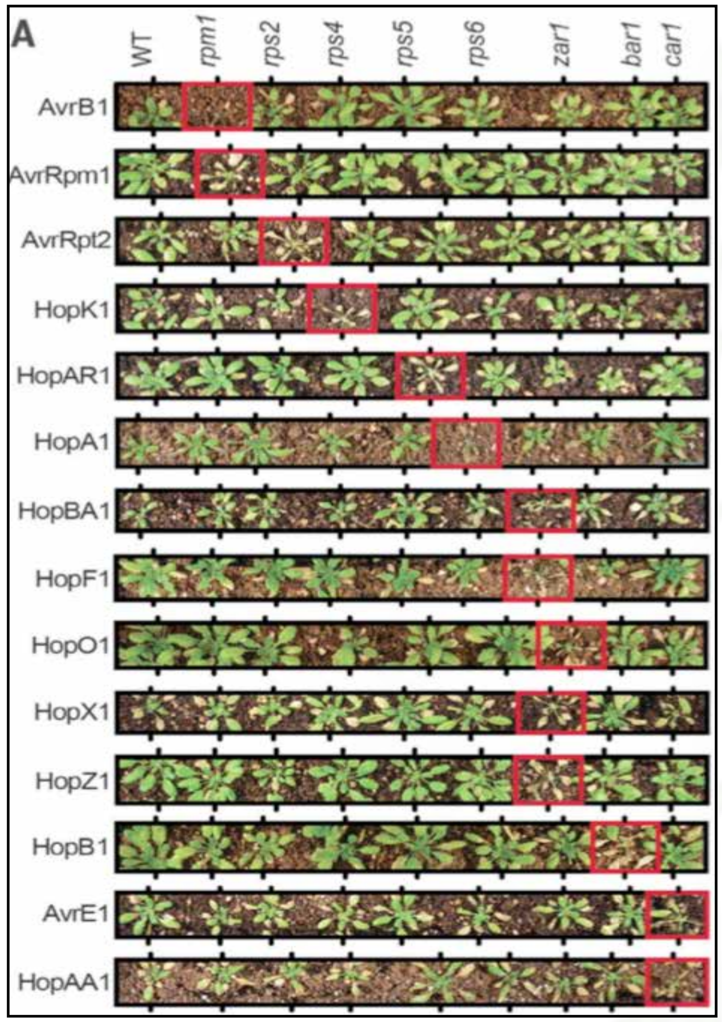

Figure 6. NLR specificity for each ETI-eliciting effector family. (A) Representative plant images after bacteria expressing each ETI-eliciting effector (left) were spray-inoculated onto wild-type (WT) or mutant A. thaliana Col-0 plants lacking a single NLR (top). Red boxes indicate loss-of-ETI interactions (HopF1r was formerly HopF2a).

collaborations, contributed in the development of novel and innovative tools, and participated in outreach activities.

Conferences, Workshops and Training events

- 4th International Conference “Plant Biotic Stresses & Resistance Mechanisms IV” at the Technische Universität of Vienna (19-20 February 2020)
- International Congress of Nematology (ICN) in 2020
- International workshop of the interaction of Arabidopsis and root-knot nematodes at RIKEN (2020)
- PCBI - Plant Cell Biology International Meeting, June 1 - 5, 2020, at OAC, Chania, Crete, Greece (postponed to 2021 due to COVID-19 pandemic)
- PAG 2021, organize systems biology and machine learning workshop.

Selected Publications

Laflamme, B., Dillon, M.M., Martel, A., Almeida, R.N.D., Desveaux, D. and Guttman, D.S. (2020) The pan-genome effector-triggered immunity landscape of a host-pathogen interaction. Science, 367, 763-768

Vong, K., Eda, S., Kadota, Y., Nasibullin, I., Wakatake, T., Yokoshima, S., Shirasu, K. and Tanaka, K. (2019) An artificial metalloenzyme biosensor can detect ethylene gas in fruits and Arabidopsis leaves. Nat Commun, 10, 5746.

Wan, L., Essuman, K., Anderson, R.G., Sasaki, Y., Monteiro, F., Chung, E.H., Osborne Nishimura, E., DiAntonio, A., Milbrandt, J., Dangl, J.L. and Nishimura, M.T. (2019) TIR domains of plant immune receptors are NAD(+)-cleaving enzymes that promote cell death. Science, 365, 799-803.

Wang, J., Wang, J., Hu, M., Wu, S., Qi, J., Wang, G., Han, Z., Qi, Y., Gao, N., Wang, H.W., Zhou, J.M. and Chai, J. (2019) Ligand-triggered allosteric ADP release primes a plant NLR complex. Science, 364.

Zhou, F., Emonet, A., Denervaud Tendon, V., Marhavy, P., Wu, D., Lahaye, T. and Geldner, N. (2020) Co-incidence of Damage and Microbial Patterns Controls Localized Immune Responses in Roots. Cell, 180, 440-453 e418

Proteomics

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

Please describe the current state of your subcommittee’s research area.

The proteomics subcommittee of MASC has tasked itself with the dissemination and visualization of protein-associated data from studies that have employed Arabidopsis. These started with data generated by proteomic surveys, but has extended to protein-protein interactions, subcellular localizations and post-translational modifications The initial development of Arabidopsis community portals mostly focused on genomics, genetics and genes. This was not surprising given the community efforts to sequence the genome and develop molecular genetic resources. A very similar process occurred in other reference organisms such as yeast and Drosophila.

With the development of mass spectrometry at the start of the 21st century and the availability of high-quality genome sequence data, a great deal of information about Arabidopsis proteins was being generated. As indicated, the Arabidopsis community portals (The Arabidopsis Information Resource and Munich Information Center for Protein Sequences) were mainly compiling gene-centric information. As a result, a number of groups working in the area of proteomics started to create data repositories that sought to capture protein-based information generated in-house and also data generated by colleagues. Much of these initial large-scale proteomic datasets resided in supplemental material that was impenetrable to the community. Thus the rise of proteomic-based portals started to occur by the mid 2000s. The researchers developing these databases became the nucleus of the proteomics subcommittee of MASC.

Recently developed Open Tools and Resources for Arabidopsis Researchers

The subcommittee has been committed to the task of proteomics data centralization and visualization. Over the past year, updates have been made to various proteomic data repositories, see list at http://www.masc-proteomics.org/. Subcommittee member Klaas Van Wijk was successful in obtaining an NSF-funded Plant Peptide Atlas project that will see plant proteomic data made available through the Institute for Systems Biology, Peptide Atlas portal (http://www.peptideatlas.org/). The objective of the Peptide Atlas is to enable the annotation of eukaryotic genomes through a thorough validation of expressed proteins.

Recent or Future 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. As the volume of data increases, some discussions about the value of these repositories has occurred. The subcommittee is examining how best to port proteomic data into ePlant e.g. abundance, protein evidence and post-translational modifications. A number of significant updates and surveys of the Arabidopsis proteome has occurred in 2019 / 2020 (see selected publications). The subcommittee intends to look at how these data can be incorporated into current community portals.

Selected Publications

McWhite CD, Papoulas O, Drew K, Cox RM, June V, Dong OX, Kwon T, Salmi ML, Roux SJ, Browning KS, Chen ZJ, Ronald PC, Marcotte EM (2020) A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. Cell. 16;181(2):460-474

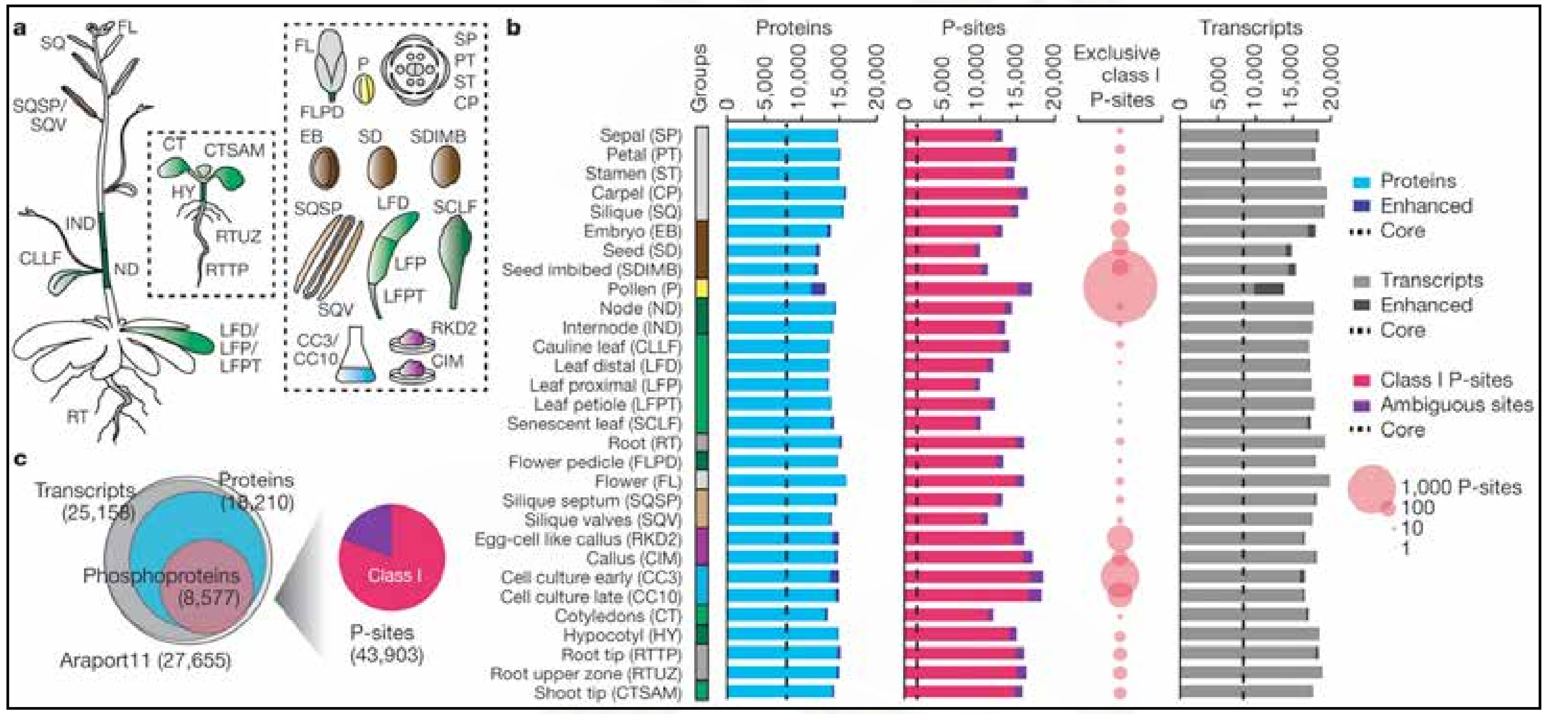

Figure 7. Schematic of tissue samples analysed, coloured according to morphology group (abbreviations defined in b): flower (light grey); seed (dark brown); pollen (yellow); stem (dark green); leaf (light green); root (dark grey); fruit (light brown); callus (magenta); cell culture (blue). b, Number of identifications at the protein, P-site and transcript levels for all tissues (n = 1 measurement per tissue). Dashed lines indicate the number of core proteins, P-sites or transcripts detected in all tissues. Tissue-enhanced proteins or transcripts are marked by a darker colour. P-sites with high-confidence amino acid localization (class I sites; more than 0.75 localization probability) are shown in pink; ambiguous site localizations are in purple. The number of P-sites exclusively detected in one tissue is shown by circles. c, Total number and overlap of identified gene loci in the transcriptome, proteome and phosphoproteome datasets compared with Araport11 (left), and the total number of identified P-sites and the proportion of class I sites (right).

Mergner J, Frejno M, List M, Papacek M, Chen X, Chaudhary A, Samaras P *et al* (2020) Mass-spectrometry-based draft of the Arabidopsis proteome. Nature 579: 409-414

Millar AH, Heazlewood JL, Giglione C, Holdsworth MJ, Bachmair A, Schulze WX (2019) The Scope, Functions, and Dynamics of Posttranslational Protein Modifications. Annual Review of Plant Biology 70: 119-151

Niehaus M, Straube H, Kunzler P, Rugen N, Hegermann J, Giavalisco P, Eubel H, Witte CP, Herde M (2020) Rapid Affinity Purification of Tagged Plant Mitochondria (Mito-AP) for Metabolome and Proteome Analyses. Plant Physiol 182: 1194-1210

Romero-Barrios N, Monachello D, Dolde U, Wong A, San Clemente H, Cayrel A, Johnson A, Lurin C, Vert G (2020) Advanced Cataloging of Lysine-63 Polyubiquitin Networks by Genomic, Interactome, and Sensor-Based Proteomic Analyses. Plant Cell 32: 123-138

Zhang H, Liu P, Guo T, Zhao H, Bensaddek D, Aebersold R, Xiong L (2019) Arabidopsis proteome and the mass spectral assay library. Sci Data 6: 278

Systems and Synthetic Biology

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Please describe the current state of your subcommittee's research area.

Research related to our subcommittee has been highly active over the last year, with many more exciting findings on the way. Proteome, protein-protein and molecular interactions are now easily identifiable and searchable through the Arabidopsis Interactions Viewer; http://bar.utoronto.ca/interactions2/ (Dong *et al*., 2020); the Loop system of plasmids are open-source and scalable and will enable rapid, modular and multiplexed vector construction for synthetic biology (Pollak *et al*., 2019), and the TuxNet tool enables the general Arabidopsis community to process RNAseq data and infer gene regulatory interactions and networks (Spurney *et al*., 2020).

Our sub-committee hosted our first spectacular conference (iPSB) in Roscoff, France in 2018, and culminated in a special issue of Molecular Plant (volume 12, issue 6). The 2nd edition of this conference will be held in 2021 in Venice, Italy, and the CSHL Network Biology conference will be held in 2021. Several workshops in this subject area were convened in the past year and have resulted in two perspective papers concerning systems and synthetic biology and its future (Argueso *et al*., 2019; Wurtzel *et al*., 2019). Finally, Arabidopsis research concerning systems and synthetic biology include the first systematic detection of chromatin-based regulatory elements in plants (Lu *et al*., 2019), mapping temporal regulatory interactions in the early N response (Brooks *et al*., 2019), stem-cell specific gene networks (Clark *et al*., 2019), the use of single cell sequencing, gene networks and mathematical modeling to elucidate a switch in xylem cell differentiation (Turco *et al*., 2019) and an overview of how to use quantitative systems biology approaches to unravel the complex network of genetic, microbial and metabolic interactions occurring during microbe-host (plant) interactions.

Recently developed Open Tools and Resources for Arabidopsis Researchers

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 Physiology. 179(4): 1893-1907.

Pollak B, Cerda A, Delmans M, Álamos S, Moyano T, West A, Gutiérrez RA, Patron NJ, Federici F, Haseloff J. (2019) Loop assembly: a simple and open system for recursive fabrication of DNA circuits. New Phytologist. 222(1):628-640.

Spurney RJ, Van den Broeck L, Clark NM, Fisher AP, de Luis Balaguer MA, Sozzani R. (2020). Tuxnet: a simple interface to process RNA sequencing data and infer gene regulatory networks. Plant Journal. 101(3):716-730.

Recent or Future activities of Subcommittee members.

A special Issue of Molecular Plant – "Plant Systems Biology" Volume 12, Issue 6, p727-892; with editorial contribution from Pascal Falter-Braun, Siobhan Brady, Rodrigo A. Gutierrez, Gloria M. Coruzzi, Gabriel Krouk

* Falter-Braun P, Brady S, Gutiérrez RA, Coruzzi GM, Krouk G. (2019). iPlant Systems Biology (iPSB): An International Network Hub in the Plant Community. Molecular Plant 12(6): 727-730

*The 2nd International Conference on Plant Systems Biology; September 21-25 2020 – due to COVID-19 concerns, please refer to the website for up-to-date information: https://meetings.embo.org/event/20-plant-systems

Conferences, Workshops and Training events

- OpenPlant Forum 2019 – Cambridge, UK https://www.openplant.org/forum

- 3rd International Conference on Plant Synthetic Biology, Bioengineering and Biotechnology, October 2019, Cambridge, UK https://www.aiche.org/sbe/conferences/international-conference-on-plant-synthetic-biology-and-bioengineering/2019

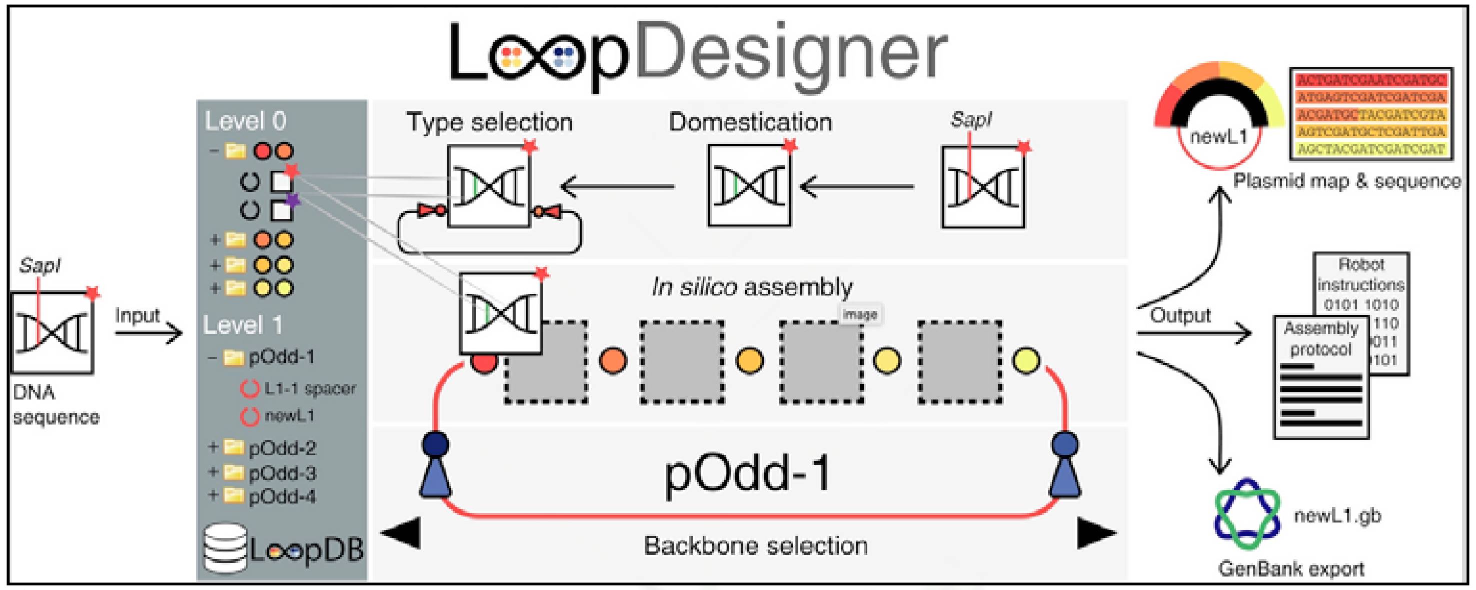


Figure 8. Design automation. A DNA sequence is submitted to LoopDesigner, which screens for BsaI and SapI sites and domesticates them to silent mutations where possible. A part type is specified for the assembly schema to save the part to the database library. To perform an in silico assembly, a receiver plasmid is selected which displays the compatible parts that can be placed in the current position of the assembly schema. As parts are included, the next compatible parts are displayed. When the assembly schema finds that all the parts required to complete the assembly are selected, the assembly simulation is performed. Then, LoopDesigner outputs the resulting plasmid map with its concurrent highlighted sequence and a protocol for Loop Type IIS reaction setup or export of GenBank sequence. Instructions to robots can be outputted if an API is provided with the required information (plasmid positions, ID mappings, robot functions) to produce the concurrent instruction file using Python scripting. The assembled part is then saved into the part library database for further assembly.

- Plant Synthetic Biology August, 2019, San Jose, USA https://plantsyntheticbiology.org

- NSR ERC Planning Workshop (2019); as a result of RiseEnAg: an Engineering Research Center for Rapid Innovations in SystEms Engineering and Agricultural Sustainability (NSF EEC #1840440)

Planned for Coming Years:

- CSHL Systems Biology: Networks (2021).
EMBO Conf. European Network Biology Conference, From Networks to Modelling: Hinxton, UK April 21-23 (2020). https://www.ebi.ac.uk/training/events/2020/2nd-european-network-biology-conference-networks-modelling

- 2nd International Plant Systems Biology Conference, Venice, September 21-25 (2020) https://meetings.embo.org/event/20-plant-systems

Products from Past Workshops:

Argueso CT, Assmann SM, Birnbaum KD, Chen S, Dinneny JR, Doherty CJ, Eveland AL, Friesner J, Greenlee VR, Law JA, Marshall-Colón A, Mason GA, O'Lexy R, Peck SC, Schmitz RJ, Song L, Stern D, Varagona MJ, Walley JW, Williams CM. (2019) Directions for research and training in plant omics. Plant Direct. 3(4), e00133.

Wurtzel ET, Vickers CE, Hansn AD, Millar AH, Cooper M, Voss-Fels KP, Nikel PI, Erb TJ. (2019) Revolutionizing agriculture with synthetic biology. Nature Plants. 5(12):1207-1210

Selected Publications

Brooks MD, Cirrone J, Pasquino AV, Swift J, Alvarez JM, Mittal S, Juang C-L, Varala K, Gutiérrez RA, Krouk G, Shasha D, Coruzzi GM. (2019) Network Walking charts transcriptional dynamics of nitrogen signaling by integrating validated and predicted genome-wide interactions. Nature Communications. 10(1):1569.

Clark NM, Buckner E, Fisher AP, Nelson EC, Nguyen TT, Simmons AR, de Luis Balaguer MA, Butler-Smith T, Sheldon PJ, Bergmann DC, Williams CM, Sozzani R. (2019) Stem-cell-ubiquitous genes spatiotemporally coordinate division through regulation of stem-cell-specific gene networks. Nature Communications. 10:5574.

Lu Z, Marand AP, Ricci WA, Ethridge CL, Zhang X, Schmitz RJ. (2019) The prevalence, evolution and chromatin signatures of plant regulatory elements. Nature Plants. 5:1250-1259.

Rodriguez PA, Rothballer M, Chowdhury SP, Nussbaumer T, Gutjahr C, Falter-Braun P. (2019). Systems Biology of Plant-Microbiome Interactions. Molecular Plant. 12(6):804-821.

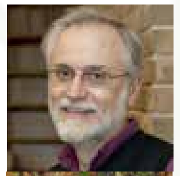
Turco GM, Rodriguez-Medina J, Siebert S, Han D, Valderamma-Gómez MÁ, Vahldick H, Shulse CN, Cole BJ, Juliano CE, Dickel DE, Savageau MA, Brady SM. (2019). Molecular Mechanisms Driving Switch Behavior in Xylem Cell Differentiation. Cell Reports. 28(2):342-351.

Arabidopsis Community Projects and Resources

Resource and Stock Centers

The Arabidopsis Biological Resource Center (ABRC)

www.abrc.osu.edu



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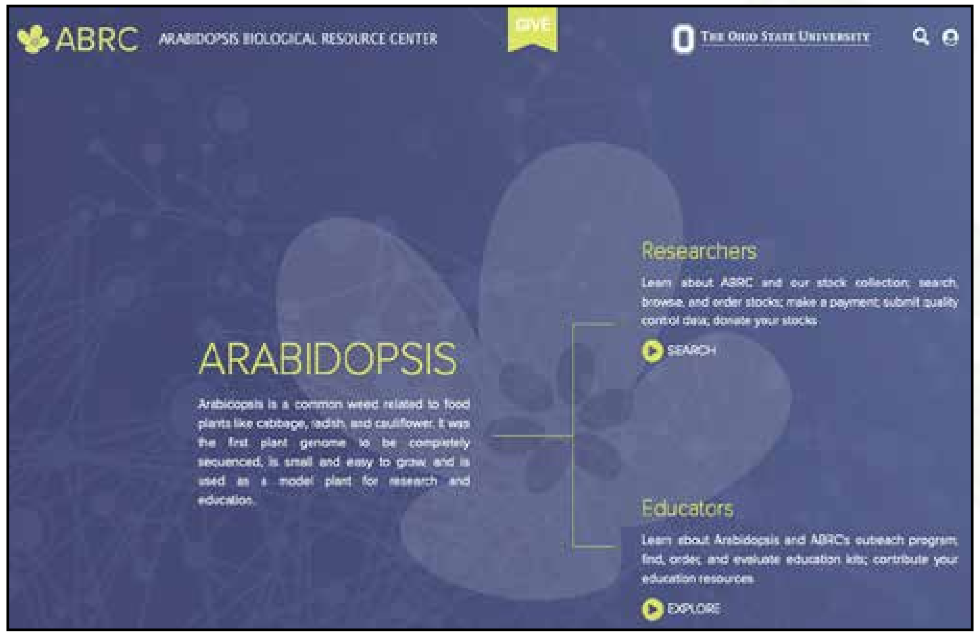
Please describe the current state of Arabidopsis research from the perspective of the country that your project or resource is based

Although demand for ABRC resources is still strong, there has been a downward trend in orders over the past 10 years. In the past 5 years, orders have stabilized indicating that there is still a base level of demand for these types of resources. Seeds and clones of Arabidopsis make up the bulk of stock distribution with the proportion of seed orders increasing from 84% in 2009 to 90% of total orders in 2019.

Resource distribution of other Brassicaceae is less than 5% of the total. In 2019, almost 50% of stock distribution was to US researchers, up from 40% five years ago. This indicates that demand for Arabidopsis seed resources in the US is robust, suggesting a strong Arabidopsis research community.



ARABIDOPSIS

Arabidopsis is a common weed related to food plants like cabbage, radish, and cauliflower. It was the first plant genome to be completely sequenced, is small and easy to grow, and is used as a model plant for research and education.

Researchers

Learn about ABRC and our stock collection; search, browse, and order stocks; make a payment; submit quality control data; donate your stocks

Educators

Learn about Arabidopsis and ABRC's outreach program; find, order, and evaluate education kits; contribute your education resources

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

ABRC launched a new web site (https://abrc.osu.edu/) in May 2019. The site has separate pathways to information for researchers and educators including stock data, ordering, payment and donation information as well as general information about Arabidopsis and ABRC. We continue to collaborate with The Arabidopsis Information Resource (TAIR) to make stock information available through the TAIR web site (https://www.arabidopsis.org/) with links out to ABRC.

Direct links have also been established from the SALK Institute Genomic Analysis Laboratory (http://signal.salk.edu/) T-DNA Express tool, 1001 Genomes (https://1001genomes.org/) web site, and the European Arabidopsis Stock Center, NASC (http://arabidopsis.info/), web site allowing users to leverage search functionality available through these resources and link directly to ABRC for stock ordering.

In 2019 ABRC distributed close to 190,000 samples to 2,260 individuals located in 47 countries. We also provided bulk seed for 2,300 seed lines to NASC and an additional 4,200 samples of seed for distribution to NASC users, where we were not able to provide bulk seed. The seed collection is now composed of more than 536,000 stocks.

Most of the *A. thaliana* seed stocks donated in 2019 were characterized mutant lines. These include a collection of embryo defective mutants donated by D. Meinke (Oklahoma State), added to a collection of chloroplast mutants recently received from R. Last (U. of Michigan). Both are part of our ongoing drive for new "legacy" stocks from retiring or re-orienting researchers for which we were recently funded (NSF CSBR). Diverse members of the Brassicaceae including accessions of *Arabis alpina, Thlaspi arvense, Brassica rapa, Erysimum cheiranthoides and Caulanthus amplexicaulis* were also received.

The non-seed portion of our collection now numbers more than 460,000 stocks. These lines include individual clones and libraries from *Arabidopsis thaliana,* and other members of the Brassicaceae, as well as constructs, host strains, antibodies, cell lines and education resources.

Non-seed resources added to the collection in 2019 include the JAtY BAC library generated by I. Bancroft, transcription factor ORF clones in bait and prey vectors donated by J. Ecker, maize clones donated by E. Grotewold and constructs from various donors. ABRC has performed quality control testing for 4,395 new and existing stocks, involving either germination testing or verifying stock identity.

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 include new resources for Arabidopsis and other Brassicaceae. Distribution is expected to continue at the current levels for most resources. Demand for education resources will likely increase following trends of the past 5 years. Quality control testing of new donations and stocks reproduced at ABRC will be carried out at similar levels to 2019.

ABRC and NASC collaboration via exchange of seed stock resources and related data will also continue. Ongoing development of our web site will include improvements to the user experience and administrative functions as well as addition of an application programming interface (API) to allow easy access to stock data. ABRC outreach continues to work with local community partners, the Ohio State University (OSU), and the broader plant science research and teaching communities to support education initiatives, especially those utilizing Arabidopsis resources.

Conferences, Workshops and Training events

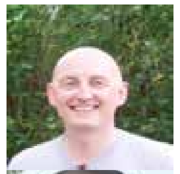
At ICAR 2019 in Wuhan, China, ABRC organized a booth in conjunction with NASC, and Dave Somers gave a presentation on the new web site in the Bioinformatics for plant research workshop. ABRC also participated in a data resources booth at Plant Biology 2019 in San Jose, CA.

Emma Knee gave a general presentation on ABRC as part of the US Culture Collection Network virtual meeting in November 2019. The ABRC advisory committee meeting was held at OSU, with a full day of presentations by ABRC staff members and a tour of the facilities. ABRC outreach and education ran booths at two local events, the Science Education Council of Ohio's annual conference and the National Science Teaching Association's regional conference in Cincinnati, OH.

In 2020 ABRC and NASC will organize a booth together at the 31st ICAR in Seattle, WA and will again participate in the data resources booth at Plant Biology 2020 in Washington, DC [ICAR2020 now delayed until 2021 and Plant Biology is going virtual: Ed]. ABRC outreach will participate in the Science Education Council of Ohio's annual conference and The Advancing Research Impact in Society Broader Impacts summit in Durham, NC.

The Nottingham Arabidopsis Stock Centre (uNASC)

http://www.Arabidopsis.info



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In 2019 we sent over 100,000 tubes of seed worldwide to 43 countries. This year's top receiving countries [previous 2018 position], are: 1st - China [3], 2nd - Germany [2] , 3rd - Spain [6] , 4th - Japan [4] , 5th - France [5] , and 6th the UK [1] . The biggest donor of stocks by far is still Germany.

The COVID-19 event saw a decline in the numbers of stocks ordered from NASC during 2020. This was particularly noticeable with respect to China during February and then some European labs from March as individual groups and departments ramped down their work. That said, orders from some countries such as Germany did not noticeably slow, and many institutes worldwide are still open as of April 2020.

Most noteworthy was the dramatic resurgence in orders (>2,000 stocks) from China during the first week of April 2020. Our exhibition stand in Wuhan at ICAR2019 was extremely well attended and demonstrated the strength and expansion of Arabidopsis research in Asia, particularly in China itself.

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 at ICAR2021 in Seattle.

RIKEN BioResource Center (RIKEN BRC)

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

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Please describe the current state of Arabidopsis research from the perspective of your project or resource

Arabidopsis has been significant plant species for plant science in Japan. The word "Arabidopsis" is shown in 74 titles out of 563 presentations in the 83rd Annual Meeting of the Botanical Society of Japan (BSJ Sep. 2019, Sendai). This model plant has been getting attention due to a novel which was serially published in a national newspaper. Shion Miura, one of the popular female writers, depicts a laboratory life of a young heroine who studies Arabidopsis mutants. Many people have learned how is the laboratory works in plant science. The novel won the BSJ Special Prize

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

RIKEN BRC has joined a project "RIKEN Integrated Symbiology (iSYM)" and started researches on plant-microbe symbiosis. Model plants such as Arabidopsis and Brachypodium are used in the project.
https://www.riken.jp/en/research/labs/isym/
https://www.yokohama.riken.jp/isym/index.html

Planned future activities of your project or resource

A series of binary vectors deposited from Dr. Tsuyoshi Nakagawa, Shimane University, is added to our Exp-Plant Catalog soon.
http://shimane-u.org/nakagawa/gbv.htm

We are planning to add Arabidopsis Transcription Factor – Glucocorticoid Receptor (TF-GR) lines to our catalog. The lines are developed at Dr. Minami Matsui laboratory in RIKEN CSRS.
https://www.embopress.org/doi/full/10.15252/msb.20177840

Conferences, Workshops and Training events

Riken BRC hosts the 13th Asian Network of Research Resource Centers (ANRRC). This International Meeting is held in November,2020.

Arabidopsis Informatics and Data Sharing Resources

The Arabidopsis Information Resource (TAIR)

www.Arabidopsis.org

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Fremont, CA 94538

Please describe the current state of Arabidopsis research from the perspective of your project or resource.

At TAIR, our view of the state of global Arabidopsis research is based on what we see through the lens of curating published literature. We import currently published 'Arabidopsis' papers as they are indexed by PubMed and use them to curate experimental gene function data. Each week, we load between 50 - 90 papers with the term 'Arabidopsis' in the title or abstract. We then review the abstracts and put the papers that seem to have functional information about Arabidopsis genes (around 41%), into our curation queue, prioritizing those with information about newly characterized genes.

As biocurators who seek to extract and organize data in meaningful ways, we share the following perspectives:
Overall, we see: 1) a steady number of papers that report on functions for previously characterized genes and 2) and an increase in the number of papers that describe high throughput experiments and contain large datasets. As the amount of papers and data increases, we at TAIR are developing strategies to increase throughput by incorporating more computation in the processing among other things. But there are things that authors can do to aid curation.

Occasionally, our import process misses relevant, curatable articles, typically because the papers either fail to mention Arabidopsis as a species or because the unique locus identifiers (e.g. AT1G01010) are not included in accessible (text) format anywhere in the paper. The high throughput papers present another challenge to curation as frequently the gene lists are attached as supplementary tables that lack metadata or are in formats that are not easily parsed such as PDF, which limits their accessibility and reuse. Issues such as absence of (accessible) identifiers in manuscripts and proliferation of unstructured datasets, highlight the need for researchers to become familiar with FAIR (Findable, Accessible, Interoperable and Reusable; https://www.force11.org/group/fairgroup/fairprinciples) data principles to ensure that their published data is compliant, as well as the need for new and better tools to make it easier for researchers to make their data FAIR.

As a start, TAIR has generated a 'cheat sheet' (https://conf.arabidopsis.org/pages/viewpage.action?pageId=22807345) to help researchers learn how they can make their published data more FAIR.

Another observation is that many more papers that include Arabidopsis genes do so as a reference for a different primary organism being studied. These are papers we import but do not curate. In these papers, Arabidopsis genes are often used to predict functions based on homology or used to find knockout mutants for heterologous gene transformation experiments. These papers highlight the important role that Arabidopsis continues to play as a model organism as researchers branch out (*pun intended*) into other plant species. As more experimental data is generated in other species, there is also a corresponding need to codify what is learned about gene functions from other plant species (especially what differs from Arabidopsis or reflect biological systems unique to those species) in order to have a comprehensive understanding of plant gene functions. To address this need, we are in the process of developing a tool to enable researchers to curate functions for any gene from any organism.

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

In the past year TAIR has made some significant operational and technical improvements, enhancements to the website and tools, and added data and resources to aid in understanding plant gene function.

Operational and Technical Changes

In May 2019 TAIR officially transitioned away from providing ordering capabilities for the ABRC. Researchers should now order stocks directly from the ABRC (https://abrc.osu.edu/). We continue to incorporate links from data pages (e.g. locus, gene, alleles, clones and germplasms) to the relevant stock centers (i.e. ABRC, NASC and RIKEN) to make finding resources easier for our community. Another significant change has been the addition of JBrowse to TAIR due to the loss of funding for the Araport (www.araport.org) project. TAIR, BAR and NCGR have joined together to ensure that the data and tools formerly provided by Araport remain available to the community. With help from members of the Araport and GMOD projects, TAIR has installed the latest version of JBrowse at TAIR (https://bit.ly/2Qhb5xC) starting with the tracks that were available at Araport. In the process, we have repaired tracks that were previously broken (e.g. Brassica Vista tracks) and also added new community data tracks for several published experiments (1,2). For those interested in making their sequence-based data public via JBrowse, TAIR welcomes your data submission. Please contact us at curator@arabidopsis.org.

In addition to the above changes, we performed software updates and technical improvements. We updated TAIR's BLAST service (https://www.arabidopsis.org/Blast/index.jsp) to the latest version of NCBI BLAST (2.9.0), and included all of the custom TAIR BLAST datasets. WU-BLAST was retired and a graphical display of alignments was added to the TAIR BLAST results display. Finally, we significantly speeded up page loading for the heavily accessed TAIR locus pages by making substantial changes to the underlying software.

PhyloGenes

In April 2019, Phoenix Bioinformatics, in collaboration with the Thomas Lab/PANTHER project at USC (www.pantherdb.org), launched PhyloGenes (www.phylogenes.org), a new web resource that facilitates inference of gene function based on phylogenetic relationships. PhyloGenes displays precomputed gene trees from PANTHER DB, alongside experimental gene function data or multiple sequence alignments. It makes use of the extensively curated information about gene function from Arabidopsis and 10 non-plant model species.

The most recent release (March 11, 2020; https://conf.arabidopsis.org/display/PHGSUP/Release+Notes) contains 40 plant species. By presenting a cohesive view of gene function in a phylogenetic context, PhyloGenes simplifies the process of assigning gene function to unknown genes. For species not included in the PhyloGenes build, users can graft protein sequences onto existing trees. TAIR now includes links out to PhyloGenes on the TAIR locus detail pages, in the Gene Families section, to view the corresponding families.

Arabidopsis MicroPublications

In October 2019, TAIR launched a partnership with the open access, peer-reviewed online journal microPublication (https://www.micropublication.org/). microPublication publishes brief, novel findings, negative and/or reproduced results, and results which may lack a broader scientific narrative. Micropublications are typically a single figure. TAIR curators review submitted works to ensure that, where possible, relevant data can be captured in TAIR. Types of data we curate from micropublications include gene functions, mutant phenotypes and expression data. Each paper is assigned a DOI and is citable. microPublications fulfill a need for a mechanism to share data that not otherwise be published such as student work from course based undergraduate research experiences. If you have questions about microPublications or are interested in serving a reviewer, send email to: contact@micropublication.org.

µP microPublication
get your data out, be cited

Gene function curation

TAIR curators continue to extract experimental gene function data from the current literature and codify the data in the form of annotations to Gene Ontology and Plant Ontology terms as well as curated gene summaries, alleles and phenotypes, and gene symbols. Along with curating recent literature, we have begun making a concentrated effort to identify and fill in gaps about missing gene function where possible. In 2019 we began by identifying sets of genes for which there were no GO annotations at all, reviewing our linked literature, and adding annotations where possible. The 'unknown' list is publicly available (https://conf.arabidopsis.org/pages/viewpage.action?pageId=22807120) and we encourage the community to contribute data if they have functional information for any of these genes. We continue to produce quarterly updates of current data for subscribers (https://www.arabidopsis.org/download/index-auto.jsp?dir=%2Fdownload_files%2FSubscriber_Data_Releases), and year old data for use by all (https://www.arabidopsis.org/download/index-auto.jsp?dir=/download_files/Public_Data_Releases). As always, we are grateful to our subscribers and data submitters for ensuring that this important resource continues to be available and up to date.

Planned future activities of your project or resource.

Aside from continuing our normal curation activities, a major goal for the coming year is to update the TAIR software stack. We plan to significantly overhaul the backend systems and replace most of the older codebase with more modern technology. This ground up redesign will enable greater flexibility, scalability, and more responsive, configurable web pages.

Conferences, Workshops and Training events

1- PAG 2020: Phoenix Bioinformatics staff organized several workshops for PAG2020 (Arabidopsis Informatics, Database Sustainability) and will continue to do so for 2021. We presented an update on TAIR during the Arabidopsis Informatics session.

2- ASPB 2019: Phoenix/TAIR co-organized the Plant Bioinformatics workshop at ASPB2019 in San Jose and presented a talk about PhyloGenes. We also presented a talk on the state of functional gene annotation at TAIR with an emphasis on what remains to be known.

3- ICAR 2019: TAIR organized the Bioinformatics resources workshop at ICAR2019 in Wuhan China and presented an update on TAIR and PhyloGenes.

Slides from TAIR presentations are available on the Phoenix Bioinformatics SlideShare (https://www.slideshare.net/PhoenixBio). We also maintain a social media presence on Twitter (@tair_news) and Facebook (https://www.facebook.com/tairnews/).

Lee TA, Bailey-Serres J. Integrative Analysis from the Epigenome to Translatome Uncovers Patterns of Dominant Nuclear Regulation during Transient Stress. Plant Cell. 2019;31(11):2573–2595. doi:10.1105/tpc.19.00463

Thieffry, A., Bornholdt, J., Ivanov,M., Peter Brodersen, P., Sandelin, A. Characterization of Arabidopsis thaliana promoter bidirectionality and antisense RNAs by depletion of nuclear RNA decay enzymes
bioRxiv 809194; doi: https://doi.org/10.1101/809194

International Arabidopsis Informatics Consortium (IAIC)

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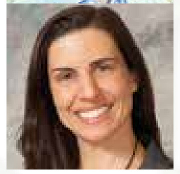

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North American Arabidopsis Steering
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Recent activities and newly developed tools and resources of your project or resource.

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, 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 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 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 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. TAIR and Araport had thus co-existed in a complementary manner, the former emphasizing functional annotation, the latter on aggregating resources.

An IAIC workshop entitled "2018 - the Future of Arabidopsis Bioinformatics", was held in May, 2018 to evaluate the 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). Most recently, after several unsuccessful NSF grant renewal applications, funding of the Araport project has been discontinued (see below).

(1) https://doi.org/10.1105/tpc.110.078519
(2) https://doi.org/10.1105/tpc.112.100669
(3) http://arabidopsisresearch.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 enable community development of Araport to replace and augment TAIR. 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, funding of project has been discontinued. Teams from The Arabidopsis Information Resource (TAIR), the National Center for Genome Resources (NCGR), and the Bio-Analytic Resource for Plant Biology (BAR) have taken over its operation and have refreshed/expanded the functionalities that were available at Araport.

Conferences, Workshops and Training events

The IAIC held a community workshop on January 13, 2020, entitled "Arabidopsis Bioinformatics" at the Plant and Animal Genomes (PAG) XXVIII conference in San Diego. The workshop featured speakers from all over the world, starting with Yijing Zhang, from the Shanghai Institutes for Biological Sciences, who shared her group's work in assembling the Plant Regulomics resource, a data-driven interface for retrieving upstream regulators from plant multi-omics data.

Korbinian Schneeberger from MPIPZ in Germany talked about their chromosome-level assemblies of seven Arabidopsis thaliana ecotype genomes and what the analysis of the data revealed about the evolution and total gene complement of this species. Andrew Farmer from the National Center for Genome Resources in New Mexico spoke about the deployment of a Genome Context Viewer (GCV) displaying the aforementioned Jiao/Schneeberger genomes, additional Arabidopsis ecotypes, and related Brassicaceae genomes, and the usefulness of GCV in exploring both macro- and micro-syntenic regions.

Larry Wu from Michigan State University described the identification of upstream, overlapping, and upstream overlapping ORFs (uORFs, oORFs, uoORFs) in Arabidopsis using the RiboSeq technique. The last two speakers, Sylva Donaldson from the BAR at the University of Toronto and Shabari Subramaniam from TAIR at Phoenix Bioinformatics in California talked about the transition of both Thalemine and JBrowse from the old Araport site to being hosted by BAR and TAIR, respectively, using the latest versions of the software.

Both tools are available to the community with updated and newly incorporated datasets. In their two talks, Sylva and Shabari also shared additional developments and new features at BAR and TAIR.

IAIC expected to hold a final workshop at ICAR 2020, scheduled for this July at the University of Washington, Seattle. However, due to the unexpect novel coronavirus-19 outbreak, ICAR 2020 has been postponed to June 2021. It is unclear if the final IAIC workshop will take place during ICAR 2021.

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) and BAR bioinformatics technician Asher Pasha, University of Toronto
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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 12 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, now delivered via the 1001 Genomes API.
* Documented subcellular localizations for 11.7k proteins, predicted localization for most of Arabidopsis proteome, from the SUBA database at the University of Western Australia.

Recent activities of your project or resource.

The news from December 2018 that Araport would not continue to be funded by the National Science Foundation in the U.S. precipitated a meeting in March, 2019 at which it was agreed that the BAR and TAIR would resuscitate the existing Thalemine and JBrowse instances, respectively, and that Araport's previous functionality would be expanded by adding a Genome Context Viewer from the National Center for Genome Resources to enable the viewing of multiple fully assembled *Arabidopsis thaliana* genomes. The Bio-Analytic Resource rolled out a revived and updated version of Araport's Thalemine at https://bar.utoronto.ca/thalemine/ in December 2019.

The BAR also published its eFP-Seq Browser at https://bar.utoronto.ca/eFP-Seq_Browser/ for exploring RNA-seq data as both read map profiles and summarized gene expression levels across two large compendia, in order to be able to quickly identify samples with the highest level of expression or where alternative splicing might be occurring (Sullivan *et al*., 2019).

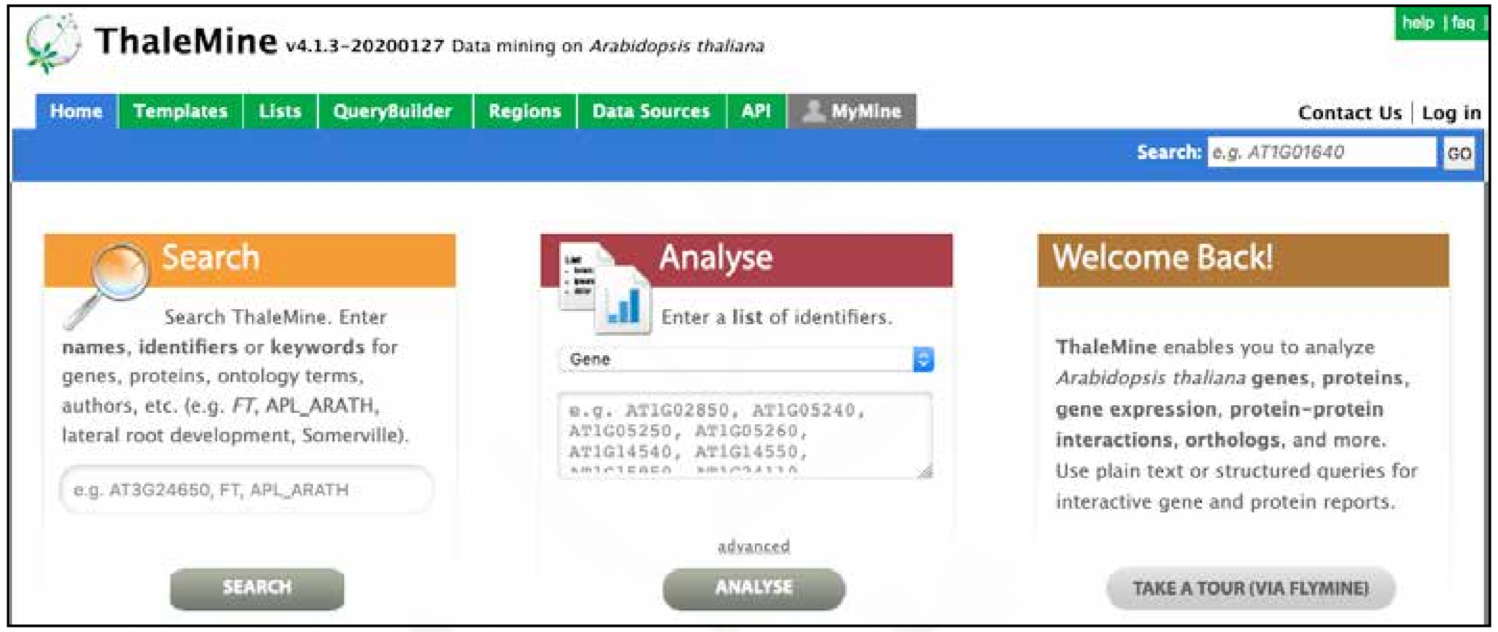
The BAR was also happy to announce its first single cell RNA-seq eFP Browser view at http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi?dataSource=Single_Cell, based on root single cell data RNA-seq from John Schiefelbein's lab at the University of Michigan (Ryu *et al*., 2019). We also added a DNA damage RNA-seq data set by Bourbousse *et al*. (2018) to the eFP Browser at http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi?dataSource=DNA_Damage, which is one of seven RNA-seq-based eFP Browser views, coming soon to ePlant.

We enabled links for 2.8 M Ecker Lab DAP-seq PDIs in our AIV2 tool (http://bar.utoronto.ca/interactions2/) to corresponding peak data in the Ecker Lab's AnnoJ Browser. The Gazzarrini and Lumba Labs at the University of Toronto (Carianopol *et al*., 2020) identified 125 SnRK1 complex interacting proteins using a meso-scale Y2H screening approach against ABA-regulated gene products and we've added these, along with hundreds of other PPIs published in the past year, into the AIV2 tool and database.

For non-Arabidopsis plant researchers, May the 4th 2019 was with you! ePlants for 15 agronomically important species became available on the BAR homepage at http://bar.utoronto.ca. We will be growing these in the future by adding more data, and we welcome comments and ideas for new data sets for them.

For maize researchers, new BAR eFP images and links to an updated gene atlas were enabled in MaizeGDB based on data from the Buell Lab (Hoopes *et al*., 2019). We collaborated to create a new eFP view for Thomas Widiez and colleagues microdissection work to generate RNA-seq data from an early timepoint in maize seed development (Doll *et al*., 2020): http://bar.utoronto.ca/efp_maize/cgi-bin/efpWeb.cgi?dataSource=Maize_Kernel.

The Mutwil Lab in Singapore published a Selaginella moellendorffii expression atlas (Ferrari *et al*., 2020). We collaborated to create an eFP Browser for it: http://bar.utoronto.ca/efp_selaginella/cgi-bin/efpWeb.cgi. Jin Zhang, Xiaohan Yang and colleagues published a nice paper on how light quality and intensity modulates the transcriptome in Kalanchoe (Zhang *et al*., 2020). We collaborated to create our first CAM plant eFP Browser, see http://bar.utoronto.ca/efp_kalanchoe/cgi-bin/efpWeb.cgi.



Search ThaleMine. Enter **names, identifiers** or **keywords** for genes, proteins, ontology terms, authors, etc. (e.g. *FT*, APL_ARATH, lateral root development, Somerville).

Enter a **list** of identifiers.

ThaleMine enables you to analyze *Arabidopsis thaliana* **genes, proteins, gene expression, protein-protein interactions, orthologs,** and more. Use plain text or structured queries for interactive gene and protein reports.

Figure 9. Thalemine hosted at BAR https://bar.utoronto.ca/thalemine/begin.do

BAR Publications (plus 2 citations* mentioned above, not in collaboration with the BAR)

Bourbousse, C., Vegesna, N., and Law, J.A. (2018). SOG1 activator and MYB3R repressors regulate a complex DNA damage network in Arabidopsis. Proc. Natl. Acad. Sci. U. S. A. 115: E12453–E12462*.

Carianopol, C.S., Chan, A.L., Dong, S., Provart, N.J., Lumba, S., and Gazzarrini, S. (2020). An abscisic acid-responsive protein interaction network for sucrose non-fermenting related kinase1 in abiotic stress response. Commun. Biol. 3: 145.

Doll, N.M., Just, J., Brunaud, V., Caïus, J., Grimault, A., Depège-Fargeix, N., Esteban, E., Pasha, A., Provart, N.J., Ingram, G.C., Rogowsky, P.M., and Widiez, T. (2020). Transcriptomics at Maize Embryo/Endosperm Interfaces Identifies a Transcriptionally Distinct Endosperm Subdomain Adjacent to the Embryo Scutellum. Plant Cell 32: 833.

Ferrari, C., Shivhare, D., Hansen, B.O., Pasha, A., Esteban, E., Provart, N.J., Kragler, F., Fernie, A., Tohge, T., and Mutwil, M. (2020). Expression Atlas of Selaginella moellendorffii Provides Insights into the Evolution of Vasculature, Secondary Metabolism, and Roots. Plant Cell 32: 853.

Hoopes, G.M., Hamilton, J.P., Wood, J.C., Esteban, E., Pasha, A., Vaillancourt, B., Provart, N.J., and Buell, C.R. (2019). An updated gene atlas for maize reveals organ-specific and stress-induced genes. Plant J. 97: 1154–1167.

Ryu, K.H., Huang, L., Kang, H.M., and Schiefelbein, J. (2019). Single-Cell RNA Sequencing Resolves Molecular Relationships Among Individual Plant Cells. Plant Physiol. 179: 1444*.

Sullivan, A. *et al*. (2019). An 'eFP-Seq Browser' for visualizing and exploring RNA sequencing data. Plant J. 100: 641–654.

Zhang, J. *et al*. (2020). Light-responsive expression atlas reveals the effects of light quality and intensity in Kalanchoë fedtschenkoi, a plant with crassulacean acid metabolism. GigaScience 9.

Planned future activities of your project or resource.

A custom eFP view in ePlant for a researcher's own RNA-seq data is in the works, along with "Gaia" (kind of like Siri or Alexa, but for Arabidopsis information) as part of 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 2019 American Society of Plant Biology (ASPB) Plant Biology conference in San Jose, as part of the Plant AgData Outreach booth and in the Plant Bioinformatics workshop; and Plant and Animal Genomes (PAG) XXVIII at the start of 2020 in San Diego, California.

The BAR principal investigator Nicholas Provart released a "Plant Bioinformatic Methods" specialization in plant bioinformatics, encompassing 4 courses on Coursera.org, see https://www.coursera.org/specializations/plant-bioinformatic-methods. These may be audited for free, or you can get a certificate for a small fee.

International Plant Phenotyping Resources

International Plant Phenotyping Network

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

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Julich Plant Phenotyping Centre

International Plant Phenotyping Network is a non-profit association (since 2015) representing the major plant phenotyping centers & practitioners within industry & academia, internationally.

IPPN 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 general public. Through workshops and symposia, IPPN established different working groups which advance specific fields of plant phenotyping research & applications and distribute all relevant information about plant phenotyping in a web-based platform (www.plant-phenotyping.org).

The purpose of the IPPN is to promote science, research and further applications in the field of plant phenotyping, focusing particularly on these goals:

- establishing a global network of institutions in order to maximize existing synergies, identify and reduce potential bottlenecks via joint projects and within topic-specific working groups;
- fostering communication and cooperation between different stakeholders from academia, industry, and the general public;
- increasing the visibility and impact of plant phenotyping beyond its own research community;
- facilitating the interdisciplinary training needed for effective plant phenotyping research and education.

Additionally, IPPN is eager to identify and initiate research projects, particularly to establish plant phenotyping in new regions and to implement advanced training activities.

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

End 2019/ beginning of 2020, the IPPN general assembly elected a new executive board, leading the organization for -at least- the next four years. For the first time in the history of the organization members from academia and also from industry are represented in this board.

Among the new board members, internationally renowned institutions are listed, like Forschungszentrum Juelich (Germany), Wageningen University & Research (Netherlands), Purdue University (USA) and University Nebraska-Lincoln (USA). On the Industry side, sensor developers & system integrators PhenoVation (Netherlands) and Phenotrait (China) are board members.

Planned future activities of your project or resource.

After the last International Plant Phenotyping Symposium (IPPS) in China (Autumn 2019) and according to the organization's internal roadmap, the next IPPS will be held in Europe in 2021. Internal voting for where exactly the venue will be is ongoing until April 2020. Preparations will start immediately afterwards.

Conferences, Workshops and Training events

Several sessions, workshops, hackathons and satellite meetings organized by IPPN's working groups within several international plant science conferences (IPAP, Rooting2020, SEB) have recently been postponed due to the outbreak of the Corona virus pandemic.
To stay informed on these, please visit IPPN's event section https://www.plant-phenotyping.org/index.php?index=580

EMPHASIS

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

Roland Pieruschka
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Julich Plant Phenotyping Centre

The European Infrastructure for Multi-scale Plant Phenomics and Simulation (EMPHASIS) is a distributed Research Infrastructure to develop and provide access to facilities and services addressing multi-scale plant phenotyping in different agro-climatic scenarios. EMPHASIS will establish an integrated European phenotyping infrastructure to analyse genotype performance under diverse environmental conditions and quantify the diversity of traits contributing to performance in diverse environmental conditions – plant architecture, major physiological functions and output, yield components and quality. EMPHASIS aims to address the technological and organizational limits of European Phenotyping, for a full exploitation of genetic and genomic resources available for crop improvement in changing climate. Inserted in the ESFRI Roadmap in 2016, EMPHASIS is in the transition from the Preparatory Phase (2017-2020) to the Implementation Phase (2020-2021) and is supposed to become operational in 2022.

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

EMPHASIS is in the process of developing its business plan in close discussion with national ministries with the final goal to enable a long term operation. Currently, ministry representatives from 14 countries have expressed their interest in supporting the implementation of EMPHASIS and a discussion was initiated to develop an Interim General Assembly as the discussion making body to develop and implement EMPHASIS and an organisation providing services to the plant science community in Europe.

Additionally, based on the landscaping analysis, which included a close interaction with Arabidopsis community, EMPHASIS started to pilot specific highly demanded services to test and illustrate the potential to generate benefits, the return of investment as well as test feasibility of these services. The pilot services include topics related to: i) access to field sites, ii) harmonisation, iii) data management, iv) harnessing innovation, v) modelling.

EMPHASIS is also active beyond plant sciences, utilizing synergies with other research infrastructures in projects such as i) CORBEL linking biological and medical infrastructures, ii) ENVRIPlus bringing together environmental and earth system research infrastructures, iii) EOSC-Life developing digital life sciences, iv) RI-VIS aiming at increasing the global visibility of European research infrastructures.

Conferences, Workshops and Training events

EMPHASIS will organize annual European Plant Phenotyping conferences starting in 2021. The first conference will be co-organized with the International Plant Phenotyping Network.

European Plant Phenotyping Network 2020

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

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Julich Plant Phenotyping Centre

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, with the aim to support the exploitation of genetic and genomic resources available for crop improvement that represents a major scientific challenge for coming decades. EPPN2020 specifically aims to facilitate the community progress 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 fifth call for transnational access enabling over 120 experiments within innovative plant phenotyping facilities in Europe. A substantial amount of the 31 facilities providing access within EPPN2020 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.

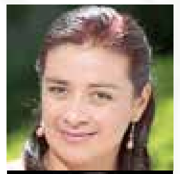
EPPN2020 will announce the final sixth call for application for access to EPPN2020 facilities in April 2020. Selected users can do the proposed experiments for free, including travel and accommodation. In total, we expect to be able to facilitate over 150 experiments.

Conferences, Workshops and Training events

EPPN2020 will host a dedicated session on related to benchmarking EPPN2020 transnational Access experiments during the SEB2021 in Antwerp.

Gramene: A comparative genomics and pathways resource for plants

http://www.gramene.org



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

Gramene provides open access to plant genomes, gene functional annotations including curated and projected metabolic and regulatory pathways, and gene expression data in a phylogenetic context, based on robust phylogenetic genes trees. In collaboration with EnsemblGenomes, Gramene hosts 67 plant reference genomes (about 2.5 million genes in total) including three Arabidopsis species (almost 100,000 genes): *A. thaliana, A. lyrata, and A. halleri*. For each reference genome sequence, we provide structural and functional gene annotations including ontology associations and protein domain assignment, genetic and structural variants, phylogenetic trees with orthologous and paralogous gene classification, whole-genome alignments, and synteny maps.

Our phylogenetic trees include 96,607 gene families comprising over 2.1 million genes or almost 2.4 million input proteins supporting homolog and ortholog assignments to Arabidopsis species. 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 (e.g., ability to select a specific GO term or InterPro domain) views to highlight homologs that share functional features.

A. thaliana serves as an anchor species within Gramene. *A. thaliana* homologs are displayed as part of the query results within the Gramene search and A. thaliana is used as the dicot model for pairwise whole-genome alignments collection. Within the past year, the alignments subset for A. thaliana grew from 57 to 66, including alignments between *A. thaliana* and each of *A. lyrata* and *A. halleri*. In addition, we host alignments between A. lyrata and each of *Medicago truncatula*, *Oryza sativa* (Japonica rice), *Theobroma cacao* (cacao), and *Vitis vinifera* (grapevine); and *A. halleri* to Japonica rice, cacao, and grapevine. Our synteny collection includes synteny maps for A. thaliana and each the following 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.

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

In collaboration with Reactome, Gramene hosts 306 metabolic and regulatory pathways curated in Japonica rice and inferred in 96 additional plant species (including the three Arabidopsis species) based on orthology. Reactome pathways are checked and peer-reviewed prior to publication to ensure factual accuracy and compliance with the data model, and a system of evidence tracking ensures that all assertions (which use community standard controlled vocabulary ontologies) are supported by primary literature. Gramene's integrated search capabilities, and interactive views facilitate visualizing gene features, gene neighborhoods, phylogenetic trees, gene expression profiles, and pathways. The homology view in the search interface allows custom pruning of the gene trees to selected species of interest, and visualizing sequence conservation to the amino acid level. The views also assist cross-referencing to other bioinformatics resources, including AraPort, TAIR and NASC for Arabidopsis.

Gramene provides tools to support integration of user data sets, in context to the reference data. These tools include a sequence assembly converter (which allows the conversion of genomic coordinates between the TAIR9 and TAIR10 genome assemblies), a genetic variant effect predictor, an advanced BioMart-based query interface, data analysis and visualization of OMICS data, multi-species pathway comparisons, and BLAST/BLAT sequence aligner. Together these reference comparative genome data and tools enable powerful cross-species comparisons among plants and reference eukaryotic species.

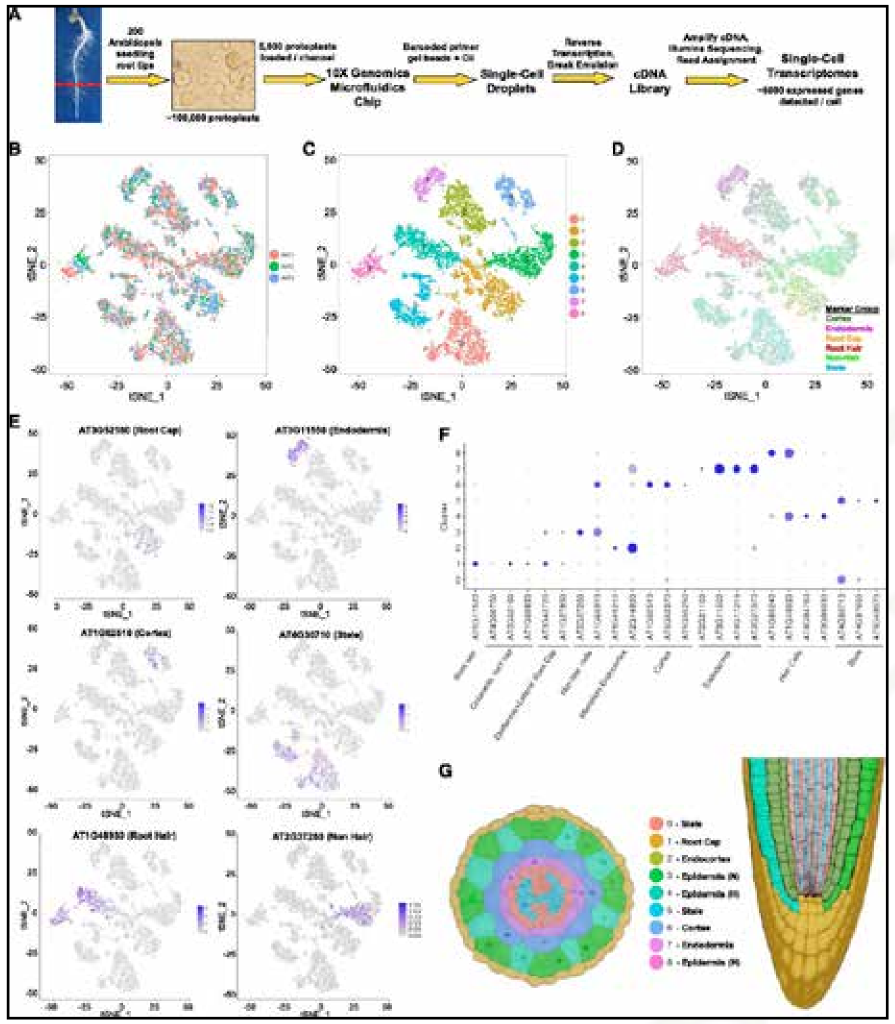

Figure 10. Isolation and cluster analysis of single-cell transcriptomes from wild-type Arabidopsis roots. A, Workflow used for scRNA-seq to obtain transcriptomes from individual Arabidopsis root cells. B, tSNE projection plot showing dimensional reduction of the distribution of 7522 individual wild-type cell transcriptomes from three biological replicates. Cell transcriptomes derived from each replicate are indicated by different colors (red = replicate 1; green = replicate 2; blue = replicate 3). C, tSNE projection plot showing nine major clusters of the 7522 individual wild-type root cell transcriptomes. D, tSNE projection plot showing the combined transcript accumulation from all marker genes tested (listed in Supplemental Table S3) on the 7522 wild-type transcriptomes, organized by the tissue/cell type of the marker gene group (cortex, endodermis, root cap, root-hair, nonhair, and stele marker gene sets). E, tSNE projection plots showing transcript accumulation for specific tissue/cell marker genes in individual cells. Color intensity indicates the relative transcript level for the indicated gene in each cell. The tissue/cell types known to preferentially express each marker gene are given in parentheses (details available in Supplemental Table S3). Additional marker gene plots are provided in Supplemental Figure S2. F, Accumulation of marker gene transcripts by cluster. This dot plot indicates the fraction of cells in each cluster expressing a given marker (dot size) and the level of marker gene expression (dot intensity) for 24 genes known to exhibit preferential expression in distinct tissue/cell types (Supplemental Table S3). G, Assignment of cell clusters to root tissues. Depictions of transverse (left) and longitudinal (right) sections of the Arabidopsis primary root showing tissues in colors corresponding to the nine-cluster plot in C. N, Nonhair cells; H, root-hair cells. Note that cells corresponding to cluster 8 are not shown on the root images, because this cluster was found to contain mature root-hair cells which are not represented in these root images.

Gramene data sets that include Arabidopsis species:

- Structural and functional annotations for 2.2 million gene models in 67 plant reference genomes including three Arabidopsis model species -A. thaliana, A. lyrata, and A. helleri, cereal, vegetable, and fruit crops (e.g., Brassicas, Fabaceas, Solanaceas), basal plants and algae.

- 96,607 phylogenetic tree families (built with 67 plant and 5 non-plant species), 299 whole-genome alignments (66 with Arabidopsis species), and 66 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 827 experiments in 24 plant species, including A. thaliana and A. lyrata.

- 306 reference metabolic and regulatory pathways curated in rice and inferred in 96 additional plant species (including the three Arabidopsis species in Gramene).

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

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

Gramene is committed to open access and reproducible science based on the FAIR (Fair, Accessible, Interoperable and Reusable) data principles. We are a phylogenomic resource, built upon best-of-class open source software, Ensembl, Reactome, and Expression Atlas infrastructure platforms.

Gramene has developed a powerful and flexible document-based architecture that enables advanced searching via a web-service accessible by a variety of programming languages; each platform supporting web-based and programmatic access through application programming interfaces (APIs).

Extensive use of ontologies, database cross-references, common data formats, metadata, community engagement and open-source software promotes interoperability within the ecosystem of informatics data and services. Gramene's genome portal utilizes the Ensembl infrastructure and is developed in collaboration with the Ensembl Genomes project (EMBL-EBI); the pathway portal, Plant Reactome (http://plantreactome.gramene.org) utilizes the Reactome infrastructure, and is developed in collaboration with OCIR; the baseline expression data from both, our genomes and pathway browsers, is a collaboration with the Expression Atlas project (EMBL-EBI). Integration across these platforms in Gramene is supported by an NSF grant IOS-1127112, and partially from USDA-ARS (8062-21000-041-00D).

Jean-Baptiste K, McFaline-Figueroa JL, Alexandre CM, Dorrity MW, Saunders L *et al*. (2019) Dynamics of Gene Expression in Single Root Cells of Arabidopsis thaliana. Plant Cell. 31(5):993-1011. doi: 10.1105/tpc.18.00785.

Ryu KH, Huang L, Kang HM, Schiefelbein J (2019). Single-Cell RNA Sequencing Resolves Molecular Relationships Among Individual Plant Cells. Plant Physiol. 179(4):1444-1456. doi: 10.1104/pp.18.01482.

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

Turco GM, Rodriguez-Medina J, Siebert S, Han D, Valderrama-Gómez MÁ *et al*. (2019) Molecular Mechanisms Driving Switch Behavior in Xylem Cell Differentiation. Cell Rep. 28(2):342-351.e4. doi: 10.1016/j.celrep.2019.06.041.

Planned future activities of your project or resource.

With future support, we will continue to maintain and build the Gramene resource, with aims to have a minimum of two releases: 1) update and expand our reference data collection of plant genomes, genetic variation, gene expression, and standardized comparative annotations, 2) enrich our Plant Reactome pathways data resource with newly curated pathways, and orthology-based projections, 3) improve the functionality of the Gramene search interface and integrate DIVE (Gupta *et al*, 2018) gene functional information, and 4) transform the community through communication and training opportunities.

Gupta A, Xu W,Jaiswal P, Taylor C, and Regala J (2018). Domain Informational Vocabulary Extraction Experiences with Publication Pipeline Integration and Ontology Curation. http://ceur-ws.org/Vol-2285/ICBO_2018_paper_43.pdf

Conferences, Workshops and Training events

In the past year, Gramene participated in 14 scientific conferences: 61st annual Maize Genetics Conference; 2019 Biocuration; 2019 CSHL Systems Biology and Engineering; 2019 CSHL Biology of Genomes; 2019 ASPB Plant Biology; 2019 International Conference in Arabidopsis Research (ICAR); 2019 CSHL Genome Informatics; 2019 Welcome Trust Plant Genomes and a Changing Environment; 3rd International Conference on Plant Synthetic Biology, Bioengineering, and Biotechnology; 2019 CSHL Plant Genomes and Biotechnology; 2019 & 2020 EU COST Integrape; 2020 Genomes Working Group CA17111; and XXVIII Plant and Animal Genomes (PAG).

We organized community outreach booths for members of the AgBioData Consortium at the PAG and ASPB conferences. We continued to host educational webinars in Gramene's YouTube channel https://goo.gl/ln9RLD.

We organized one pathway curation jamborees and one virtual gene structural annotation jamboree for faculty (predominantly from primarily undergraduate institutions or PUIs), graduate students, and maize researchers.

For the later, we hosted four 3-hour long live webinars, and made the video-recordings, as well as our training material available in a google drive (shorturl.at/oBHVZ). Other plant education activities geared to K-12 students and faculty included hands-on activities to celebrate Fascination of Plants Day at Bayville Elementary School, Science Night and a DNA workshop for Science Olympiad participants at Franklin K-8 School, Saturday DNA at CSHL DNA Learning Center, panels on Ethics in Genetic Engineering at SUNY Stony Brook, and Food and Climate at CSHL.

In the next year, we plan on continuing our outreach, education and training activities, including attending the PAG, ASPB and CSHL Biology of Genomes meetings.

The Global Plant Council

globalplantcouncil.org/

Isabel Mendoza-Poudereux
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Recent activities and newly developed tools and resources of your project or resource.

The Global Plant Council (GPC) is a coalition of national, regional and international research organizations and professional societies representing plant, crop, agricultural, and environmental sciences across the globe.

GPC promotes plant science across borders and disciplines: it aims to support those directly involved in research, but also in education and training, to increase awareness of the key role of plant research in science and society.

The GPC website (http://www.globalplantcouncil.org) is the central stone of the GPC online communication strategy. It is daily updated with relevant news, events and resources that are shared thereafter through our social media channels that gather almost 20.000 followers.

GPC launched this year the ECRi, or Early-Career Researcher (ECR) International Network, a collection of activities addressed to help the plant science ECRs with 4 essential pillars: job hunting, grant writing, dissemination and networking

The first science communication workshop hosted by GPC was held in June 2019, and revolve on how to promote "your" science to the media and general public. This training was part of the Arabidopsis Conference in Wuhan, China (ICAR19)

Planned future activities of your project or resource.

We had planned to provide a GPC-hosted workshop on science communication at the 30th June 2020 in Torino (Italy) as part of the Plant Biology Europe 2020 conference. However this meeting has now been postponed until June 28th- July 1st 2021.

Global Plant Council

The Global Plant Council (GPC) is a coalition of organizations representing the plant, crop, agricultural, and environmental sciences across the globe, representing thousands of experts.

Analysis of Arabidopsis Publications

Outlook for 2020

In the 2019 MASC Annual Report we reported for the first time that the number of publications that included Arabidopsis had slipped below those publications that included rice. This trend continues into this report as the number of rice publications move further ahead of those that include 'Arabidopsis'. The number of Arabidopsis publications has plateaued since 2013 and with current trends will be soon overtaken by the number of publications that include maize/corn or wheat/Triticum. We speculated last year that this represents a general global change in emphasis from discovery-led to more applied plant science research and that the progress that has been made with Arabidopsis has been transitioned to other plant species. However thse trends are undoubtedly also linked to technical improvements that has made analysis of more complex genotypes and growing conditions more routine.

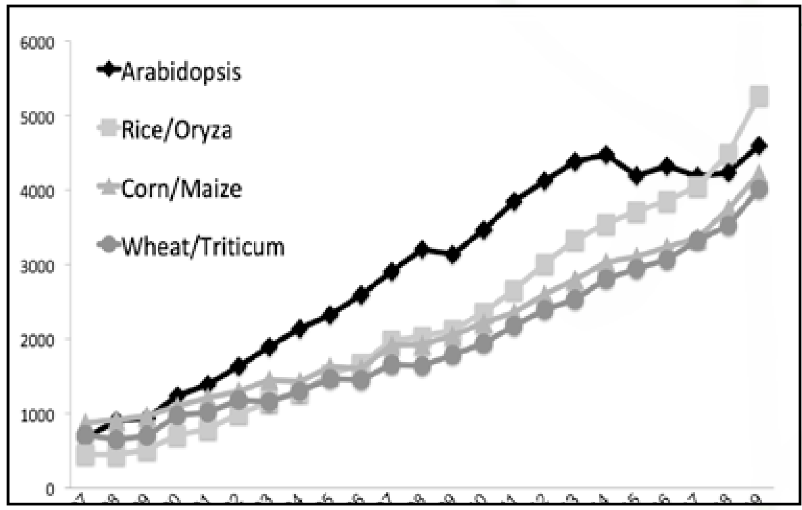

Figure 11. Papers published in Pubmed journals globally with Arabidopsis, rice/oryza, corn/maize or wheat/triticum in the Title/ Abstract.

Despite the plateau in the number of papers containing 'Arabidopsis' China continues to buck-the-trend with 2019 seeing a continuing increase in its number of publications (Figure 12). The other four nations with the highest number of publications remain the same as in 2018 as the number of their outputs have levelled. A significant positive conclusion to be drawn from Figure 11 and Figure 12 is that the numbers have not declined over the past five years so perhaps the amount of global Arabidopsis research has reached a status-quo.

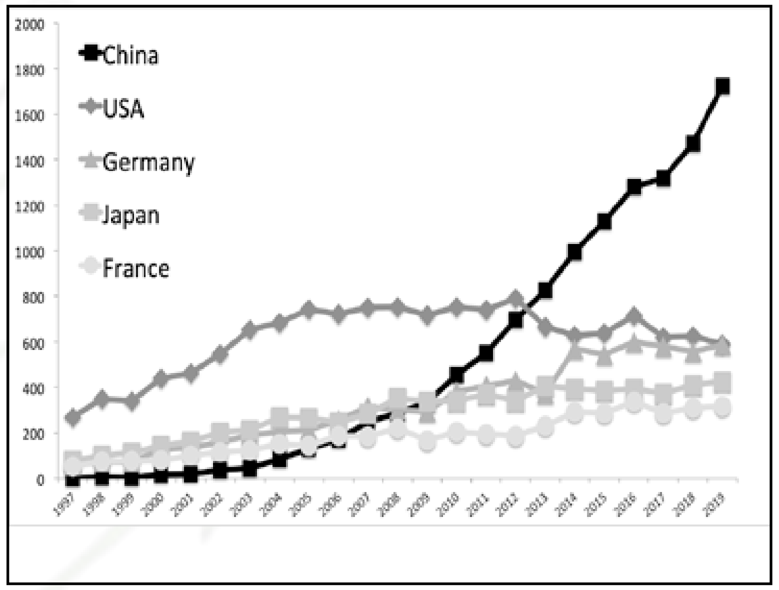

Figure 12. Papers published in Pubmed journals with Arabidopsis in the Title/Abstract since 2011. Globally These countries are have the highest number of publications.

Figure 13 shows the proportional changes in the number of Arabidopsis publications between 2011 and 2019 for the 30 countries included in the 2020 MASC report. Between 2011 and 2015 27 of 29 countries showed an increase in the number of their Arabidopsis publications (Figure 13, any green colour) whilst 7 of these increases were greater than two-fold (darkest green).

However between 2015 and 2019 the number of countries with an increase was 22 of 30, with just 2 of these with the higher increase (darkest green). This reduction in number of countries that have higher increases in the number of Arabidopsis publications corresponds to the plateau in the overall number of publications (figure 11).

In 2019 many high-profile "Cell-Nature-Science" (CNS) publications featured Arabidopsis research, documenting a number of firsts in plant science. These include the discovery in plant nuclei of liquid–liquid phase separations of polyadenylation complexes [1], defining the control and organization of the cambial stem cells that are the pregenitors of all woody tissues [2], identifying molecular controls of autophagy [3], engineering a synthetic switch for control of stomatal opening [4] or defining the first complete blueprint for immunity pan-NLRomes [5].

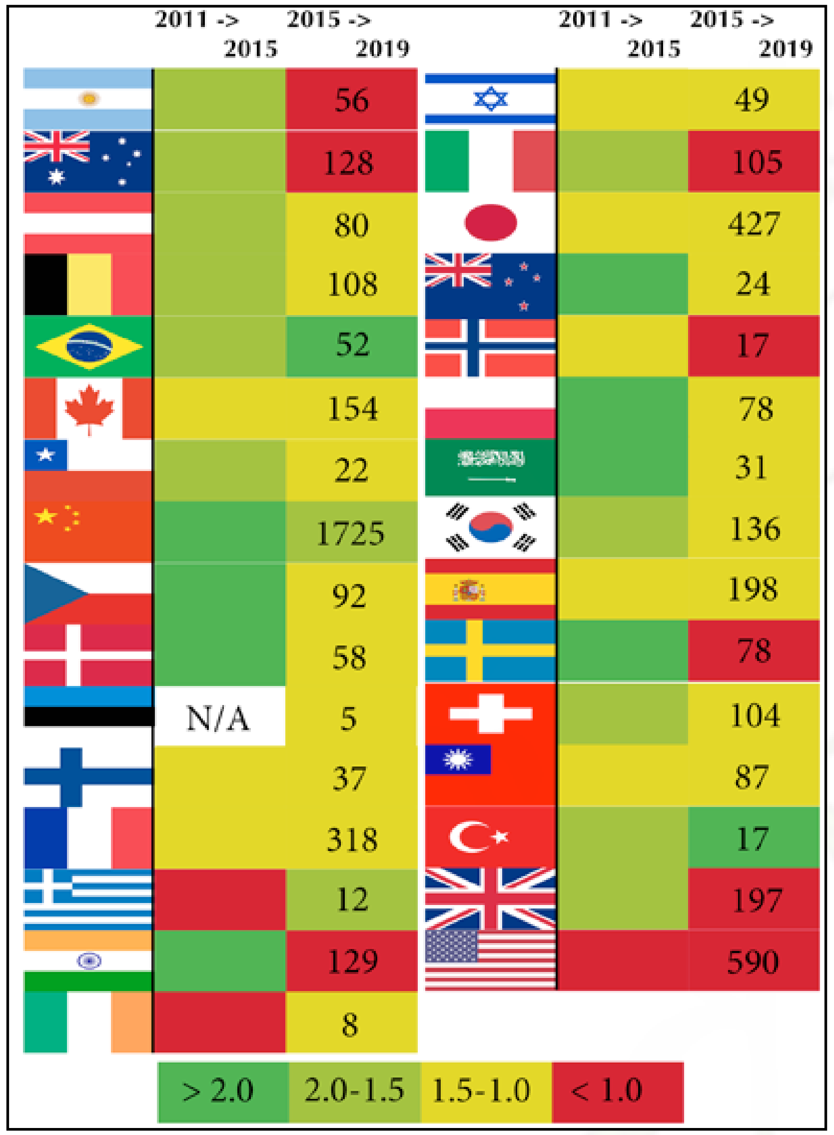

Figure 13 Change in the number of papers published in PubMed journals with Arabidopsis in the Title/Abstract between 2011 and 2015 or between 2015 and 2019. Countries are those included in this report. The proportional change in the number of publications between years are colour-coded as follows: Dark green (>2.0), Green (1.5 – 2.0), Lime Green (1.5 – 1.0), Red (<1.0). The following terms were used in the PubMed search box: Arabidopsis[Title/Abstract] AND COUNTRY AND (“journal article”[Publication Type] OR “review”[Publication Type]) AND YEAR[DP]. The number of publications in 2019 is documented in the right-hand box.

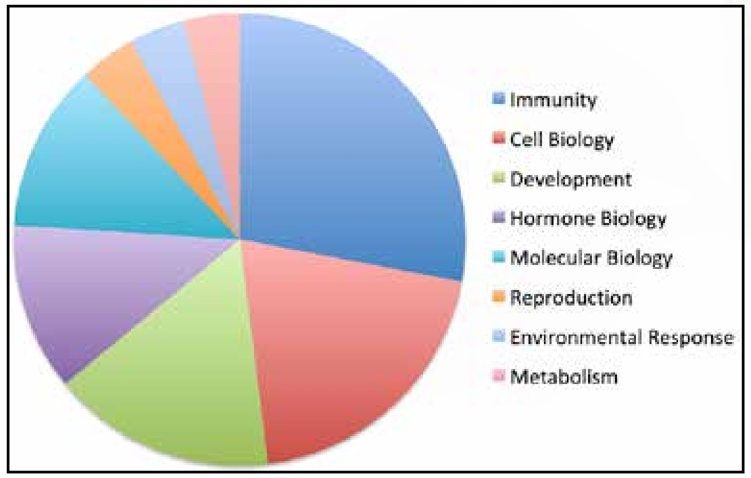

Figure 14 Broad categories of 2019 Cell-Nature-Science publications that feature research performed in Arabidopsis

This breadth of topics covered across CNS publications shows that research in Arabidopsis continues to be influential in many areas of plant science (figure 14). There is no assumption that CNS papers are of higher quality than those published elsewhere and their success and longevity will be judged in the fullness of time.

Importantly the corresponding authorship of the 2019 CNS papers are spread around the globe with 13 led from Europe, 7 from the USA and 5 from China, although of course most of these papers are cross-border collaborations.

[1]- Fang, X., Wang, L., Ishikawa, R. *et al.* Arabidopsis FLL2 promotes liquid–liquid phase separation of polyadenylation complexes. Nature 569, 265–269 (2019). doi:10.1038/s41586-019-1165-8

[2]- Miyashima, S., Roszak, P., Sevilem, I. *et al.* Mobile PEAR transcription factors integrate positional cues to prime cambial growth. Nature 565, 490–494 (2019). doi: 10.1038/s41586-018-0839-y

[3]- Marshall RS, Hua Z, Mali S, McLoughlin F, Vierstra RD. ATG8-Binding UIM Proteins Define a New Class of Autophagy Adaptors and Receptors. Cell. ;177(3):766-781.e24. doi: 10.1016/j.cell.2019.02.009

[4]- Papanatsiou M, Petersen J, Henderson L, Wang Y, Christie JM, Blatt MR. Optogenetic manipulation of stomatal kinetics improves carbon assimilation, water use, and growth. Science. 363(6434):1456-1459. doi: 10.1126/science.aaw0046

[5]- Van de Weyer AL, Monteiro F, Furzer OJ, Nishimura MT, Cevik V, Witek K, Jones JDG, Dangl JL, Weigel D, Bemm F. A Species-Wide Inventory of NLR Genes and Alleles in Arabidopsis thaliana. Cell. 178(5):1260-1272.e14. doi: 10.1016/j.cell.2019.07.038

MASC Country Reports

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

Argentina

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Argentina

Please describe the current state of Arabidopsis research in your country

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

Arico D, Legris M, Castro L, *et al*. Neighbour signals perceived by phytochrome B increase thermotolerance in Arabidopsis. Plant Cell Environ. 2019;42(9):2554-2566. doi:10.1111/pce.13575

Cabello JV, Chan RL. Arabidopsis and sunflower plants with increased xylem area show enhanced seed yield. Plant J. 2019;99(4):717-732. doi:10.1111/tpj.14356

Godoy Herz MA, Kubaczka MG, Brzyzek G, *et al*. Light Regulates Plant Alternative Splicing through the Control of Transcriptional Elongation. Mol Cell. 2019;73(5):1066-1074.e3. doi:10.1016/j.molcel.2018.12.005

Gómez MS, Falcone Ferreyra ML, Sheridan ML, Casati P. Arabidopsis E2Fc is required for the DNA damage response under UV-B radiation epistatically over the microRNA396 and independently of E2Fe. Plant J. 2019;97(4):749-764. doi:10.1111/tpj.14158

Lescano I, Bogino MF, Martini C, *et al*. Ureide Permease 5 (AtUPS5) Connects Cell Compartments Involved in Ureide Metabolism. Plant Physiol. 2020;182(3):1310-1325. doi:10.1104/pp.19.01136

Lorenzo CD, Alonso Iserte J, Sanchez Lamas M, *et al*. Shade delays flowering in Medicago sativa. Plant J. 2019;99(1):7-22. doi:10.1111/tpj.14333

Luccioni L, Krzymuski M, Sánchez-Lamas M, Karayekov E, Cerdán PD, Casal JJ. CONSTANS delays Arabidopsis flowering under short days. Plant J. 2019;97(5):923-932. doi:10.1111/tpj.14171

Perotti MF, Ribone PA, Cabello JV, Ariel FD, Chan RL. AtHB23 participates in the gene regulatory network controlling root branching, and reveals differences between secondary and tertiary roots. Plant J. 2019;100(6):1224-1236. doi:10.1111/tpj.14511

Ré DA, Cambiagno DA, Arce AL, *et al*. CURLY LEAF Regulates MicroRNA Activity by Controlling ARGONAUTE 1 Degradation in Plants. Mol Plant. 2020;13(1):72-87. doi:10.1016/j.molp.2019.10.003

Righini S, Rodriguez EJ, Berosich C, Grotewold E, Casati P, Falcone Ferreyra ML. Apigenin produced by maize flavone synthase I and II protects plants against UV-B-induced damage. Plant Cell Environ. 2019;42(2):495-508. doi:10.1111/pce.13428

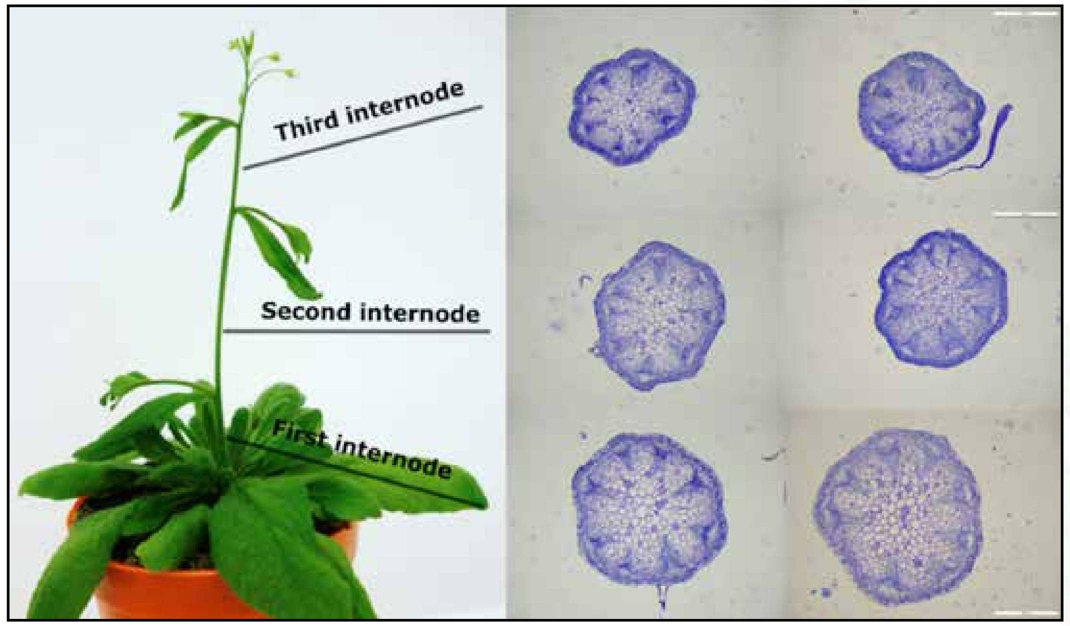

Figure 15. Illustrative photograph of Arabidopsis plants signaling first, second and third internodes. Stem cross-sections were obtained from the three internodes of untreated (left) or weight-treated plants (right) and stained with toluidine blue. Scale bars represent 0.5 mm.

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.

Please describe the current state of Arabidopsis research in your country

Australia has a strong tradition in plant research and in particular with regards to Arabidopsis functional genomics. Many institutions such as the Plant Industry Division of the Commonwealth Scientific and Industrial Research Organisation (CSIRO) and major Universities are engaged in Arabidopsis research. The CSIRO's Division of Plant Industry funds major programs in Plant Genomics and University researchers are funded mainly through the Australian Research Council's (ARC's) Discovery, Linkage Grant Schemes, or the Grains Research and Development Corporation of Australia (GRDC).

The ARC Center of Excellence Scheme funds a number of Centres in Australia that carry out Arabidopsis research, such as Plant Energy Biology (https://plantenergy.edu.au/research/people), Translational Photosynthesis (https://photosynthesis.org.au/) and more recently, Plant Success in Nature and Agriculture. Such Centres have allowed highly strategic and collaborative reseach projects (nationally and internationally) to be carried out. This has strengthened Australian plant science capabilities, trained numerous students and post-docs and generated substantial resources to ensure Australia remains internationally competitive in plant science research.

Conferences, Workshops and Outreach 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.

Upcoming Events:

The International Congress on Plant Molecular Biology (IPMB), Cairns Convention Centre, Queensland, 24th Oct 2021 (https://ipmb2021.org/). Australia is excited to be hosting the 13th International IPMB in 2021. We expect over 1000 researchers to attend plenary and concurrent sessions to discuss recent major impact discoveries from basic molecular biology to crop biotechnology.

COMBIO 2020 Melbourne has been rescheduled for 2022, National conference that includes several symposia dedicated to plant science and Arabidopsis research (www.asps.org.au).

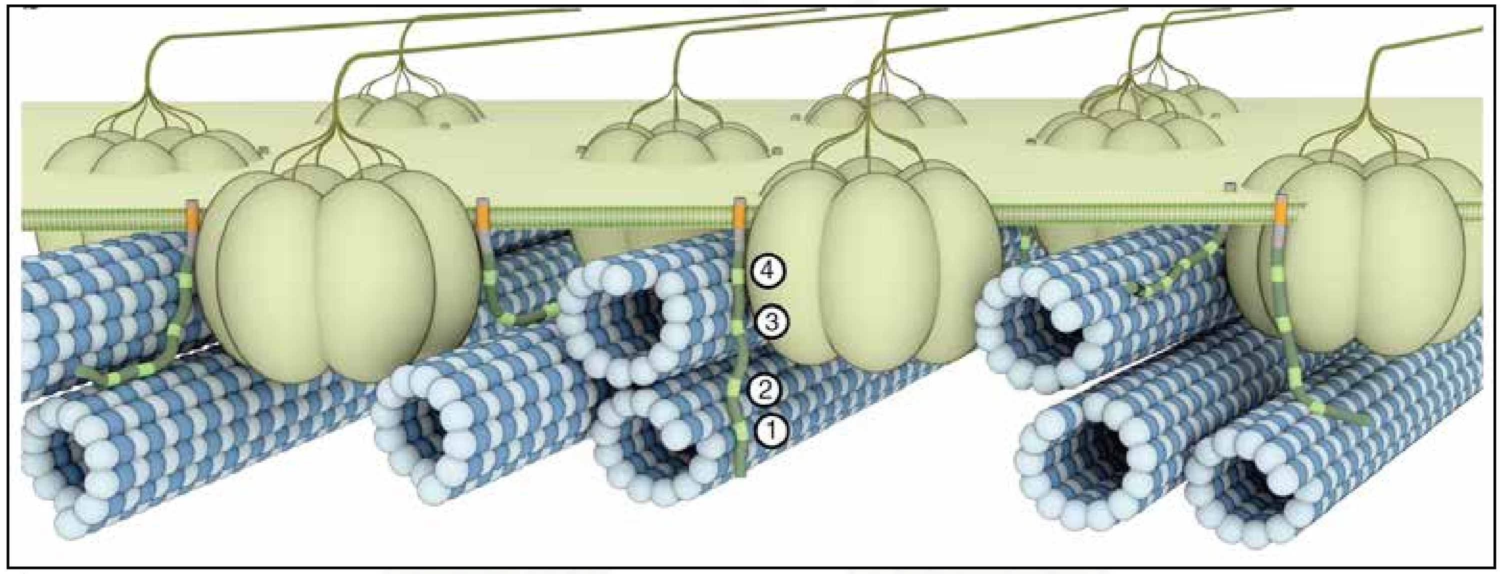

Figure 16. CC1 localization in its cellular context as part of the cellulose synthase complex (CSC). While the CSCs migrate along cortical microtubules during cellulose production, CC1 is involved in microtubule array organization via its cytosolic N-terminus. Similar to the Tau binding behavior, the CC1-microtubule interaction is dynamic and the microtubule-binding motifs (green) are potentially able to bind several tubulin dimers, distributed over one or several microtubules, thereby affecting microtubule bundling or dynamics. The individual components of the cartoon representation are drawn to scale, except for CC1 thickness and omission of its apoplastic domain. Membrane association and length of CC1, as well as the microtubule diameter, determine possible interaction modes

Selected Publications

Bhatia Sun YK, Yao J, Scaffidi A, Melville KT, Davies SF, Bond CS, Smith SM, Flematti GR, Waters MT. Divergent receptor proteins confer responses to different karrikins in two ephemeral weeds. Nat Commun. 2020 Mar 9;11(1):1264.

Chen W, Taylor MC, Barrow RA, Croyal M, Masle J. Loss of Phosphoethanolamine N-Methyltransferases Abolishes Phosphatidylcholine Synthesis and Is Lethal. Plant Physiol. 2019 Jan;179(1):124-142. doi: 10.1104/pp.18.00694.

Gonzalez-Bayon R, Shen Y, Groszmann M, Zhu A, Wang A, Allu AD, Dennis ES,§ Peacock WJ, Greaves IK. Senescence and Defense Pathways Contribute to Heterosis. Plant Physiol. 2019 May;180(1):240-252. doi: 10.1104/pp.18.01205

Gutmann B, Royan S, Schallenberg-Rüdinger M, Lenz H, Castleden IR, McDowell R, Vacher MA, Tonti-Filippini J, Bond CS, Knoop V, Small ID. The Expansion and Diversification of Pentatricopeptide Repeat RNA-Editing Factors in Plants. Mol Plant. 2020

James AM, Haywood J, Leroux J, Ignasiak K, Elliott AG, Schmidberger JW, Fisher MF, Nonis SG, Fenske R, Bond CS, Mylne JS. The macrocyclizing protease butelase 1 remains autocatalytic and reveals the structural basis for ligase activity. Plant J. 2019 Jun;98(6):988-999

Kesten C, Wallmann A, Schneider R, McFarlane HE, Diehl A, Khan GA, van Rossum BJ, Lampugnani ER, Szymanski WG, Cremer N, Schmieder P, Ford KL, Seiter F, Heazlewood JL, Sanchez-Rodriguez C, Oschkinat H, Persson S. The companion of cellulose synthase 1 confers salt tolerance through a Tau-like mechanism in plants. Nat Commun. 2019 Feb 20;10(1):857.

Li L, Lavell A, Meng X, Berkowitz O, Selinski J, van de Meene A, Carrie C, Benning C, Whelan J, De Clercq I, Wang Y. Arabidopsis DGD1 SUPPRESSOR1 Is a Subunit of the Mitochondrial Contact Site and Cristae Organizing System and Affects Mitochondrial Biogenesis. Plant Cell. 2019 Aug;31(8):1856-1878.

O'Leary BM, Oh GGK, Lee CP, Millar AH. Metabolite Regulatory Interactions Control Plant Respiratory Metabolism via Target of Rapamycin (TOR) Kinase Activation. Plant Cell. 2020 Mar;32(3):666-682.

Sweetman C, Waterman CD, Rainbird BM, Smith PMC, Jenkins CD, Day DA, Soole KL. AtNDB2 Is the Main External NADH Dehydrogenase in Mitochondria and Is Important for Tolerance to Environmental Stress. Plant Physiol. 2019 Oct;181(2):774-788.

Zhao C, Wang Y, Chan KX, Marchant DB, Franks PJ, Randall D, Tee EE, Chen G, Ramesh S, Phua SY, Zhang B, Hills A, Dai F, Xue D, Gilliham M, Tyerman S, Nevo E, Wu F, Zhang G, Wong GK, Leebens-Mack JH, Melkonian M, Blatt MR, Soltis PS, Soltis DE, Pogson BJ, Chen ZH. Evolution of chloroplast retrograde signaling facilitates green plant adaptation to land. Proc Natl Acad Sci U S A. 2019 Mar 12;116(11):5015-5020.

Major Funding Sources

Australian Research Council (https://www.arc.gov.au/).The Australian Reseach Council provides a number of Grants (Discovery, Linkage) and Fellowships (DECRA, Future Fellowship) to support fundamental research.

The Grains Research and Development Corporation (GRDC) - http://www.grdc.com.au/ is responsible for planning, investing and overseeing research and development, to improve the profitability across the grains industry. The GRDC supports translational research to improve yield and yield stability.

Austria

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Please describe the current state of Arabidopsis research in your country

Arabidopsis research in Austria 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.maxperutzlabs.ac.at/research/research-groups#c369), the Institute of Science and Technology, Austria (IST Austria) (https://ist.ac.at/en/research/), the Austrian Institute of Technology (AIT) (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=209112&L=1&MP=208727-210133), the University of Vienna (www.univie.ac.at/mosys) and the University of Graz (https://botanik.uni-graz.at/de/forschung/molecular-plant-physiology/).

More than 20 research groups focus on molecular genetics (including population, epi-, and developmental genetics), RNA-, chromosome-, cell-, and glycobiology as well as stress and hormone signaling. There are vivid collaboration activities between the research groups sharing experimental tools provided by sequencing, proteomic, genome editing, phenotyping, imaging and computational facilities (https://www.viennabiocenter.org/facilities/, https://ist.ac.at/en/research/scientific-service-units/ and https://boku.ac.at/wissenschaftliche-initiativen/vibt/das-vibt-imaging-center). Furthermore, the recent establishment of the Austrian plant phenotyping network (APPN) aims to support phenotyping for fundamental and applied plant research, from Arabidopsis to trees and from subcellular to the level of whole plant architecture (https://appn.at/expertise/).

While most Arabidopsis groups are strong in fundamental research the AIT has recently started a translational European wide project to uncover and promote tolerance to temperature and water stress in the native European oilseed Brassicaceae, *Camelina sativa* (UNTWIST).

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

Major update to AraPheno
https://arapheno.1001genomes.org)

Major update to AraGWAS
https://aragwas.1001genomes.org

APPN (Austrian Plant Phenotyping Network)
https://appn.at/

Conferences, Workshops and Outreach events

Participation of the Childrens's University in Vienna, Lower and Upper Austria and the Austrian Radio channel Ö1 (https://boku.ac.at/en/lehrentwicklung/kinderboku/themen/aktivitaeten-fuer-kinder)

Open Campus at the IST Austria including stands on Arabidopsis (https://ist.ac.at/en/education/ist-for-kids/)

Participation at the Fascination of Plants Day on the 17th of May, 2019 from the Gregor Mendel Institute of Molecular Plant Biology (GMI) of the Austrian Academy of Sciences

Selected Publications

Dünser K, Gupta S, Herger A, Feraru MI, Ringli C, Kleine-Vehn J. Extracellular matrix sensing by FERONIA and Leucine-Rich Repeat Extensins controls vacuolar expansion during cellular elongation in Arabidopsis thaliana. EMBO J. 2019;38(7):e100353. doi:10.15252/embj.2018100353

Feraru E, Feraru MI, Barbez E, *et al*. PILS6 is a temperature-sensitive regulator of nuclear auxin input and organ growth in Arabidopsis thaliana. Proc Natl Acad Sci U S A. 2019;116(9):3893-3898. doi:10.1073/pnas.1814015116

Plotnikova A, Kellner MJ, Schon MA, Mosiolek M, Nodine MD. MicroRNA Dynamics and Functions During Arabidopsis Embryogenesis. Plant Cell. 2019;31(12):2929-2946. doi:10.1105/tpc.19.00395

Marhava P, Hoermayer L, Yoshida S, Marhavý P, Benková E, Friml J. Re-activation of Stem Cell Pathways for Pattern Restoration in Plant Wound Healing. Cell. 2019;177(4):957-969.e13. doi:10.1016/j.cell.2019.04.015

Retzer K, Akhmanova M, Konstantinova N, *et al*. Brassinosteroid signaling delimits root gravitropism via sorting of the Arabidopsis PIN2 auxin transporter. Nat Commun. 2019;10(1):5516.
doi:10.1038/s41467-019-13543-1.

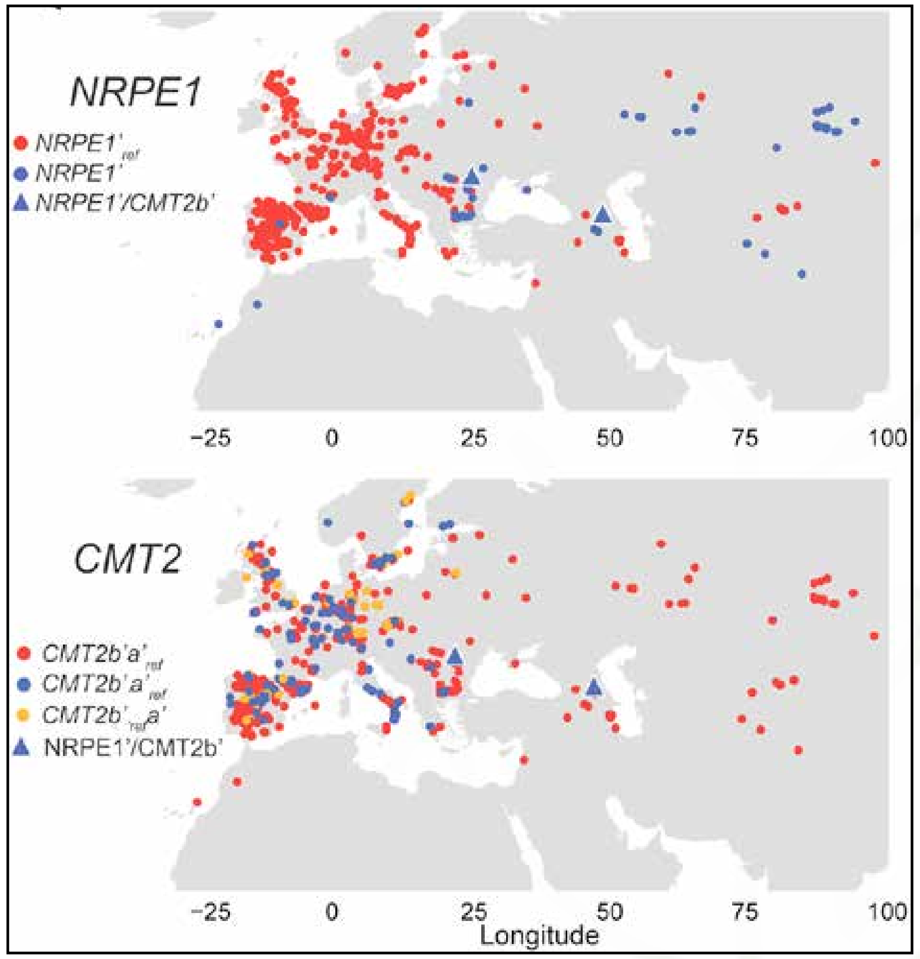

Figure 17 Geographical distribution of NRPE1 and CMT2 alleles.Maps show the distribution of NRPE1′, CMT2b′, and CMT2a′ alleles, and the frequency of non-reference alleles along to longitude.

Sasaki E, Kawakatsu T, Ecker JR, Nordborg M. Common alleles of CMT2 and NRPE1 are major determinants of CHH methylation variation in Arabidopsis thaliana. PLoS Genet. 2019;15(12):e1008492. Published 2019 Dec 30. doi:10.1371/journal.pgen.1008492.

Schoberer J, König J, Veit C, *et al*. A signal motif retains Arabidopsis ER-a-mannosidase I in the cis-Golgi and prevents enhanced glycoprotein ERAD. Nat Commun. 2019;10(1):3701. doi:10.1038/s41467-019-11686-9

Sims J, Copenhaver GP, Schlögelhofer P. Meiotic DNA Repair in the Nucleolus Employs a Nonhomologous End-Joining Mechanism. Plant Cell. 2019;31(9):2259-2275. doi:10.1105/tpc.19.00367

Waidmann S, Ruiz Rosquete M, Schöller M, *et al*. Cytokinin functions as an asymmetric and anti-gravitropic signal in lateral roots. Nat Commun. 2019;10(1):3540. doi:10.1038/s41467-019-11483-4

Zhu Q, Gallemí M, Pospíšil J, Žádníková P, Strnad M, Benková E. Root gravity response module guides differential growth determining both root bending and apical hook formation in Arabidopsis. Development. 2019;146(17):dev175919. doi:10.1242/dev.175919

Major 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)

FEBS Fellowships (https://www.febs.org/our-activities/fellowships/)

Belgium

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Please describe the current state of Arabidopsis research in your country

Research on *Arabidopsis thaliana* remains a pillar for fundamental plant science in Belgium. This is also illustrated by the challenge to reduce the list of Arabidopsis publications in this report to a maximum number of 10.

Nevertheless, also in Belgium plant scientists feel an increasing pressure from funding agencies, universities, and research institutes to focus on more applied research aspects. This entails for instance research on crop plants, or projects addressing topics that are relevant for climate change.

FWO and ERC are the two main funding bodies that still promote basic research, while a number of funding initiatives by FWO and other organizations are aimed at applied research. Succeeding in these calls often means submitting projects that do not focus on Arabidopsis as a model plant. This being said, it is likely that Arabidopsis will remain a major tool to generate and test hypothesis even in applied research projects.

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

- New version of PLAZA
https://bioinformatics.psb.ugent.be/plaza/

- Belgian Galaxy launched last year (Flemish funding)
https://usegalaxy.be

Conferences, Workshops and Outreach events

Conferences for 2019 have been covered in the 2019 report. As far as I'm aware, conferences for 2020 have been postponed to 2021 due to the ongoing COVID-19 crisis.

Selected Publications

Decaestecker W, Buono RA, Pfeiffer ML, Vangheluwe N, Jourquin J, Karimi M, Van Isterdael G, Beeckman T, Nowack MK, Jacobs TB. CRISPR-TSKO: A Technique for Efficient Mutagenesis in Specific Cell Types, Tissues, or Organs in Arabidopsis. Plant Cell. 2019 Dec;31(12):2868-2887. doi: 10.1105/tpc.19.00454.

Dejonghe W, Sharma I, Denoo B, De Munck S, Lu Q, Mishev K, Bulut H, Mylle E, De Rycke R, Vasileva M, Savatin DV, Nerinckx W, Staes A, Drozdzecki A, Audenaert D, Yperman K, Madder A, Friml J, Van Damme D, Gevaert K, Haucke V, Savvides SN, Winne J, Russinova E. Disruption of endocytosis through chemical inhibition of clathrin heavy chain function. Nat Chem Biol. 2019 Jun;15(6):641-649. doi: 10.1038/s41589-019-0262-1. Epub 2019 Apr 22. PMID: 31011214

Hander T, Fernández-Fernández ÁD, Kumpf RP, Willems P, Schatowitz H, Rombaut D, Staes A, Nolf J, Pottie R, Yao P, Gonçalves A, Pavie B, Boller T, Gevaert K, Van Breusegem F, Bartels S, Stael S. Damage on plants activates Ca2+-dependent metacaspases for release of immunomodulatory peptides. Science. 2019 Mar 22;363(6433). pii: eaar7486. doi: 10.1126/science.aar7486. PMID: 30898901

Huang J, Willems P, Wei B, Tian C, Ferreira RB, Bodra N, Martínez Gache SA, Wahni K, Liu K, Vertommen D, Gevaert K, Carroll KS, Van Montagu M, Yang J, Van Breusegem F, Messens J. Mining for protein S-sulfenylation in Arabidopsis uncovers redox-sensitive sites. Proc Natl Acad Sci U S A. 2019 Oct 15;116(42):21256-21261. doi: 10.1073/pnas.1906768116. Epub 2019 Oct 2. PMID: 31578252

Li T, Natran A, Chen Y, Vercruysse J, Wang K, Gonzalez N, Dubois M, Inzé D. A genetics screen highlights emerging roles for CPL3, RST1 and URT1 in RNA metabolism and silencing. Nat Plants. 2019 May;5(5):539-550. doi: 10.1038/s41477-019-0419-7. Epub 2019 May 10. PMID: 31076735

Lu KJ, van 't Wout Hofland N, Mor E, Mutte S, Abrahams P, Kato H, Vandepoele K, Weijers D, De Rybel B. Evolution of vascular plants through redeployment of ancient developmental regulators. Proc Natl Acad Sci U S A. 2020 Jan 7;117(1):733-740. doi: 10.1073/pnas.1912470117. Epub 2019 Dec 24. PMID: 31874927

Ramakrishna P, Ruiz Duarte P, Rance GA, Schubert M, Vordermaier V, Vu LD, Murphy E, Vilches Barro A, Swarup K, Moirangthem K, Jørgensen B, van de Cotte B, Goh T, Lin Z, Vos U, Beeckman T, Bennett MJ, Gevaert K, Maizel A, De Smet I. EXPANSIN A1-mediated radial swelling of pericycle cells positions anticlinal cell divisions during lateral root initiation. Proc Natl Acad Sci U S A. 2019 Apr 23;116(17):8597-8602. doi: 10.1073/pnas.1820882116. Epub 2019 Apr 3. PMID: 30944225

Ramon M, Dang TVT, Broeckx T, Hulsmans S, Crepin N, Sheen J, Rolland F. Default Activation and Nuclear Translocation of the Plant Cellular Energy Sensor SnRK1 Regulate Metabolic Stress Responses and Development. Plant Cell. 2019 Jul;31(7):1614-1632. doi: 10.1105/tpc.18.00500. Epub 2019 May 13. PMID: 31123051

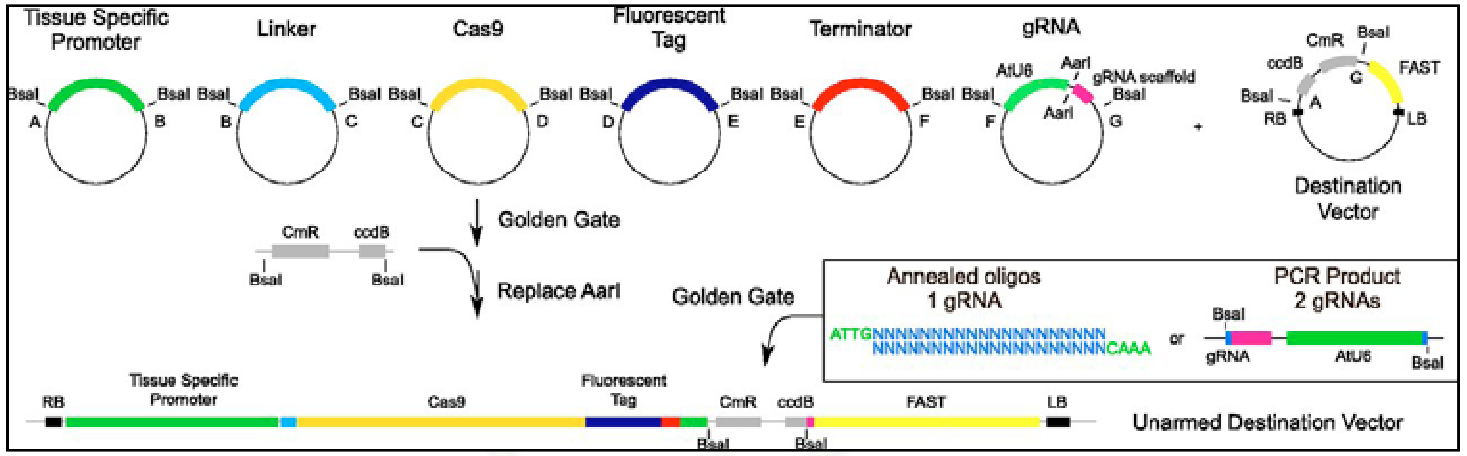

Figure 18. Six entry modules are combined in a binary destination vector, containing a FAST screenable marker cassette, via Golden Gate assembly. The six entry modules contain a tissue-specific promoter, a cloning linker, the Cas9 nuclease, a fluorescent tag, a terminator, and a module containing an AtU6-26 promoter driving the expression of an unarmed gRNA scaffold. These modules replace the ccdB and CmR selectable markers, allowing for the negative selection of the destination vector in ccdB-sensitive E. coli cells. The resulting vector can be directly "armed" with one or two gRNAs upon predigestion with AarI. Alternatively, the AarI restriction sites can be replaced by a PCR product containing two BsaI sites flanking ccdB and CmR expression cassettes. In a single Golden Gate reaction, a pair of annealed oligonucleotides are cloned, resulting in an expression vector containing one gRNA. Alternatively, Golden Gate cloning of a PCR product containing a first gRNA attached to an AtU6-26 promoter and the spacer sequence of the second gRNA results in an expression vector containing two gRNAs.

Vanholme R, Sundin L, Seetso KC, Kim H, Liu X, Li J, De Meester B, Hoengenaert L, Goeminne G, Morreel K, Haustraete J, Tsai HH, Schmidt W, Vanholme B, Ralph J, Boerjan W. COSY catalyses trans-cis isomerization and lactonization in the biosynthesis of coumarins. Nat Plants. 2019 Oct;5(10):1066-1075. doi: 10.1038/s41477-019-0510-0. Epub 2019 Sep 9. PMID: 31501530

Vanhaelewyn L, Viczián A, Prinsen E, Bernula P, Serrano AM, Arana MV, Ballaré CL, Nagy F, Van Der Straeten D, Vandenbussche F. Differential UVR8 Signal across the Stem Controls UV-B-Induced Inflorescence Phototropism. Plant Cell. 2019 Sep;31(9):2070-2088. doi: 10.1105/tpc.18.00929. Epub 2019 Jul 9. PMID: 31289115

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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Please describe the current state of Arabidopsis research in your country

In Brazil the number of institutions using Arabidopsis in their research is growing each year. At the moment, at least fifteen different institutions are using it as a model plant. We are seeing 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 investigate gene functions.

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.

Conferences, Workshops and Outreach events

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, Cuiabá, Mato Grosso Brazil, from June 9 to 12, 2019.
Nature Conference: Advances in Metabolic Communication

October 15–18, 2019
Belmond Copacabana Palace, Rio de Janeiro, Brazil

Selected Publications

Batista-Silva W, Heinemann B, Rugen N, Nunes-Nesi A, Araújo WL, Braun HP, Hildebrandt TM. (2019) The role of amino acid metabolism during abiotic stress release. Plant Cell. Environ. 42:1630–1644. doi: 10.1111/pce.13518.

da Fonseca-Pereira P, Souza PVL, Hou LY, Schwab S, Geigenberger P, Nunes-Nesi A, Timm S, Fernie AR, Thormählen I, Araújo WL, Daloso DM (2019) Thioredoxin h2 contributes to the redox regulation of mitochondrial photorespiratory metabolism. Plant Cell Environ 43(1):188-208 doi:10.1111/pce.13640

Dantas LLB, Calixto CPG, Dourado MM, Carneiro MS, Brown JWS and Hotta CT (2019) Alternative Splicing of Circadian Clock Genes Correlates With Temperature in Field-Grown Sugarcane. Front. Plant Sci. 10:1614. doi: 10.3389/fpls.2019.01614

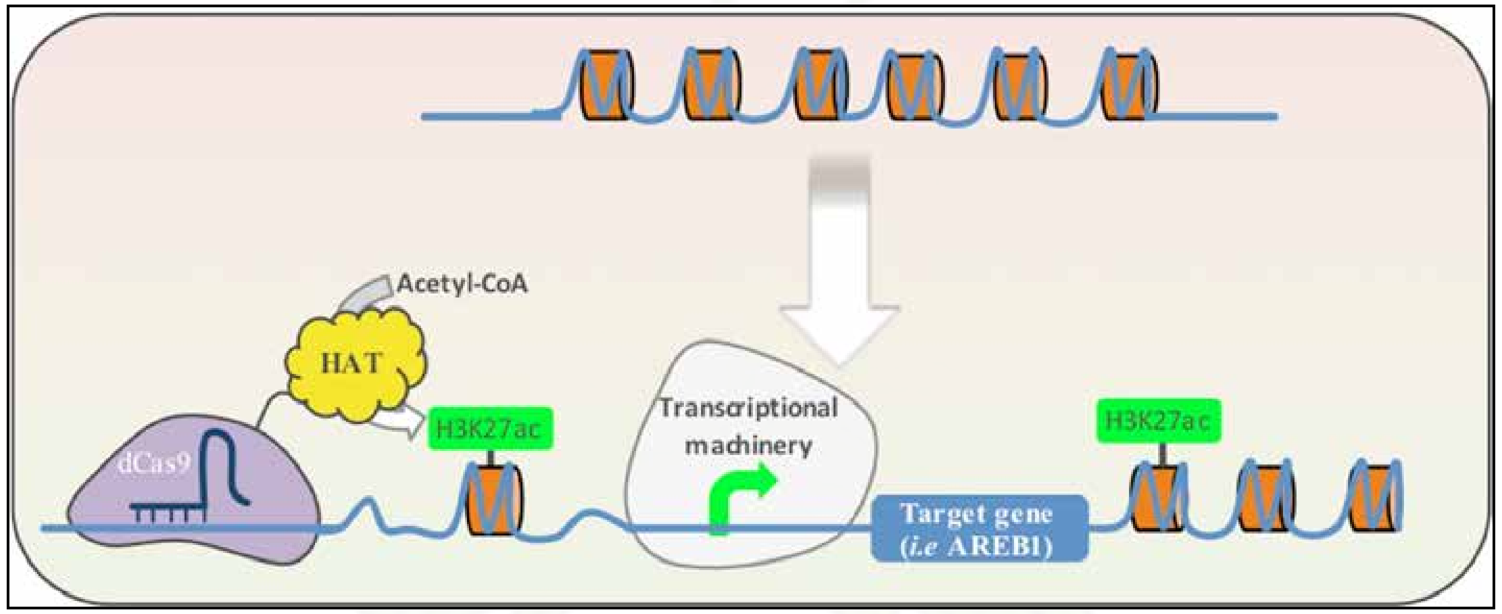

Figure 19. Schematic illustration of a model for dCas9HAT function in transcriptional activation of a target gene. Upper: the histone compaction (in orange) induces DNA condensation and limits transcription. Below: the dCas9HAT in complex with a single guide RNA (in dark blue) binds DNA on a target locus. The histone acetyl-transferase (HAT) triggers histone acetylation on the lysine 27 (H3K27ac) and induces local DNA relaxation. The DNA relaxation strengthens the interaction of the transcriptional machinery and /or transcriptional enhancers with the target locus

de Souza Chaves I, Feitosa-Araújo E, Florian A, Medeiros DB, da Fonseca-Pereira P, Charton L, Heyneke E, Apfata JAC, Pires MV, Mettler-Altmann T, Araújo WL, Neuhaus HE, Palmieri F, Obata T, Weber APM, Linka N, Fernie AR, Nunes-Nesi A (2019) The mitochondrial NAD+ transporter (NDT1) plays important roles in cellular NAD+ homeostasis in Arabidopsis thaliana. Plant J. 100(3):487-504. doi: 10.1111/tpj.14452.

Li, B., Ferreira, M.A., Huang, M. *et al*. The receptor-like kinase NIK1 targets FLS2/BAK1 immune complex and inversely modulates antiviral and antibacterial immunity. Nat Commun 10, 4996 (2019). https://doi.org/10.1038/s41467-019-12847-6

Lima, V.F., Medeiros, D.B., Souza, L.P., Gago, J., Fernie, A.R. and Daloso, D.M. (2019) The sucrose-to-malate ratio correlates with the faster CO_2 and light stomatal responses of angiosperms compared to ferns. New Phytol. 223(4), 1873–1887. Doi: 10.1111/nph.15927

Lima-Melo Y, Gollan PJ, Tikkanen M, Silveira JAG, Aro EM. (2019) Consequences of photosystem-I damage and repair on photosynthesis and carbon use in Arabidopsis thaliana. Plant J. 97(6):1061-1072. doi: 10.1111/tpj.14177.

Oliveira, R.A.d.C., de Andrade, A.S., Imparato, D.O. *et al*. Analysis of Arabidopsis thaliana Redox Gene Network Indicates Evolutionary Expansion of Class III Peroxidase in Plants. Sci Rep 9, 15741 (2019). https://doi.org/10.1038/s41598-019-52299-y

Roca Paixão JF, Gillet FX, Ribeiro TP, Bournaud C, Lourenço-Tessutti IT, Noriega DD, Melo BP, de Almeida-Engler J, Grossi-de-Sa MF. (2019) Improved drought stress tolerance in Arabidopsis by CRISPR/dCas9 fusion with a Histone AcetylTransferase. Sci Rep 9: 8080 doi: 10.1038/s41598-019-44571-y.

Yoshida T, dos Anjos L, Medeiros DB, Araújo WL, Fernie AR, Daloso DM. 2018. Insights into ABA-mediated regulation of guard cell primary metabolism revealed by systems biology approaches. Progress in Biophysics and Molecular Biology. 146: 37-49 doi: 10.1016/j.pbiomolbio.2018.11.006.

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)

Canada

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

- eFP-Seq Browser
https://bar.utoronto.ca/eFP-Seq_Browser

- Update of Araport's ThaleMine
https://bar.utoronto.ca/thalemine

Selected Publications

The Gazzarrini and Lumba Labs (Carianopol *et al*.2019, doi:10.1038/s42003-020-0866-8) identified 125 SnRK1 complex interacting proteins using a meso-scale Y2H screening approach against ABA-regulated gene products.

The Desveaux Lab (Cao *et al*. 2019, doi:10.1111/tpj.14425) generated an ABA-T3SE interactome network (ATIN) between P. syringae Type 3 Secreted Effectors (T3SEs) and Arabidopsis proteins encoded by ABA-regulated genes in order to further understand how plant pathogens can manipulate endogenous hormone signaling pathways. ATIN consists of 476 PPIs between 97 Arabidopsis ABA-regulated gene products and 56 T3SEs from four pathovars of P. syringae, as determined using Y2H.

Also re. plant-pathogen interactions, The Guttman and Desveaux Labs (Laflamme *et al*. 2020, doi:vi10.1126/science.aax4079) published an analysis of the plant pan-genome immunity landscape using their PsyTEC compendium, which consisted of 529 representative P. syringae T3SEs screened against Arabidopsis to identify those which trigger an immune response. The results showed that relatively few genes (including two novel ones) in Arabidopsis recognize the majority of P. syringae effectors.

The Provart Lab published its eFP-Seq Browser at https://bar.utoronto.ca/eFP-Seq_Browser/ for exploring RNA-seq data as both read map profiles and summarized gene expression levels across two large compendia (Sullivan *et al*. 2019, doi:10.1111/tpj.14468), in order to be able to quickly identify samples with the highest level of expression or where incidents of alternative splicing may be occurring. The Provart Lab also rolled out a revived and updated version of Araport's Thalemine at https://bar.utoronto.ca/thalemine/ as part of a multi-lab effort to resuscitate Araport.

Major Funding Sources

- National Science and Engineering Research Council (NSERC) (http://www.nserc-crsng.gc.ca)
- Genome Canada (http://www.genomecanada.ca/en/)
- New Frontiers in Research Fund (https://www.sshrc-crsh.gc.ca/funding-financement/nfrf-fnfr/index-eng.aspx)

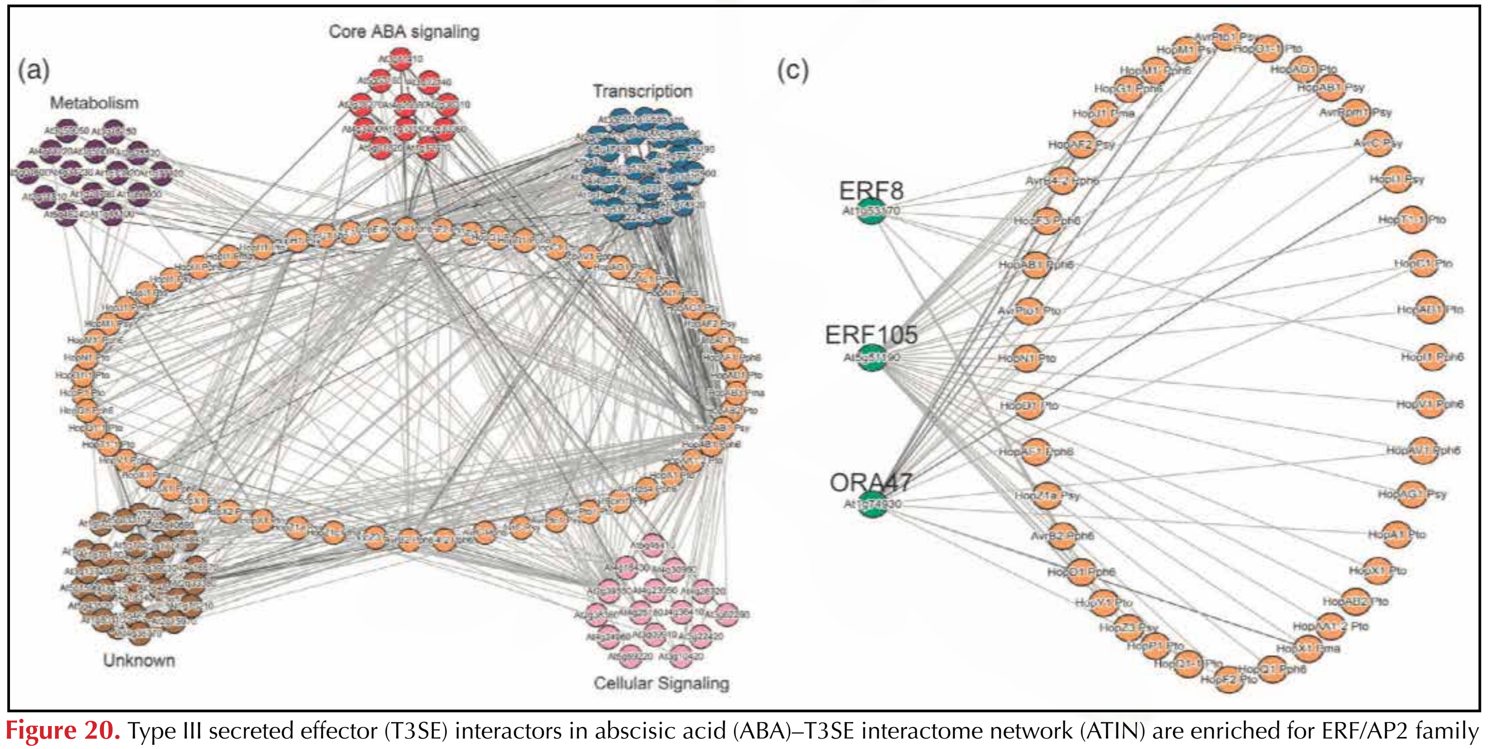

Figure 20. Type III secreted effector (T3SE) interactors in abscisic acid (ABA)–T3SE interactome network (ATIN) are enriched for ERF/AP2 family transcription fac- tors. (a) T3SE interactors can be grouped into five functional categories.

Chile

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Universidad Andres Bello, Chile.

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

Pollak B, Cerda A, Delmans M, Álamos S, Moyano T, West A, Gutiérrez RA, Patron NJ, Federici F, Haseloff J. Loop assembly: a simple and open system for recursive fabrication of DNA circuits. New Phytol. 2019 Apr;222(1):628-640. doi: 10.1111/nph.15625.

This method provides a simple generalized solution for DNA construction with standardized parts. The cloning system is provided under an OpenMTA license for unrestricted sharing and open access.

Conferences, Workshops and Outreach events

January 9th, 2019
Seminar: Orange on top: Is there a mutual exclusion between anthocyanin and carotenoids biosynthesis in petunia flowers?
This seminar was held on campus Las Palmeras – Universidad de Chile. Santiago Chile.
It was presented by Dr. Julian Verdonk, Wageningen University. Netherlands.
Organizers: Universidad de Chile.

March, 27th – 29th, 2019.
Symposium: First International Symposium of Food, Nutrition, Physical Fitness and Health
The symposium was held at INTA, Universidad de Chile. Santiago – Chile.
The meeting committee included several fieds associated to nutrition and health: Healty and sustainable food, nutritional genomics, Nutrition and physical activity, influence of socio-economic factors on nutrition, and urban planification, physical activity and nutrition.
The key note speakers were Dr. Alejandra Chavez-Santoscoy (Mexico), Eduardo Guerra Hernandez (Spain), Jesús Rodríguez Huertas (Spain), Dr. Bruno Gualaro (Brazil), Dr. Leandro Pereira (Brazil), Dra. Diana Parra (USA), Stefan Martens (Italy).
Organizers: Centro de investigación en Alimentos para el Bienestar en el Ciclo Vital and the Proyecto de Consolidación de la Internacionalización de la Investigación y Postgrado de la Universidad de Chile,

April 22th – 25th, 2019
EMBO Workshop: Integrative biology: From molecules to ecosystems in extreme environments (w19-107)
EMBO Workshops are meetings that cover different and evolving aspects of life-science-related subject areas and bring scientists together to present and discuss their latest findings.

Organizers: Eric Schimer, University of Edinburg, UK., Rodrigo Gutierrez, Pontificia Universidad Católica de Chile, CL, Francisca Blanco, Universidad Andres Bello, CL, Stephan Pollman, Universidad Politecnica de Madrid, ES, Laurence Lejay, INRA, Montpelier, FR

July 22th – 23th, 2019
3rd SCIENTIFIC MEETING ON VEGETAL BIOLOGY AND BIOTECHNOLOGY DIGV-UTAL
The meeting was held in Salón Bicentenario de la U. de Talca, Campus Lircay, Talca –
Chile.
The meeting included four thematical areas: Biotic and abiotic stress, phytogenetics resources, Vegetal development, and Ecology and molecular evolution.
Organizer: Ph.D. program on Sciences, mention plant genetics on Instituto de Ciencias
Biológicas on Universidad de Talca – Chile.

June 12th, 2019
Conference: "Sorting of Small RNAs into exosomes secreted by human cells"
The conference was held at Las Palmeras, Universidad de Chile. Santiago – Chile.
Seminar presented by Randy Schekman, Ph.D., Nobel price of Physiology/medicine 2013.
Organizers: Universidad de Chile.

October 16-18th, 2019
Conference: 2nd Energy, Efficiency and Environmental Sustainability 2019
This coneference was held at Universidad de La Serena. La Serena – Chile.
Key Note Speakers:
Gianluca Li Puma, PhD. Loughborough University, UK
Mohamed El-Roz, PhD. Caen University, France
María Bernechea, PhD. University of Zaragoza, Spain.
Organizers: Universidad de La Serena and Centro de Estudios Avanzandos en Zonas Áridas.

September 13th, 2019
Seminar: Domestication of a Y chromosome in papaya
The seminar was held at Facultad de Ciencias Agronómicas of Universidad de Chile. Santiago – Chile.
The seminar was presented by Ray Ming, PhD. Its research is based on the genomic analysis of Papaya and the determination of sex. Dr Ming participated in the sequencing of the papaya genome.
Organizers: Departamento de Producción Agrícola, Facultad de Ciencias Agronómicas, Universidad de Chile and Departamento de Ciencias Vegetales, Facultad de Agronomía e Ingeniería Forestal, Pontificia Universidad Católica de Chile

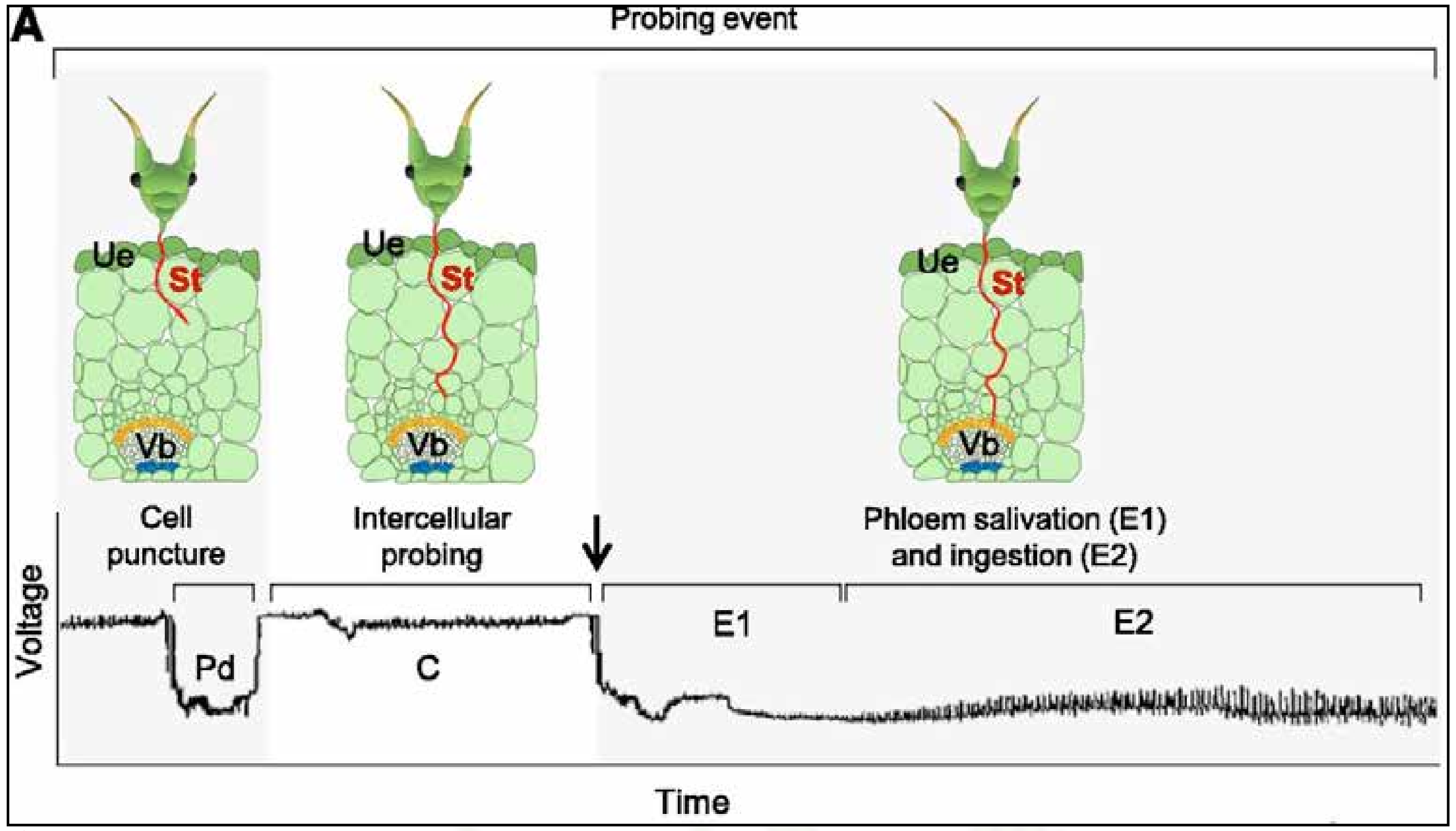

Figure 21. Determination of Sampling Time for Early Aphid Infestation Stage.
EPG was performed to evaluate the feeding behavior of M. persicae using Arabidopsis (wild-type Col-0) as a host with the aim of determining the proper sampling time related to the early infestation stage.
(A) Schematic representation of the biological activities of the aphid stylet inside the host plant and its corresponding EPG waveform. The arrow points to the potential drop related to the stylet entry into the sieve elements. C, intercellular probing; E1, phloem salivation; E2, phloem ingestion; Pd, cell puncture (potential drop); St, stylet; Ue, upper epidermis; Vb, vascular bundle.

December 4th, 2019
Seminar: "Vegetable improvement of the cherry tree: current status and perspectives"
This seminar was held at the research building of Universidad Andres Bello. Santiago – Chile.
Seminar presented by José Quero-García PhD., from INRA (Bordeaux, France) an international expert on genetic improvement of cherry trees. The presentation was based on their findings on the generation of QTLs linked to agronomical characteristics and their usage in programs of assisted selection.
Organizer: Laboratorio de Genómica Funcional & Bioinformática, Departamento de Producción Agrícola. Universidad de Chile.

Selected Publications

Alvarez JM, Moyano TC, Zhang T, Gras DE, Herrera FJ, Araus V, O'Brien JA, Carrillo L, Medina J, Vicente-Carbajosa J, Jiang J, Gutiérrez RA. Local Changes in Chromatin Accessibility and Transcriptional Networks Underlying the Nitrate Response in Arabidopsis Roots. Mol Plant. 2019 Dec 2;12(12):1545-1560. doi: 10.1016/j.molp.2019.09.002. Epub 2019 Sep 14.

García Bossi J, Kumar K, Barberini ML, Domínguez GD, Rondón Guerrero YDC, Marino-Busljе C, Obertello M, Muschietti JP, Estevez JM. The role of P-type IIA and P-type IIB Ca2+-ATPases in plant development and growth. J Exp Bot. 2020 Feb 19;71(4):1239-1248. doi: 10.1093/jxb/erz521.

Garrido-Bigotes A, Valenzuela-Riffo F, Figueroa CR. Evolutionary Analysis of JAZ Proteins in Plants: An Approach in Search of the Ancestral Sequence. Int J Mol Sci. 2019 Oct 12;20(20):5060. doi: 10.3390/ijms20205060.

Rubilar-Hernández C, Osorio-Navarro C, Cabello F, Norambuena L. PI4KIII□ Activity Regulates Lateral Root Formation Driven by Endocytic Trafficking to the Vacuole. Plant Physiol. 2019 Sep;181(1):112-126. doi: 10.1104/pp.19.00695. Epub 2019 Jul 8.

Parra-Rojas JP, Largo-Gosens A, Carrasco T, Celiz-Balboa J, Arenas-Morales V, Sepúlveda-Orellana P, Temple H, Sanhueza D, Reyes FC, Meneses C, Saez-Aguayo S, Orellana A. New steps in mucilage biosynthesis revealed by analysis of the transcriptome of the UDP-rhamnose/UDP-galactose transporter 2 mutant. J Exp Bot. 2019 Oct 15;70(19):5071-5088. doi: 10.1093/jxb/erz262.

Silva-Sanzana C, Celiz-Balboa J, Garzo E, Marcus SE, Parra-Rojas JP, Rojas B, Olmedo P, Rubilar MA, Rios I, Chorbadjian RA, Fereres A, Knox P, Saez-Aguayo S, Blanco-Herrera F. Pectin Methylesterases Modulate Plant Homogalacturonan Status in Defenses against the Aphid *Myzus persicae.* Plant Cell. 2019 Aug;31(8):1913-1929. doi: 10.1105/tpc.19.00136. Epub 2019 May 24.

Sunitha S, Loyola R, Alcalde JA, Arce-Johnson P, Matus JT, Rock CD. The Role of UV-B light on Small RNA Activity During Grapevine Berry Development.
G3 (Bethesda). 2019 Mar 7;9(3):769-787. doi: 10.1534/g3.118.200805.

Timmermann T, Poupin MJ, Vega A, Urrutia C, Ruz GA, González B. Gene networks underlying the early regulation of Paraburkholderia phytofirmans PsJN induced systemic resistance in Arabidopsis PLoS One. 2019 Aug 22;14(8):e0221358. doi: 10.1371/journal.pone.0221358. eCollection 2019.

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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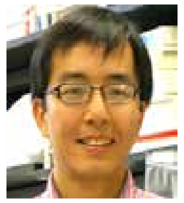


Please describe the current state of Arabidopsis research in your country

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 research papers published by Chinese researchers.

According to the 2019 MASC Report, about one-third of all Arabidopsis papers published in 2018 were from China. 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 are no such funding programs towards Arabidopsis research. As a result, Arabidopsis is often used as an easily manipulated model system to test crop gene functions. Nevertheless, the number of Arabidopsis papers published in 2018 by Chinese researchers ranks only after rice papers, and more than those of maize or wheat.

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 2019.

- AraShare: A community biological resource center
http://www.arashare.cn/

- Plant Transcriptional Regulatory Map (includes updated PlantTFDB and additional resources)
http://plantregmap.cbi.pku.edu.cn/

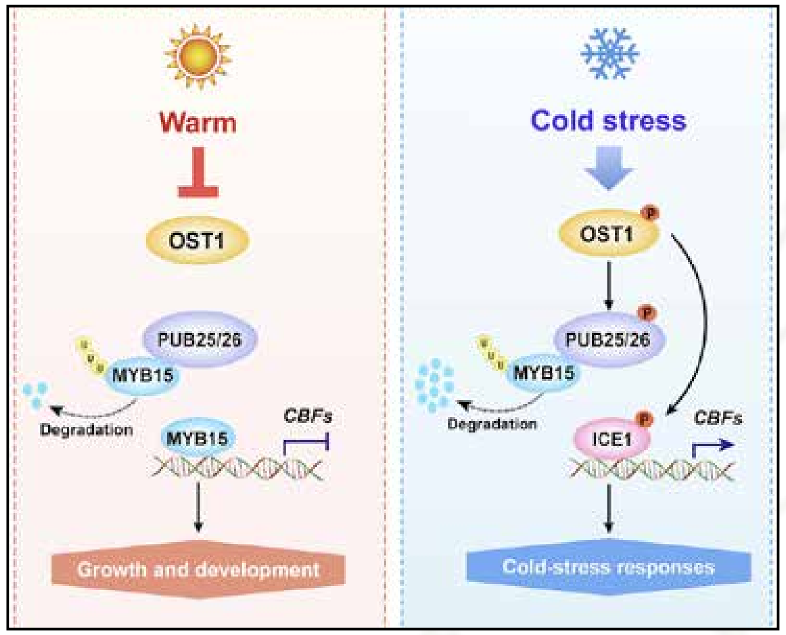


Figure 22. UB25 and PUB26 promote plant freezing tolerance by degrading the cold signaling negative regulator MYB15

- AHD2.0: Arabidopsis hormone database 2.0
https://bigd.big.ac.cn/ahd/

- LSD3.0: Arabidopsis leaf senescence database 3.0
https://bigd.big.ac.cn/lsd/

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

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

- Shoot cell type-specific expression ebrowser
http://jiaolab.genetics.ac.cn/shootapex.html

Conferences, Workshops and Outreach events

Major conferences held in 2019
- 30th International Conference on Arabidopsis Research (ICAR2019), June 16-21, 2019, Wuhan, Hubei

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

- 21st International Conference on Nitrogen Fixation (ICNF2019), October 10-15, 2019 Wuhan, Hubei

- 2019 National Congress of Plant Biology, October 11-14, 2019 Chengdu, Sichuan (http://www.ncpb.net/2019/)

Selected Publications

Li W, Song T, Wallrad L, Kudla J, Wang X, Zhang W. (2019) Tissue-specific accumulation of pH-sensing phosphatidic acid determines plant stress tolerance. Nat Plants. 2019 Sep;5(9):1012-1021.

Cui Y, Cao W, He Y, Zhao Q, Wakazaki M, Zhuang X, Gao J, Zeng Y, Gao C, Ding Y, Wong HY, Wong WS, Lam HK, Wang P, Ueda T, Rojas-Pierce M, Toyooka K, Kang B-H, Jiang L. (2019) A whole-cell electron tomography model of vacuole biogenesis in Arabidopsis root cells. Nat. Plants 5(1):95-105.

He J, Chen Q, Xin P, Yuan J, Ma Y, Wang X, Xu M, Chu J, Peters RJ, Wang G. (2019) CYP72A enzymes catalyse 13-hydrolyzation of gibberellins. Nat. Plants 5(10): 1057-1065.

Li H, Cai Z, Wang X, Li M, Cui Y, Cui N, Yang F, Zhu M, Zhao J, Du W, He K, Yi J, Tax FE, Hou S, Li J, Gou X. (2019) SERK receptor-like kinases control division patterns of vascular precursors and ground tissue stem cells during embryo development in Arabidopsis. Mol. Plant 12(7): 984-1002.

Qiu Q, Mei H, Deng X, He K, Wu B, Yao Q, Zhang J, Lu F, Ma J, Cao X. (2019) DNA methylation repels targeting of Arabidopsis REF6. Nat. Commun. 10(1): 2063.

Tian C, Wang Y, Yu H, He J, Wang J, Shi B, Du Q, Provart NJ, Meyerowitz EM, Jiao Y. (2019) A gene expression map of shoot domains reveals regulatory mechanisms. Nat. Commun. 10(1): 141.

Wang J, Hu M, Wang J, Qi J, Han Z, Wang G, Qi Y, Wang H-W, Zhou J-M, Chai J. (2019) Reconstitution and structure of a plant NLR resistosome conferring immunity. Science 364(6435): eaav5870.

Wang J, Wang J, Hu M, Wu S, Qi J, Wang G, Han Z, Qi Y, Gao N, Wang H-W, Zhou J-M, Chai J. (2019) Ligand-triggered allosteric ADP release primes a plant NLR complex. Science 364(6435): eaav5868.

Wang X, Ding Y, Li Z, Shi Y, Wang J, Hua J, Gong Z, Zhou JM, Yang S. (2019) PUB25 and PUB26 promote plant freezing tolerance by degrading the cold signaling negative regulator MYB15. Dev. Cell 51(2): 222-235.

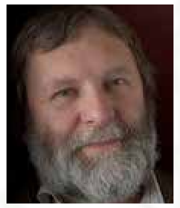
You Y, Zhai Q, An C, Li C. (2019) LEUNIG_HOMOLOG mediates MYC2-dependent transcriptional activation in cooperation with the coactivators HAC1 and MED25. Plant Cell 31(9): 2187-2205.

Zhong S, Liu M, Wang Z, Huang Q, Hou S, Xu YC, Ge Z, Song Z, Huang J, Qiu X, Shi Y, Xiao J, Liu P, Guo YL, Dong J, Dresselhaus T, Gu H, Qu L-J. (2019) Cysteine-rich peptides promote interspecific genetic isolation in Arabidopsis. Science 364(6443): eaau9564.

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

Please describe the current state of Arabidopsis research in your country

Arabidopsis driven research in Czech Republic is qualitatively but also quantitatively expanding over the last decade. An important aspect of that is that for medium/small country as Czech republic is, Arabidopsis driven basic plant research is not centralized only in the capital. In fact historically first steps in Czech plant molecular biology were done already in 80ies – before the political regime change – at the Institute of Biophysics, Czech Academy of Sciences (CAS) in Brno, which is still very active, currently especially in the fields of plant molecular epigenetics and plant developmental biology.

Over the last decade supply of EU structural funds supported expansion of not only plant science in Brno, but also in Olomouc – in these two cities existing university and Academy departments grew in quality of plant research and new joint institutes focused on the plant science were established and are stabilized over the last years. CEITEC (https://www.ceitec.eu/ - also with the participation of Masaryk university and Mendel agricultural university in respect to plant sciences) in Brno is a multidisciplinary center which includes "Genomics and Proteomics of Plant Systems" division encompassing 8 research groups with topics focused on understanding the evolutionary-based strategies of plants. The knowledge acquired by –omic approaches, combined with research experience in the areas of developmental and stress biology of plants, is subsequently used to develop new agricultural, biotechnology and biomedical applications.

In Olomouc "The Center of the Region Haná for Biotechnological and Agricultural Research" (CRH – includes Palacký university and Inst. of Exp. Botany, CAS in respect to plant sciences) is a scientific workplace focused on plant research and plant biotechnology development. Local scientists belong to world´s top experts in reading genetic information of barley, wheat and other plants important for nutrition of the ever-growing human population. Another important focus is plant cell biology. Based on the results of basic research, they suggest procedures that enable breeders to obtain varieties of new generation with the desired properties, especially higher yield and resistance to drought, temperature fluctuations and other stress factors.

In the capital Prague and south Bohemian city Ceské Budejovice no new EU funded big infrastructures supporting plant research were developed, but traditionally at the Charles university in Prague plant biology research at Departments of experimental plant biology and at the Department of botany is well developing with a great focus on cell and developmental biology of Arabidopsis (ERC grant to Matyáš Fendrych from the Department of exp. Plant Bilogy) and plant ecological genomics of Brassicaceae (ERC grant to Filip Kolár from the Department of Botany).

At the Department of experimental plant biology of the University of South Bohemia partially Arabidopsis driven research is focused on the photosynthesis and regulation of gas exchange (stomata development and regulation also under the stress). The Institute of Experimental Botany in Prague (belongs to Czech Academy of Sciences) serves since the middle of the last century as a crystallization point of basic laboratory plant biology research focused on plant genetics, physiology, phytopathology and biotechnology. However, IEB is also active in applied research – esp. in apple breeding. Most of the work in this institute is based on and driven by the Arabidopsis research. The Institute of Plant Molecular Biology (IPMB of the Czech Academy of Sciences) was founded in 1990 when several genetically oriented teams split from the Institute of Experimental Botany in Prague and moved to Ceské Budejovice. This Institute contributes significantly to Czech national programs of plant biotechnology and plant protection against biotic stresses, and provides expertise on the diagnosis of quarantined plant viruses to the Ministry of Agriculture and the State Phytosanitary Administration, and on genetically modified crops to the Ministry of the Environment.

Applied plant crop production research in Czech republic is not only done in several crop specialized institutes and breeding stations, but is partially centralized and coordinated by the Crop Research Institute in Prague which uses also Arabidopsis driven wisdom to be applied for crops.

PSI (Photon Systems Instruments - https://psi.cz/) company located close to Brno is contributing worldwide to the development of spectral methods to monitor plant physiology in the lab and field, but also development internationally very successful cultivation and phenotyping platforms. Currently, PSI's main product lines include: (1) devices for chlorophyll fluorescence measurement and advanced imaging; (2) high-tech photobioreactors and other algal cultivators; (3) intelligent growth chambers and cultivation rooms; (4) customized PlantScreenTM Phenotyping Systems; (5) a range of novel LED light sources for plant cultivation and research; and (6) hand-held devices for monitoring chlorophyll fluorescence kinetics, plant reflective indices and spectral characteristics of natural and artificial light.
Overall it is obvious that in Czech republic both basic as well as applied plant research based on Arabidopis model is flourishing over the last years and that the country also contributes to the methodology-instrumental advancement in plant biology studies.

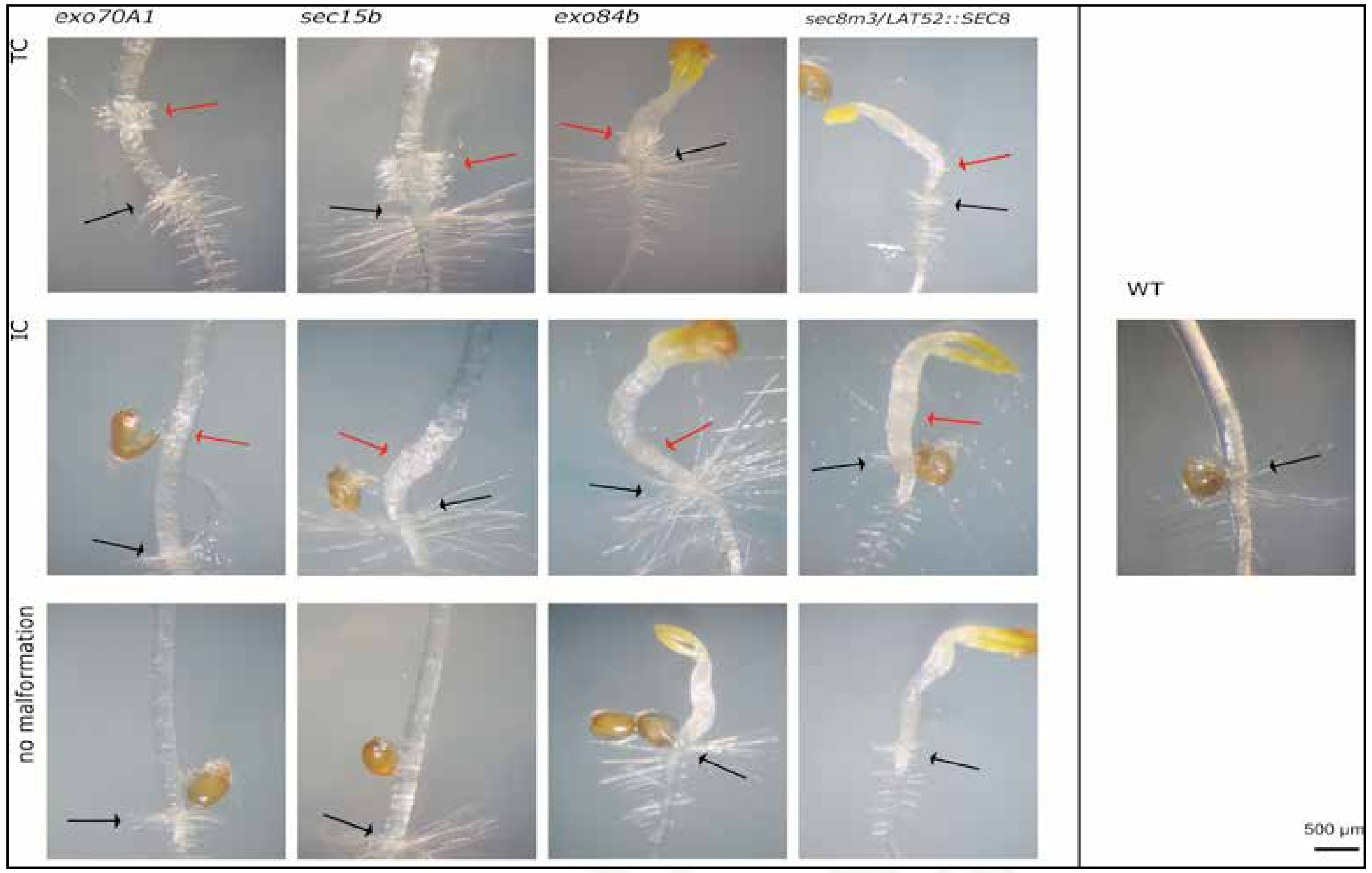

Figure 23. Phenotypic defects of etiolated hypocotyls in exocyst mutants. Typical phenotypic deviations—ectopic collet-like structures with or without developed hairs (phenotypes TC and IC) and shortened hypocotyls without malformations in 7-day-old exo70A1, sec15b, exo84b, and sec8m3/LAT52::SEC8 mutant seedlings. Black arrows, collet hairs; red arrows, ectopic collet-like structures. A WT seedling is shown alongside for comparison.

Conferences, Workshops and Outreach events

- Plant Biology CS 2019

Every three years, the Czech Society of Experimental Plant Biology and Plant Physiology section of the Slovak Botanical Society jointly organize meetings, which are hosted by alternating Czech and Slovak university cities. The conference titled "Plant Biology CS, 2019" took place in Ceské Budejovice (at the joint campus of the University of South Bohemia and Biology Centre of the Czech Academy of Sciences) from 25th to 30th August 2019. It was an international meeting of high quality (most plenary and key note speakers were experts in the fields from abroad) and lot of contributions were based on Arabidopsis research.

- Plant Development and Production Biology under Global Climate Change

This was an advanced international meeting with plenary and key note speakers being prominent experts in respective fields and lot of contributions were driven by Arabidopsis research. Meeting was held in Brno, September 9th-11th 2019, and was also organized to commemorate 100 years anniversary of Mendel Agricultural University in Brno establishment.

Selected Publications

Adamusová K, Khosravi S, Fujimoto S, Houben A, Matsunaga S, Fajkus J, Fojtová M. Two combinatorial patterns of telomere histone marks in plants with canonical and non-canonical telomere repeats. Plant J. Dec 13. doi: 10.1111/tpj.14653. 2019

Janková Drdová E, Klejchová M, Janko K, Hála M, Soukupová H, Cvrcková F, Žárský V. Developmental plasticity of Arabidopsis hypocotyl is dependent on exocyst complex function. J Exp Bot. 70(4):1255-1265. doi: 10.1093/jxb/erz005. 2019

Küpper H, Benedikty Z, Morina F, Andresen E, Mishra A, Trtílek M. Analysis of OJIP Chlorophyll Fluorescence Kinetics and QA Reoxidation Kinetics by Direct Fast Imaging. Plant Physiol. 179(2):369-381. doi: 10.1104/pp.18.00953. Epub 2018 Dec 18. 2019

Leontovycová H, Kalachova T, Trdá L, Pospíchalová R, Lamparová L, Dobrev PI, Malínská K, Burketová L, Valentová O, Janda M. Actin depolymerization is able to increase plant resistance against pathogens via activation of salicylic acid signalling pathway. Sci Rep. 2019 Jul 18;9(1):10397. doi: 10.1038/s41598-019-46465-5.

Mandáková T, Pouch M, Brock JR, Al-Shehbaz IA, Lysak MA. Origin and Evolution of Diploid and Allopolyploid Camelina Genomes Were Accompanied by Chromosome Shattering. Plant Cell. 2019 Nov;31(11):2596-2612. doi: 10.1105/tpc.19.00366. Epub 2019 Aug 26.

Nowicka A, Tokarz B, Zwyrtková J, Dvorák Tomaštíková E, Procházková K, Ercan U, Finke A, Rozhon W, Poppenberger B, Otmar M, Niezgodzki I, Krecmerová M, Schubert I, Pecinka A. Comparative analysis of epigenetic inhibitors reveals different degrees of interference with transcriptional gene silencing and induction of DNA damage. Plant J. doi: 10.1111/tpj.14612. 2019

Oulehlová D, Kollárová E, Cifrová P, Pejchar P, Žárský V, Cvrcková F. Arabidopsis Class I Formin FH1 Relocates between Membrane Compartments during Root Cell Ontogeny and Associates with Plasmodesmata. Plant Cell Physiol. 2019 Aug 1;60(8):1855-1870. doi: 10.1093/pcp/pcz102.

Schorová Š, Fajkus J, Záveská Drábková L, Honys D, Schrumpfová PP. The plant Pontin and Reptin homologues, RuvBL1 and RuvBL2a, colocalize with TERT and TRB proteins in vivo, and participate in telomerase biogenesis. Plant J. Apr;98(2):195-212. doi: 10.1111/tpj.14306. 2019

Skalák J, Vercruyssen L, Claeys H, Hradilová J, Cerný M, Novák O, Placková L, Saiz-Fernández I, Skaláková P, Coppens F, Dhondt S, Koukalová Š, Zouhar J, Inzé D, Brzobohatý B. Multifaceted activity of cytokinin in leaf development shapes its size and structure in Arabidopsis. Plant J. 2019 Mar;97(5):805-824. doi: 10.1111/tpj.14285.

Zdarska M, Cuyacot AR, Tarr PT, Yamoune A, Szmitkowska A, Hrdinová V, Gelová Z, Meyerowitz EM, Hejátko J. ETR1 Integrates Response to Ethylene and Cytokinins into a Single Multistep Phosphorelay Pathway to Control Root Growth. Mol Plant. 2019 Oct 7;12(10):1338-1352. doi: 10.1016/j.molp.2019.05.012. Epub 2019 Jun 7.

Major Funding Sources

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

1. Czech Science Foundation/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
Both institutions support also bilateral projects with selected countries.

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

3. Technology Agency of the Czech Republic
http://www.tacr.cz/english/

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

Denmark

Michael Palmgren
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University of Copenhagen, Department of Plant and Environmental Sciences

Please describe the current state of Arabidopsis research in your country

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.

Selected Publications

Hoffmann RD, Olsen LI, Ezike CV, Pedersen JT, Manstretta R, López-Marqués RL, Palmgren M (2019) Roles of plasma membrane proton ATPases AHA2 and AHA7 in normal growth of roots and root hairs in Arabidopsis thaliana. Physiol Plant. 166: 848-861.

Hunziker P, Halkier BA, Schulz A (2019) Arabidopsis glucosinolate storage cells transform into phloem fibres at late stages of development. J Exp Bot. 70: 4305-4317.

Millard PS, Weber K, Kragelund BB, Burow M (2019) Specificity of MYB interactions relies on motifs in ordered and disordered contexts. Nucleic Acids Res. 47: 9592-9608.

Nielsen M, Ard R, Leng X, Ivanov M, Kindgren P, Pelechano V, Marquardt S (2019) Transcription-driven chromatin repression of Intragenic transcription start sites. PLoS Genet. 15: e1007969.

Nintemann SJ, Palmgren M, López-Marqués RL (2019) Catch You on the Flip Side: A Critical Review of Flippase Mutant Phenotypes. Trends Plant Sci. 24: 468-478

Paulsen PA, Custódio TF, Pedersen BP (2019) Crystal structure of the plant symporter STP10 illuminates sugar uptake mechanism in monosaccharide transporter superfamily. Nat Commun. 10: 407

Theorin L, Faxén K, Sørensen DM, Migotti R, Dittmar G, Schiller J, Daleke DL, Palmgren M, López-Marqués RL, Günther Pomorski T (2019) The lipid head group is the key element for substrate recognition by the P4 ATPase ALA2: a phosphatidylserine flippase. Biochem J. 476: 783-794

Xu D, Hunziker P, Koroleva O, Blennow A, Crocoll C, Schulz A, Nour-Eldin HH, Halkier BA (2019) GTR-Mediated Radial Import Directs Accumulation of Defensive Glucosinolates to Sulfur-Rich Cells in the Phloem Cap of Arabidopsis Inflorescence Stem. Mol Plant. 12: 1474-1484.

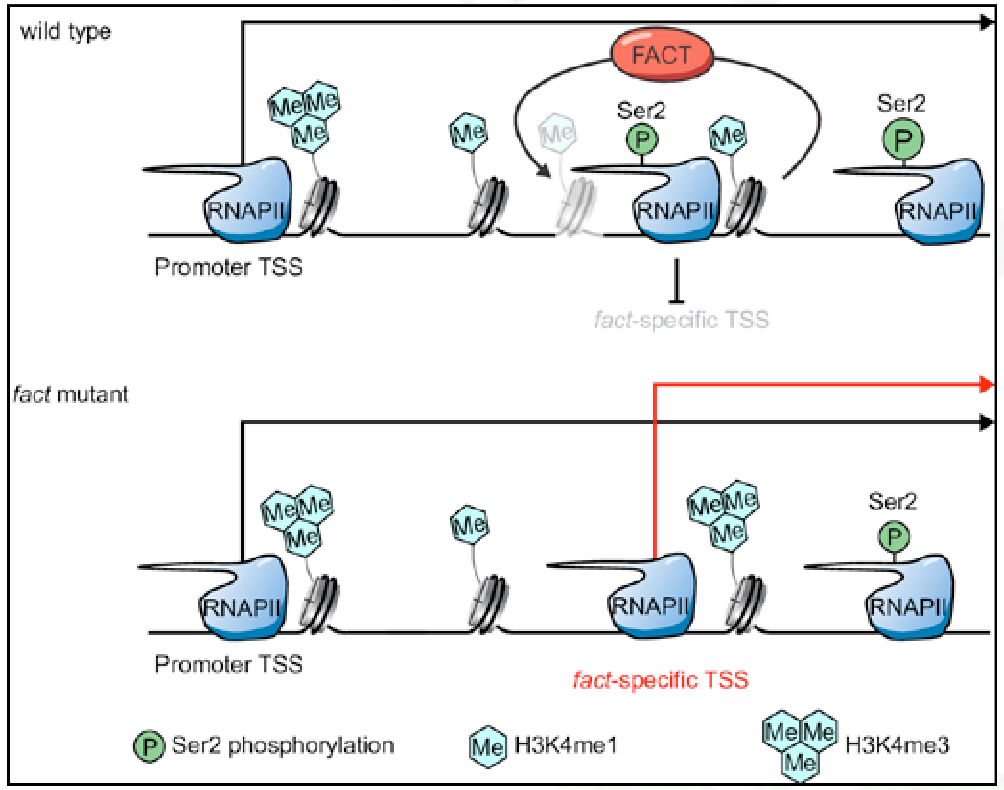
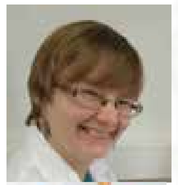


Figure 24. Cartoon summarizing FACT-dependent chromatin repression of intragenic TSSs in Arabidopsis. (A) In wild type Arabidopsis, RNAPII initiates transcription from canonical promoters of genes containing fact-specific TSS. Specific histone signatures such as H3K4me3 (blue tri-hexagon) are associated with TSSs at promoters, while RNAPII CTD Ser2 phosphorylation (green circle) and H3K4me1 (blue hexagon) are associated with RNAPII elongation zones. Repressed intragenic fact-specific TSSs are enriched for H3K4me1 in their repressed state. (B) fact-specific TSSs initiate transcription (red arrow) in fact mutants. Only a subset of intragenic sites marked with H3K4me1 represents fact-specific TSSs, indicated by a H3K4me1-marked nucleosome at a position without evidence for transcriptional initiation in fact mutants. Activation of fact-specific intragenic TSSs correlates with reduced H3K4me1 level and an increase of the H3K4me3 promoter signature.

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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Please describe the current state of Arabidopsis research in your country

Arabidopsis research is mostly carried out in TalTech and University of Tartu in Estonia. Researchers in TalTech study the role of the ABCE1 protein and its homologs in RNA silencing and the function of Arabidopsis myosins. In the Institute of Technology at the University of Tartu, researchers focus on the signalling pathways that mediate stomatal responses to environmental cues. Custom-built devices that enable parallel recording of stomatal conductance in multiple intact Arabidopsis plants are used to characterise plant stomatal behaviour.

Several independent research directions are pursued in the institute, including identification and detailed characterisation of the role of genes that control stomatal movements in response to changes in CO2 concentration and relative air humidity; and assessing potential interactions between signalling pathways that control stomatal development and movements. In the Department of Botany at the University of Tartu, Arabidopsis is used as a model to study the effects of cultivation density on individual and group performance.

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

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

Conferences, Workshops and Outreach events

- The New Phytologist Next Generation Scientists 2020 meeting that was supposed to take place from 3-6 August in Tartu, Estonia has been postponed to 2021 due to COVID-19
https://www.newphytologist.org/nextgenevents/2020

Figure 25. Postponed but will take place in 2021 in Tartu
https://www.newphytologist.org/nextgenevents/2020

Selected Publications

In 2019, there were no publications with leading authors from Estonia, but Estonian Arabidopsis researchers contributed to several collaboration papers.

Dittrich M, Mueller HM, Bauer H, Peirats-Llobet M, Rodriguez PL, Geilfus C-M, Carpentier SC, Rasheid KASA, **Kollist H, Merilo E**, *et al* (2019) The role of Arabidopsis ABA receptors from the PYR/PYL/RCAR family in stomatal acclimation and closure signal integration. Nat Plants 5: 1002–1011

Huang S, Waadt R, **Nuhkat M, Kollist H**, Hedrich R, Roelfsema MRG (2019) Calcium signals in guard cells enhance the efficiency by which abscisic acid triggers stomatal closure. New Phytol 224: 177–187

Julian J, Coego A, Lozano-Juste J, Lechner E, Wu Q, Zhang X, **Merilo E**, Belda-Palazon B, Park S-Y, Cutler SR, *et al* (2019) The MATH-BTB BPM3 and BPM5 subunits of Cullin3-RING E3 ubiquitin ligases target PP2CA and other clade A PP2Cs for degradation. Proc Natl Acad Sci 116: 15725–15734

Sun Y, Harpazi B, Wijerathna-Yapa A, **Merilo E**, Vries J de, Michaeli D, Gal M, Cuming AC, **Kollist H**, Mosquna A (2019) A ligand-independent origin of abscisic acid perception. Proc Natl Acad Sci 116: 24892–24899

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

Finland

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Please describe the current state of Arabidopsis research in your country

The largest users of Arabidopsis in research: University of Helsinki, University of Turku, University of Oulu. Despite many groups focusing on plants with agricultural relevance Arabidopsis continues to be the major tool and model for basic research. Arabidopsis also continues to serve as a reference species and is used to establish conceptual models prior to testing in crop species.

Research concentrating on strategies using Arabidopsis continues to be funded in Finland with major funding coming from the Academy of Finland, thus basic research continues to thrive in Finland in particular in the fields plant development, plant-environment interactions and photosynthesis.

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

The National Plant Phenotyping facility (NaPPI; https://www.helsinki.fi/en/infrastructures/national-plant-phenotyping) is a shared phenotyping facility with University of Helsinki part concentrating on Arabidopsis. NaPPi is part of the European Plant Phenotyping Network (EPPN).

Conferences, Workshops and Outreach events

The Academy of Finland-funded Centre of Excellence in the Molecular Biology of Primary Producers organized the conference “Plants in a Changing World” in Helsinki, November 6-8, 2019.

Selected Publications

Abou-Saleh RH, Hernandez-Gomez MC, Amsbury S, Miyashima S, Roszak P, Sevilem I, Toyokura K, Blob B, Heo JO, Mellor N, *et al* 2019. Mobile PEAR transcription factors integrate positional cues to prime cambial growth. Nature 565(7740): 490-494

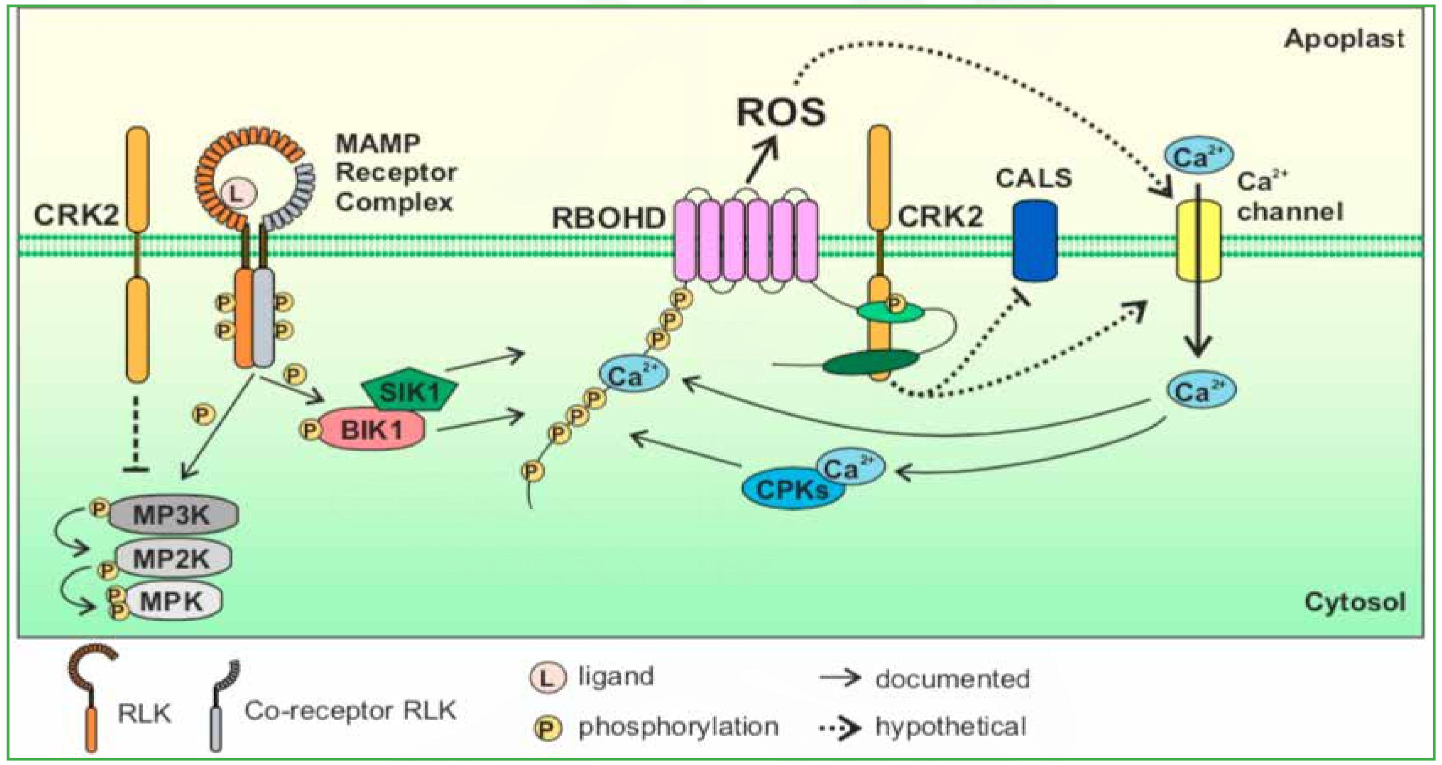

Figure 26. Schematic model for MAMP-triggered RBOHD activation. MAMPs are recognized by MAMP receptor complexes. RBOHD N-terminus is phosphorylated by BIK1 and SIK1 and apoplastic ROS production is induced. Apoplastic ROS production by RBOHD leads to Ca2+ influx into the cytosol. Ca2+-binding to RBOHD N-terminus and to CPKs leads to Ca2+-dependent activation of RBOHD. We found that CRK2 also contributes to the activation of RBOHD via phosphorylation of its C-terminus at S703. CRK2 can also mediates inhibition of MAPK activation and callose deposition via CALS after MAMPperception. MPK,mitogen-activatedproteinkinase;MP2K,MPKK;MP3K,MPKKK. plants taken 18 h after the end of a 6 h exposure to O3.

Durian G, Jeschke V, Rahikainen M, Vuorinen K, Gollan PJ, Brosché M, Salojärvi J, Glawischnig E, Winter Z, Li S, Noctor G, Aro EM, Kangasjärvi J, Overmyer K, Burow M, Kangasjärvi S. 2020. PROTEIN PHOSPHATASE 2A-B′□ Controls Botrytis cinerea Resistance and Developmental Leaf Senescence. Plant Physiol 182(2):1161-1181

Gerotto C, Trotta A, Bajwa AA, Mancini I, Morosinotto T, Aro EM. 2019. Thylakoid Protein Phosphorylation Dynamics in a Moss Mutant Lacking SERINE/THREONINE PROTEIN KINASE STN8. Plant Physiol 180(3):1582-1597

Hunter K, Kimura S, Rokka A, Tran HC, Toyota M, Kukkonen JP, Wrzaczek M. 2019. CRK2 enhances salt tolerance by regulating callose deposition in connection with PLD□1. Plant Physiology 180(4): 2004-2021.

Kimura S, Hunter K, Vaahtera L, Tran HC, Vaattovaara A, Rokka A, Stolze SC, Harzen A, Citterico M, Meißner L, Wilkens MMT, Hamann T, Toyota M, Nakagami H, Wrzaczek M. 2020. CRK2-mediated control of ROS production by phosphorylation of the RBOHD C-terminus in Arabidopsis. Plant Cell. https://doi.org/10.1105/tpc.19.00525

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(7740): 485-489

Yan D, Yadav SR, Paterlini A, Nicolas WJ, Petit JD, Brocard L, Belevich I, Grison MS, Vaten A, Karami L, El-Showk S, Lee JY, Murawska GM, Mortimer J, Knoblauch M, Jokitalo E, Markham JE, Bayer EM, Helariutta Y. 2019. Sphingolipid biosynthesis modulates plasmodesmal ultrastructure and phloem unloading. Nat Plants 5(6): 604-615

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

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

- PHENOSCOPE (http:// www.ijpb.versailles.inra.fr/en/plateformes/ppa/index. html) and PHENOPSIS (www1.montpellier.inra.fr/ibip/lepse/english/ressources/ phenopsis.htm) are high-throughput automated phenotyping platforms at Versailles and Montpellier.
- SPS tools for Functional Genomics https://www6.inra.fr/saclay-plant-sciences_eng/Infrastructures).

- Plant Genomic center, https://cnrgv.toulouse.inra.fr/Library/Arabidopsis

- PHENOPSIS DB is an information system (http://bioweb.supagro.inra.fr/phenopsis/ Accueil.php?lang=En)

- IPS2: FlagDB++ v6.3 : Plant genomes DB, http://tools.ips2.u-psud.fr/projects/FLAGdb++/ HTML/index.shtml

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

- ChloroKb decoding the chloroplast, LPCV, Grenoble, 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/

- The TULIP summer school 2019 “Biological interactions : from genes to ecosystems “2019 (6 to 12 July in the French Pyrenees) Pic du Midi de Bigorre, https://www.labex-tulip.fr/labex-tulip_eng/Training-and-higher-education/Summer-School/Summer-School-2019

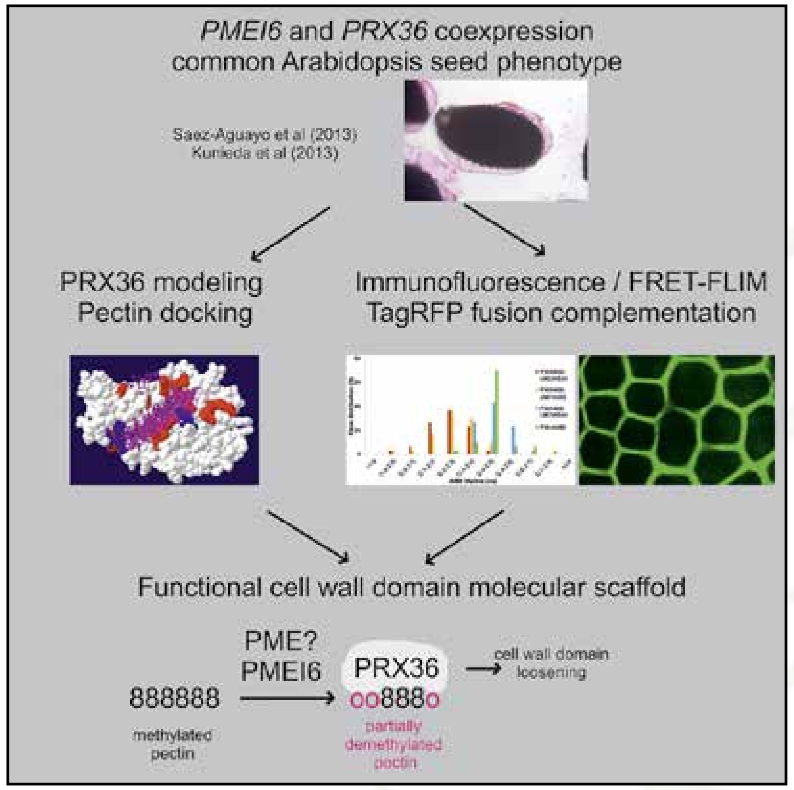

Figure 27 Pectin Demethylesterification Generates Platforms that Anchor Peroxidases to Remodel Plant Cell Wall Domains

- 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

- Molecular Basis of a Sustainable Agriculture: Focus for Montpellier-2020, Plant Nutrition and Development, 5-6 May 2020, Montpellier, https://sites.google.com/view/mbsagro/home

- 20th International Symposium on Iron Nutrition and Interactions, juin 29 - juillet 3, Reims, https://www.isinip2020.fr

- XII INTERNATIONAL SYMPOSIUM ON THE PLANT HORMONE ETHYLENE (ETHYLENE2020) - 29 JUNE TO 3 JULY 2020, Toulouse, http://ethylene2020.inp-toulouse.fr/en/index.html

- The TULIP summer school 2020 “Biological interactions : from genes to ecosystems 11 to 17 July in the French Pyrenees) https://www.labex-tulip.fr/labex-tulip_eng/Training-and-higher-education/Summer-School/Summer-School-2020

- SPS Summer School 2020, “Plant cell walls in development, plant-microbe interactions and for the bioeconomy”, July 5-11, 2020 – Versailles (France), https://www6.inrae.fr/saclay-plant-sciences/Formation/Ecoles-d-ete/Ecole-d-ete-2020

Selected Publications

Ariel, Federico; Lucero, Leandro; Christ, Aurelie; Mammarella, Maria Florencia; Jegu, Teddy; Veluchamy, Alaguraj; Mariappan, Kiruthiga; Latrasse, David; Blein, Thomas; Liu, Chang; Benhamed, Moussa; Crespi, Martin (2019) R-Loop Mediated trans Action of the APOLO Long Noncoding RNA. Molecular cell, DOI:10.1016/j.molcel.2019.12.015

Chantreau M, Poux C, Lensink MF, Brysbaert G, Vekemans X, Castric V. (2019) Asymmetrical diversification of the receptor-ligand interaction controlling self-incompatibility in Arabidopsis Elife. 2019 Nov 25;8. pii: e50253. doi: 10.7554/eLife.50253.

Francoz, E; Ranocha, P; Le Ru, A; Martinez, Y; Fourquaux, I; Jauneau, A; Dunand, C; Burlat, V (2019) Pectin Demethylesterification Generates Platforms that Anchor Peroxidases to Remodel Plant Cell Wall Domains DEVELOPMENTAL CELL Volume: 48 Issue: 2 Pages: 261-+ DOI: 10.1016/j.devcel.2018.11.016

Gao, Fei; Robe, Kevin; Bettembourg, Mathilde; Navarro, Nathalia; Rofidal, Valerie; Santoni, Veronique; Gaymard, Frederic; Vignols, Florence; Roschzttardtz, Hannetz; Izquierdo, Esther; Dubos, Christian The Transcription Factor bHLH121 Interacts with bHLH105 (ILR3) and Its Closest Homologs to Regulate Iron Homeostasis in Arabidopsis (2019) The Plant cell, Volume:32Issue:2 Pages:508-524, DOI:10.1105/tpc.19.00541

Khanday, I; Skinner, D; Yang, B ; Mercier, R; Sundaresan, V (2019) A male-expressed rice embryogenic trigger redirected for asexual propagation through seeds NATURE Volume: 565 Issue: 7737 Pages: 91-+ DOI: 10.1038/s41586-018-0785-8

Medici, A; Szponarski, W; Dangeville, P; Safi, A; Dissanayake, IM; Saenchai, C; Emanuel, A; Rubio, V; Lacombe, B ; Ruffel, S ; Tanurdzic, M; Rouached, H; Krouk, G (2019) Identification of Molecular Integrators Shows that Nitrogen Actively Controls the Phosphate Starvation Response in Plants PLANT CELL Volume: 31, Issue: 5, Pages: 1171-1184 DOI: 10.1105/tpc.18.00656

Michaeli, S; Clavel, M; Lechner, E; Viotti, C; Wu, J ; Dubois, M ; Hacquard, T; Derrien, B ; Izquierdo, E; Lecorbeiller, M (2019) The viral F-box protein P0 induces an ER-derived autophagy degradation pathway for the clearance of membrane-bound AGO1 PNAS, Volume: 116, Issue: 45, Pages: 22872-22883, DOI: 10.1073/pnas.1912222116

Morel, P ; Chambrier, P; Boltz, V; Chamot, S ; Rozier, F; Bento, SR ; Trehin, C ; Monniaux, M; Zethof, J ; Vandenbussche, M (2019) Divergent Functional Diversification Patterns in the SEP/AGL6/AP1 MADS-Box Transcription Factor Superclade The PLANT CELL, Volume: 31, Issue: 12, Pages: 3033-3056, DOI: 10.1105/tpc.19.00162

Platre, MP ; Bayle, V ; Armengot, L ; Bareille, J; Marques-Bueno, MD; Creff, A; Maneta-Peyret, L ; Fiche, JB; Nollmann, M ; Miege, C ; Moreau, P; Martiniere, A; Jaillais, Y (2019) Developmental control of plant Rho GTPase nano-organization by the lipid phosphatidylserine SCIENCE, Volume: 364 Issue: 6435 Pages: 57-+DOI: 10.1126/science.aav9959

Voxeur, A ; Habrylo, O; Guenin, S; Miart, F ; Soulie, MC ; Rihouey, C ; Pau-Roblot, C ; Domon, JM ; Gutierrez, L ; Pelloux, J ; Mouille, G; Fagard, M; Hofte, H ; Vernhettes, S. (2019) Oligogalacturonide production upon Arabidopsis thaliana-Botrytis cinerea interaction PNAS; Volume: 116, Issue: 39, Pages: 19743-19752 DOI: 10.1073/pnas.1900317116

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. Thematic calls can also be opened by these research organizations for their research laboratories to support emerging or risky projects or to facilitate the development of interdisciplinary projects.

- The French national research agency, ANR (http://www. agence-nationale-recherche.fr/en/about-anr/about-the- french-national-research-agency/), provides funding for project-based research. In 2019, the overall score of funding was around 15% of the submitted ANR projects.

- European funding:

http://erc.europa.eu/funding- and-grants Marie-Curie research programmes

http:// ec.europa.eu/research/mariecurieactions/ EMBO http://www.embo.org/funding-awards

Greece

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Please describe the current state of Arabidopsis research in your country

Although the Arabidopsis research community in Greece is small, it remains active producing fascinating results and managing still to acquire funding support.

Despite the impact on basic research, Arabidopsis is the primary model plant species opening new horizons regarding the applied research related to agronomically important species including trees and cultivated plants.

Conferences, Workshops and Outreach events

41st Conference of the Hellenic Society of Biological Sciences, 9 – 11 May 2019, Katerini

70th Conference of the Hellenic Society of Biochemistry and Molecular Biology, 29 November - 1 December 2019, Eugenides Foundation, Athens

Selected Publications

Daras G, Alatzas A, Tsitsekian D, Templalexis D, Rigas S, Hatzopoulos P. (2019) Detection of RNA-protein interactions using a highly sensitive non-radioactive electrophoretic mobility shift assay. Electrophoresis 40:1365-1371

Daras G, Rigas S, Alatzas A, Samiotaki M, Chatzopoulos D, Tsitsekian D, Papadaki V, Templalexis D, Banilas G, Athanasiadou AM, Kostourou V, Panayotou G, Hatzopoulos P. (2019) LEFKOTHEA Regulates Nuclear and Chloroplast mRNA Splicing in Plants. Dev Cell. 50: 767-779.

Valassakis C, Dervisi I, Agalou A, Papandreou N, Kapetsis G, Podia V, Haralampidis K, Œconomidou VA, Spaink HP, Roussis A. (2019) Novel interactions of Selenium Binding Protein family with the PICOT containing 2 proteins AtGRXS14 and AtGRXS16 in Arabidopsis thaliana. Plant Science 281: 102-112.

Major Funding Sources

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

- General Secretariat for Research and Technology (GSRT) www.gsrt.gr/central.

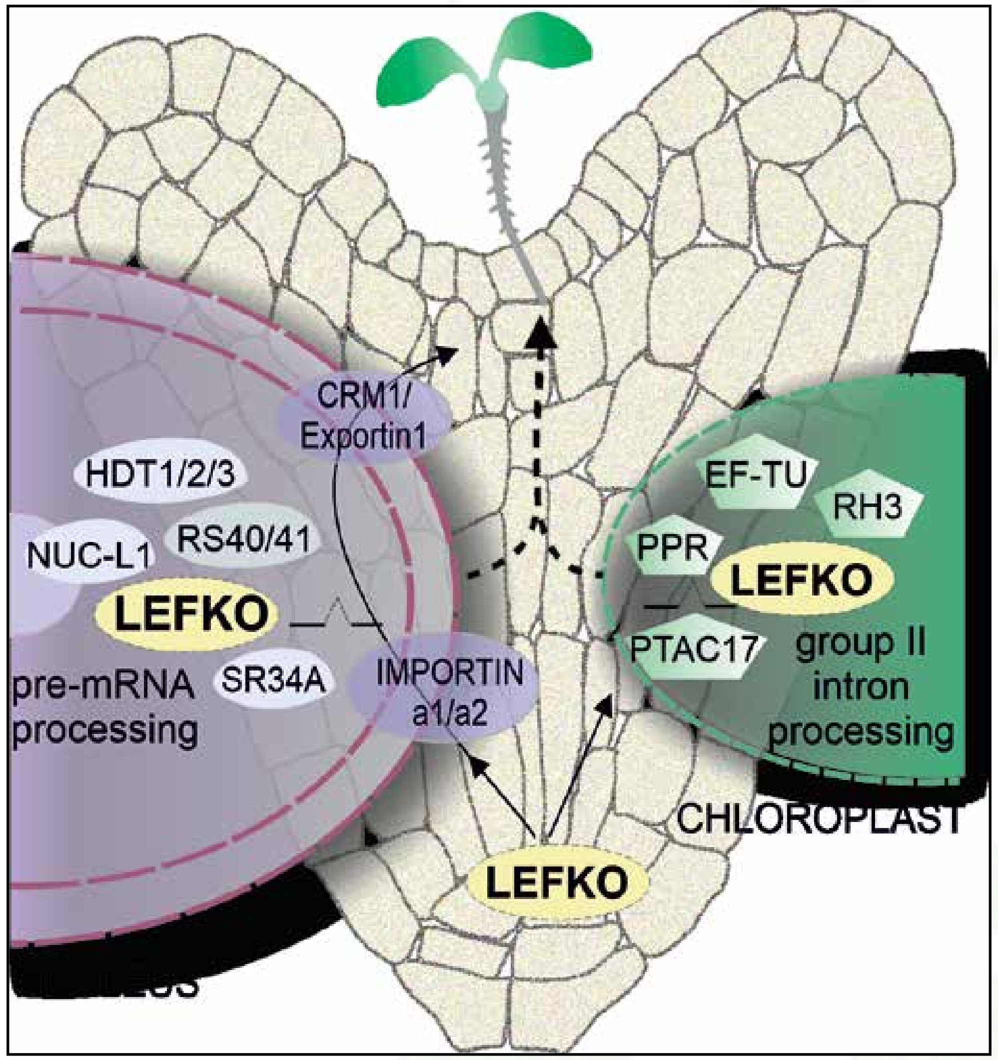
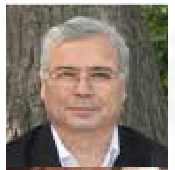
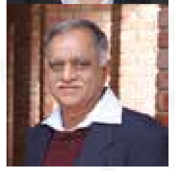


Figure 28 Schematic model of LEFKOTHEA splicing role in plant growth.
In the cytoplasm, ribosomes translate LEFKOTHEA mRNA to protein. Driven by the N-terminal transit peptide, LEFKO is targeted to chloroplasts where it directly regulates the splicing of group II introns. The nucleocytoplasmic partitioning of LEFKO is controlled by the NLS and NES motifs. In the nucleus, LEFKO physically interacts with spliceosomal components to accomplish nuclear pre-mRNA splicing

India





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Please describe the current state of Arabidopsis research in your country

In India, although there is no dedicated financial support for Arabidopsis research from the Government funding agencies, scientists can compete for grants dedicated for basic science and many projects are regularly funded on Arabidopsis exclusively; many more projects use Arabidopsis as a system to validate genes from crop plants. Consequently, the overall quality of publications on Arabidopsis research done in India has improved considerably; it is quite visible from the articles published from India in 2019. In fact many interesting articles in high impact journals have already appeared in the first few months of 2020 that we wish to include in next year's report.”

The Dr. Jiten Thakur's group at NIPGR, New Delhi, has been involved in understanding of the functioning of Mediator, a huge multiprotein complex required for transcriptional regulation by studying the interaction map of Arabidopsis Mediator complex and expounded its structural topology.

Dr. Sudip Chattopadhyay has nucleated a group at NIT, Durgapur, on light signalling in Arabidopsis. In the past year, his group has demonstrated the antagonistic role of a bHLH (MYC2) transcription factor and HY5 in light regulated Arabidopsis seedling development. Their study has revealed that expression of HY5 is negatively regulated by MYC2 primarily in blue light, wheeras HY5 negatively regulates MYC2 expression under multiple wavelengths of light.

Dr. Sourav Datta's group, at IISER, Bhopal, is mainly focusing on the role of BBX family of zinc finger transcription factors in postgerminative seedling growth, UV-B tolerance and flowering. They have recently shown that HY5 transcript levels are enhanced by over-expression of BBX31 in UV light, in a UVR8-dependent manner, suggesting that BBX31 might regulate HY5 transcription.

Dr. Kishore Panigrahi and co-workers, at NISER, Bhubaneswar, using microarray analysis, have shown that expression of genes encoding components involved in light, hormone and clock pathways (including PIF4, COL9, EPR1, CIP1, ARF18, ARR6, SAUR9 and TOC1) changes in Arabidopsis root under various light intensities, indicating their putative role in light intensity mediated root development.

Dr. Utpal Nath's group at IISc, Bangalore has done commendable work on the role of TCP proteins in leaf development in Arabidopsis. Employing biochemical and genetic tools, they have demonstrated that TCP4 not only stimulates auxin response but also directly activates HAT2 gene, encoding a HD-ZIP II transcription factor, imparting differentiation competence.

Dr. Kalika Prasad at IISER, Thiruvanathapuram, has been exploring the role of PLETHORA (PLT) genes in organ regeneration. As part of this broader objective, recently, his group has addressed the question how multicellular organisms regenerate their tissues or organs once they are damaged. They have elucidated the molecular mechanism of organ regeneration potential using root tip as a model system and shown that the dosage of gradient-expressed PLT2 transcription factor determines the regeneration potential and organ size.

Dr. A.K. Sarkar at NIPGR, New Delhi, has analysed the evolutionary relationship and functional sugnificance of Gibberellic Acid Stimulated Transcript (GAST)-like genes that encode small polypeptides and play diverse roles in regulating plant growth and development.

Dr. Ashverya Laxmi's recent work at NIPGR, New Delhi, revealed how glucose signaling helps plants develop memory against heat stress signal to respond better to subsequent heat stress treatments. This work has provided novel information about seedling adaptation and survival under heat stress conditions and fetched novel insights in to the mechanistic basis of plant plasticity.

The focus of Dr. Ashis Nandi's group at JNU, New Delhi, is to understand the immune machinery of plants. Previously, they reported the identification of FLD/RSI1 as an essential component of infection memory development. In an attempt to reveal the broader roles of FLD, they have identified the role of FLD in modulating ET/JA signaling and defense against necrotrophic pathogens.

Dr. Jyothi Vadassery, at NIPGR, New Delhi, is working on the identification of calcium channels in plant-insect interaction. Her group has identified a CYCLIC NUCLEOTIDE GATED CHANNEL19 (CNGC19) that activates herbivory-induced Ca2+ flux and consequently plant defense; loss in CNGC19 function causes decrease in defense against herbivory.

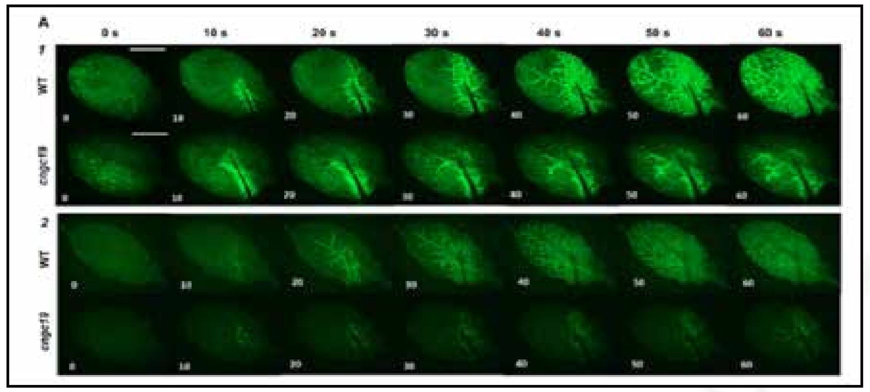

Figure 29. BiFC Changes in distribution of wound-induced cytosolic Ca2+ levels in leaves of the wild type and cyclic nucleotide-gated channels mutant (cngc19). A GFP-based calcium sensor for imaging calcium dynamics, GCaMP3, was employed as Ca2+ reporter by mobilizing it in both the wild type and mutant backgrounds.
In wild type, the Ca2+ signal starts near the wound site and then move to the vasculature and eventually spreads to the entire leaf lamina within 60 s (Upper panel). In contrast, in cngc19 mutant, there is not only aberrant but even reduced Ca2+ signal transmission through the vasculature. The lower panel simply shows the fluorescence image with linear brightness-contrast correction.

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

Dr. A.K. Sarkar's group at NIPGR, New Delhi, has devised an improved and cost-effective protocol to isolate sufficient quantity of high-quality mRNA and miRNAs from plant tissues derived by Laser Capture Microdisection (LCM); Gautam *et al.* (2019) Methods Mol. Biol. 1933: 89-98. doi: 10.1007/978-1-4939-9045-0_5.

Conferences, Workshops and Outreach events

National Arabidopsis meeting (NAM) is an annual feature now and it was held from October 29-31, 2019 at NISER, Bhubaneswar, where most people working on Arabidopsis in India participated.

Selected Publications

Chakraborty M, Gangappa SN, Maurya JP, Sethi V, Srivastava AK, Singh A, Dutta S, Ojha M, Gupta N, Sengupta M, Ram H, Chattopadhyay S (2019) Functional interrelation of MYC2 and HY5 plays an important role in Arabidopsis seedling development. Plant J. 99: 1080-1097.

Challa KR, Rath M, Nath U (2019) The CIN-TCP transcription factors promote commitment to differentiation in Arabidopsis leaf pavement cells via both auxin-dependent and independent pathways. PLoS Genet. 15: e1007988.

Durgaprasad K, Roy MV, Venugopal M A, Kareem A, Raj K, *et al.* (2019) Gradient expression of transcription factor imposes a boundary on organ regeneration potential in plants. Cell Rep. 29: 453-463.e3.

Kumar A, Singh A, Kumar P, Sarkar AK (2019) Giberellic acid-stimulated transcript proteins evolved through successive conjugation of novel motifs and their subfunctionalization. Plant Physiol. 180: 998-1012.

Kumari S, Yadav S, Patra D, Singh S, Sarkar AK, Panigrahi KCS (2019) Uncovering the molecular signature underlying the light intensity-dependent root development in Arabidopsis thaliana. BMC Genomics. 20(1): 596.

Maji S, Dahiya P, Waseem M, Dwivedy N, Bhat DS, Dar T, Thakur JK (2019) Interaction map of Arabidopsis Mediator complex expounding its topology. Nucleic Acids Res. 47: 3904-3920.

Meena MK, Prajapati R, Krishna D, Divakaran K, Pandey Y, Reichelt M, Mathew MK, Boland W, Mithöfer A, Vadassery J (2019) The Ca2+ channel CNGC19 regulates Arabidopsis defense against Spodoptera herbivory. Plant Cell 31: 1539-1562.

Sharma M, Banday Z, Shukla BN, Laxmi A (2019) Glucose regulated Arabidopsis HLP1 acts as a key molecule in governing thermomemory. Plant Physiol. 180: 1-20.

Vadde BVL, Challa KR, Sunkara P, Hegde AS, Nath U (2019) The TCP4 transcription factor directly activates TRICHOMELESS1 and 2 and suppresses trichome initiation. Plant Physiol. 181: 1587-1599.

Yadav A, Bakshi S, Yadukrishnan P, Lingwan M, Dolde U, Wenkel S, Masakapalli SK, Datta S (2019) The B-box containing microprotein miP1a/BBX31 regulates photomorphogenesis and UV-B protection in Arabidopsis. Plant Physiol. 179: 1876-1892.

Major Funding Sources

- Department of Biotechnology (DBT), Government of India http://dbtindia.nic.in/index.asp
- Department of Science &Technology (DST), Government of India http://www.dst.gov.in/scientific-programme/serindex.htm
- Science and Engineering Research Board (SERB), Government of India http://www.serb.gov.in/home.php
- 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/

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Please describe the current state of Arabidopsis research in your country

Most research funding agencies in Ireland are focused on near-term applied research. However, research on model organisms such as Arabidopsis thaliana has been funded by Science Foundation Ireland (SFI) if it is considered either oriented basic or applied research, while fellowship funding is available from the Irish Research Council (IRC) for basic research, including on Arabidopsis.

There is strong pressure from funding agencies via funding calls in Ireland for the research community to focus on applied research. There is a need to grow the Arabidopsis research community in Ireland to a larger scale, which can best be achieved through international partnerships combined with the recruitment priorities of the universities in Ireland. We look forward to welcoming ICAR2022 to Belfast and hope that this event can raise the profile of Arabidopsis and plant science in Ireland. http://icar2022.arabidopsisresearch.org/

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

Łangowski L, Goñi O, Quille P, Stephenson S, Carmody N, Feeney E, Barton D, Østergaard L and SO'Connell S (2019) A Plant Biostimulant From the Seaweed Ascophyllum nodosum (Sealicit) Reduces Podshatter and Yield Loss in Oilseed Rape Through Modulation of IND Expression. Sci Rep 9(1):16644

Zuniga-Soto E, Fitzpatrick DA, Doohan FM and Mullins E (2019) Insights into the transcriptomic response of the plant engineering bacterium Ensifer adhaerens OV14 during transformation. Scientific reports. Jul 17;9(1):1-7.

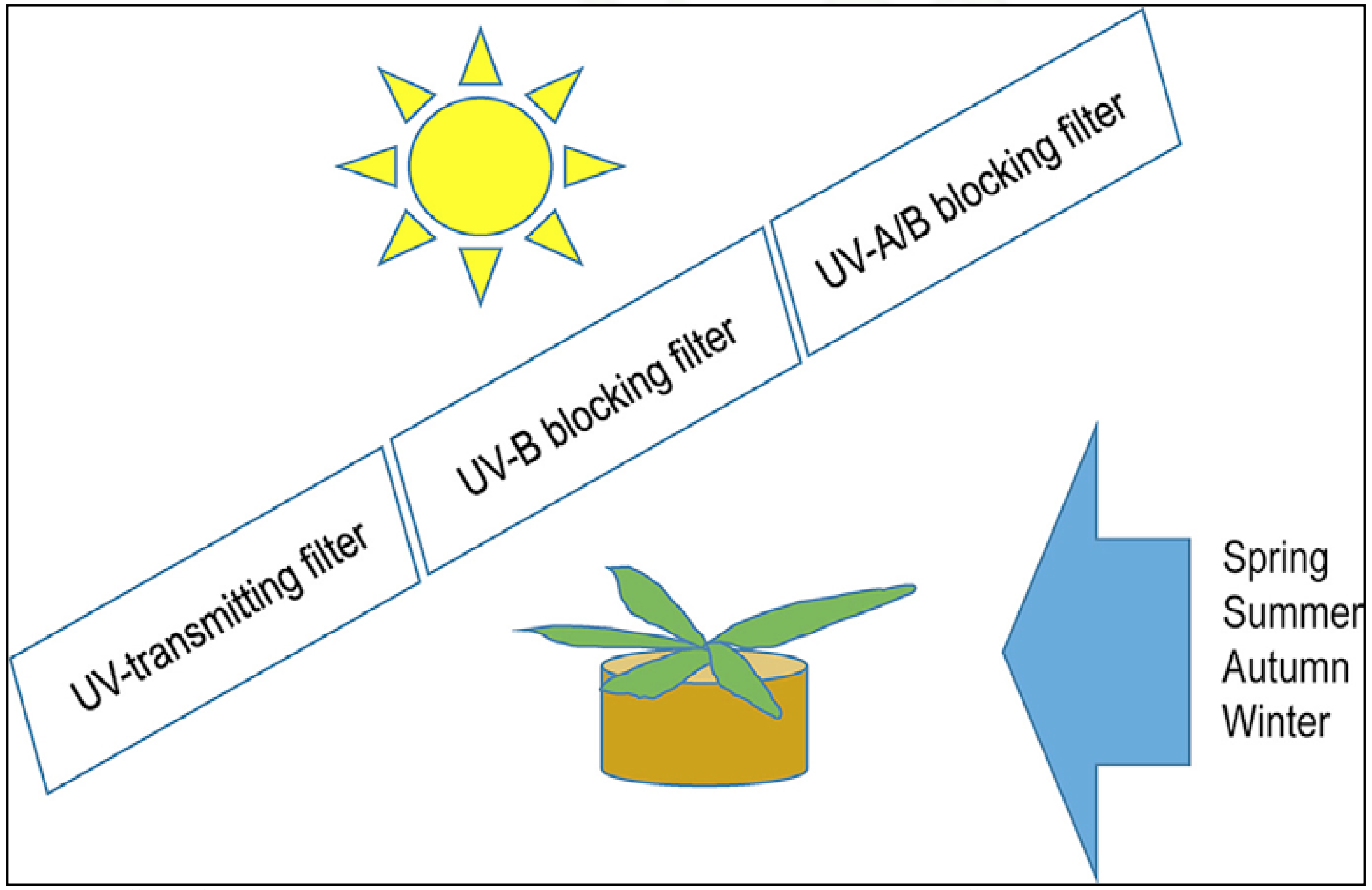

Figure 30. Effects of natural solar UV-B radiation on three Arabidopsis accessions are strongly affected by seasonal weather conditions.

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 doi:10.1093/molbev/msz063

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 doi:10.1105/tpc.18.00663

Duszynska, D., Vilhjalmsson, B., Bravo, R.C., Swamidatta, S., Juenger, T.E., Donoghue, M.T., Comte, A., Nordborg, M., Sharbel, T.F., Brychkova, G., McKeown, P.C. and Spillane 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. doi:10.1007/s00497-019-00369-6

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 doi:10.1016/j.plaphy.2018.06.016

Major Funding Sources

- Foundation Ireland (SFI); Department of Agriculture, Fisheries and Food; Irish Research Council for Science, Engineering and Technology; and the European Union.

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 Johnathan Dalzell, School of Biological Sciences, Queens University Belfast, Northern Ireland.

14. Dr. Emmanualle Graciet, School of Biology, National University of Ireland Maynooth, Ireland.

Israel

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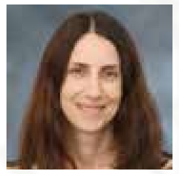

Please describe the current state of Arabidopsis research in your country

Study of Arabidopsis and of additional plant models and crops is conducted in various labs located in major research centers and universities across the country: The Hebrew University of Jerusalem, Tel Aviv University, the Weizmann Institute of Science, Ben Gurion University of the Negev, Bar Ilan University and the Technion - Israel Institute of Technology. Applied research is primarily conducted at the Agriculture Research Organization/ Volcani Center. Areas of Arabidopsis research include plant physiology, biochemistry, metabolomics, cell biology, development and functional genomics. Current Arabidopsis research projects are supported by grants from the ISF, ERC, BSF and GIF.

Conferences organized by the Israeli Society of Plant Sciences aim to promote scientific interactions and collaborations between students across the country. International conferences in these disciplines are also organized and hosted by Israeli scientists. .

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

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

- Protocols and automation scripts for measuring circadian rhythms of fluorescence: http://www.rachelgreenlab.com/resources.html

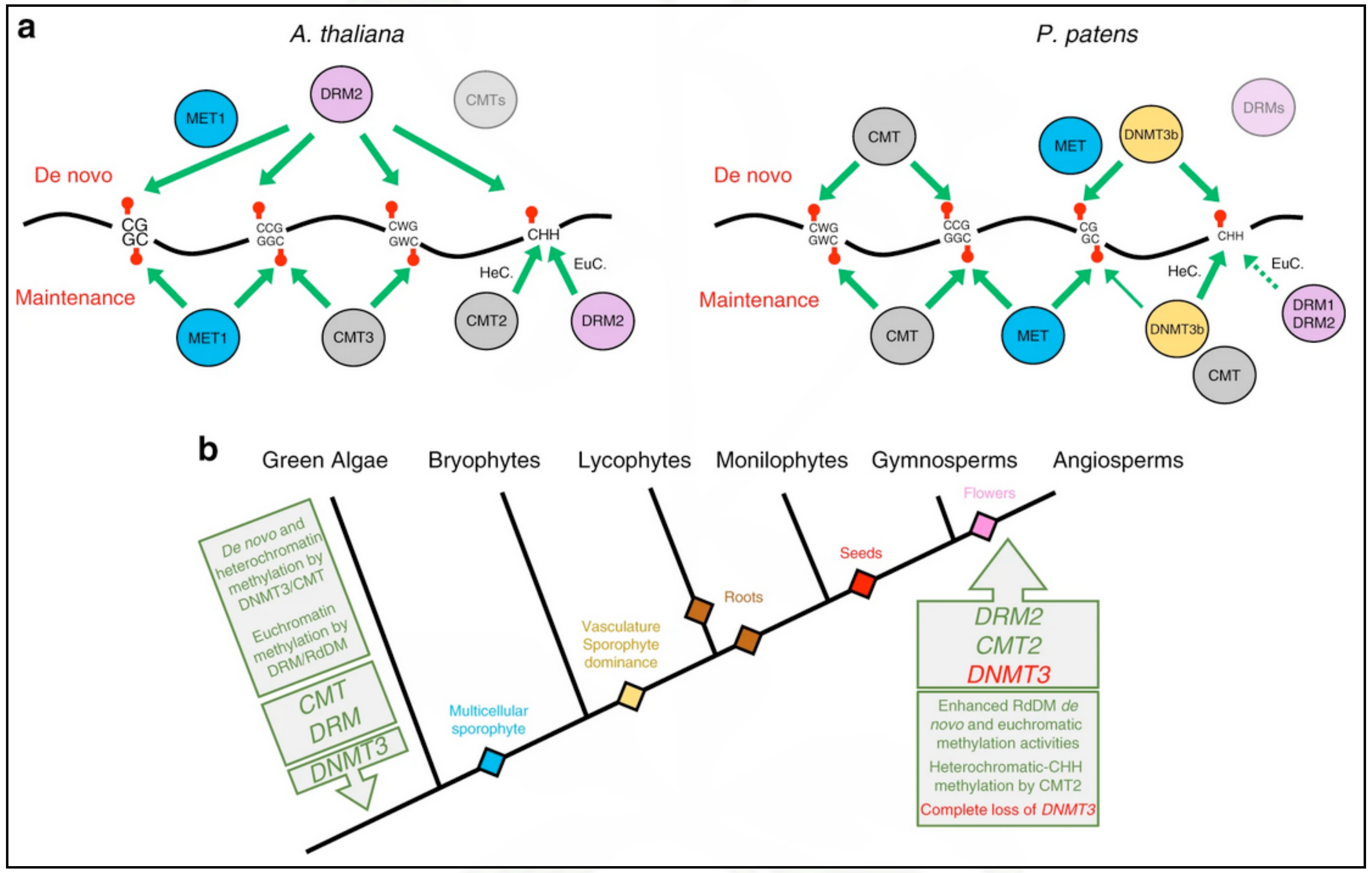

Figure 31. Mechanisms and evolution of plant DNMTs. a DNMT methylation mechanisms are illustrated based on current knowledge. Black line represents the DNA with different cytosine subcontexts embedded in it. Lollipops represent methylation. Arrows width is corresponding qualitatively to the relative level of methylation mediated by indicated DNMTs. HeC. = heterochromatin, EuC. = euchromatin. De novo and maintenance methylation activities are shown above and below the DNA, respectively. De novo methylation in P. patens is based on our RPS transgene results. Future studies would need to check the de novo methylation activity of CMTs and DRMs (masked ovals) in Arabidopsis (angiosperms) and P. patens (basal/DNMT3-encoding plants), respectively. b Schematic illustration of the evolution of plant DNMTs and their function based on previous and our studies. Backbone of phylogenetic tree is inspired by https://langdalelab.com/

Conferences, Workshops and Outreach events

- The Israeli Society of Plant Sciences Conference, February 13th, 2019, Sde-Boker
- ICPMB 2019: Mitochondria - The Energy Hubs of Living Organisms, 10-15.3.2019, Ein-Gedi.
- Plant Genomics, March 18-19, 2019, The Israel Academy of Sciences and Humanities, Jerusalem
- 9th ILANIT/FISEB Conference, 17-20 February 2020, Eilat
- The Batsheva de Rothschild Seminar on Physics & Biology of Plant Growth March 30 - April 2, 2020, Ein Gedi, Israel - POSTPONED

Selected Publications

Cohen A, Hacham Y, Welfe Y, Khatib S, Avice JC, Amir R: Evidence of a significant role of glutathione reductase in the sulfur assimilation pathway. Plant J 2019.

Dakhiya Y, Green RM: Thermal imaging as a noninvasive technique for analyzing circadian rhythms in plants. New Phytol 2019, 224:1685-1696.

Hazak O, Mamon E, Lavy M, Sternberg H, Behera S, Schmitz-Thom I, Bloch D, Dementiev O, Gutman I, Danziger T, *et al*.: A novel Ca2+-binding protein that can rapidly transduce auxin responses during root growth. PLoS Biol 2019, 17:e3000085.

Lieberman-Lazarovich M, Yahav C, Israeli A, Efroni I: Deep Conservation of cis-Element Variants Regulating Plant Hormonal Responses. Plant Cell 2019, 31:2559-2572.

Luria G, Rutley N, Lazar I, Harper JF, Miller G: Direct analysis of pollen fitness by flow cytometry: implications for pollen response to stress. Plant J 2019, 98:942-952.

Majhi BB, Sreeramulu S, Sessa G: BRASSINOSTEROID-SIGNALING KINASE5 Associates with Immune Receptors and Is Required for Immune Responses. Plant Physiol 2019, 180:1166-1184.

Murik O, Chandran SA, Nevo-Dinur K, Sultan LD, Best C, Stein Y, Hazan C, Ostersetzer-Biran O: Topologies of N(6) -adenosine methylation (m(6) A) in land plant mitochondria and their putative effects on organellar gene expression. Plant J 2020, 101:1269-1286.

Soltabayeva A, Srivastava S, Kurmanbayeva A, Bekturova A, Fluhr R, Sagi M: Early Senescence in Older Leaves of Low Nitrate-Grown Atxdh1 Uncovers a Role for Purine Catabolism in N Supply. Plant Physiol 2018, 178:1027-1044.

Sun Y, Harpazi B, Wijerathna-Yapa A, Merilo E, de Vries J, Michaeli D, Gal M, Cuming AC, Kollist H, Mosquna A: A ligand-independent origin of abscisic acid perception. Proc Natl Acad Sci U S A 2019, 116:24892-24899.

Vela-Corcia D, Aditya Srivastava D, Dafa-Berger A, Rotem N, Barda O, Levy M: MFS transporter from Botrytis cinerea provides tolerance to glucosinolate-breakdown products and is required for pathogenicity. Nat Commun 2019, 10:2886.

11. Yaari R, Katz A, Domb K, Harris KD, Zemach A, Ohad N: RdDM-independent de novo and heterochromatin DNA methylation by plant CMT and DNMT3 orthologs. Nat Commun 2019, 10:1613.

Major Funding Sources

- ISF: https://www.isf.org.il
- BSF and NSF-BSF: https://www.bsf.org.il/
- ERC: https://erc.europa.eu/
- GIF: http://www.gif.org.il/Pages/default.aspx

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Please describe the current state of Arabidopsis research in your country

There are just over 20 groups, large and small, currently working on Arabidopsis in Italy. They work mainly in Universities and the Institutes of the National Research Council (CNR) distributed throughout the country, in cities such as Rome, Milan, Naples, Bologna, Padova, Pisa, Verona, Bari, Cosenza, l'Aquila, Lecce, Perugia, Ancona, Potenza, Sassari, and Palermo.

Authors from these laboratories conducting diversified research on Arabidopsis published more than 80 papers in 2019 with Italian scientists as lead or co-authors. Research is mainly focused on plant responses to environment and abiotic stress, oxygen sensing and signalling, plant root and reproductive development, seed germination, plant metabolism and defense responses.

Research on Arabidopsis is funded almost exclusively by small Italian grants awarded to individual research groups by the Universities, such as in Rome and Milan, or local regional grants. Unfortunately, as in previous years, the Italian Ministry of Education, University and Research, has continued to decrease funding for basic research thus causing a reduction in the amount of work produced on Arabidopsis.

International funding, such as European grants or Human frontiers grants (one recently attributed to L. Conti from the University of Milan) are exceptions. Despite all of this, research activities cover most topics related of Arabidopsis and the results obtained are published in high impact journals.

Conferences, Workshops and Outreach events

04-06/09/2019 - Jointed SIBV-SBI Congress. Conference. Padua, Italy. http://www.sibv.eu/congressi-ed-eventi/congresso-congiunto-sbi-sibv

-Meet Me Tonight - 27-28th September 2019. Outreach activity. Giardini Indro Montanelli. Milan, Italy. http://www.meetmetonight.it/il-programma/

-International Workshop in Posttranscriptional modifications September 2019, Biosciences Dept. Milano University, Italy Organizing committee, 50 participants,

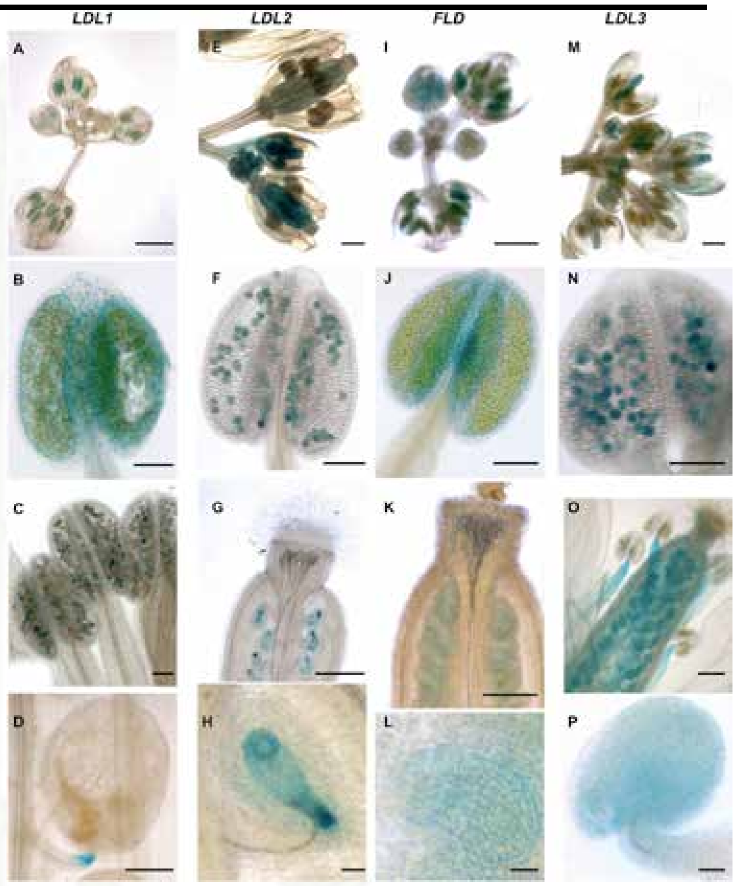

Figure 32 Promoter activity of Arabidopsis LDL/FLD genes during reproductive development. Histochemical GUS staining of LDL/FLD::GFP-GUS Arabidopsis transgenic plants in inflorescences is shown. Bars indicate 1 mm in (A,E,G,I,K,M,O), 100 µm in (B–D,F,J,N), and 20 µm in (H,L,P).

Selected Publications

Alfieri A, Doccula FG, Pederzoli R, Grenzi Matteo, Bonza MC, Luoni L, Candeo A, Romano Armada N, Barbiroli A, Valentini G, Schneider TR, Bassi A, Bolognesi M, Nardini M, Costa A. The structural bases for agonist diversity in an Arabidopsis thaliana glutamate receptor-like channel. Proc Natl Acad Sci U S A. 2019; 117: 752-760.

Caselli F, Beretta VM, Mantegazza O, Petrella R, Leo G, Guazzotti A, Herrera-Ubaldo H, de Folter S, Mendes MA, Kater MM, Gregis V. REM34 and REM35 Control Female and Male Gametophyte Development in Arabidopsis thaliana Front Plant Sci. 2019 Oct 24;10:1351.

Di Mambro R, Svolacchia N, Dello Ioio R, Pierdonati E, Salvi E, Pedrazzini E, Vitale A, Perilli S, Sozzani R, Benfey PN, Busch W, Costantino P, Sabatini S. The Lateral Root Cap Acts as an Auxin Sink that Controls Meristem Size. Current Biology. 2019;29(7):1199-1205.

Locci F, Benedetti M, Pontiggia D, Citterico M, Caprari C, Mattei B, Cervone F, De Lorenzo G "An Arabidopsis Berberine Bridge Enzyme-Like Protein Specifically Oxidizes Cellulose Oligomers And Plays A Role In Immunity". Plant Journal. 2019; 98: 540-554.

Martignago D, Bernardini B, Polticelli F, Salvi D, Cona A, Angelini R, Tavladoraki P. The Four FAD-Dependent Histone Demethylases of Arabidopsis Are Differently Involved in the Control of Flowering Time. Front Plant Sci. 2019; 10, 669.

Mattioli R, Francioso A, d'Erme M, Trovato M, Mancini P, Piacentini L, Casale AM, Wessjohann L, Gazzino R, Costantino P, Mosca L. Anti-inflammatory activity of polyphenolic extract from Arabidopsis thaliana in Alzheimer's disease models. Int. J. Mol. Sci. 2019 20:708

Teardo E, Carraretto L, Moscatiello R, Cortese E, Vicario M, Festa M, Maso L, De Bortoli S, Calì T, Vothknecht UC, Formentin E, Cendron L, Navazio L, Szabo I. A chloroplast-localized mitochondrial calcium uniporter transduces osmotic stress in Arabidopsis. Nature Plants. 2019 Jun;5(6):581-588.

Termolino P, Falque M, Aiese Cigliano R, Cremona G, Paparo R, Ederveen A, Martin OC, Consiglio FM, Conicella C. Recombination suppression in heterozygotes for a pericentric inversion induces the interchromosomal effect on crossovers in Arabidopsis. Plant Journal. 2019;100(6):1163-1175.

Weits DA, Kunkowska AB, Kamps NCW, Portz KMS, Packbier NK, Nemec Venza Z, Gaillochet C, Lohmann JU, Pedersen O, van Dongen JT, Licausi F. An apical hypoxic niche sets the pace of shoot meristem activity. Nature. 2019 May;569(7758):714-717

Zaffagnini M, Marchand CH, Malferrari M, Murail S, Bonacchi S, Genovese D, Montalti M, Venturoli G, Falini G, Baaden M, Lemaire SD, Fermani S, Trost P. Glutathionylation primes soluble glyceraldehyde-3-phosphate dehydrogenase for late collapse into insoluble aggregates. Proc Natl Acad Sci U S A. 2019;116(51):26057-26065.

Major Funding Sources

-Local funding from:

- Sapienza University of Rome :
https://www.uniroma1.it/sites/default/files/field_file_allegati/progetti_piccoli_medi_e_grandi_0.pdf
- Progetto di Ateneo Ricerche Universitarie 2019 "Priming of defense responses in the trade-off between plant immunity and growth." Coordinator: Simone Ferrari.

- Progetto di Ateneo Ricerche Universitarie 2019 "Molecular dynamics underlying PME activity in plant immunity. Coordinator:Vincenzo Lionetti.

- Progetto di Ateneo Ricercehe Universitarie 2019 "Interplay between proline and ROS in the fine tuning of root-meristem size in Arabidopsis. Coordinator Maurizio Trovato

- Progetto di Ateneo Ricerche Universitarie 2018/2019 "Molecular Mechanisms in developmental boundary formation. Coordinator: Sabrina Sabatini
-Roma Tre University of Rome Research-Grant to Department of Science, University 'Roma Tre'-'Dipartimenti di Eccellenza'

- University of Milan:
http://eng.dbs.unimi.it/ecm/home/research/funded-research-projects
Study of the physiological role played by the aminoacid-binding domain of the Arabidopsis Glutamate Receptor-like channel GLR3.3 in long-distance communication". Coordinator: Alex Costa.

The Italian Ministry of Education, University and Research funded:

- PRIN2017(2019-2022) Regulatory signals and redox systems in plant growth-defence trade off. Code: 2017ZBBYNC Coordinator: Giulia De Lorenzo
https://www.miur.gov.it/documents/20182/424391/DD+n.1063+del+31-05-2019+-+ALLEGATO+A+-+LS9.pdf/8ba4cf5b-4a28-bebd-3f1b-f535de5f79c4?version=1.0&t=1559563731935

- PRIN 2017 (2019-2022) MIUR PRIN 2017 "SOUP: Signaling the Organelle Unfolded Protein response". Code: PRIN 2017FBS8YN. P.I. Coordinator: Paolo Pesaresi.
https://expertise.unimi.it/individual?uri=http%3A%2F%2Firises.unimi.it%2Fresource%2Fproject%2F43234

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

- MSCA RISE (2016-2020) SEXSEED project - "Sexual Plant Reproduction – Seed formation" - Horizon2020-MSCA RISE 2016 - European Union (EU)- project n. 690946 - Project P.I Lucia Colombo
https://cordis.europa.eu/project/id/690946/it

- Human Frontier Science Program Organization - RGP0011/2019 - An integrative approach to decipher flowering time dynamics under drought stress. Coordinator Lucio Conti
https://www.hfsp.org/awardees/awards?field_award_type_target_id=All&field_countries_target_id&field_nationalities_target_id&page=3

Japan

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RIKEN BRC

Please describe the current state of Arabidopsis research in your country

Arabidopsis has been used by many plant researchers as a model higher plant to understand the life phenomena of higher plants and to identify key factors and regulatory networks in environmental response and development. Because various useful resources such as multiple mutants have been developed and are available from stock centers. In addition, translational research to apply the knowledge obtained from Arabidopsis to various crops and trees has been increasing.

New Resources and Software tools available for Arabidopsis Researchers that have been initiated or funded in 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)
- PlaSMA Plant Specialized Metabolome Annotation (http://plasma.riken.jp/)

Distribution and Redistribution

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

Other RIKEN CSRS developed tools and resources:

- AtGenExpress Arabidopsis Gene Expression profile database (http://bit.ly/1P2YT8v)
- KNApSacK Comprehensive species-metabolite relationship database (http://bit.ly/1LfFkyZ) (NAIST)
- Plant-PrAS (Plant-Protein Annotation Suite) database of physicochemical and structural properties, and novel functional region in plant proteomes (http://plant-pras.riken.jp/)
- MassBank Public repository of mass spectral data for sharing spectra among research communities (http://www.massbank.jp/en/about.html)
- Plant-PrAS (Plant-Protein Annotation Suite) (http://plant-pras.riken.jp/)
- RIPPS (RIKEN Plant Phenotyping System) (https://academic.oup.com/pcp/article/59/10/2030/5043525)
- The Chloroplast Function Database III (https://plant.rtc.riken.jp/color/c/index.html)
- Arabidopsis nuclear-encoded chloroplast protein mutant seeds (https://epd.brc.riken.jp/en/archives/4909)
- Arabidopsis sORF Database HanaDB-At (http://hanadb01.bio.kyutech.ac.jp/hanadb-at/)
- Hormone-like peptides in Arabidopsis (http://hanadb01.bio.kyutech.ac.jp/peptide/)
- Hormonome platform and RIKEN Plant Hormone Research Network (http://hormones.psc.riken.jp/)

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

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

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

- KOMICS Kazusa Metabolomics Database portal (http://www.kazusa.or.jp/komics/en/)
- MassBase: a plant metabolome database (http://bit.ly/1Rlf9Dd)
- MS-MS Fragment Viewer database (http://bit.ly/1QWjPUm)
- Plant GARDEN Plant Genome And Resource Database ENtry (https://plantgarden.jp)
- PGDBj Plant Genome DataBase Japan (http://pgdbj.jp/?ln=en)
- KaPPA-View4 for integration of transcriptome and metabolome data on metabolic maps (http://kpv.kazusa.or.jp/)
- CoP: a database for plant co-expressed gene network (http://webs2.kazusa.or.jp/kagiana/cop0911/)
- RnR: a database for regulatory network in T87 cultured cells of Arabidopsis thaliana (http://webs2.kazusa.or.jp/kagiana/rnr0912/indexff.html)

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

- nekko: a portal site for Rhizophagus irregularis genome (http://nekko.nibb.ac.jp)
- Japanese Morning Glory Genome Database: (http://ipomoeanil.nibb.ac.jp)
- The Plant Organelles Database 3: (http://podb.nibb.ac.jp/Organellome/)
- PHYSCObase: (http://moss.nibb.ac.jp/physco.html)

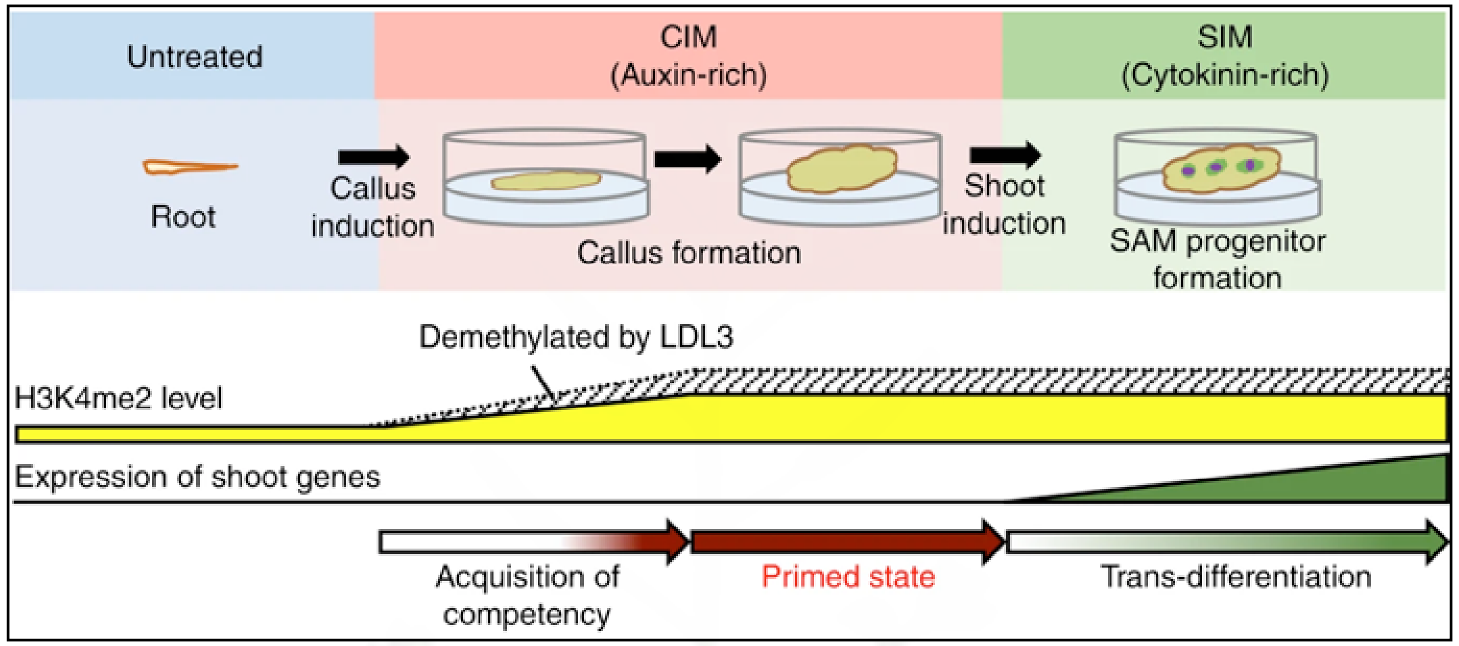

Figure 33 Schematic of the acquisition of shoot regenerative competency. LDL3 is up-regulated and erases H3K4me2 marks of downstream genes during callus formation, although the total amount of H3K4me2 is still increased. The removal of H3K4me2 mediated by LDL3 does not immediately alter the gene expression of callus tissue, but is primed for subsequent shoot induction, which allows the genes for shoot initiation to be activated. The shaded area indicates the H3K4me2 removed by LDL3 during callus formation

Conferences, Workshops and Outreach events

-May 11-14, 2019: "Principles of pluripotent stem cells underlying plant vitality", Tohoku Univ. (http://www.tfc.tohoku.ac.jp/event/4226.html)
- May 21-30, 2019: EMBO Practical Course "Functional live imaging of plants", Nagoya Univ. (https://meetings.embo.org/event/19-plant-live-imaging)
- Mar. 19-21, 2020: 61st Annual Meeting of Japanese Society of Plant Physiologists. Osaka Univ. (https://jspp.org/annualmeeting/61/e_greeting.php)
- May 21-30, 2020: EMBO practical course "Functional Imaging of Plants". Nagoya Univ.
- Dec. 7-10, 2020: Cold Spring Harbor Asia Conference "Integrative Epigenetics in Plants", Awaji Yumebutai Conference Center (http://www.csh-asia.org/2020meetings/epiplant.html)
- May/June 2021: International Symposium on Sustainable Resource Science, Yokohama, Japan
- ICAR2023 will be held in Japan for the first time in 13 years since ICAR2010.

Selected Publications

Fujii, S., Tsuchimatsu, T., Kimura, Y., Ishida, S., Tangpranomkorn, S., Shimosato-Asano, H., Iwano, M., Furukawa, S., Itoyama, W., Wada, Y., Shimizu, K.K., Takayama, S. (2019) A stigmatic gene confers interspecies incompatibility in the Brassicaceae. Nature Plants 5: 731–741

Hoshino, R., Yoshida, Y., Tsukaya, H. (2019) Multiple steps of leaf thickening during sun-leaf formation in Arabidopsis. Plant J. 100:738-753.

Ishihara, H., Sugimoto, K., Tarr, P.T., Temman, H., Kadokura, S., Inui, Y., Sakamoto, T., Sasaki, T., Aida, M., Suzuki, T., Inagaki, S., Morohashi, K., Seki, M., Kakutani, T., Meyerowitz, E.M., Matsunaga, S. (2019) Primed histone demethylation regulates shoot regenerative competency. Nature Commun. 10: 1786.

Ishikawa, M., Morishita, M., Higuchi, Y., Ichikawa, S., Ishikawa, T., Nishiyama, T., Kabeya, Y., Hiwatashi, Y., Kurata, T., Kubo, M., Shigenobu, S., Tamada, Y., Sato, Y., Hasebe, M. (2019) Physcomitrella STEMIN transcription factor induces stem cell formation with epigenetic reprogramming. Nature Plants. 5:681-690.

Kidokoro, S., Kim, J.S., Ishikawa, T., Suzuki, T., Shinozaki, K., Yamaguchi-Shinozaki, K. (2020) DREB1A/CBF3 is repressed by transgene-induced DNA methylation in the Arabidopsis ice1-1 mutant. Plant Cell. (in press) doi: 10.1105/tpc.19.00532.

Ota, R., Ohkubo, Y., Yamashita, Y., Ogawa-Ohnishi, M., Matsubayashi, Y. (2020) Shoot-to-root mobile CEPD-like 2 integrates shoot nitrogen status to systemically regulate nitrate uptake in Arabidopsis. Nature Commun. 11: 641.

Soyano, T., Shimoda, Y., Kawaguchi, M, Hayashi, M. (2019) A shared gene drives lateral root development and root nodule symbiosis pathways in Lotus. Science 366:1021-1023.

Seto, Y., Yasui, R., Kameoka, H., Tamiru, M., Cao, M., Terauchi, R., Sakurada, A., Hirano, R., Kisugi, T., Hanada, A., Umehara, M., Seo, E., Akiyama, K., Burke, J., Takeda-Kamiya, N., Li, W., Hirano, Y., Hakoshima, T., Mashiguchi, K., Noel, J.P., Kyozuka, J., Yamaguchi, S. (2019) Strigolactone perception and deactivation by a hydrolase receptor DWARF14. Nature Commun. 10:191.

Toriba, T., Tokunaga, H., Shiga, T., Nie, F., Naramoto, S., Honda, E., Tanaka, K., Taji, T., Itoh, J.I., Kyozuka, J. (2019) BLADE-ON-PETIOLE genes temporally and developmentally regulate the sheath to blade ratio of rice leaves. Nature Commun. 10:619.

Tsugawa, H, Nakabayashi, R., Mori, T., Yamada, Y., Takahashi, M., Rai, A., Sugiyama, R., Yamamoto, H., Nakaya, T., Yamazaki, M., Kooke, R., Bac-Molenaar, J.A., Oztolan-Erol, N., Keurentjes, J.J.B., Arita, M., Saito, K. (2019) A cheminformatics approach to characterize metabolomes in stable-isotope-labeled organisms. Nature Methods. 16: 295–298.

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/2218avZ)

- 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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Please describe the current state of Arabidopsis research in your country

Agriculture and horticulture play major roles in the New Zealand economy, with major crops including ryegrass, clover and other forage crops for dairy cattle and fruits such as apple and kiwifruit. In this context, Arabidopsis is largely used as an easily manipulated model for the identification and testing of gene function, with information translated into other species.

However, within New Zealand universities, Arabidopsis is also used for basic research into plant growth and development.

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

Genome sequence from *Pachycladon cheesemanii,* a New Zealand member of the Brassicaceae that originated 1-3.5 million years ago. Useful for evolutionary studies with A. thaliana. Sequence data are available from the NCBI Bioproject database (www.ncbi.nlm.nih.gov/bioproject) under ID: PRJNA475190.

Conferences, Workshops and Outreach events

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

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

Queenstown Molecular Biology Week-Plant Satellite, Queenstown, New Zealand, 3-4 September 2020 (but likely to be cancelled due to Corona Virus)

Selected Publications

Soffe R, Bernach M, Remus-Emsermann MNP and Nock V (2019). Replicating Arabidopsis model leaf surfaces for phyllosphere microbiology. Sci Rep 9, 14420

Dong Y, Gupta S, Sievers R, Wargent J J, Wheeler D, Putterill J, Macknight R, Gecgev T, Mueller-Roeber B and Dijkwel PP (2019). Genome draft of the Arabidopsis relative Pachycladon cheesemanii reveals novel strategies to tolerate New Zealand’s high ultraviolet B radiation environment. BMC Genomics, 20:838

Figure 34 Twenty-eight-day-old *A. thaliana* and 38-day-old *P. cheesemanii* plants after a 5-day UV-B treatment. A. thaliana (28 days old) and P. cheesemanii (38 days old) plants were grown in long day conditions and subsequently transferred to UV-B-supplemented white light for 5 days (UV-B-5-day) or to white light only (control). a *A. thaliana* Col-0 b *A. thaliana* Kondara c *P. cheesemanii Kingston* d *P. cheesemanii* Wye creek plants grown under control conditions. e *A. thaliana* Col-0 f *A. thaliana* Kondara g *P. cheesemanii* Kingston h *P. cheesemanii* Wye creek plants after UV-B treatment. i-l Enlarged insets are shown for UV-B-treated plants (e-h) only. Arrows indicate necrotic lesions (white), leaf curling (green) and glossy appearance (yellow), respectively. Scale bars, 3.5 cm

Sun X, Malhis N, Zhao B, Gsponer J, Rikkerink EHA. 2020. Computational disordered analysis in ethylene response factors uncovers binding motifs critical to their diverse functions. International Journal of Molecular Sciences, 21: 74

Cyril Hamiaux, Lesley Larsen, Hui Wen Lee, Zhiwei Luo, Prachi Sharma, Bill C. Hawkins, Nigel B. Perry, Kimberley C. Snowden; Chemical synthesis and characterization of a new quinazolinedione competitive antagonist for strigolactone receptors with an unexpected binding mode. Biochem J 476: 1843–1856.

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

Watkin, SAJ, Keown JR, Richards E, Goldstone DC, Devenish SRA and Pearce FG (2018) Plant DHDPR forms a dimer with unique secondary structure features that preclude higher-order assembly. Biochemistry Journal 475:137-150 doi: 10.1042/BCJ20170709.

Major Funding Sources

- The Marsden Fund administered by the Royal Society of New Zealand (http://www.royalsociety.org.nz/programmes/funds/marsden/)

- Ministry for Business, Innovation and Employment (MBIE; http://www.mbie.govt.nz/) through:

Core funding to Crown Research Institutes

- The Endeavour fund (http://www.mbie.govt.nz/info-services/science-innovation/investment-funding/current-funding/2018-endeavour-round)

- The Catalyst Fund (http://www.mbie.govt.nz/info-services/science-innovation/investment-funding/current-funding/catalyst-fund)

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

Norway

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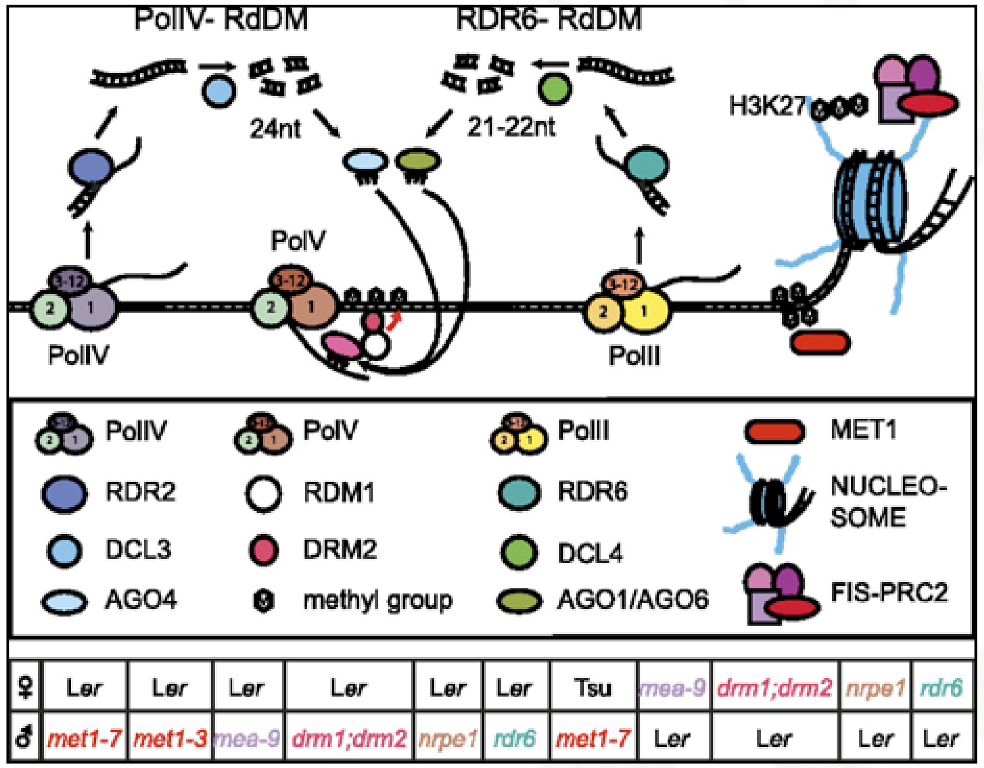
Please describe the current state of Arabidopsis research in your country

The Arabidopsis community in Norway consists of groups based in Bergen, Hamar, Oslo, Stavanger, Ås, Tromsø and Trondheim. Main focus areas of research are developmental processes, response to biotic and abiotic stress as well as photosynthesis. Topics of particular interest include peptide-based and cell wall signaling processes, epigenetics and gametophytic development, jasmonic acid-based defense responses and adaptation to cold stress. Of particular interest is the translation of relevant research findings to tree species of commercial interest due to the sizeable commercial interest in forestry in Norway.



♀	Ler	Ler	Ler	Ler	Ler	Ler	Tsu	mea-9	drm1;drm2	nrpe1	rdr6
♂	met1-7	met1-3	mea-9	drm1;drm2	nrpe1	rdr6	met1-7	Ler	Ler	Ler	Ler

Figure 35. Summary of the epigenetic mechanisms postulated to govern the regulation of imprinted gene expression. Canonical (PolIV-RdDM) and noncanonical (RDR6-RdDM) forms utilize small RNAs of different origins to mediate de novo DNA methylation in all sequence contexts as well as maintenance of CHH methylation (where C denotes cytosine and H denotes all bases except G). MET1 is the main methyltransferase responsible for the maintenance of CG methylation. The FIS-PRC2 complex mediates trimethylation of the 27th amino acid (Lys) on the tail of histone 3 (H3K27me3). Mutants (Col-0 background) of the various pathways investigated in this study are listed together with the wild-type cross partner (Ler -1or Tsu-1).

Despite the small overall size of the community the members continue to generate high quality outputs (exemplified by the publications listed), that attract significant interest.

Selected Publications

Blagojevic D, Lee Y, Brede DA, Lind OC, Yakovlev I, Solhaug KA, Fossdal CG, Salbu B, Olsen JE (2019) Comparative sensitivity to gamma radiation at the organismal, cell and DNA level in young plants of Norway spruce, Scots pine and Arabidopsis thaliana. Planta. 2019; 250(5): 1567-1590. doi: 10.1007/s00425-019-03250-y.

Engelsdorf T, Kjaer L, Gigli-Bisceglia N, Vaahtera L, Bauer S, Miedes E, Wormit A, James L, Chairam I, Molina A, Hamann T (2019) Functional characterization of genes mediating cell wall metabolism and responses to plant cell wall integrity impairment. BMC Plant Biol. 2019; 19(1): 320. doi: 10.1186/s12870-019-1934-4.

Grytten I, Rand KD, Nederbragt AJ, Storvik GO, Glad IK, Sandve GK (2019) Graph Peak Caller: Calling ChIP-seq peaks on graph-based reference genomes. PLoS Comput Biol. 2019; 15(2): e1006731. doi: 10.1371/journal.pcbi.1006731.

Hornslien KS, Miller JR, Grini PE (2019) Regulation of Parent-of-Origin Allelic Expression in the Endosperm. Plant Physiol. 2019; 180(3): 1498-1519. doi: 10.1104/pp.19.00320.

Olsson V, Joos L, Zhu S, Gevaert K, Butenko MA, De Smet I (2019) Look Closely, the Beautiful May Be Small: Precursor-Derived Peptides in Plants. Annu Rev Plant Biol. 2019; 70: 153-186. doi: 10.1146/annurev-arplant-042817-040413.

Zakhartsev M (2019) Using a Multi-compartmental Metabolic Model to Predict Carbon Allocation in Arabidopsis thaliana. Methods Mol Biol. 2019; 2014: 345-369. doi: 10.1007/978-1-4939-9562-2_27.

Major Funding Sources

- Norwegian Research Council

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

Poland

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Please describe the current state of Arabidopsis research in your country

Arabidopsis is undoubtedly an important object of scientific research in Poland. The total value of signed contracts for projects on this model plant by the National Science Center Poland in 2019 was 2,973,265 EUR. The net value of other ongoing NCN-funded Arabidopsis projects that have started in previous years was 9,471,097 EUR.

Similarly to other countries, in Poland Arabidopsis has dual use as a model to study basic processes in plants and a very practical system facilitating functional studies for crop species. Due to the multidisciplinary character of plant research and complexity of studied subjects our scientists cooperate internationally. Such example could be the work of Lopez *et al*. published in 2019, that results from Polish-American co-operation.

Lopez VA, Park BC, Nowak D, Sreelatha A, Zembek P, Fernandez J, Servage KA, Gradowski M, Hennig J, Tomchick DR, Pawłowski K, Krzymowska M, Tagliabracci VS (2019) A Bacterial Effector Mimics a Host HSP90 Client to Undermine Immunity. Cell 179: 205-218.e221

The authors report the discovery of bacterial effector kinase HopBF1, which has the ability to modulate plant host immunity by phosphorylation of the HSP90 protein. The work describes a new, previously unknown phenomenon in the interaction between the plant and the pathogen.

In 2019, two important scientific conferences were held in Poland. The first is the 44th Federation of European Biochemical Societies Conference, during which plant-related subjects (including Arabidopsis)were widely discussed. The second conference was the 9th Polish Society of Experimental Plant Biology Conference. Here, works on Arabidopsis were very strongly represented by both Polish scientists and international leaders.
In particular flowering, seed formation, epigenetics, interactions of plants with biotic and abiotic factors were discussed.

The subject of plant responses to stress is very actively explored in Poland. This is also reflected by increasing number of papers in this field published every year.

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

Web application AFproject - a joint effort to benchmark, improve and simplify alignment-free sequence analysis. [http://afproject.org/app/]
Zielezinski *et al*. Benchmarking of alignment-free sequence comparison methods. Genome Biology, 2019, 20, p144. doi: 10.1186/s13059-019-1755-7

Conferences, Workshops and Outreach events

- 44th Federation of European Biochemical Societies Conference – Krakow, Poland, July 6-11, 2019

- 9th Polish Society of Experimental Plant Biology Conference - Torus, Poland, September 9–12, 2019

Selected Publications

Research conducted on Arabidopsis:

Kwasniak-Owczarek M, Kazmierczak U, Tomal A, Mackiewicz P, Janska H. 2019. Deficiency of mitoribosomal S10 protein affects translation and splicing in Arabidopsis mitochondria. Nucleic Acids Research 47(22): 11790-11806.

Kwasnik A, Wang VY-F, Krzyszton M, Gozdek A, Zakrzewska-Placzek M, Stepniak K, Poznanski J, Tong L, Kufel J. 2019. Arabidopsis DXO1 links RNA turnover and chloroplast function independently of its enzymatic activity. Nucleic Acids Research 47(9): 4751-4764.

Maszkowska J, D□bski J, Kulik A, Kistowski M, Bucholc M, Lichocka M, Klimecka M, Sztatelman O, Szyma□ska KP, Dadlez M, *et al*. 2019. Phosphoproteomic analysis reveals that dehydrins ERD10 and ERD14 are phosphorylated by SNF1-related protein kinase 2.10 in response to osmotic stress. Plant, Cell & Environment 42(3): 931-946.

Mazur R, Mostowska A, Szach J, Gieczewska K, Wójtowicz J, Bednarska K, Garstka M, Kowalewska Ł. 2019. Galactolipid deficiency disturbs spatial arrangement of the thylakoid network in Arabidopsis thaliana plants. Journal of Experimental Botany 70(18): 4689-4704.

Olszak M, Truman W, Stefanowicz K, Sliwinska E, Ito M, Walerowski P, Rolfe S, Malinowski R. 2019. Transcriptional profiling identifies critical steps of cell cycle reprogramming necessary for Plasmodiophora brassicae-driven gall formation in Arabidopsis. Plant J 97(4): 715-729.

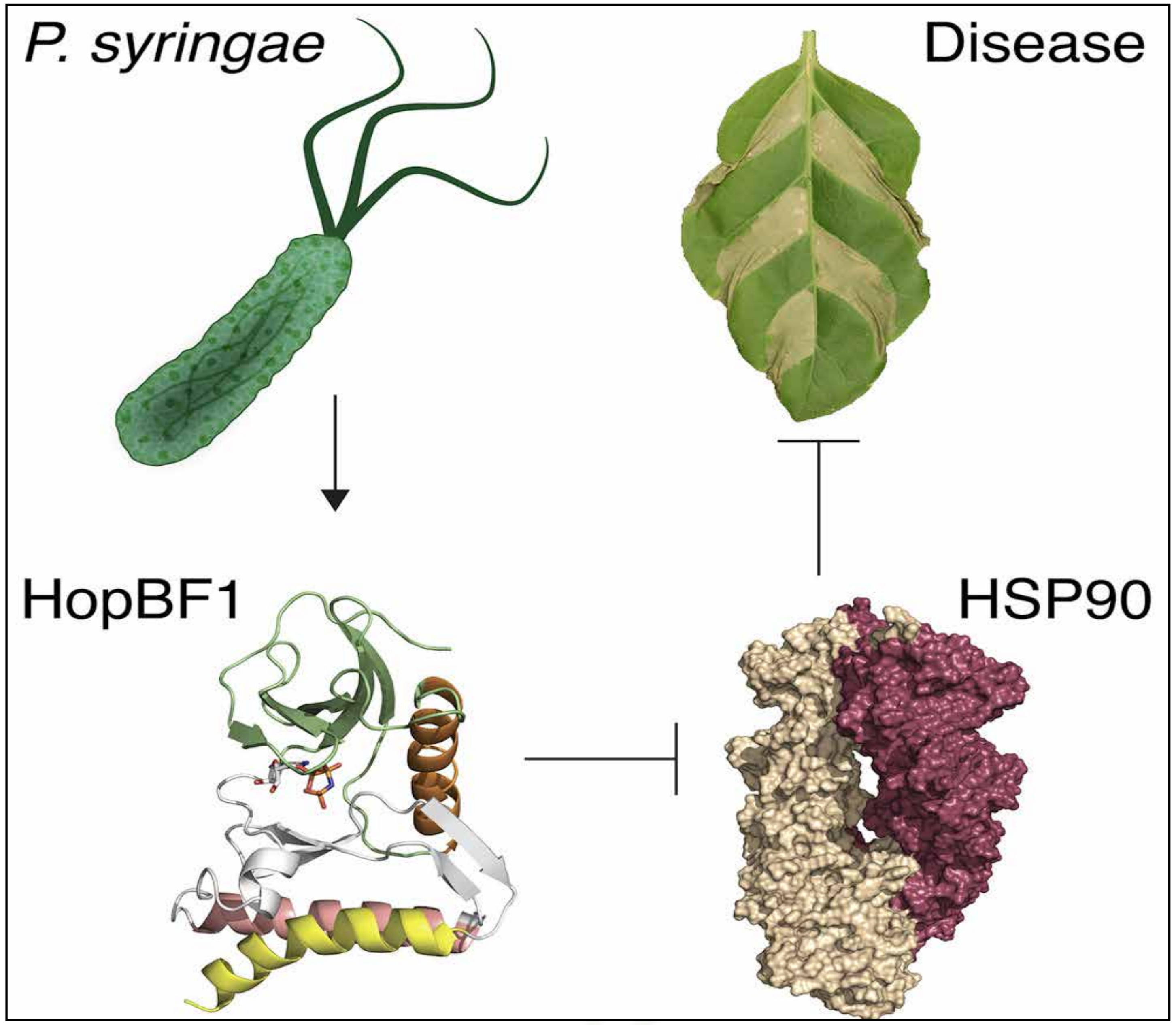


Figure 36. A Bacterial Effector Mimics a Host HSP90 Client to Undermine Immunity

Rozp□dek P, Nosek M, Domka A, Wa□ny R, J□drzejczyk R, Tokarz K, Pilarska M, Niewiadomska E, Turnau K. 2019. Acclimation of the photosynthetic apparatus and alterations in sugar metabolism in response to inoculation with endophytic fungi. Plant, Cell & Environment 42(4): 1408-1423.

You Y, Sawikowska A, Lee JE, Benstein RM, Neumann M, Krajewski P, Schmid M. 2019. Phloem Companion Cell-Specific Transcriptomic and Epigenomic Analyses Identify MRF1, a Regulator of Flowering. The Plant Cell 31(2): 325-345.

Research conducted on other plant species:

Lopez VA, Park BC, Nowak D, Sreelatha A, Zembek P, Fernandez J, Servage KA, *et al.* 2019. A Bacterial Effector Mimics a Host HSP90 Client to Undermine Immunity. Cell 179(1): 205-218.e221.

Pawela A, Banasiak J, Biała W, Martinoia E, Jasi□ski M. 2019. MtABCG20 is an ABA exporter influencing root morphology and seed germination of Medicago truncatula. The Plant journal : for cell and molecular biology 98(3): 511-523.

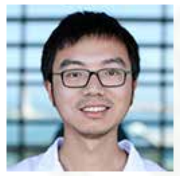
Major Funding Sources

- National Science Centre Poland
https://www.ncn.gov.pl/

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

- The National Centre for Research and Development
https://www.ncbr.gov.pl

Saudi Arabia



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

Please describe the current state of Arabidopsis research in your country

King Abdullah University of Science and Technology (KAUST) conduct most of the Arabidopsis research in Saudi Arabia. KAUST established a center (Center for Desert Agriculture, CDA) to encourage the seven plant science groups working together. The CDA researchers use model plant Arabidopsis to study the basic biological questions and also translate these knowledges to crops, aim to resolve the significant challenges in the Kingdom and the world.

The research mainly focuses on plant-microbe interaction (Professor Heribert Hirt), root development and growth/defense trade-offs (Professor Ikram Blilou), genome editing (Professor Magdy Mahfouz) and carotenoid-related metabolic pathways (Professor Salim Al-Babili).

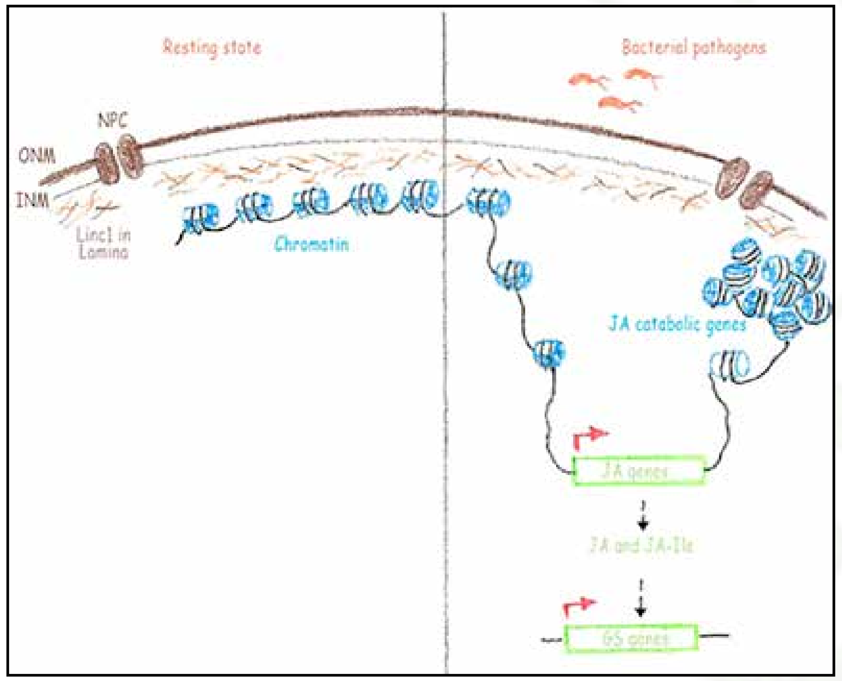

Figure 37. Hypothetical working model for the role of LINC1 in plant immunity. Linc1 is present in nuclear lamina and acts as a sort of scaffold to hold the chromatin. When necessary, such as during a pathogen infection, Linc1 facilitates the open conformation of the genes required for defense, such as the JA biosynthetic and signaling genes and closed conformation of certain other genes such as the JA catabolic genes resulting the accumulation of JA and JA-Ile. The increased amounts of JA and JA-Ile inturn switch on the expression of glucosinolate genes. ONM, outer nuclear membrane; INM, inner nuclear membrane; NPC, nuclear pore complex; JA, jasmonic acid; JA-Ile, jasmonic acid- isoleucine; Gs, glucosinate genes.

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/

Selected Publications

Abuauf, H., Haider, I., Jia, K.-P., Ablazov, A., Mi, J., Blilou, IHan B, Jiang Y, Cui G, *et al.*, (2020). CATION-CHLORIDE CO-TRANSPORTER 1 (CCC1) mediates plant resistance against Pseudomonas syringae. Plant Physiology, pp.01279.2019.

Ali Z, Mahfouz MM, Mansoor S, (2020). CRISPR-TSKO: A Tool for Tissue-Specific Genome Editing in Plants. Trends in Plant Science 25, 123-6.

Eida AA, Alzubaidy HS, De Zélicourt A, *et al.*, (2019). Phylogenetically diverse endophytic bacteria from desert plants induce transcriptional changes of tissue-specific ion transporters and salinity stress in Arabidopsis thaliana. Plant Science 280, 228-40.

Jarad M, Mariappan K, Almeida-Trapp M, *et al.*, (2020). The Lamin-Like LITTLE NUCLEI 1 (LINC1) Regulates Pattern-Triggered Immunity and Jasmonic Acid Signaling. Frontiers in Plant Science 10.

Jia K-P, Dickinson AJ, Mi J, *et al.*, (2019). Anchorene is a carotenoid-derived regulatory metabolite required for anchor root formation in Arabidopsis. Science Advances 5, eaaw6787.

Jiang Y, Han B, Zhang H, *et al.*, (2019). MAP4K4 associates with BIK1 to regulate plant innate immunity. EMBO reports 20, e47965.

Julkowska MM, Saade S, Agarwal G, *et al.*, (2019). MVApp—Multivariate Analysis Application for Streamlined Data Analysis and Curation. Plant Physiology 180, 1261-76.

Long Y, Stahl Y, Weidtkamp-Peters S, Blilou I, (2020) Visualizing Protein Associations in Living Arabidopsis Embryo. In: Bayer M, ed. Plant Embryogenesis: Methods and Protocols. New York, NY: Springer US, 167-88.

Major Funding Sources

- King Abdullah University of Science and Technology.

South Korea

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

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

Conferences, Workshops and Outreach events

In 2019
- Cold spring harbor Asia conference on plant cell and development
https://www.csh-asia.org/2019meetings/plant.html
- Annual Conference of the Korean Society of Plant Biologists
- KSPB Winter conference
http://www.kspb.kr/bbs/board.php?bo_table=05_01&wr_id=90&sst=wr_hit&sod=asc&sop=and&page=1

Selected Publications

Do THT, Choi H, Palmgren M, Martinoia E, Hwang JU, Lee Y. (2019) Arabidopsis ABCG28 is required for the apical accumulation of reactive oxygen species in growing pollen tubes. Proc Natl Acad Sci U S A. 116(25):12540-12549.

Hwang K, Susila H, Nasim Z, Jung JY, Ahn JH. (2019) Arabidopsis ABF3 and ABF4 Transcription Factors Act with the NF-YC Complex to Regulate SOC1 Expression and Mediate Drought-Accelerated Flowering. Mol Plant. 12(4):489-505.

Lee HG, Seo PJ. (2019) MYB96 recruits the HDA15 protein to suppress negative regulators of ABA signaling in Arabidopsis. Nat Commun. 10(1):1713.

Lee DW, Lee S, Lee J, Woo S, Razzak MA, Vitale A, Hwang I. (2019) Molecular Mechanism of the Specificity of Protein Import into Chloroplasts and Mitochondria in Plant Cells. Mol Plant. 12(7):951-966.

Kim MH, Jeon J, Lee S, Lee JH, Gao L, Lee BH, Park JM, Kim YJ, Kwak JM. (2019) Proteasome subunit RPT2a promotes PTGS through repressing RNA quality control in Arabidopsis. Nat Plants. 2019 Dec;5(12):1273-1282.

Kim H, Yu SI, Jung SH, Lee BH, Suh MC. (2019) The F-Box Protein SAGL1 and ECERIFERUM3 Regulate Cuticular Wax Biosynthesis in Response to Changes in Humidity in Arabidopsis. Plant Cell. 31(9):2223-2240.

Lee MH, Jeon HS, Kim SH, Chung JH, Roppolo D, Lee HJ, Cho HJ, Tobimatsu Y, Ralph J, Park OK. (2019) Lignin-based barrier restricts pathogens to the infection site and confers resistance in plants. EMBO J. 38(23):e101948.

Kim EJ, Lee SH, Park CH, Kim SH, Hsu CC, Xu S, Wang ZY, Kim SK, Kim TW. (2019) Plant U-Box40 Mediates Degradation of the Brassinosteroid-Responsive Transcription Factor BZR1 in Arabidopsis Roots. Plant Cell. 31(4):791-808.

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(1):37-51.

Song JH, Kwak SH, Nam KH, Schiefelbein J, Lee MM. (2019) QUIRKY regulates root epidermal cell patterning through stabilizing SCRAMBLED to control CAPRICE movement in Arabidopsis. Nat Commun. 10(1):1744. doi: 10.1038/s41467-019-09715-8.

Major Funding Sources

- National Research Funding (Korea)
https://www.nrf.re.kr/
- Rural Development Agency (Korea)
https://www.rda.go.kr/

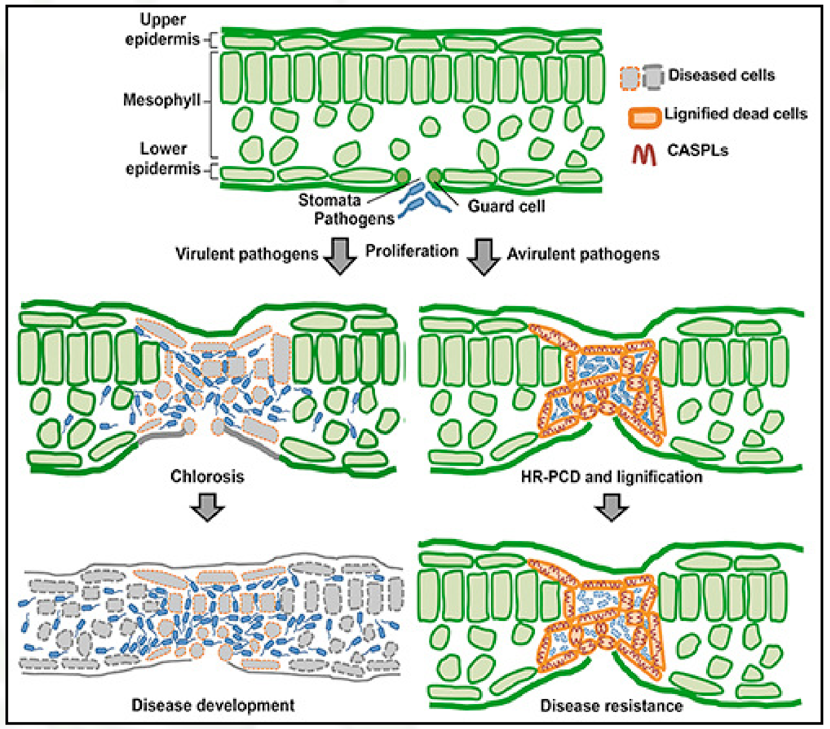

Figure 38. Plants employ a multilayered immune system, but the exact mechanisms of how plants restrict pathogen growth remain unclear. In this study, the phenolic polymer and cell wall component lignin is shown to form a mechanical barrier against avirulent pathogens, thereby conferring disease resistance in plants. Lignification is induced during incompatible plant-pathogen interactions in Arabidopsis. Lignin spatially restricts and encompasses bacteria in the extracellular space. Lignin deposition enhances disease resistance. Casparian strip organizer proteins CASPL1D1 and CASPL4D1 are required for pathogen-induced lignification.

Spain

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Please describe the current state of Arabidopsis research in your country

Authors from laboratories studying Arabidopsis in Spain published about 350 papers in the last year, which is similar to that seen in recent years. However, the proportion of papers that use previous knowledge initially obtained in Arabidopsis but use other plant species as a central object of study is growing. Indeed, since 2008, funded plant science has changed in Spain towards more applied approaches; however, Arabidopsis still is predominant among the financed lines of plant science research.

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

A reproducible epigenomic analysis pipeline using Galaxy and Jupyter, packaged into Docker images to facilitate transparency and reuse was developed for different Brassicaceae species, as described in Payá-Milans M, Poza-Viejo L, San Martín-Uriz P, Lara-Astiaso D, Wilkinson MD and Crevillén P (2019) Genome-wide analysis of the H3K27me3 epigenome and transcriptome in Brassica rapa. Gigascience 8: 1-13.

Conferences, Workshops and Outreach events

- The "International Symposium on Plant Photobiology" was organized in Barcelona by members of the Centre for Research in Agricultural Genomics, including Profs Jaume Martínez-García and Elena Monte, and Dr Jordi Moreno-Romero (June 3-8, 2019).

- The "Small Molecules in Plant Research: Chemistry and Biology Come Together" symposium was organized by plant biologists lead by Prof. Antonio Granell in Valencia (December 10-11, 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 Crevillén P, Gómez-Zambrano A, López JA, Vázquez J, Piñeiro M and Jarillo JA (2019) Arabidopsis YAF9 histone readers modulate flowering time through NuA4-complex-dependent H4 and H2A.Z histone acetylation at FLC chromatin. New Phytologist 222: 1893-1908.

García-León M, Cuyas L, El-Moneim DA, Rodríguez L, Belda-Palazón B, Sánchez-Quant E, Fernández Y, Roux B, Zamarreño AM, García-Mina JM, Nussaume L, Rodriguez PL, Paz-Ares J, Leonhardt N and Rubio V (2019) Arabidopsis ALIX regulates stomatal aperture and turnover of abscisic acid receptors. Plant Cell 31: 2411-2429.

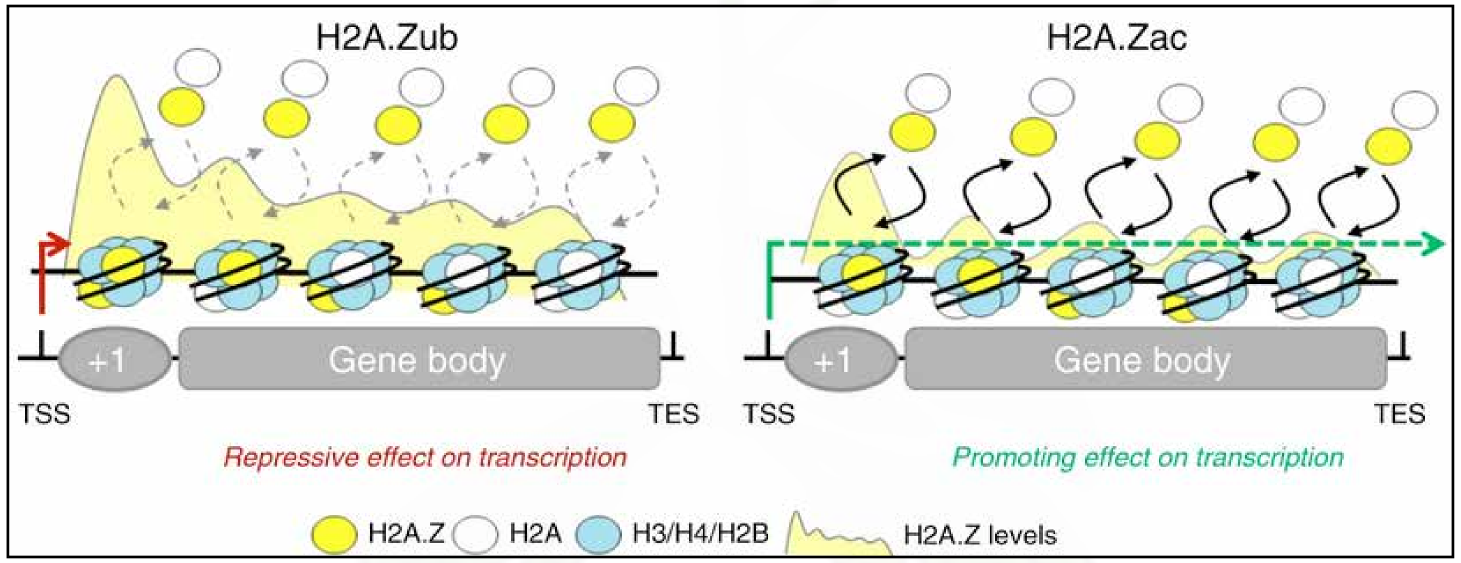

Figure 39. Proposed model for H2A.Z-mediated gene regulation in which monoubiquitination of H2A.Z is required for transcriptional repression (left) and acetylation of H2A.Z for transcriptional activation, while H2A.Z levels along the genes are consequence of the transcriptional activity, where transcriptional repression leads to accumulation of H2A.Z (left) and active transcription to decreased levels of H2A.Z (right).

Gómez-Zambrano A, Merini W and Calonje M (2019) The repressive role of Arabidopsis H2A.Z in transcriptional regulation depends on AtBMI1 activity. Nature Communications 10: 2828.

González B and Vera P (2019) Folate metabolism interferes with plant immunity through 1C methionine synthase-directed genome-wide DNA methylation enhancement. Molecular Plant 12: 1227-1242.

Guzmán-Benito I, Donaire L, Amorim-Silva V, Vallarino JG, Esteban A, Wierzbicki AT, Ruiz-Ferrer V and Llave C (2019) The immune repressor BIR1 contributes to antiviral defense and undergoes transcriptional and post-transcriptional regulation during viral infections. New Phytologist 224: 421-438.

Hernández-García J, Briones-Moreno A, Dumas R and Blázquez MA (2019) Origin of gibberellin-dependent transcriptional regulation by molecular exploitation of a transactivation domain in DELLA proteins. Molecular Biology and Evolution 36: 908-918.

Julian J, Coego A, Lozano-Juste J, Lechner E, Wu Q, Zhang X, Merilo E, Belda-Palazon B, Park SY, Cutler SR, An C, Genschik P and Rodriguez PL (2019) The MATH-BTB BPM3 and BPM5 subunits of Cullin3-RING E3 ubiquitin ligases target PP2CA and other clade A PP2Cs for degradation. Proceedings of the National Academy of Sciences USA 116: 15725-15734.

Molina-Contreras MJ, Paulisic S, Then C, Moreno-Romero J, Pastor-Andreu P, Morelli L, Roig-Villanova I, Jenkins H, Hallab A, Gan X, Gomez-Cadenas A, Tsiantis M, Rodríguez-Concepción M and Martínez-García JF (2019) Photoreceptor activity contributes to contrasting responses to shade in Cardamine and Arabidopsis seedlings. Plant Cell 31: 2649-2663.

Sequeira-Mendes J, Vergara Z, Peiro R, Morata J, Araguez I, Costas C, Mendez-Giraldez R, Casacuberta JM, Bastolla U and Gutierrez C (2019) Differences in firing efficiency, chromatin, and transcription underlie the developmental plasticity of the Arabidopsis DNA replication origins. Genome Research 29: 784-797.

Wilson-Sánchez D, Lup SD, Sarmiento-Mañús R, Ponce MR and Micol JL (2019) Next-generation forward genetic screens: using simulated data to improve the design of mapping-by-sequencing experiments in Arabidopsis. Nucleic Acids Research 47: e140.

Major Funding Sources

- About 80 grants from the State Research Agency of Spain (Ministry of Science and Innovation) fund Arabidopsis research projects at individual laboratories.

Sweden

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Please describe the current state of Arabidopsis research in your country

The major funding bodies, including both private foundations and governmental agencies, all support basic research devoted to plant sciences and many of the grantees use Arabidopsis as their main model system. Most funders have one call per year and award project grants to support research and salary or stipend over a few years, with occasional calls for larger grants aimed at specific research areas. Typically, larger research grants are awarded to groups of and are used to support basic core facilities in major research facilities (as listed above), enabling access also to smaller research groups to carry out most type of research.

In recent time several larger individual competitive grants have been awarded to Arabidopsis researcher. In 2019 both Prof. Markus Schmid, UPSC, Department of Plant Physiology, Umeå University and Prof. Claudia Köhler, LCPU, Department of Plant Biology, Swedish University of Agricultural Sciences, Uppsala - both were appointed Wallenberg Scholars and received a grant of SEK 18 million each from the Wallenberg Foundations as a five-year grant for free research. Earlier years, for instance Prof. Ove Nilsson, UPSC, Swedish University of Agricultural Sciences, Umeå (Wallenberg Scholar 2012) and Dr. Charles Melnyk, LCPU, Department of Plant Biology, Swedish University of Agricultural Sciences, Uppsala (Wallenberg Academy Fellow 2016) was awarded larger grants for their research from the private Knut and Alice Wallenberg Foundation.

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

- 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”

- New Phenotyping Platform for Trees Biology has just been inaugurated at Umeå Plant Science Centre shorturl.at/fjsKU

- The Swedish Metabolomics Centre in Umeå is a national resource, http://www.swedishmetabolomicscentre.se/

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

- Plant Research and Higher Education in Southern Sweden
https://www.plantlink.se/

- The Linnean Centre for Plant Biology in Uppsala
https://lcpu.se/

Conferences, Workshops and Outreach events

18 May 2019, Fascination of Plants Day with events taking place across Swedish Plant Science hubs https://plantday18may.org/category/europe/sweden/

28 - 30 August 2019, the Scandinavian Plant Physiology Society (SPPS) conference was held in Umeå, Sweden

Selected Publications

Batista, R.A.; Moreno-Romero, J.; Qiu, Y.; *et al.* (2019) The MADS-box transcription factor PHERES1 controls imprinting in the endosperm by binding to domesticated transposons ELIFE e50541:8

Dukic, E.; Herdean, A.; Cheregi, O.; *et al.* (2019) K+ and Cl- channels/transporters independently fine-tune photosynthesis in plants Sci Rep 9:8639

Johnsson, C.; Jin, X.; Xue, W.; *et al.* (2019) The plant hormone auxin directs timing of xylem development by inhibition of secondary cell wall deposition through repression of secondary wall NAC-domain transcription factors Physiol Plant 165:673-689

Kloth, K.J.; Abreu, I.N.; Delhomme, N.; *et al.*(2019) PECTIN ACETYLESTERASE9 Affects the Transcriptome and Metabolome and Delays Aphid Feeding Plant Physiol 181:1704-1720

Lakehal, A.; Chaabouni, S.; Cavel, E.; *et al.* (2019) A Molecular Framework for the Control of Adventitious Rooting by TIR1/AFB2-Aux/IAA-Dependent Auxin Signaling in Arabidopsis Mol Plant 12:1499-1514

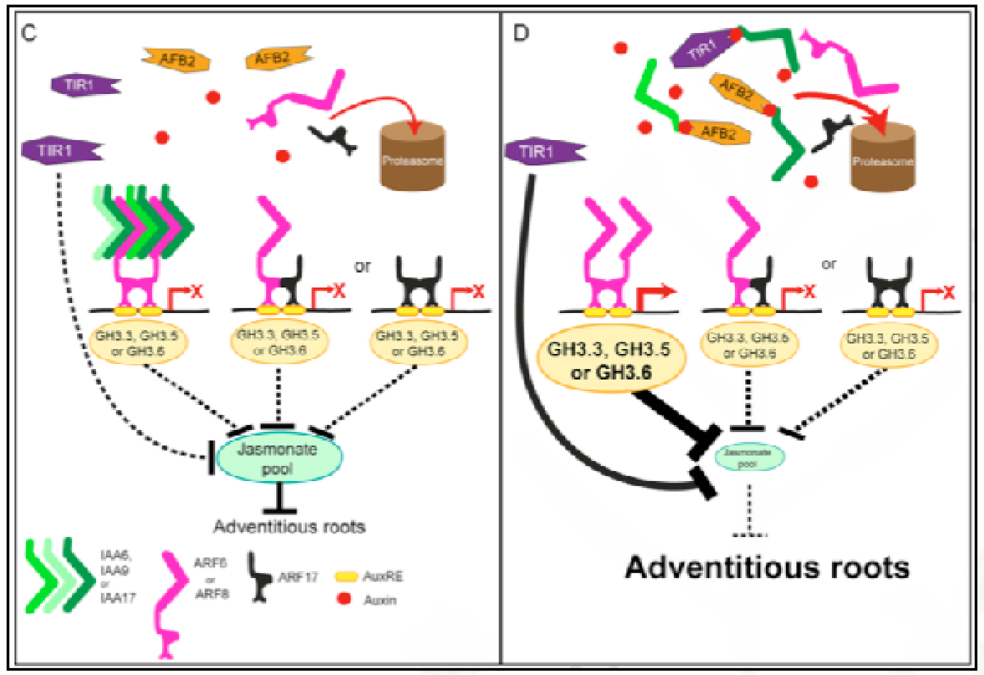


Figure 40. TIR1/AFB2-Aux/IAA6/9/17-ARF6/8 and ARF17 signaling module is involved in the control of adventitious root initiation upstream of GH3.3, GH3.5 and GH3.6 (C) Adventitious root initiation is controlled by a subtle balance of ARF activators and repressor acting upstream of JA signaling (Gutierrez *et al.*,). Under steady-state conditions there is a balance between the positive regulators ARF and ARF and the negative regulator ARF. The three ARFs are regulated at the transcriptional and post- transcriptional levels and their proteasome-dependent degradation possibly contributes to maintain their balance. IAA, IAA and IAA protein repress the transcriptional activity of ARF and ARF. The negative regulator ARF either interacts with ARF and/or ARF to inhibit their transcriptional activity or competes for the AuxRE elements in the promotors of the GH genes. TIR protein controls JA biosynthesis through a pathway yet to be identified. (D) When the auxin content increases the Aux/IAA proteins form an auxin coreceptor complex with TIR and/or AFB and are sent for degradation through the S proteasome. In this case, the transcriptional activity of ARF and ARF is released. Therefore, the balance is shifted towards the positive regulators and results in the induction of GH gene expression. The negative effect of TIR on JA biosynthesis is accentuated. The increased conjugation of JA by the three GH enzymes combined to the downregulation of JA biosynthesis will reduce the JA pool and subsequently downregulate JA signaling, resulting in increased AR initiation.

Vain, T.; Raggi, S.; Ferro, N.; *et al.* (2019) Selective auxin agonists induce specific AUX/IAA protein degradation to modulate plant development Proc Natl Acad Sci U S A 116:6463-6472

Van Moerkercke, A.; Duncan, O.; Zander, M.; *et al.* (2019) A MYC2/MYC3/MYC4-dependent transcription factor network regulates water spray-responsive gene expression and jasmonate levels Proc Natl Acad Sci U S A 116:23345-23356

You, Y.; Sawikowska, A.; Lee, J.E.; *et al.* (2019) Phloem Companion Cell-Specific Transcriptomic and Epigenomic Analyses Identify MRF1, a Regulator of Flowering Plant Cell 31:325-345

Zan, Y. and Carlborg, Ö. (2019) A Polygenic Genetic Architecture of Flowering Time in the Worldwide Arabidopsis thaliana Population Mol Biol Evol 36:141-154

A more applied (maize) paper, already well cited:

Markovic, D.; Colzi, I.; Taiti, C.; *et al.* (2019) Airborne signals synchronize the defenses of neighboring plants in response to touch J Exp Bot. 70:691-700

Major Funding Sources

- The Swedish Research Council (VR); http://www.vr.se
VR supports researcher-initiated, basic research

- The Swedish Foundation for Strategic Research; http://www.stratresearch.se
Supports strategic research in natural science, engineering and medicine

- The Swedish Agency for Innovation Systems (VINNOVA); http://www.vinnova.se
Promotes sustainable growth by funding needs-driven research and the development of effective innovation systems

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

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

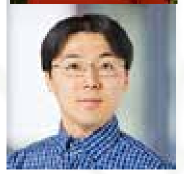
- Carl Trygger's Foundation for Scientific Research; http://www.carltryggersstiftelse.se/
A private foundation supporting research within the areas of agriculture, forestry, biology, chemistry and physics

- The Kempe Foundations; http://www.kempe.com
Private foundations devoted to support scientific research in Northern Sweden

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

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

Switzerland



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Please describe the current state of Arabidopsis research in your country

Switzerland hosted the 11th Tri-National Arabidopsis Meeting in April 2019. Sessions on "From Arabidopsis to Crops" and "Technology Development" highlighted the progress on the MASC roadmap "From Bench to Bountiful Harvests". The conference had world-wide attendants, which originally started by three countries Austria, Germany and Switzerland. Publications in high-impact journals are regularly produced from Switzerland, such as on plant defense and root development in 2019-2020.

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

- Kakui H, Yamazaki M, Hamaya NB, Shimizu KK, Pollen Grain Counting Using a Cell Counter (2020) In: Pollen and Pollen Tube Biology: Methods and Protocols, Anja Geitmann (editor), MIMB, Humana Press, IN PRESS

Conferences, Workshops and Outreach events

- 11th TNAM (Tri-National Arabidopsis Meeting), 10-12 Apr 2019, Zurich
https://www.tnam2019.ethz.ch/

- 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/

- Summer schools
https://swissplantscienceweb.unibas.ch/en/education/summer-schools/
• Microbiomes in soil, plant, animal and human health (for PhDs and postdoc fellows): 11-16 July 2019 (Bern University, One Health - Interfaculty Research Cooperation)
• Improving health at the interfaces between environment, plants, animals and humans (for Bachelor and Master students): 26-30 August 2019 (Bern University, One Health - Interfaculty Research Cooperation)

- PSC Symposium 2019, Plant Response to Environment across Scales,
11 Dec 2019, Zurich
https://www.plantsciences.uzh.ch/en/outreach/conferences/plantresponseacrossscales.html

- SwissPLANT symposium 2020, 29 – 31 Jan 2020, Ovronnaz
https://swissplantscienceweb.unibas.ch/en/events/swissplant/

- Lausanne Genomics Days 2020, 10 – 11 Feb 2019, Lausanne https://biologie.cuso.ch/index.php?id=1741&L=0&tx_displaycontroller[showUid]=5156

Workshops

- OrgN2020: International workshop on organic nitrogen and plant nutrition, 2-6 Feb 2020, Monte Verità
http://www.botany.unibe.ch/orgn2020/

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

Berhin A, de Bellis D, Franke RB, Buono RA, Nowack MK, Nawrath C (2019) The Root Cap Cuticle: A Cell Wall Structure for Seedling Establishment and Lateral Root Formation. Cell. 2019 Mar 7;176(6):1367-1378.e8.

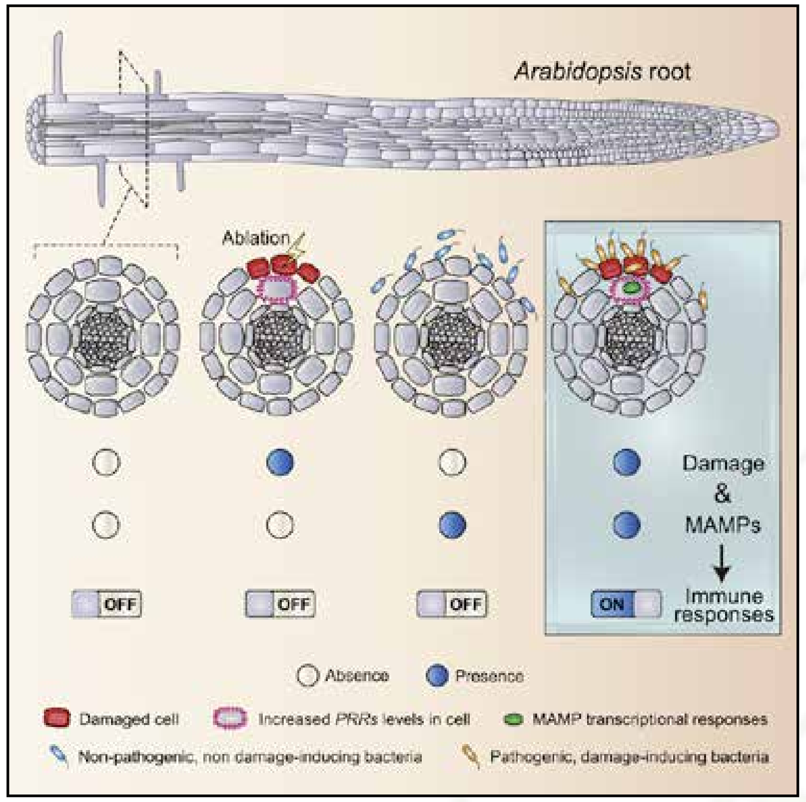

Figure 41: Co-incidence of Damage and Microbial Patterns Controls Localized Immune Responses in Roots

Fernández I, Cosme M, Stringlis IA, Yu K, de Jonge R, van Wees SM, Pozo MJ, Pieterse CMJ, van der Heijden MGA (2019) Molecular dialogue between arbuscular mycorrhizal fungi and the nonhost plant Arabidopsis thaliana switches from initial detection to antagonism New Phytol. 2019 Jul;223(2):867-881.

Grob S, Grossniklaus U (2019) Invasive DNA elements modify the nuclear architecture of their insertion site by KNOT-linked silencing in Arabidopsis thaliana Genome Biol. 2019 Jun 11;20(1):120.

Kesten C, Gámez-Arjona FM, Menna A, Scholl S, Dora S, Huerta AI, Huang HY, Tintor N, Kinoshita T, Rep M, Krebs M, Schumacher K, Sánchez-Rodríguez C (2019) Pathogen-induced pH changes regulate the growth-defense balance in plants. EMBO J. 2019 Dec 16;38(24):e101822.

Kurenda A, Nguyen CT, Chételat A, Stolz S, Farmer EE (2019) Insect-damaged Arabidopsis moves like wounded Mimosa pudica Proc Natl Acad Sci U S A. 2019 Dec 17;116(51):26066-26071.

Lorenzo-Orts L, Witthoeft J, Deforges J, Martinez J, Loubéry S, Placzek A, Poirier Y, Hothorn LA, Jaillais Y, Hothorn M (2019) Concerted expression of a cell cycle regulator and a metabolic enzyme from a bicistronic transcript in plants Nat Plants. 2019 Feb;5(2):184-193.

Schreier TB, Umhang M, Lee SK, Lue WL, Shen Z, Silver D, Graf A, Müller A, Eicke S, Stadler-Waibel M, Seung D, Bischof S, Briggs SP, Kötting O, Moorhead GBG, Chen J4, Zeeman SC (2019) LIKE SEX4 1 Acts as a Amylase-Binding Scaffold on Starch Granules during Starch Degradation Plant Cell. 2019 Sep;31(9):2169-2186.

Xiao Y, Stegmann M, Han Z, DeFalco TA, Parys K, Xu L, Belkhadir Y, Zipfel C, Chai J (2019) Mechanisms of RALF peptide perception by a heterotypic receptor complex. Nature. 2019 Aug;572(7768):270-274.

Yasuhiro Sato, Rie Shimizu-Inatsugi, Misako Yamazaki, Kentaro K. Shimizu & Atsushi J. Nagano (2019) Plant trichomes and a single gene GLABRA1 contribute to insect community composition on field-grown Arabidopsis thaliana BMC Plant Biology volume 19, Article number: 163 (2019)

Zhou F, Emonet A, Dénervaud Tendon V, Marhavy P, Wu D, Lahaye T, Geldner N (2020) Co-incidence of Damage and Microbial Patterns Controls Localized Immune Responses in Roots Cell. 2020 Feb 6;180(3):440-453.e18. doi: 10.1016/j.cell.2020.01.013

Major Funding Sources

- Swiss National Science Foundation (SNSF) http://www.snf.ch/en/Pages/default.aspx
- European Research Council (ERC), https://erc.europa.eu/
- SystemsX.ch, http://www.systemsx.ch/
- Syngenta (Plant Science Center - Syngenta Fellowship), https://www.plantsciences.uzh.ch/en/research/fellowships/syngenta.html
- Research and Innovation Staff Exchange (RISE) of European Commission http://ec.europa.eu/research/mariecurieactions/about/research-innovation-staff-exchange_en
- State Secretariat for Education, Research, and Innovation (SERI), https://www.sbfi.admin.ch/sbfi/en/home.html
- University Research Priority Program of Evolution in Action: From Genomes to Ecosystems (directors: Beat Keller, Ueli Grossniklaus, University of Zurich) http://www.evolution.uzh.ch/en.html
- Japan Science and Technology Agency (JST), Core Research for Evolutional Science and Technology (CREST), https://www.jst.go.jp/kisoken/crest/en/

Taiwan

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Please describe the current state of Arabidopsis research in your country

In recent years plant/agricultural researchers in Taiwan have focused several important global challenges, such as intensifying climate change, depletion of natural resources. These problems make it urgent to undertake the agricultural transformation and industrial upgrading. Thus, advancing agricultural modernization and innovation are important. In 2018, weather was better than earlier years in Taiwan, making it a bumper harvest year for agriculture. The invested money for basic research and advancing agricultural translation research in Taiwan are several billions of US dollars, which was a new high over the last 20 years.

Currently, scientific researchers in Taiwan more than 70% using Arabidopsis as a model plant to first test ideas and theories, and then translating to agriculture research. The main mission for all plant researchers is 1) to discover important mechanisms and to solve biological critical questions, and 2) to create edge-cutting and innovative technologies and to translate it into an industry. For example, we solve a long-standing question of plant biology on protein import machinery into chloroplasts, where photosynthesis is taking place. A key part identified to link the outer and inner membrane translocons of chloroplast. Evolutionary analyses further suggest that this chloroplast protein import machinery in a plant is from a bacterial protein secretion system.

We have already completed many foundational works, seen many historic changes, and achieved a number of successes in 2019 and believe that we can continue and stay strong and successes in 2020.

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

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/)

7. Forestry and Resource Conservation, National Taiwan University (http://ntuf.cc.ntu.edu.tw)

8. Taiwan Rice Insertional Mutants Database

Conferences, Workshops and Outreach events

1. NPAS Seminar: 2019 Asia-Pacific drosophila neurobiology conference

2. Stem cells & developmental biology mini-symposium -division of life sciences

3. AS-NIH-TMU Joint Neuroscience Symposium
4. IBC Biophysics mini-symposium - From Physics to Diseases

5. Mini-symposium on protein structure and function

6. Joint Meetings: Abcam Epigenetics Conference and 14th Asia Epigenome Meeting (AEM) / 3rd Taipei Epigenetics and Chromatin Meeting (TECM)

7. The 17th international symposium on rice functional genomics (ISRFG 2019)

8. Radiocaesium in Agricultural Environment and Internal Radiation dose from Foods in Fukushima after the Nuclear Accident of 2011

9. Application of Organic or Inorganic Materials to Soils for Development of Sustainable Agriculture

10. 2019 IMB Symposium

11. 2020 UW Madison-Academia Sinica Stem Cell & Regenerative Medicine Symposium: Biology, Technology & Regulation

12. The 12th Shang-Fa Yang memorial lecture

13. The 13th Shang-Fa Yang memorial lecture

Selected Publications

Angkawijaya, A.E., Nguyen, V.C., and Nakamura, Y. (2019). LYSOPHOSPHATIDIC ACID ACYLTRANSFERASES 4 and 5 are involved in glycerolipid metabolism and nitrogen starvation response in Arabidopsis. New Phytol 224, 336-351.

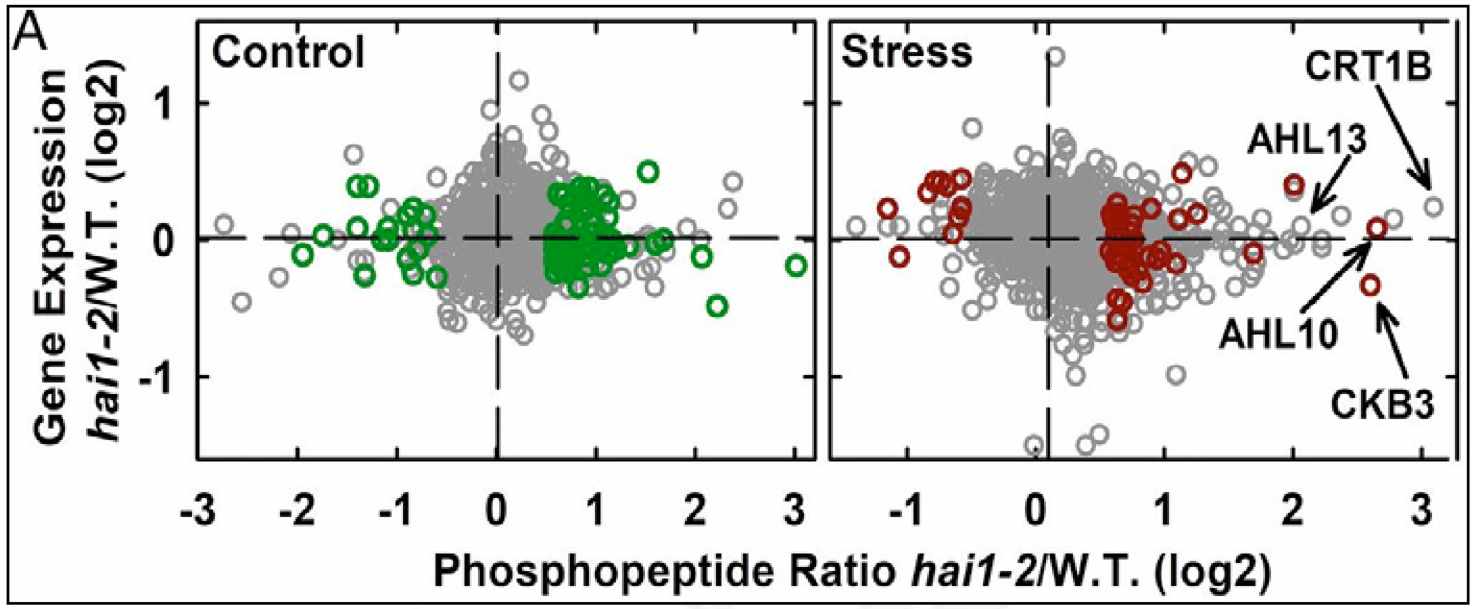

Figure 42: Phosphoproteomics of *hai1-2* identifies a set of HAI1-affected phosphoproteins, including AHL10. (A) Phosphopeptide abundance versus gene expression for *hai1-2* compared with wild type. Dark green or red symbols indicate phosphopeptides with significantly increased or decreased abundance (unadjusted $P \leq 0.05$ by one sample t-test and fold change ≥1.5) in hai1-2 compared with wild type for control and stress (–1.2 MPa, 96 h) treatments (Datasets S2 and S3). Other phosphopeptide data are plotted using gray symbols.

Cho, H.Y., Lu, M.J., and Shih, M.C. (2019). The SnRK1-eIFiso4G1 signaling relay regulates the translation of specific mRNAs in Arabidopsis under submergence. New Phytol 222, 366-381.

Hsu, C.W., Lo, C.Y., and Lee, C.R. (2019). On the postglacial spread of human commensal Arabidopsis thaliana: journey to the East. New Phytol 222, 1447-1457.

Jang, G.J., Yang, J.Y., Hsieh, H.L., and Wu, S.H. (2019). Processing bodies control the selective translation for optimal development of Arabidopsis young seedlings. Proc Natl Acad Sci U S A 116, 6451-6456.

Li, Y., Xu, X., Lee, M.H., Chu, M.W., and Chien, C.L. (2019). Observation of half-quantum flux in the unconventional superconductor beta-Bi2Pd. Science 366, 238-241.

Michniewicz, M., Ho, C.H., Enders, T.A., Floro, E., Damodaran, S., Gunther, L.K., Powers, S.K., Frick, E.M., Topp, C.N., Frommer, W.B., *et al*. (2019). TRANSPORTER OF IBA1 Links Auxin and Cytokinin to Influence Root Architecture. Dev Cell 50, 599-609 e594.

Pecher, P., Moro, G., Canale, M.C., Capdevielle, S., Singh, A., MacLean, A., Sugio, A., Kuo, C.H., Lopes, J.R.S., and Hogenhout, S.A. (2019). Phytoplasma SAP11 effector destabilization of TCP transcription factors differentially impact development and defence of Arabidopsis versus maize. PLoS Pathog 15, e1008035.

Wang, T., Schreiber, C., Elbaz, D., Yoshimura, Y., Kohno, K., Shu, X., Yamaguchi, Y., Pannella, M., Franco, M., Huang, J., *et al*. (2019). A dominant population of optically invisible massive galaxies in the early Universe. Nature 572, 211-214.

Wong, M.M., Bhaskara, G.B., Wen, T.N., Lin, W.D., Nguyen, T.T., Chong, G.L., and Verslues, P.E. (2019). Phosphoproteomics of Arabidopsis Highly ABA-Induced1 identifies AT-Hook-Like10 phosphorylation required for stress growth regulation. Proc Natl Acad Sci U S A 116, 2354-2363.

Zhang, W., Wang, G., Xu, Z.G., Tu, H., Hu, F., Dai, J., Chang, Y., Chen, Y., Lu, Y., Zeng, H., *et al*. (2019). Lactate Is a Natural Suppressor of RLR Signaling by Targeting MAVS. Cell 178, 176-189 e115.

Major Funding Sources

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

Turkey

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Please describe the current state of Arabidopsis research in your country

Majority of the plant science in Turkey focus on crop plants such as wheat, barley or other economically important legumes. This is not surprising since Turkey is among the gene centers of wheat and some other crops and has a large arable land, which is roughly 1/5 of total of EU28 (Costa *et al*. 2019). Also, Turkey has rich plant diversity due to diverse habitat types and in recent years plant scientist has focused on biology of endemic plant species that reside in these habitats.

When one checks the seed banks (NASC or ABRC) for ecotypes from Turkey, the results are very limited (2 different localities) (TAIR database as 28.03.2020), although Turkey is roughly 3 times larger than UK. Hence, natural variation in Turkey is highly under-represented in seed banks and inevitably in studies that investigate natural variation of Arabidopsis. Distribution map of NASC natural ecotypes stock given in Figure 45 clearly shows lack of ecotypes from Turkey in seeds banks, while Germany, UK, Spain, Sweden and France take the lead in the land area normalized list (seed bank entries per 100.000 km2).

Since Turkey is very rich in plant biodiversity (ex: Turkey has equal or more number of plant species when compared to EU28 combined) and habitat diversity it can be reckoned that Arabidopsis natural variation in Turkey should also have the potential to be high. By considering this potential recently there is an initiative to create a collection of Arabidopsis from different geographical regions of Turkey.

There are only few laboratories that utilize Arabidopsis as a model for physiological or molecular studies. However, in the recent years, some laboratories also started to utilize Arabidopsis-related model species (ARMS) that are found in Turkey to elucidate differential responses between Arabidopsis and its extremophile relatives at biochemical and molecular level. Some example plant species are extreme halophyte Schrenkiella parvula (Eutrema parvulum) that is found around Salt Lake (central Anatolia, Turkey) (Uzilday *et al*., 2015, Yalcinkaya *et al*. 2019) or *Arabis alpina*, which is an artic-alpine species.

Moreover, it is believed that *Arabis alpina* originates from Anatolian mountains (Ansell *et al*. 2011). The number of these examples can be increased, but, overall, it can be concluded that Turkey has a biodiversity potential that can be synergistically exploited in conjugation with Arabidopsis and tools it provide to researchers.

Conferences, Workshops and Outreach events

4th National Plant Physiology Symposium (UBFS2020) - https://ubfs2020.aku.edu.tr/

Selected Publications

Akkaya, Ö., & Arslan, E. (2019). Biotransformation of 2, 4-dinitrotoluene by the beneficial association of engineered Pseudomonas putida with Arabidopsis thaliana. 3 Biotech, 9(11), 408.

Arslan, E., & Akkaya, Ö. (2020). Biotization of Arabidopsis thaliana with Pseudomonas putida and assessment of its positive effect on in vitro growth. In Vitro Cellular & Developmental Biology-Plant, 1-9.

Demircan, N., Cucun, G., & Uzilday, B. (2020). Mitochondrial alternative oxidase (AOX1a) is required for the mitigation of arsenic-induced oxidative stress in Arabidopsis thaliana. Plant Biotechnology Reports, 1-11.

Eroglu, S., Karaca, N., Vogel-Mikus, K., Kavcic, A., Filiz, E., & Tanyolac, B. (2019). The conservation of VIT1-dependent iron distribution in seeds. Frontiers in plant science, 10, 907.

Gören-Saglam, N., Harrison, E., Breeze, E., Öz, G., & Buchanan-Wollaston, V. (2020). Analysis of the impact of indole-3-acetic acid (IAA) on gene expression during leaf senescence in Arabidopsis thaliana. Physiology and Molecular Biology of Plants, 1-13.

Kayihan, D.S., Kayihan, C., & Çiftçi, Y.Ö. (2019). Moderate level of toxic boron causes differential regulation of microRNAs related to jasmonate and ethylene metabolisms in Arabidopsis thaliana. Turkish Journal of Botany, 43(2), 167-172.

Niron, H., & Türet, M. (2019). A Putative Common Bean Chalcone O-Methyltransferase Improves Salt Tolerance in Transgenic Arabidopsis thaliana. Journal of Plant Growth Regulation, 1-13.

Pandey, A., Khan, M. K., Hakki, E. E., Gezgin, S., & Hamurcu, M. (2019). Combined Boron Toxicity and Salinity Stress—An Insight into Its Interaction in Plants. Plants, 8(10), 364.

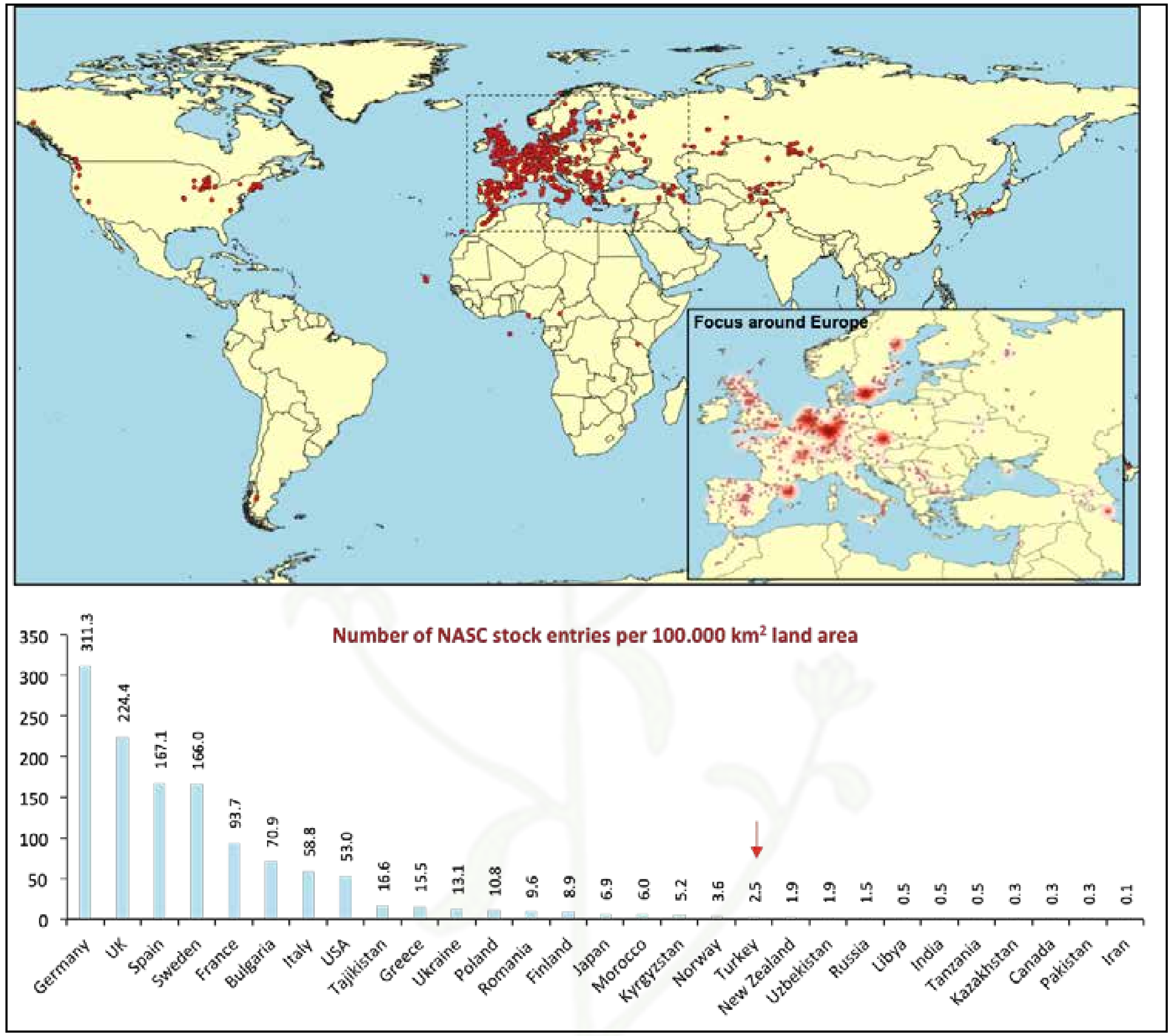

Figure 43: Distribution of NASC natural ecotype collection across the world (Data provided by Marcos Castellanos-Uribe, Operations Manager at NASC). Focus around Europe shows concentration of the collection on specific regions. Chart below shows number of NASC stock entries per 100.000 km2 land area. Note that countries with less than 100.000 km2 land area were omitted from the list.

Surgun-Acar, Y., & Zemheri-Navruz, F. (2019). 24-Epibrassinolide promotes arsenic tolerance in Arabidopsis thaliana L. by altering stress responses at biochemical and molecular level. Journal of plant physiology, 238, 12-19.

Yalcinkaya, T., Uzilday, B., Ozgur, R., & Turkan, I. (2019). The roles of reactive carbonyl species in induction of antioxidant defence and ROS signalling in extreme halophytic model Eutrema parvulum and glycophytic model Arabidopsis thaliana. Environmental and experimental botany, 160, 81-91

Major Funding Sources

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

United Kingdom

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Please describe the current state of Arabidopsis research in your country

The UK is a world leader in the quality of plant science research papers as judged by citation rate. This excellence is supported by over 600 research groups who conduct some aspect of research using Arabidopsis. However one challenge for these researchers are the limited funding opportunities to obtain support for discovery-led plant science research. Outside of individual fellowships, UKRI-BBSRC responsive mode is the only scheme that will support postdoctoral research of this nature. In total this supports around 15 grants/year that total ~£8M. This has significantly reduced since 2014 when there are a clear switch to support for more applied research in plant science. Currently UK excellence is being maintained but this is in danger as the proportion of available funding for discovery-led research declines. GARNet have explored this issue with UKRI-BBSRC and produced a document with recommendations, the primary of which is to engage researchers to engage with BBSRC as they are 'open-for-business' for discovery-led plant science applications. https://www.garnetcommunity.org.uk/sites/default/files/GARNish_BBSRC_Piece.pdf

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

- The Eurasian Arabidopsis Stock Centre (uNASC) is based at the University of Nottingham. http://Arabidopsis.info/

- 3D RNA-Seq Analysis Tool: Researchers at the James Hutton Institute, University of Dundee have developed the 3D RNA-Seq Analysis Tool for the comprehensive differential expression, alternative splicing analysis and visualisation of RNASeq Data. http://ics.hutton.ac.uk/3drnaseq/

- BBSRC-funded Wheat and Rice Transformation facility at NIAB. They have capacity to transfer 100 genes inthese important crops and invite Arabidopsis researchers to submit their genes of interest. https://www.niab.com/research/agricultural-crop-research/plant-biotechnology

Conferences, Workshops and Outreach events

- CellWall2019: University of Cambridge. July 7th-12th 2019. http://cellwall2019.org/

- IS-MPMI University of Glasgow: July 14th-18th 2019. https://www.ismpmi.org/Congress/2019/Pages/default.aspx

- 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

~~- Our Plants, Our Future. BSPP IYPH Conference: April 20th-21st 2020~~ COVID19 postponement ~~https://www.bspp.org.uk/conferences/our-plants-our-future/~~

~~- Genetics Society Arabidopsis Meeting: Durham University. April 21st-22nd 2020~~ COVID19 postponement ~~https://www.dur.ac.uk/conference.booking/details/?id=1403~~

- Sainsbury Lab Symposium: Pluripotency in plant development. SLCU September 23rd-25th 2020 https://www.slcu.cam.ac.uk/SLS20

- BSPP20: Protecting Plants, Protecting Life: December 7th-9th 2020 https://www.bspp.org.uk/conferences/bspp2020-protecting-plants-protecting-life/

- ICAR2022 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 20th-24th 2022.** http://icar2022.Arabidopsisresearch.org

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/

Fang X, Wang L, Ishikawa R, Li Y, Fiedler M, Liu F, Calder G, Rowan B, Weigel D, Li P, Dean C (2019) Arabidopsis FLL2 promotes liquid-liquid phase separation of polyadenylation complexes. Nature. doi: 10.1038/s41586-019-1165-8

Greenwood M, Domijan M, Gould PD, Hall AJW, Locke JCW (2019) Coordinated circadian timing through the integration of local inputs in Arabidopsis thaliana. PLoS Biol. doi: 10.1371/journal.pbio.3000407

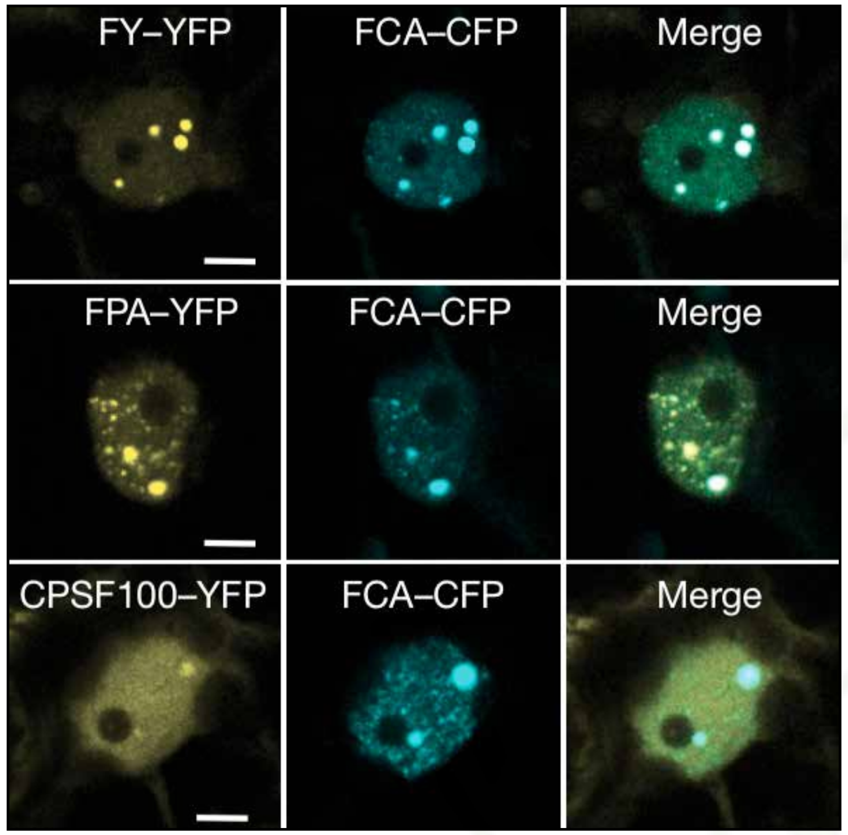


Figure 44: Colocalization of FY–YFP, FPA–YFP and CPSF100–YFP with FCA–CFP in tobacco leaf nuclei. Images are representative of three independent experiments. Scale bars, 5 µm.

He S, Vickers M, Zhang J, Feng X. Natural depletion of histone H1 in sex cells causes DNA demethylation, heterochromatin decondensation and transposon activation (2019) Elife. doi: 10.7554/eLife.42530

Isner JC, Olteanu VA, Hetherington AJ, Coupel-Ledru A, Sun P, Pridgeon AJ, Jones GS, Oates M, Williams TA, Maathuis FJM, Kift R, Webb AR, Gough J, Franklin KA, Hetherington AM (2019) Short- and Long-Term Effects of UVA on Arabidopsis Are Mediated by a Novel cGMP Phosphodiesterase. Curr Biol. doi: 10.1016/j.cub.2019.06.071

Kirchhelle C, Garcia-Gonzalez D, Irani NG, Jérusalem A, Moore I (2019) Two mechanisms regulate directional cell growth in Arabidopsis lateral roots. Elife doi: 10.7554/eLife.47988

Lawrence EJ, Gao H, Tock AJ, Lambing C, Blackwell AR, Feng X, Henderson IR (2019) Natural Variation in TBP-ASSOCIATED FACTOR 4b Controls Meiotic Crossover and Germline Transcription in Arabidopsis. Curr Biol. doi: 10.1016/j.cub.2019.06.084

Papanatsiou M, Petersen J, Henderson L, Wang Y, Christie JM, Blatt MR (2019) Optogenetic manipulation of stomatal kinetics improves carbon assimilation, water use, and growth. Science. doi: 10.1126/science.aaw0046

Smit ME, McGregor SR, Sun H, Gough C, Bågman AM, Soyars CL, Kroon JT, Gaudinier A, Williams CJ, Yang X, Nimchuk ZL, Weijers D, Turner SR, Brady SM, Etchells JP (2019) A PXY-Mediated Transcriptional Network Integrates Signaling Mechanisms to Control Vascular Development in Arabidopsis. Plant Cell. doi: 10.1105/tpc.19.00562

Yang W, Schuster C, Prunet N, Dong Q, Landrein B, Wightman R, Meyerowitz EM (2019) Visualization of Protein Coding, Long Noncoding, and Nuclear RNAs by Fluorescence in Situ Hybridization in Sections of Shoot Apical Meristems and Developing Flowers. Plant Physiol. doi: 10.1104/pp.19.00980

Yasrab R, Atkinson JA, Wells DM, French AP, Pridmore TP, Pound MP (2019) RootNav 2.0: Deep learning for automatic navigation of complex plant root architectures. Gigascience. doi: 10.1093/gigascience/giz123

Major Funding Sources

- Biotechnology and Biological Sciences Research Council (BBSRC) https://bbsrc.ukri.org/

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

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

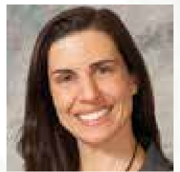
- Natural Environment Research Council http://www.nerc.ac.uk

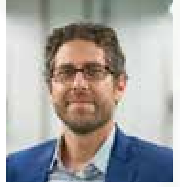
- The Gates Foundation http://www.gatesfoundation.org/

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

- The Newton Fund https://www.newtonfund.ac.uk/

United States of America





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With additoonal input from the North American *Arabidopsis* Steering Committee (NAASC)
https://www.araport.org/community/group/naasc
1. Jose Dinneny, Stanford University (2015 - 2020) NAASC Treasurer
2. Elizabeth Haswell, Washington University- St. Louis (2015 - 2020) Representative to MASC
3. Roger Innes, Indiana University (2016 - 2021) NAASC President
4. Peter McCourt, University of Toronto (2016 - 2021)
5. Sean Cutler, University of California, Riverside (2017 - 2022)
6. Jennifer Nemhauser, University of Washington, Seattle (2017 - 2022) NAASC Vice-President
7. Federica Brandizzi, Michigan State University (2018 - 2023)
8. Anna Stepanova, NC State University (2018 - 2023) NAASC Secretary
9. Siobhan Braybrook, UCLA (2019 - 2024)
10. Keith Slotkin, Donald Danforth Plant Science Center & Univ. of Missouri-Columbia (2019 - 2024)
11. Joanna Friesner, (2006- current) NAASC Executive Director

Please describe the current state of Arabidopsis research in your country

Due to the COVID-19 pandemic, in the spring of 2020, Arabidopsis biology (Research and Education, see below) across the United States underwent an unprecedented pause. To promote social distancing and reduce the pressure on our healthcare system, nearly all research and education using live Arabidopsis plants was halted in mid-March. The dual mission of Arabidopsis biology has continued from home. Laboratories have refocused their efforts on training, analyzing data and writing manuscripts. NAASC, the ICAR 2020/2021 planning committee, thanks all of the dedicated researchers and educators for sacrificing the efficiency of their programs for the health of their communities.

Due to the need to practice social distancing, we have postponed ICAR 2020 to 2021. ICAR 2021 will be held on June 21-25, 2021 in Seattle, Washington State, USA. We have retained the existing URL (http://icar2020.arabidopsisresearch.org) to avoid confusion in accessing conference information and updates. NAASC is working hard to transfer as much of the exciting schedule of ICAR 2020 as possible to the 2021 meeting. The theme of ICAR 2021 will continue to emphasize 'Arabidopsis as a nexus for Discovery, Innovation, Application and Impact'. Due to the Seattle ICAR's postponement, the subsequent schedule of future ICAR meetings has shifted (see below). The organizers of ICAR 2020/2021 sincerely thank Geraint Parry, GARNet Coordinator, Motoaki Seki, MASC Japanese Country Representative, and their respective organizing committees for their willingness to shift dates.

ICAR 2021 - June 21-25th in Seattle, USA,
ICAR 2022 – June 20-24th in Belfast, Northern Ireland
ICAR 2023 – Dates to be announced later, Japan

Arabidopsis is used in the United States for both research and education, and the line between these two often blurs. The primary funder of Arabidopsis research continues to be the U.S. National Science Foundation (NSF), with the Divisions of Integrative and Organismal Systems and Molecular & Cellular Biosciences providing the majority of funding. Arabidopsis research is now also being supported under the new 'Understanding the Rules of Life' initiative, which sits within NSF's 10 Big Ideas and seeks to predict an organism's phenotype by crossing different scales of research. One shift within the community, which has been happening over several years, is the movement away from laboratory groups that exclusively study Arabidopsis, and towards research groups that study multiple plants, including Arabidopsis, to leverage the available genetic and genomic resources. Highlights of recent research accomplishments are listed below. In addition, we recommend the following White Paper which discusses the future of Arabidopsis bioinformatics:

Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future, International Arabidopsis Informatics Consortium, Plant Direct, Volume 3 / Issue 1, e00109, doi: 10.1002/pld3.109

The use of Arabidopsis in Education & Outreach has quickly grown, in part due to the NSF's Broader Impact mission, the availability and low cost of educational kits from the Arabidopsis Biological Resource Center (ABRC), and community support for education and outreach from the American Society of Plant Biologists (ASPB). There are more diverse opportunities for funding Education & Outreach in plant biology than ever before, including ASPB's BLOOME grants and NSF's new initiative 'Reintegrating Biology'. In addition to Education & Outreach, ASPB supports the whole plant biology community through their education of lawmakers, annual awards and community interaction portal called Plantae.

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

- Mass-spectrometry-based draft of the Arabidopsis proteome
https://www.nature.com/articles/s41586-020-2094-2

- Improved 'transcript-based' annotation of Arabidopsis transposable elements
https://www.biorxiv.org/content/10.1101/2020.02.20.956714v1

- An Improved Recombineering Toolset for Plants
http://www.plantcell.org/content/32/1/100

Conferences, Workshops and Outreach events

1(1) ICAR 2020 (6-10 July) Postponed to ICAR 2021 (June 21-25): The 31st International Conference on Arabidopsis Research (ICAR 2020, http://icar2020.arabidopsisresearch.org) was being organized by NAASC to be held this summer, 2020 at the University of Washington, Seattle, USA. However, it became clear by spring that, due to the global COVID-19 pandemic, holding the ICAR this year would not be feasible. NAASC worked with local University partners and with the organizers for ICAR 2021-Belfast and ICAR 2022-Japan to collaboratively develop a plan to postpone each of the three ICARs by one year.

On March 23, 2020, we made this joint statement: Due to the current global COVID-19 situation we have collaboratively decided to postpone the upcoming International Conferences on Arabidopsis Research (ICAR) by one year such that ICAR 2020 becomes ICAR 2021-Seattle, followed by ICAR 2022-Belfast and ICAR 2023-Japan.

Therefore we hope you will be excited to sign up for ICAR 2021-Seattle (June 21-25, 2021), as well as ICAR 2022-Belfast (June 20-24, 2022), and ICAR 2023-Japan (date TBA).

Our rationale is this: as the gravity of this global pandemic is becoming clearer, we have come to realize that it would be inadvisable to convene ICAR 2020 this July. Because the safety and health of our community are more important than convening this summer, we believe it would be irresponsible to host a large international conference where there is a substantial risk to our participants (and by extension, our friends, colleagues, and families back at home).

Members of the worldwide Arabidopsis and plant science research communities have watched the tragic global spread of the COVID-19 disease that has affected many aspects of our daily and scientific lives. With respect to this year's International Conference on Arabidopsis Research (ICAR 2020), the North American Arabidopsis Steering Committee (NAASC) started planning a set of options in February, in case it became clear that this year's conference, scheduled for July, in Seattle, USA, should not be held.

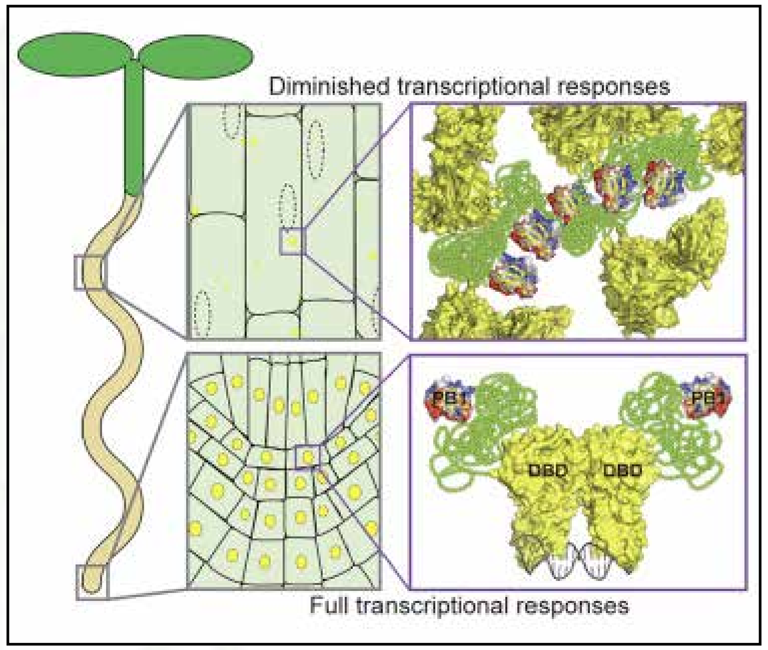

Figure 45: Nucleo-cytoplasmic Partitioning of ARF Proteins Controls Auxin Responses in *Arabidopsis thaliana*.

The organizers of ICAR 2020-Seattle, ICAR 2021-Belfast, UK, and ICAR 2022- Japan, convened to discuss how best to collaboratively support the global Arabidopsis community in these unprecedented and challenging times. We know that ICAR is our community's primary annual convening, where cutting-edge research is shared and collaborations are established and strengthened. We don't take lightly the amount of effort that has already been extended for ICAR 2020, including a diverse program consisting of 32 community-organized sessions that were chosen as part of a community competition, and 24 platform speakers invited from the international community. We also considered the planning undertaken by the UK and Japanese Arabidopsis communities for ICARs 2021 and 2022. Ultimately, we agreed we must prioritize our community's health and safety by postponing ICAR 2020.

The Arabidopsis community is tightly linked and interdependent. Our multinational cooperation began solidly in the early 1990's via the joint efforts by researchers in many nations to sequence the Arabidopsis genome and continued in the 2000's and beyond. Our collaborative partnerships remain vital today, even as regional research and educational objectives may shift to reflect evolving priorities, advances in technologies, and local funding realities, among other considerations.

Thank you for understanding the difficult position we are in with respect to this unexpected crisis. We hope that you, and those closest to you, remain healthy, and that as a community, we can continue to support each other as much as possible.

Signed by:

- Joanna Friesner, NAASC Executive Director, Lead ICAR 2020/2021 Organizer; on behalf of the North American Arabidopsis Steering Committee (NAASC)
- Geraint Parry, GARNet Coordinator and Lead Organiser of ICAR2022; on behalf of the GARNet leadership group
- Motoaki Seki, MASC Japanese Country Representative and a lead organizer of ICAR 2023; on behalf of the ICAR 2023 Organizing Committee in Japan

Support for ICAR 2020/2021 organization is, in part, provided by the U.S. National Science Foundation under Grant No. #1518280. Any opinions, findings, & conclusions or recommendations expressed in this event, or in resulting work, are those of the participants & do not necessarily reflect the views of the NSF.

(2) Addtional US meetings/workshops in 2019: Phenome: Tucson, Arizona; Crops in Silico- Symposium and Hackathon; Modeling across species, including Arabidopsis; Urbana, Illinois; Gordon Research Conference on Epigenetics; Holderness, New Hampshire; FASEB The Mechanisms in Plant Development: Olean, New York; ASPB Plant Synthetic Biology: San Jose, California

Selected Publications

Patricia Baldrich, Brian D. Rutter, Hana Zand Karimi, Ram Podicheti, Blake C. Meyers, Roger W. Innes (2019) Plant Extracellular Vesicles Contain Diverse Small RNA Species and Are Enriched in 10- to 17-Nucleotide "Tiny" RNAs. The Plant Cell. doi: 10.1105/tpc.18.00872

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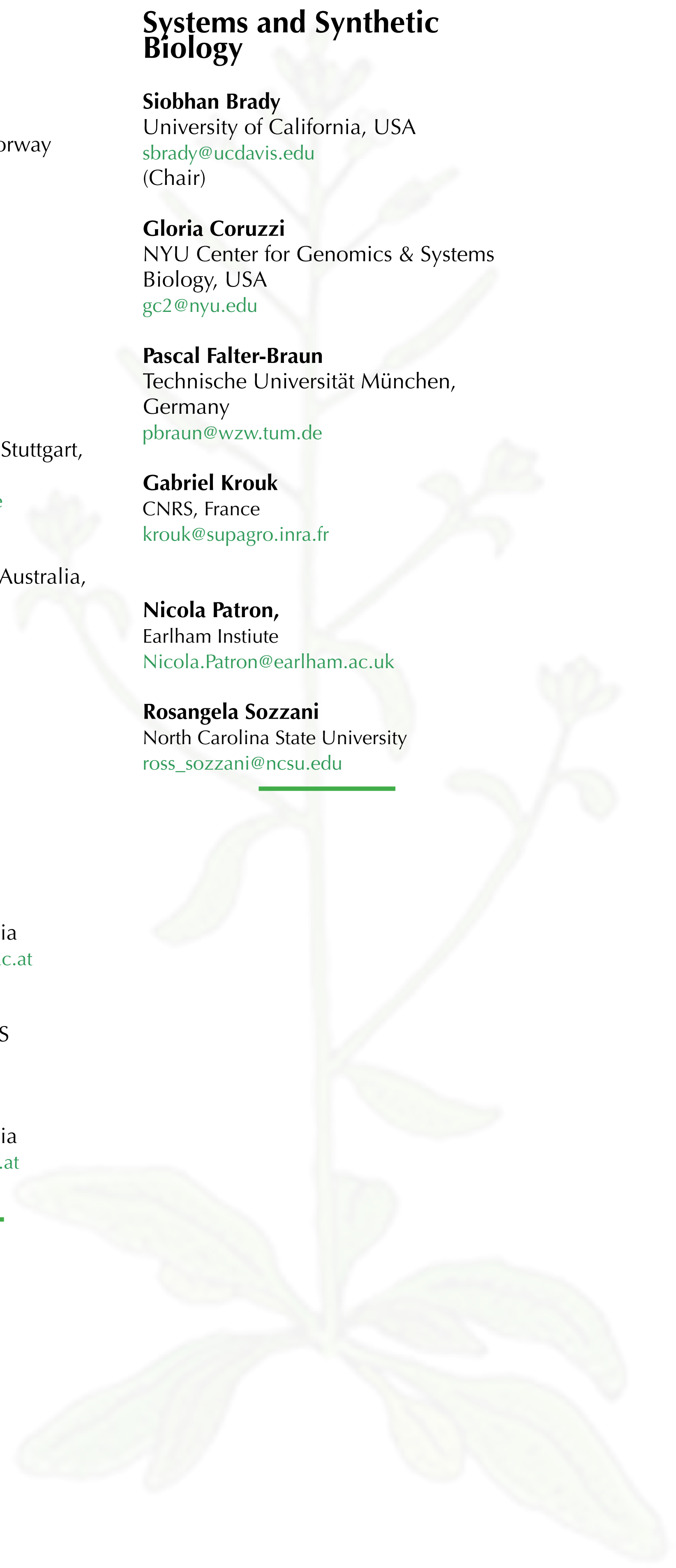

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